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DISSERTATION

Titel der Dissertation

Developmental Cycle, Transcriptome and Metabolic Features of the Chlamydial Symbiont *Protochlamydia amoebophila*

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Doktorin der Naturwissenschaften (Dr. rer.nat.)

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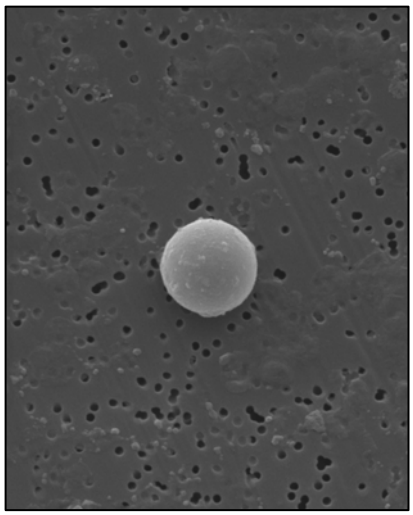
Introduction & Outline



Scanning electron micrograph shows a single *Protochlamydia amoebophila* cell.

INTRODUCTION

Chlamydiae

The discovery of chlamydiae goes back to the year 1907 as Halberstädter and von Prowazek described transmission of trachoma from human to orang-utans by inoculating their eyes with conjunctival epithelial scrapings. They found in infected cells intracytoplasmatic inclusions containing small dense particles of different sizes, thought that these particles are protozoa and called them “Chlamydozoa” (Halberstädter & Prowazek, 1907) (Figure 1). In the next 50 years, many efforts were initiated to culture these unusual organisms and finally Tang *et al*. successfully isolated the trachoma agent from chick-embryo yolk sacs which had been inoculated with material from infected human eyes (Tang *et al.*, 1957). Because of their obligate intracellular existence, chlamydiae were considered for almost 10 years after their initial isolation as large viruses, until chlamydiae were finally identified as closely related group of gram-negative intracellular bacteria and have been placed in their own order *Chlamydiales*, with one family *Chlamydiaceae*, and a single genus *Chlamydia* (Moulder *et al.*, 1984). These organisms have for long been considered to be human and animal pathogens with a relatively narrow host range but the application of new diagnostic methods resulted in the detection of chlamydiae even in birds, amphibians and reptiles demonstrating a less strict host specificity of *Chlamydiaceae* than previously thought (Corsaro & Venditti, 2004; Horn, 2008). Today, *Chlamydiaceae* are classified according to their molecular phylogeny in two genera. The genus *Chlamydia* contains the three species *C. trachomatis, C. muridarum, C. suis* and the genus *Chlamydophila* consists of six species (*C. pneumoniae, C. pecorum, C. felis, C. abortus, C. caviae, C. psittaci*) (Everett *et al.*, 1999).

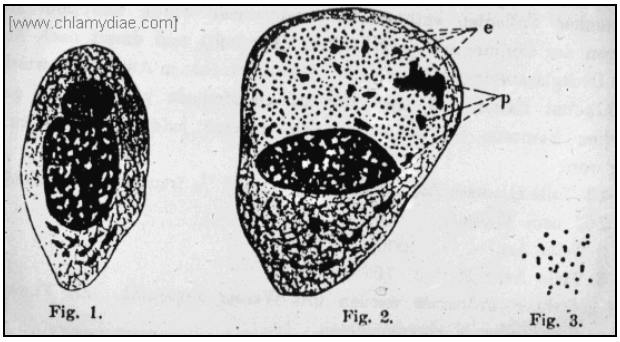


Figure 1. Original drawings of inclusion bodies by Halberstaedter and von Prowazek´s. Image was taken from www.chlamydiae.com and shows a normal conjunctival epithelial cell (left), an infected cell (middle), and free chlamydial particles (right).

Diversity within the *Chlamydiales*

The recent isolation of obligate intracellular *Chlamydia*-like organisms from several unexpected clinical and environmental sources changed our perception of the diversity of the phylum *Chlamydiae* dramatically and resulted in the description of seven novel chlamydial families. These families, termed *Simkaniaceae*, *Waddliaceae*, *Rhabdochlamydiaceae*, *Criblamydiaceae*, *Piscichlamydiaceae,* *Clavochlamydiaceae,* and *Parachlamydiaceae,* represent evolutionary early diverging sister groups of the *Chlamydiaceae* (Fritsche *et al.*, 1993; Kahane *et al.*, 1993; Rurangirwa *et al.*, 1999; Amann *et al.*, 1997; Kostanjsek *et al.*, 2004; Draghi *et al.*, 2004; Karlsen *et al.*, 2008; Kuo *et al.*, 2008; Thomas *et al.*, 2006a) (Figure 2).

In contrast to the well-known chlamydiae, members of the newly identified *Chlamydia*-like organisms are extremely widespread in the environment and thrive in a remarkably different group of host organisms including fish, insects, crustaceans, molluscs, and protozoa (Horn, 2008). Interestingly, molecular diversity studies of the *Chlamydiales* in environmental samples indicate that the actual diversity of these organisms is even higher and that many novel lineages within this order still await their isolation in appropriate host organisms (Corsaro *et al.*, 2002; Corsaro *et al.*, 2003; Horn & Wagner, 2001; Ossewaarde & Meijer, 1999).

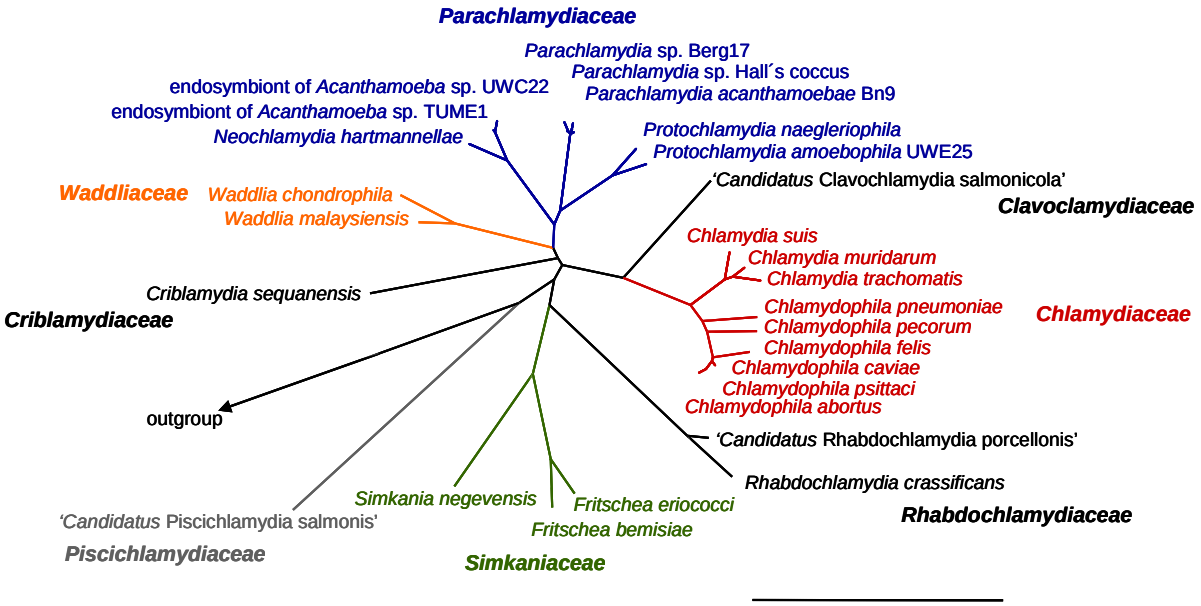


Figure 2. Phylogeny of chlamydiae. 16S rRNA-based phylogenetic tree showing the affiliation and diversity of chlamydial organisms. Tree calculation was performed using the neighbour joining algorithm (jukes cantor distance correction) implemented in the ARB program package (Ludwig *et al.*, 2004). Scale bar represents 10% estimated evolutionary distance.

Members of the family *Simkaniaceae* are divided into the two genera *Simkania* and *Fritschea.* The single member of *Simkania*, *Simkania negevensis*, was originally discovered in a contaminated laboratory cell culture (Kahane *et al.*, 1993). The original host remained unknown but recent studies demonstrated that *S. negevensis* is able to propagate in free-living amoebae (Kahane *et al.*, 2002; Kahane & Friedman, 1995; Michel *et al.*, 2005). Members of the genus *Fritschea* (*Fritschea eriococci* and *Fritschea bemisiae*) were initially detected in bacteriocytes of the insect species *Bemisia tabaci* and *Eriococcus spurious* (Everett *et al.*, 2005; Thao *et al.*, 2003). *Waddlia chondrophila* and *Waddlia malayensis* represent the family *Waddliaceae* which were found in an aborted bovine fetus and urine samples from a fruit bat, respectively (Chua *et al.*, 2005; Rurangirwa *et al.*, 1999). As shown by Michel and coworkers, *Waddlia chondrophila* is also able to grow in free-living amoebae (Michel *et al.*, 2004).

In the year 2004, Kostanjsek *et al*. identified '*Candidatus* Rhabdochlamydia porcellionis' in hepatopancreatic cells of the woodlouse *Porcellio scaber* and grouped these *Chlamydia*-like bacteria into the family *Rhabdochlamydiaceae* (Kostanjsek *et al.*, 2004), three years later the second member of this family, *Rhabdochlamydia crassificans*, was detected in crustaceans (Corsaro *et al.*, 2007).

The three families *Criblamydiaceae, Piscichlamydiaceae, and Clavochlamydiaceae* consist of only one described member each and were obtained recently from an unknown host by *Acanthamoeba* co-culture and identified in fish, respectively (Draghi *et al.*, 2004; Karlsen *et al.*, 2008; Thomas *et al.*, 2006b).

The majority of *Chlamydia*-like isolates, however, belongs to the family *Parachlamydiaceae* which consists of the three genera *Parachlamydia*, *Neochlamydia*, and *Protochlamydia* (Amann *et al.*, 1997; Collingro *et al.*, 2005b; Fritsche *et al.*, 1993; Fritsche *et al.*, 2000; Horn *et al.*, 2000). All known members of the family *Parachlamydiaceae* were described as endosymbionts of free-living amoebae belonging to the genera *Acanthamoeba* and *Hartmanella* (Figure 3).

Free-living amoebae as hosts for bacterial pathogens

Free-living amoebae of the genus *Acanthamoeba* are considered cosmopolitan and live almost everywhere. These protozoa were detected in soil, fresh-, marine- and tap water, air-conditioning units, on plants and animals, and inside vertebrates (Rodriguez-Zaragoza, 1994). They normally feed on bacteria, controlling therefore bacterial populations in the environment, and multiply as free-living trophozoits. Under environmental stress, a resting cyst form can be developed protecting them from inhospitable conditions (Page, 1988). Acanthamoebae are opportunistic human pathogens causing *Acanthamoeba* keratitis (a blinding corneal infection associated with contaminated contact lenses), cutaneous lesions or

chronic granulomatous amoebic encephalitis (GAE). The latter two diseases occur predominantly in immunodeficient patients (Khan, 2006; Marciano-Cabral & Cabral, 2003). Furthermore, amoebae are carriers of a remarkably high number of bacteria which can resist digestion by these protozoa. Several of these microbes also multiply in the amoebae and ultimately lyse them (Birtles *et al.*, 1997; Essig *et al.*, 1997; Greub & Raoult, 2002a; Greub & Raoult, 2004; Molmeret *et al.*, 2005; Rowbotham, 1980). As many of these facultative and obligate intracellular bacteria are important pathogens of humans, it has been speculated that virulence mechanisms developed by bacteria to survive and multiply in the predatory amoebae have also enabled them to infect other eukaryotic hosts including humans (Greub & Raoult, 2004; Harb *et al.*, 2000; Horn *et al.*, 2004; Pagnier *et al.*, 2008) as demonstrated for *Legionella pneumophila* (Cirillo *et al.*, 1994; Harb *et al.*, 2000) and *Mycobacterium avium* (Cirillo *et al.*, 1997). Consequently, free-living amoebae have been considered as “Trojan horses” of the microbial world by serving as carriers of pathogenic bacteria from the environment to humans (Barker & Brown, 1994). The fact that *Chlamydia*-like bacteria such as *S. negevensis*, *W. chondrophila* but also *C. pneumoniae* which naturally infect higher eukaryotes, are also able to infect and replicate within amoebae (Essig *et al.*, 1997; Kahane *et al.*, 2001; Michel *et al.*, 2004), is consistent with the postulate that common virulence mechanisms are used to successfully infect amoebal and higher eukaryotic cells.

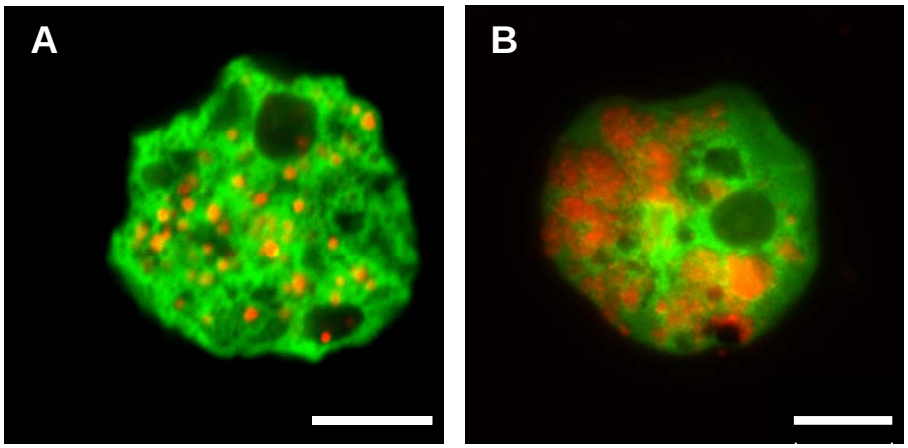


Figure 3. *Acanthamoeba castellanii* Neff infected with *Chlamydia*-like bacteria. Fluorescence *in situ* hybridization with rRNA-targeted oligonucleotide probes of an amoeba trophozoite infected with (A) *Protochlamydia amoebophila* and (B) *Parachlamydia acanthamoebae*. Amoebae are labelled green, chlamydiae are labelled red. Scale bars correspond to 10 µm.

Approximately 25% of environmental as well as clinical (corneal samples) *Acanthamoeba* isolates were shown to harbour non-cultivable bacterial endosymbionts demonstrating that

endosymbiosis occurs commonly in amoebae (Fritsche *et al.*, 1993). In contrast to many of the associations described above, these infections are stable and have no obvious disadvantages for the host. Such a stable symbiotic interaction of obligate intracellular bacteria with amoebae was described for members of four distinct evolutionary lineages within the *Alphaproteobacteria*, the *Betaproteobacteria*, the *Bacteroidetes* and the *Chlamydiae* (Amann *et al.*, 1997; Birtles *et al.*, 1997; Fritsche *et al.*, 1993; Fritsche *et al.*, 1999; Fritsche *et al.*, 2000; Heinz *et al.*, 2007; Horn *et al.*, 1999; Horn *et al.*, 2000; Horn *et al.*, 2001; Horn *et al.*, 2002; Horn & Wagner, 2004). The worldwide distribution of only four well-separated obligate intracellular symbiont lineages of acanthamoebae suggests that this type of interaction has evolved several times during evolution, but that these events only rarely occurred (Horn & Wagner, 2004). However, the number of characterized amoebal isolates is still rather limited and more isolates need to be investigated to confirm this hypothesis. Additionally, the limited diversity of obligate bacterial endosymbionts in amoeba might also reflect that most amoebal isolates were obtained by using highly similar cultivation approaches. Possibly, the application of innovative amoeba isolation approaches would lead to the isolation of other amoeba with novel symbionts.

While most amoebal isolates harbour only one bacterial endosymbiont, a recent study reports the first description of an amoeba isolate harbouring two phylogenetically different endosymbionts (belonging to the *Betaproteobacteria* and *Chlamydiae*) (Heinz *et al.*, 2007). This finding is particularly interesting as amoeba have been postulated, based on comparative genomic analysis, as hot spots for lateral gene transfer between intracellular bacteria (Ogata *et al.*, 2006), although the genome of *P. amoebophila* contains only few genes for which a recent lateral acquisition can be proposed (Horn *et al.*, 2004).

The intracellular life of chlamydiae

Characteristic to all members of the *Chlamydiales* is the unique biphasic developmental cycle which was first described at the level of light microscopy in the early 1930s by Bedson and Bland (Bedson, 1932). During the developmental cycle, chlamydiae alternate between two morphologically and physiologically distinct forms, the elementary bodies (EBs) and the reticulate bodies (RBs). Intermediate bodies (IBs) represent the transition states between both developmental forms (Hatch, 1999; Matsumoto, 1988; Moulder, 1991; Ward, 1988).

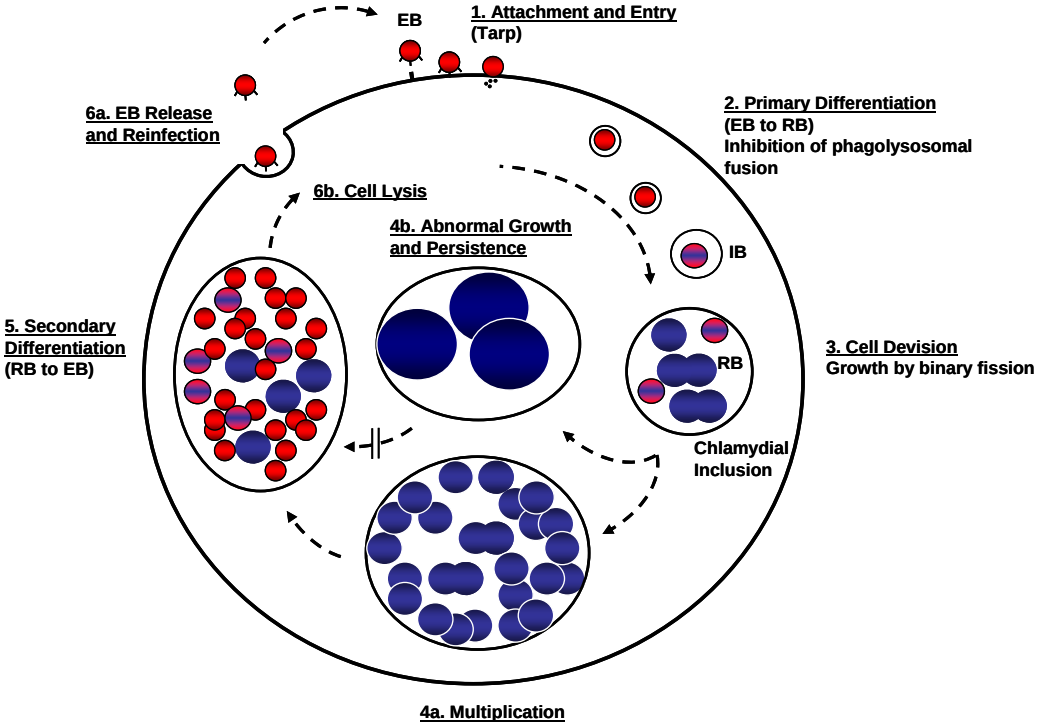


Figure 4. The chlamydial developmental cycle. Modified from (Abdelrahman & Belland, 2005).

EBs (approximately 0.3-0.6 µm in size) and RBs (approximately 1 µm in size) of most chlamydiae are coccoid, some newly identified *Chlamydia*-like organisms, however, have been shown to possess elongated, rod-shaped or even star-like shaped EBs (Corsaro *et al.*, 2007; Karlsen *et al.*, 2008; Kostanjsek *et al.*, 2004; Thomas *et al.*, 2006a). The primary role of the spore-like, infectious EB is to survive outside of the host cell until re-infection of new host cells. The EBs are well-adapted to the extracellular environment possessing highly condensed DNA (Barry *et al.*, 1992; Hatch, 1999) and are believed to be metabolically inactive (RNA/DNA ratio of 1:1) (Hatch, 1999; Ward, 1988). They are osmotically stable and poorly permeable because of the highly cross-linked major outer membrane protein (MOMP)

and other envelope proteins (Hackstadt *et al.*, 1985; Hatch *et al.*, 1984; Newhall & Jones, 1983; Newhall, 1987).

The first contact of the EB with a susceptible host cell takes place for most chlamydial species through reversible electrostatic interactions of the bacteria with heparan sulfate containing glycosaminoglycans on the cell surface (Chen *et al.*, 1996; Stephens *et al.*, 2001; Su *et al.*, 1996; Wuppermann *et al.*, 2001; Zhang & Stephens, 1992). Subsequently, host actin recruitment and entry of the EB into a host membrane bound vacuole, termed inclusion, is caused by an irreversible interaction with unidentified host cell receptors, rapidly followed by signalling events (tyrosine phosphorylation of host cell proteins) and release of a type III secretion system exported protein (Tarp; translocated actin-recruiting phosphoprotein) (Birkelund *et al.*, 1997; Carabeo *et al.*, 2002; Clifton *et al.*, 2004; Dautry-Varsat *et al.*, 2005; Fawaz *et al.*, 1997) (Figure 4/1). EBs trigger their own internalization by eukaryotic cells very efficiently and this process has been termed “parasite-specified endocytosis” (Byrne & Moulder, 1978; Hackstadt, 1999). Although the processes involved in attachment and uptake differ between chlamydial strains and species, generally the entire event of actin recruitment and internalization is finished for most species after approximately 1.5 min (Dautry-Varsat *et al.*, 2005). Since Tarp is not encoded in the *P. amoebophila* genome, the protein which is used by *Chlamydia*-like bacteria to initiate host actin recruitment and internalization into the eukaryotic cell is not known (Horn *et al.*, 2004).

Almost simultaneously with attachment and entry of the EB into the host cell, reduction of MOMP and cystein-rich proteins causes a decrease in rigidity (Hatch *et al.*, 1986) allowing an increase in size and development of EB to RB. The differentiation from EB to RB includes gene expression in particular for ribosome assembly, chromosome decondensation and inclusion maturation (Abdelrahman & Belland, 2005; Belland *et al.*, 2003; Shaw *et al.*, 2000; Wichlan & Hatch, 1993) (Figure 4/2).

The RB represents the metabolically active stage which divides by binary fission within the non-fusogenic inclusion (Taraska *et al.*, 1996; van Ooij *et al.*, 2000) (Figure 4/3 and 4/4a). RBs are highly transcriptionally active (RNA/DNA ratio of 3:1) (Ward, 1988) and maximum expression of genes involved in cell division, type three secretion system assembly, energy metabolism, protein folding, DNA replication and DNA repair could be measured during this stage (Belland *et al.*, 2003; Mäurer *et al.*, 2007; Nicholson *et al.*, 2003).

After several rounds of logarithmic multiplication, a yet unknown signal triggers secondary differentiation of RBs to EBs and the population becomes increasingly asynchronous (Figure 4/5). Expressed late-cycle genes encode components for the highly disulfide-cross-linked outer-membrane complex, genes involved in the condensation of the chromosome and a

large number of genes with unknown function which were only found in chlamydiae (Abdelrahman & Belland, 2005; Belland *et al.*, 2003; Hatch, 1999; Nicholson *et al.*, 2003).

Under cell culture conditions, the duration of the complete developmental cycle depends on the strain as well as on the type of host cell and is between 48 h and 84 h for pathogenic chlamydiae (Belland *et al.*, 2003; Hatch, 1999; Mäurer *et al.*, 2007; Nicholson *et al.*, 2003; Wolf *et al.*, 2000) and between 24 h and 15 days for *Chlamydia*-like bacteria (Greub & Raoult, 2002b; Greub *et al.*, 2005b; Kahane *et al.*, 2001; Kahane *et al.*, 2002). Under unfavourable conditions such as nutrient deficiency, immunological responses or antibiotic treatment, chlamydiae have evolved a remarkable strategy to persist for long time in a viable but non-cultivable state within their host cells (Beatty *et al.*, 1994; Hogan *et al.*, 2004) which is suggested to be involved in chronic chlamydial disease (Hogan *et al.*, 2004) (Figure 4/4b). Persistent chlamydiae show a characteristic altered growth mode including enlarged and pleomorphic RBs that are inhibited in binary fission and differentiation to EBs while still replicating their chromosomes. After removal of the growth inhibitory factor, the differentiation to mature EBs can be continued (Beatty *et al.*, 1995; Hogan *et al.*, 2004) and EBs are released from the infected host cell either by host-cell lysis or exit cells without concomitant death of the host cell by fusion of the inclusion membrane with the host cell membrane (exocytosis) (Hybiske & Stephens, 2007; Hybiske & Stephens, 2008; Todd & Caldwell, 1985) (Figures 4/6 and 5).

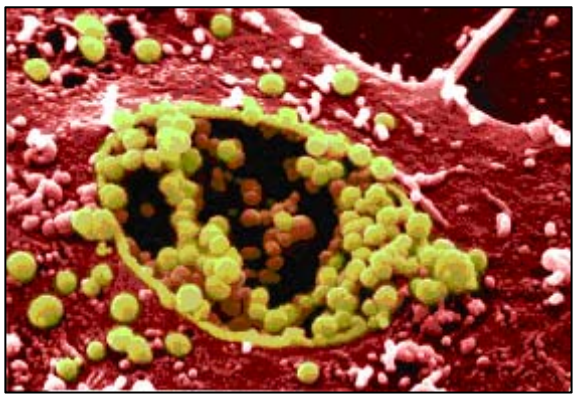


Figure 5. Host cell burst caused by chlamydiae. Scanning electron microscopy micrograph was taken from http://www.mkuntze.de/images/chlamydien_3.jpg and shows chlamydial elementary bodies (EBs) in green.

Pathogenic potential of *Chlamydiaceae*

Because of the medical relevance in humans and animals, members of the *Chlamydiaceae* are also referred to as pathogenic chlamydiae. Pathogenic chlamydiae include two of the most prevalent and successful human pathogens worldwide. *Chlamydia trachomatis* is the causative agent of trachoma and is the world´s leading preventable cause of blindness with about 8 million people blinded as a result of this disease (Schachter, 1999; Thylefors *et al.*, 1995; WHO, 2008). Additionally, *C. trachomatis* is the most common sexually transmitted bacterial pathogen, with over 90 million new cases each year worldwide (WHO, 2001). *Chlamydophila pneumoniae* infects a majority of humans at some time in their lives causing a range of serious respiratory diseases (Grayston *et al.*, 1986; Schachter, 1999) and it has been estimated that *C. pneumoniae* is responsible for 2 to 43% of all cases of community-acquired pneumonia (CAP) (Wellinghausen *et al.*, 2006). Furthermore, *C. pneumoniae* has recently been associated with several chronic diseases of unknown cause, such as coronary artery disease, multiple sclerosis, asthma and Alzheimer´s disease (Mahony *et al.*, 2003) but despite intense research efforts, the etiologic role of *C. pneumoniae* in these diseases is still unclear (Cao *et al.*, 2007; Johnston & Martin, 2005; Mussa *et al.*, 2006; Paradowski *et al.*, 2007; Stratton & Wheldon, 2006).

Infections of humans can also be caused by *Chlamydophila psittaci* associated with psittacine birds leading to psittacosis with very severe clinical symptoms (Schachter, 1999) and *Chlamydophila abortus* which is the causative agent of enzootic abortion of ewes (EAE) or ovine enzootic abortion (OEA) in sheep (Aitken, 2000; Longbottom & Coulter, 2003). Contact with sheep infected with the EWE abortion agent can be of particular risk to pregnant women (Longbottom & Coulter, 2003).

Epidemiology of *Chlamydia*-like bacteria

The close phylogenetic affiliation of *Chlamydia*-like bacteria to pathogenic chlamydiae, which comprise some of the most successful human and animal pathogens, raises the question whether these newly identified and widespread bacteria might also be of relevance for human or veterinary medicine. Based on a number of serological and molecular studies (Corsaro & Venditti, 2004; Corsaro & Greub, 2006) as well as on the observation that novel chlamydiae are able to infect mammalian cells *in vitro* (Collingro *et al.*, 2005a; Friedman *et al.*, 2003; Greub *et al.*, 2003c; Kocan *et al.*, 1990), an association between *Chlamydia*-like organisms and human and animal diseases is strongly supported, in particular for members of the *Parachlamydiaceae*, *Simkaniaceae* and *Waddliaceae*.

Parachlamydiaceae infections in humans

In several studies human exposure to *Parachlamydiaceae* has been associated with health problems. First indication of a possible pathogenic potential of *Chlamydia*-like bacteria was the isolation of the *Parachlamydia acanthamoeba* strain Hall´s coccus from acanthamoebae which were involved in an outbreak of humidifier fever in a print shop in the United States (Birtles *et al.*, 1997; Lewis, 1990). In the following years, serological and molecular studies have demonstrated that *P. acanthamoebae* [including type strain Bn_9, isolate $Berg_{17}$, Hall´s coccus and several unnamed isolates (Everett *et al.*, 1999)] is not only associated with human respiratory diseases, including community-acquired pneumonia, bronchitis, and aspiration pneumonia but might also play a role in atherosclerosis and human miscarriage (Baud *et al.*, 2008; Baud *et al.*, 2009; Birtles *et al.*, 1997; Corsaro *et al.*, 2001; Corsaro *et al.*, 2002; Greub *et al.*, 2003a; Greub *et al.*, 2003b; Greub *et al.*, 2006; Marrie *et al.*, 2001). Due to the presence of *P. acanthamoebae* in immunodeficient patients, the organism has recently been suggested to act as an opportunistic human respiratory pathogen which normally does not harm its host but can affect people with a suppressed immune system (Greub *et al.*, 2003a; Greub *et al.*, 2003b; Marrie *et al.*, 2001). *P. acanthamoebae* can infect and proliferate in a range of simian and human cell lines as well as in primary human macrophages (Casson *et al.*, 2006; Collingro *et al.*, 2005a; Greub *et al.*, 2003c), although its proliferation is markedly reduced compared to proliferation in its natural amoebal host (Collingro *et al.*, 2005a; Greub *et al.*, 2003c) and differences in host cell defence could be observed (Greub *et al.*, 2005a). This clearly contrasts to findings that legionellae and *Mycobacterium avium* grown within amoebae subsequently exhibit enhanced growth in monocytes and enhanced entry into macrophages, respectively (Cirillo *et al.*, 1997; Cirillo *et al.*, 1999).

Our knowledge on the pathogenicity of other members of the *Parachlamydiaceae* is still sparse. Only *Protochlamydia naegleriophila* was recently detected in a clinical sample of an immunocompromised pneumonia patient (Casson *et al.*, 2008), however again no prove for its function as causative agent of human diseases is available.

Prevalence of *Simkaniaceae* in human respiratory disease

Of all *Chlamydia*-like organisms, *Simkania negevensis* is the most extensively studied member regarding its pathogenic potential. *S. negevensis* is well-adapted for survival and proliferation in higher eukaryotic host cells and macrophages as well as in free-living amoebae (Kahane *et al.*, 1998; Kahane *et al.*, 2001; Kahane *et al.*, 2008). Its role as an emerging human respiratory pathogen was supported in several worldwide epidemiological studies demonstrating the detection of the organism in clinical specimens of bronchiolitis and pneumonia patients (Friedman *et al.*, 2006; Kahane *et al.*, 1998; Kahane *et al.*, 2007a; Kumar *et al.*, 2005). Additionally, the presence of *S. negevensis* DNA in arterial biopsy

specimens (Friedman *et al.*, 2003) and an involvement in acute rejection of lung transplanted recipients has been reported (Husain *et al.*, 2007). Conversely, serological studies showed also a high seroprevalence of *S. negevensis* in healthy individuals suggesting a common exposure of humans to these organisms which obviously does not always affect human health (Friedman *et al.*, 2006; Kahane *et al.*, 2007b). Further investigations of co-presence of other known respiratory pathogens are therefore needed to clarify the role of *S. negevensis* in the establishment of a severe respiratory infection.

Infection of higher animals and humans by members of *Waddliaceae* and *Rhabdochlamydiaceae*

Waddlia chondrophila has been shown to be associated with several cases of aborted fetuses in bovines in the United States and in Germany (Dilbeck-Robertson *et al.*, 2003; Dilbeck *et al.*, 1990; Henning *et al.*, 2002; Rurangirwa *et al.*, 1999). Furthermore, recent studies demonstrate a strong association between the presence of *W. chondrophila* IgG antibodies and early human fetal death (Baud *et al.*, 2007; Baud *et al.*, 2008). In this context it is interesting to note that *W. chondrophila* is able to enter and rapidly multiply in human macrophages (Goy *et al.*, 2008).

DNA of *Rhabdochlamydia*-related organisms, which are known as symbionts of insects and crustaceaea, has been detected in samples of patients suffering from uveitis (Corsaro & Venditti, 2004). However, the presence of *Chlamydia*-like endosymbionts in arthropods is not considered to play a major role in the epidemiology of chlamydial infections so far (Corsaro & Greub, 2006).

***Chlamydia*-like bacteria involved in fish diseases**

'*Candidatus* Piscichlamydia salmonis', '*Candidatus* Clavochlamydia salmonicola' and some still unnamed *Chlamydia*-like bacteria have been described recently to cause infections in salmonid fish (gill epitheliocystis) (Draghi *et al.*, 2004; Karlsen *et al.*, 2008; Meijer *et al.*, 2006) with up to 100% mortality in cultured fish (Nowak & LaPatra, 2006). It is tempting to speculate, that these bacteria are transmitted via protozoan hosts as several free-living amoebae have been found to be implicated in systemic diseases of fish (Bermingham & Mulcahy, 2006; Corsaro & Venditti, 2004; Draghi *et al.*, 2004; Dykova *et al.*, 1995; Dykova *et al.*, 1998; Dykova *et al.*, 2003). However, *in vitro* proliferation of these novel *Chlamydia*-like organisms in amoebae is not documented so far.

Whether *Chlamydia*-like organisms are in fact causing agents of human and veterinary infectious diseases is still questionable, as no animal model has yet been established and

the organism has not been isolated directly from samples of diseased patients. The growing body of molecular and serological evidence strenghtens the causative role of *Chlamydia*-like bacteria in several diseases, however, the sole presence of DNA from *Chlamydia*-like bacteria in patients does not provide convincing evidence of disease causation as discussed in Frederick´s and Relman´s revisions of Koch´s postulates for sequence-based identification of microbial pathogens (Fredericks & Relman, 1996). Therefore, a causal relationship, if existent, remains to be demonstrated.

***Protochlamydia amoebophila* UWE25 as a model organism for *Chlamydia*-like bacteria**

P. amoebophila UWE25 was originally described as a gram-negative endosymbiont of an *Acanthamoeba* sp. isolated from a soil sample in western Washington State, USA (Fritsche *et al.*, 1993; Fritsche *et al.*, 2000). Based on its 16S rRNA gene sequence, this organism was classified as a member of the family *Parachlamydiaceae*. It shows the characteristic chlamydial developmental stages with coccoid EBs and RBs and is in contrast to other members of the *Parachlamydiaceae* located in single inclusions which are dispersed throughout the amoebal cytoplasm (Collingro *et al.*, 2005b; Fritsche *et al.*, 2000) (Figure 3). As *P. amoebophila* had a cytopathic effect on its original host amoebae, but was shown to form stable associations with various other acanthamoebae as well as with the social amoeba *Dictyostelium discoideum* (Fritsche *et al.*, 1998; Skriwan *et al.*, 2002), this symbiont was transferred for further propagation in the lab to the *Acanthamoeba* sp. UWC1 (Fritsche *et al.*, 1998; Gautom & Fritsche, 1995).

Since 2004, the complete genome sequence of *P. amoebophila* is available and still represents the only published genome sequence of a *Chlamydia*-like bacterium (Horn *et al.*, 2004).

General biological aspects of *P. amoebophila*

The *P. amoebophila* genome provided novel insights into the evolution of the *Chlamydiae* (*Chlamydia*-like bacteria are thought to have diverged from *Chlamydiaceae* about 700 million years ago) and their intracellular life style (Horn *et al.*, 2004). It represents the second largest genome (approximately 2.5 Mbp) among all published genomes of obligate intracellular bacteria and is about twice as large as the 12 analyzed genomes of pathogenic chlamydiae (Azuma *et al.*, 2006; Carlson *et al.*, 2005; Kalman *et al.*, 1999; Read *et al.*, 2000; Read *et al.*, 2003; Shirai *et al.*, 2000; Stephens *et al.*, 1998; Thompson *et al.*, 2005; Thomson *et al.*, 2008). The genome revealed marked differences to the highly reduced genomes of *Chlamydiaceae* which are well-adapted to multicellular host organisms and indicated that *P.*

amoebophila possesses a considerably higher metabolic capability (Horn *et al.*, 2004). The genome of *P. amoebophila* encodes not only several well-known chlamydial virulence factors (type III secretion system, Inc proteins and a protease-like activity factor (CPAF)) but encodes several additional virulence proteins which are absent in pathogenic chlamydiae such as a type IV secretion system, leucine rich repeat proteins as well as a hemolysin protein.

The G+C content of *P. amoebophila* (35.8%) is lower than the G+C content of all other sequenced *Chlamydiaceae* species (39-41%) and no recent lateral gene transfer could be detected with the exception of the type IV secretion system (G+C content >42%) acquired from an unknown donor (Greub *et al.*, 2004; Horn *et al.*, 2004). Furthermore, *P. amoebophila* possesses three ribosomal RNA (rRNA) operons, likely permitting a faster response to environmental changes (Klappenbach *et al.*, 2000), compared to *Chlamydiaceae* species which possess only one or two rRNA operons. 35 transfer RNA (tRNA) genes and corresponding tRNA synthetases for the production of all aminoacyl tRNAs are encoded in the genome sequence. In total, 2,031 putative genes were identified and classified into 38% functionally characterized proteins (based on derived amino acid sequence homology to proteins of other organisms), 31% not yet functionally characterized proteins, and 31% unknown proteins without homology to any publicly available sequence. 46% of the predicted genes are shared among all chlamydial genomes, thus representing the core gene set for structural, metabolic, and regulatory capabilities of chlamydiae. However, slightly more than half of the predicted genes are absent from all other chlamydial genomes, indicating that they encode *P. amoebophila*-specific functions which might be important for survival in a fluctuating environment and likely define a broader host tropism of these organisms (Horn *et al.*, 2004).

Chlamydial Metabolism

The intimate relationship of chlamydiae with their eukaryotic host cells led to several adaptations of the bacterial metabolism to that of the host cell in order to effectively exploit the host organism. Within the relatively safe host compartment intracellular bacteria have access to the universal energy-rich metabolic intermediates and accordingly the establishment of a symbiosis have enabled the bacteria to reduce major metabolic pathways (Zientz *et al.*, 2004). *Chlamydiaceae* are therefore not able to synthesize purines, pyrimidines, NAD^+ and several cofactors *de novo*, they are auxotrophic for most amino acids and lack key enzymes of several biosynthetic pathways (McClarty, 1999). To compensate for missing metabolic intermediates and nucleotides, chlamydiae encode a wide variety of transporter proteins (McClarty, 1999; Tjaden *et al.*, 1999; Winkler & Neuhaus, 1999).

However, genome sequencing revealed that chlamydiae are still able to synthesize essential precursor metabolites during glycolysis, the pentose phosphate pathway and the tricarboxylic acid (TCA) cycle and produce energy in form of ATP during oxidative phosphorylation independently from the host. This surprising finding has changed the view of chlamydiae as real “energy parasites” (Iliffe-Lee & McClarty, 1999; Kalman *et al.*, 1999; Read *et al.*, 2000; Shirai *et al.*, 2000; Stephens *et al.*, 1998). Recent proteome and transcriptome studies have shown that genes involved in energy metabolism are maximally expressed during middle and later stages of the developmental cycle, while in its early stages a dependence on host cell ATP exists, which is imported by constitutively expressed ADP/ATP translocases (Nicholson *et al.*, 2003; Shaw *et al.*, 2002).

Core metabolic pathways and energy production in *P. amoebophila*

P. amoebophila shows a remarkably higher metabolic capability compared to its pathogenic relatives, but nevertheless relies on the import of host-derived metabolites (Horn *et al.*, 2004; Horn *et al.*, 2006) (Figure 6). Like pathogenic chlamydiae, *P. amoebophila* encodes a glucose-6-phosphate transporter (*uhpC*) for the import of phosphorylated glucose. However, unlike pathogenic chlamydiae, *P. amoebophila* encodes a glucokinase and is thus additionally able to generate phosphorylated glucose (glucose-6-P) independently from its amoeba host cell. Glucose-6-P is then converted during glycolysis to pyruvate via fructose-1,6-bisphosphate using a pyrophosphate-dependent phosphofructokinase (*pfkA*) and energy in form of four ATP molecules can be generated during this process. The *P. amoebophila* genome encodes additionally all genes required for metabolism of the storage compound glycogen which is believed to drive the glycolytic pathway during primary and secondary differentiation steps when host-derived molecules and ATP are not accessible (McClarty, 1999).

The pentose phosphate pathway is generally an alternative to glycolysis and serves to generate NADPH and pentose sugars. *P. amoebophila* is, like pathogenic chlamydiae, equipped with the complete gene set for enzymes of this pathway. Furthermore, *P. amoebophila* possesses all enzymes involved in the TCA cycle which provides essential precursors (oxaloacetate, 2-oxoglutarate, and succinyl-CoA) for biosynthesis of many compounds including some amino acids. Oxidation of acetyl-CoA to CO_2 and generation of NADH, $FADH_2$, and GTP can therefore be carried out independently from the host cell.

In addition to the minimal respiratory chain present in *Chlamydiaceae*, by which electrons are transferred by a Na^+-translocating NADH oxidoreductase (*nqrA-F*) and a succinate dehydrogenase (*sdhA-C*) via the quinone pool to the cytochrome bd complex *(cydA,B*) establishing a proton motif force (PMF) used for ATP synthesis by a V-type ATPase (*ntpA, B,*

D, E, I, K) (Stephens, 1999), *P. amoebophila* encodes a H^+-translocating NADH oxidoreductase (*nuoA-N*), a cytochrome C, and a cytochrome C oxidase (*cyoA-E*) (Figure 6). The additional NADH oxidoreductase might enable *P. amoebophila* to generate a PMF which can subsequently be used by an additional F-type ATPase (*atpA-H*). Furthermore, *P. amoebophila* produces menaquinone on its own which is suggested to be used in the quinine pool of the respiratory chain instead of host-derived ubiquinone. Due to the presence of an F- as well as a V-type ATPase *P. amoebophila* should be able to gain significantly more energy by oxidative phosphorylation than *Chlamydiaceae* (Horn *et al.*, 2004; Horn *et al.*, 2006).

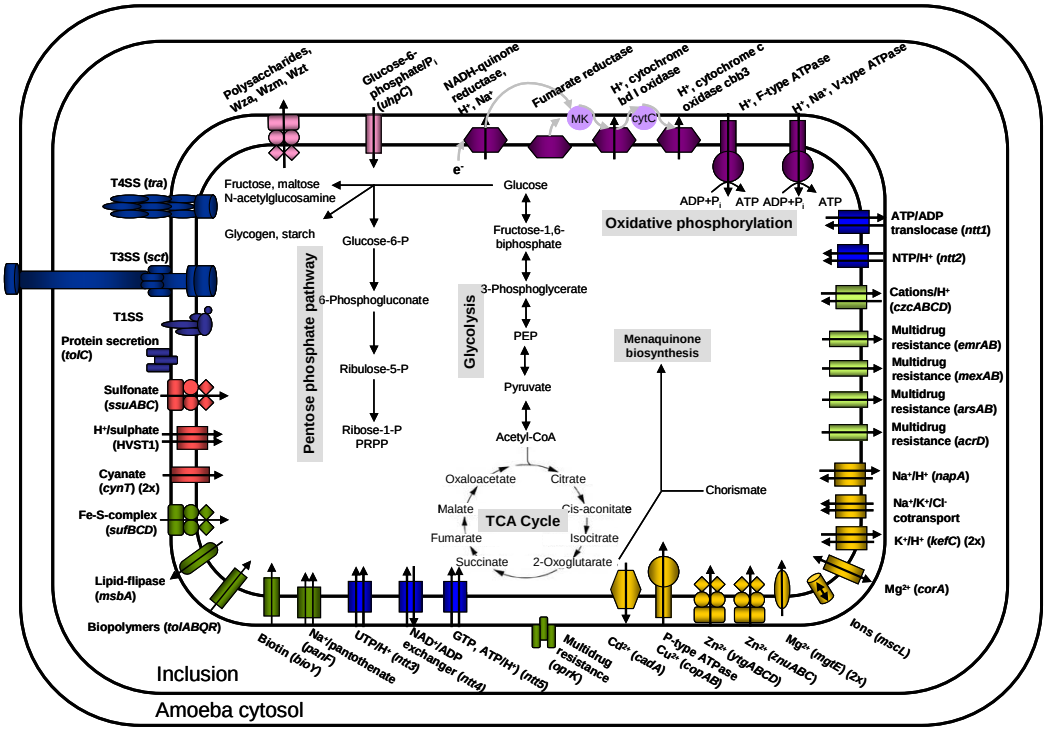


Figure 6. Major metabolic pathways and transport proteins of *P. amoebophila*. Modified from (Horn *et al.*, 2006).

Nucleotide and amino acid metabolism and transport

The obligate intracellular lifestyle of chlamydiae has resulted in the loss of genes essential for *de novo* synthesis of nucleotides and thus requires compensatory transport mechanisms for the import of different metabolites from the cytosolic host nucleotide pool (Moran, 2002; Moulder, 1991). For this purpose, several highly specific nucleotide transport proteins (NTT) could be identified in chlamydiae (Winkler *et al.*, 1999; Winkler & Neuhaus, 1999) and although chlamydiae are able to generate ATP on their own, *P. amoebophila* encodes five NTT proteins (*ntt1-5*). Heterologous expression of the five nucleotide transporters of *P. amoebophila* in *E. coli* revealed that they have concerted substrate specificities and together

represent a machinery to efficiently tap the nucleotide and NAD^+ pool of the host (Haferkamp *et al.*, 2004; Haferkamp *et al.*, 2006; Schmitz-Esser *et al.*, 2004) (Figure 6).

Chlamydiae also lack key components for *de novo* synthesis of most amino acids. Whereas *Chlamydiaceae* show strain-to-strain variation in amino acid requirements, they are generally able to synthesize only aspartate, glycine, and glutamate which can be easily converted from intermediate molecules during metabolism (Hatch, 1975; Kalman *et al.*, 1999; Kuo & Grayston, 1990; McClarty, 1999; Stephens *et al.*, 1998), *P. amoebophila* possesses specific enzymes for the production of six amino acids (glycine, serine, proline, glutamate, glutamine, and aspartate). To counterbalance the missing essential amino acids, a variety of specific amino acid transporters (four isoforms of tyrosine/tryptophan transporters [*tyrP_1-4*], a methionine transporter [*metINQ*], four alanine transporter isoforms [*dagA*], a glutamate transporter [*gltT*], and a proline transporter [*putB*]) as well as two general amino acid transporters (*aaaT*, *braB*) and two oligopeptide ABC transporters (*oppA-F*) are encoded in the genome (Figure 7).

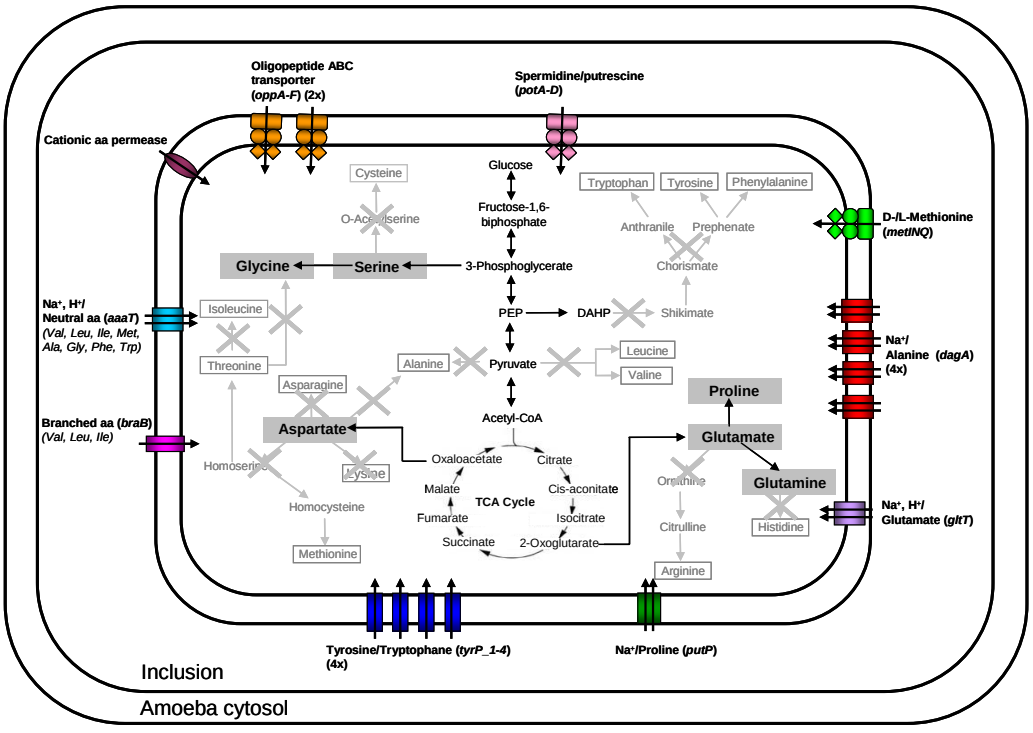


Figure 7. Major amino acid pathways and amino acid transport proteins of *P. amoebophila*. Modified from (Horn *et al.*, 2006).

In summary, *P. amoebophila* is according to in *silico* genome analysis - like its pathogenic counterparts - strongly dependent on its host cell and has to acquire a number of molecules including amino acids, nucleotides and NAD^+ from the host cell cytosol. However, *P. amoebophila* is much better adapted to a less stable environment than its pathogenic

relatives and this is reflected in a higher number of rRNA operons, a more effective respiratory chain and a complete TCA cycle (Collingro *et al.*, 2005b; Horn *et al.*, 2004; Horn *et al.*, 2006). The presence of several chlamydial virulence factors and transporters in the genome of *P. amoebophila* suggests that the last common ancestor of *Parachlamydiaceae* and *Chlamydiaceae* was already adapted to intracellular survival in early unicellular eukaryotes, which possibly served as "training ground" for free-living bacteria to become adapted intracellular pathogens (Harb *et al.*, 2000; Marciano-Cabral & Cabral, 2003; Marrie *et al.*, 2001; Molmeret *et al.*, 2005).

It was the aim of this thesis to contribute to a better understanding of the biology of *Chlamydia*-like bacteria, which were first identified in the early 1990s. The topics investigated in this thesis range from the diversity and pathogenic potential of these conspicuous microorganisms to their developmental cycle, transcriptome and single cell metabolism. The results obtained in this thesis are discussed in detail in the following chapters.

OUTLINE

Chapter II reports on the characterization of eight novel environmental *Acanthamoebae* isolates and their obligate intracellular symbionts. Phylogenetic analysis of the symbionts revealed their affiliation to four evolutionary lineages of amoeba symbionts recognized previously and suggests the existence of only a limited number of phylogenetically different groups of obligate intracellular endosymbionts of acanthamoebae worldwide.

Chapter III describes a novel nested and semi-nested PCR approach targeting the 16S rRNA gene of *Chlamydia*-like bacteria. This assay was used to screen respiratory samples from patients with community-acquired pneumonia (CAP). *Protochlamydia amoebophila*, *Waddlia chondrophila*, and '*Candidatus* Rhabdochlamydia porcellionis'-related sequences were detected for the first time in human respiratory samples raising the question whether these *Chlamydia*-like bacteria are involved in respiratory disease.

Chapter IV gives a comprehensive description of the biphasic developmental cycle of *P. amoebophila* in two different *Acanthamoeba* hosts. Fluorescence *in situ* hybridization, immunofluorescence and quantitative real-time PCR revealed a well-balanced symbiotic interaction between host and symbiont and completion of the reproductive growth cycle of *P. amoebophila* after 4 days in both host amoebae. Iron depletion induced abnormal cell growth, most similar to the persistent forms of *Chlamydiaceae*, which thus might reflect an ancient strategy of *Chlamydiales* to overcome inhospitable conditions.

Chapter V illustrates the development, validation and application of a microarray in order to analyze the global gene expression profile of *P. amoebophila* during infection of *Acanthamoeba*. The transcriptome data demonstrate that 61% of the genes in the *P. amoebophila* genome are transcribed *in vivo* and enzyme transcripts involved in core metabolism, molecule uptake and host-cell manipulation were observed. 52% of those genes which have no homologues in pathogenic chlamydiae are transcribed and likely represent *P. amoebophila*-specific functions which are important for survival in amoeba hosts. The microarray data provide novel insights into the complex host-symbiont interaction and future application of the developed chip during synchronous infection will decipher gene expression patterns linked with the different stages of the developmental cycle or environmental stresses.

Chapter VI describes stable isotope Raman microspectroscopy as a new single-cell approach to differentiate between reticulate (RBs) and elementary bodies (EBs) of *P. amoebophila* and to directly observe metabolic traits of these bacteria. With this technique it could be demonstrated that both growth stages take up phenylalanine within their amoebal host cell and also consume this amino acid extracellularly for several weeks. In addition, EBs were shown to be able to energize their cytoplasmic membrane outside of the host and remain infective even after three weeks of host-free incubation. This newly discovered feature is in contrast to textbook knowledge and raises interesting hypothesis regarding the infectivity and ecological success of environmentally transmitted chlamydiae.

Chapter VII shortly summarizes in English as well as in German the findings presented in this thesis.

The **Appendix** includes a list of the author's publications, oral and poster presentations given by the author, acknowledgments, and the curriculum vitae.

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Chapter II

Diversity of bacterial endosymbionts of environmental *Acanthamoeba* isolates

Image was taken from www.dgpgroup.com.

Diversity of bacterial endosymbionts of environmental *Acanthamoeba* isolates

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Running title: Bacterial endosymbionts of *Acanthamoeba* spp.

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Acanthamoeba sp. EI1, EI2 and EI3 were isolated and identified by S.H., *Acanthamoebae* sp EI4, EI5 were isolated and identified by V.M.H., EI6 and EIDS3 by E.H. E.R.T. isolated and identified *Acanthamoebae* sp 5a2 and performed the transmission electron microscopy. S.S.-E. wrote the manuscript.

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ABSTRACT

Free-living amoebae are frequent hosts for bacterial endosymbionts. In this study, the symbionts of eight novel environmental *Acanthamoeba* strains isolated from different locations worldwide were characterized. Phylogenetic analysis revealed that they were related to either of four evolutionary lineages of amoeba symbionts recognized previously. This study provides evidence for the existence of only a small number of phylogenetically well separated groups of obligate intracellular endosymbionts of acanthamoebae with global distribution.

INTRODUCTION

Free-living amoebae are widespread protozoa including phylogenetically diverse genera like *Acanthamoeba*, *Hartmanella* and *Naegleria*. They occur in various habitats including soil, water and the air (Finn *et al.*, 2006; Rodriguez-Zaragoza, 1994) and in many engineered environments like water supplies and air-conditioning units (Marshall *et al.*, 1997). Free-living amoebae are opportunistic pathogens, causing keratitis or encephalitis, and important predators of prokaryotic and eukaryotic microorganisms with a great influence on microbial community composition (Finn *et al.*, 2006; Rodriguez-Zaragoza, 1994). By grazing on microbes, free-living amoebae also contribute to plant growth, soil mineralization and nutrient cycles (Bonkowski, 2004; Clarholm, 2002; Rodriguez-Zaragoza, 1994).

Apart from being a food source of free-living amoebae, some bacteria are able to survive phagocytosis and multiply within amoebae. The association between these bacteria and their amoeba hosts can be either transient (in the case of facultative intracellular bacteria) or stable (in the case of obligate intracellular bacteria). A wide range of well-known bacterial and eukaryotic pathogens are able to infect amoebae and exploit them for multiplication (Collingro *et al.*, 2004; Greub *et al.*, 2004; Molmeret *et al.*, 2005). Free-living amoebae may thus serve as environmental reservoir and vectors for the transmission of pathogenic bacteria to humans (Albert-Weissenberger *et al.*, 2007; Barker & Brown, 1994) and might represent evolutionary training grounds facilitating the adaptation of bacteria to survival within eukaryotic cells (Allary *et al.*, 2007; Collingro *et al.*, 2004; Harb *et al.*, 2000; Molmeret *et al.*, 2005; Ogata *et al.*, 2006).

Stable associations of bacteria with amoebae leading to long-term symbiotic interactions were described for members of four evolutionary lineages within the *Alphaproteobacteria* (Birtles *et al.*, 2000; Fritsche *et al.*, 1999; Xuan *et al.*, 2007), the *Betaproteobacteria* (Beier *et al.*, 2002; Heinz *et al.*, 2007), the *Bacteroidetes* (Cole *et al.*, 2001; Xuan *et al.*, 2007) and the *Chlamydiae* (Amann *et al.*, 1997; Birtles *et al.*, 1997; Fritsche *et al.*, 2000; Heinz *et al.*, 2007). The different lifestyles of these obligate intracellular bacteria – either directly in the amoeba cytoplasm or enclosed in host-derived vacuoles – suggests fundamentally different mechanisms of host cell interactions. However, with the exception of chlamydia-related amoeba symbionts (Abd *et al.*, 2008; Collingro *et al.*, 2004; Greub & Raoult, 2002; Greub *et al.*, 2003; Greub *et al.*, 2005), our knowledge about obligate intracellular symbionts of amoebae is still scarce. In this study, eight novel *Acanthamoeba* strains and their symbionts were analyzed.

Isolation of acanthamoebae

Ten different amoeba strains were isolated from soil and lake sediment samples from Austria, Tunisia, and Dominica, respectively, using non-nutrient agar plates seeded with live or heat-inactivated *Escherichia coli* or *Saccharomyces cerevisiae* as described previously (Table 1; (Heinz *et al.*, 2007). Amoeba isolates were axenized and tentatively classified as *Acanthamoeba* spp. based on morphological criteria characteristic for this genus (cell size, contractile vacuole, needle-like pseudopodia, and appearance of the nucleus (Page, 1976). Out of these ten isolates, eight contained intracellular bacteria as revealed by staining with the fluorescent DNA dye 4', 6-diamidine-2'-phenylindol- dihydrochloride (DAPI). Isolates EI1, EI2 and EI6 harboured coccoid bacteria, whereas isolates EI3, EI4, EI5, 5a2 and EIDS3 contained rod-shaped bacteria (Table 1). The two *Acanthamoeba* isolates without intracellular bacteria were not analysed further.

Simultaneous isolation of DNA from amoeba hosts and their bacterial endosymbionts was performed as described previously (Heinz *et al.*, 2007). The 18S rRNA genes were amplified using primers targeting conserved 18S rRNA gene regions (Supplementary Table 1), cloned using the TOPO TA kit (Invitrogen Life Technologies) and sequenced on an ABI 3130 XL genetic analyzer using the BigDye Terminator kit v3.1. For each isolate three to six clones were analyzed and found to be identical (99.8-100% sequence similarity). The software Pintail (Ashelford *et al.*, 2005) indicated that the obtained sequences were not chimeric. All 18S rRNA sequences showed highest sequence similarity with members of the genus *Acanthamoeba* (96.6-99.7%); similarity values to other genera were below 90% (Table 1). Using the 95% similarity threshold value for the definition of *Acanthamoeba* 18S rRNA sequence types (Stothard *et al.*, 1998) the isolates *Acanthamoeba* spp. EI1, EI2, EI3, 5a2, EIDS3 and EI6 could be assigned to the sequence type T4; *Acanthamoeba* spp. EI4 and EI5 could be assigned to sequence type T2. Consistently, phylogenetic analysis using the ARB software package (Ludwig *et al.*, 2004) revealed a well-supported relationship of the new amoeba isolates with the genus *Acanthamoeba* and the genotypes T2 and T4, respectively (Fig. 1). The eight *Acanthamoeba* isolates containing endosymbionts were deposited at the American Type Culture Collection ATCC (Table 1).

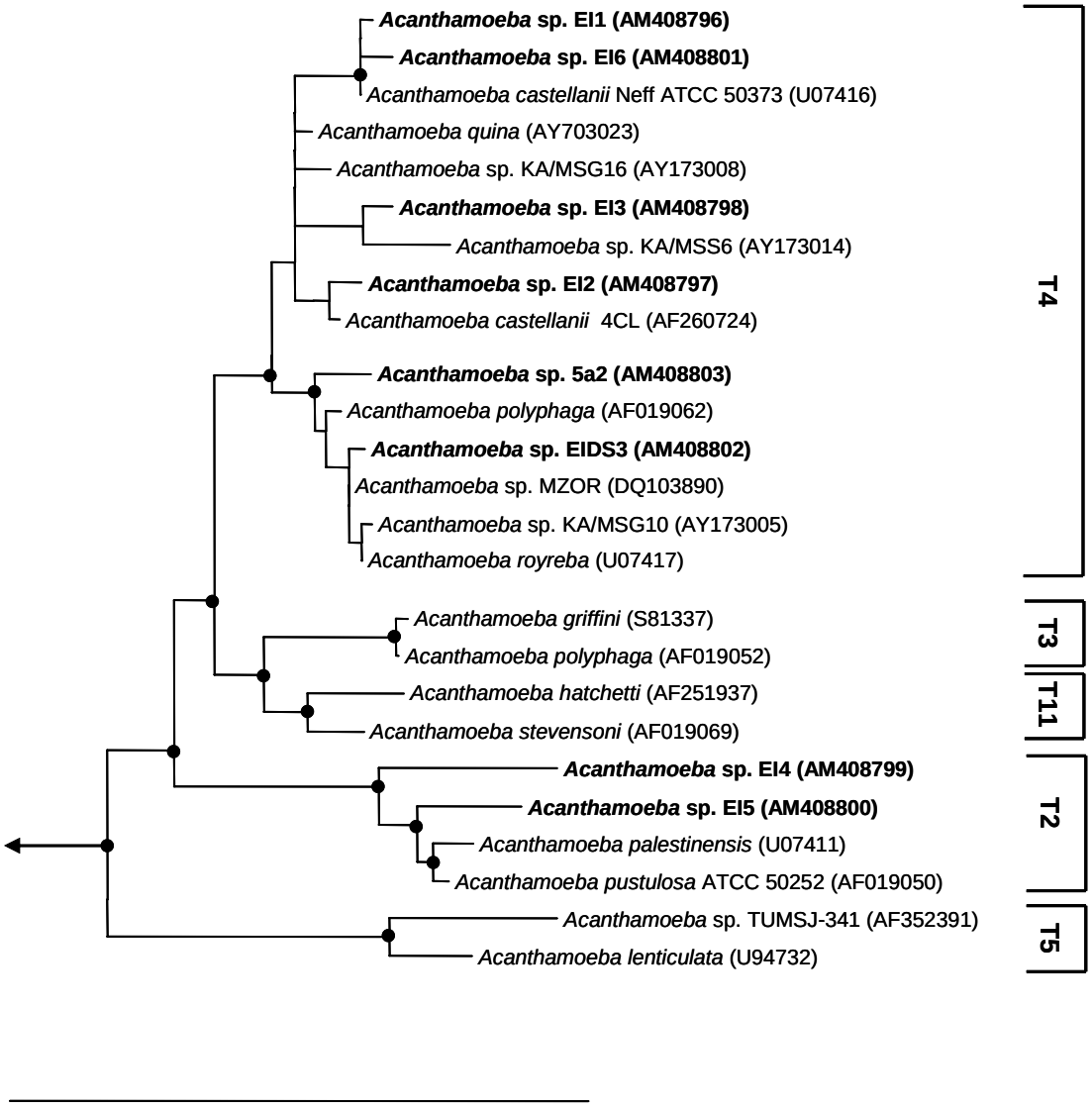


Figure 1. Phylogenetic relationships of *Acanthamoeba* host cells. An 18S rRNA based TREE-PUZZLE tree (HKY nucleotide substitution model; (Strimmer & von Haeseler, 1996) is shown. A filter considering only positions which are conserved in at least 50% of all amoebal 18S rRNA sequences was used for tree calculations. Selected *Acanthamoeba* 18S rRNA sequence types (Stothard *et al.*, 1998) are indicated. Black dots represent nodes with TREE-PUZZLE support and PHYLIP maximum parsimony bootstrap values (1.000 resamplings; (Felsenstein, 1989)) greater than 80%. GenBank accession numbers are given in brackets. Arrow, to outgroup; bar, 10% estimated evolutionary distance.

Identification of bacterial endosymbionts

In order to identify the bacterial endosymbionts of the recovered *Acanthamoeba* isolates, their near full-length 16S rRNA gene sequences (1388-1549 bp) were amplified (Supplementary Table 1) and cloned. For each symbiont three to six clones were sequenced and found to be identical (99.9-100% sequence similarity); the software Pintail indicated that the obtained 16S rRNA sequences were not chimeric. Comparative sequence analysis revealed that all sequences are highly similar to previously described obligate endosymbionts of free-living amoebae (Table 1).

Three of the identified symbionts (in isolates EI1, EI2, and EI6) showed highest 16S rRNA sequence similarity (98.9-99.5%) to members of the *Parachlamydiaceae* (Table 1) and thus belong to the genera *Parachlamydia* and *Protochlamydia* within this family according to the proposed taxonomy of *Chlamydiae* (Collingro *et al.*, 2005; Everett *et al.*, 1999; Katoh & Toh, 2008). Hereafter, these bacteria are accordingly referred to as *Parachlamydia* sp. EI1, *Parachlamydia* sp. EI6 and *Protochlamydia* sp. EI2.

Three *Acanthamoeba* endosymbionts (in isolates EI4, 5a2 and EIDS3) showed highest 16S rRNA sequence similarity to a group of amoeba symbionts within the *Bacteroidetes* (98.3-99.3%; Table 1), whose only described representative is '*Candidatus* Amoebophilus asiaticus TUMSJ-321' (Cole *et al.*, 2001). With the exception of a group of arthropod symbionts related to '*Candidatus* Cardinium hertigii' (Zchori-Fein & Perlman, 2004), similarity of these bacteria to other members of the *Bacteroidetes* was below 85%. These symbionts were thus named '*Candidatus* Amoebophilus EI4', '*Candidatus* Amoebophilus 5a2', and '*Candidatus* Amoebophilus EIDS3'.

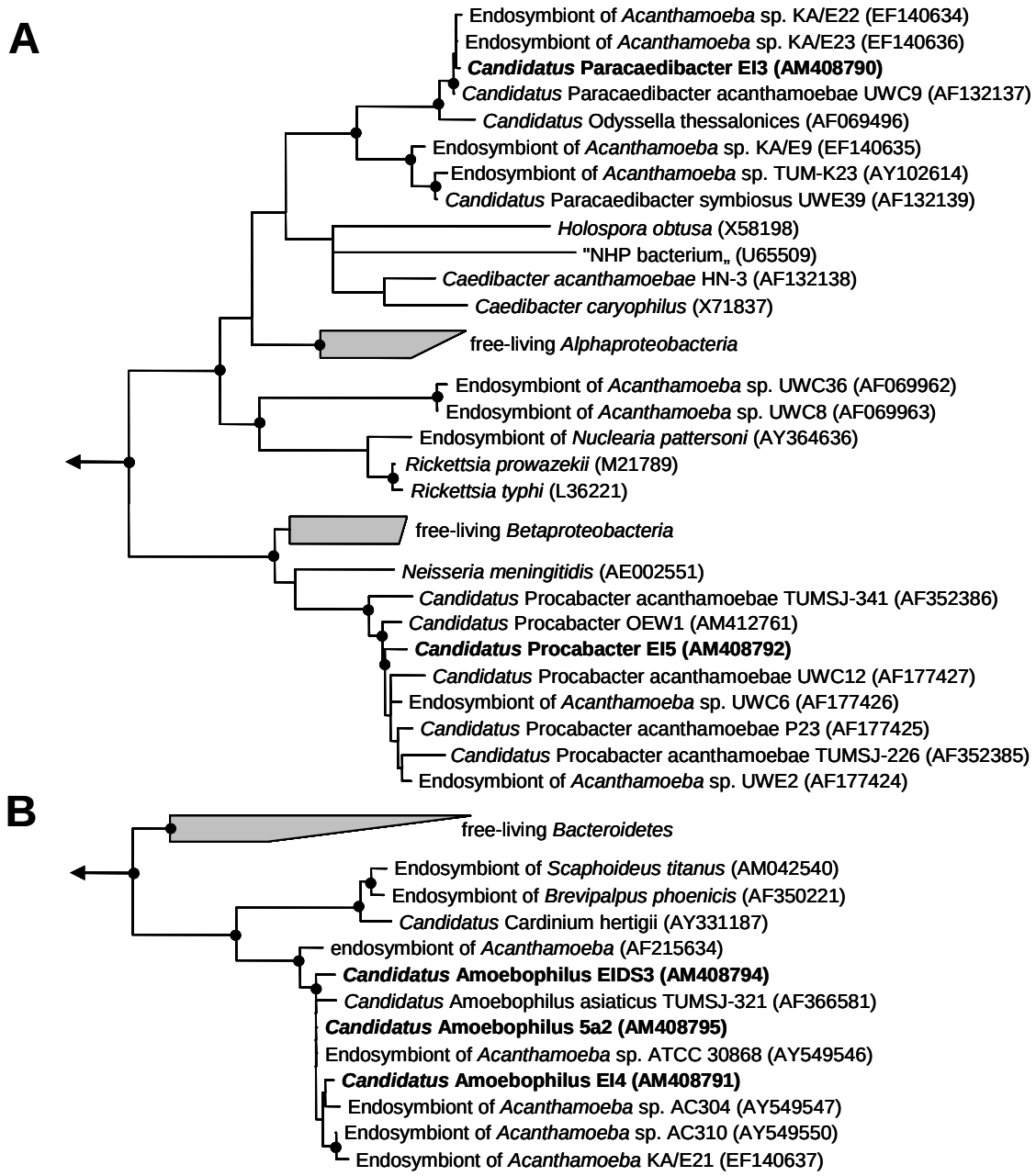
Endosymbiont of *Acanthamoeba* sp. EI3 was most similar to the alphaproteobacterial *Acanthamoeba* symbiont '*Cand.* Paracaedibacter acanthamoebae UWC9' (99.7% sequence similarity; Table 1; (Fritsche *et al.*, 1999)); the similarity to other members of the *Alphaproteobacteria* was significantly lower (83-92%). The endosymbiont of *Acanthamoeba* sp. EI3 is therefore tentatively referred to as '*Candidatus* Paracaedibacter EI3'.

Endosymbiont of *Acanthamoeba* sp. EI5 shared highest similarity with a group of betaproteobacterial endosymbionts of free-living amoebae, particularly with '*Cand*. Procabacter acanthamoebae Page23' (97.3%; Table 1; (Beier *et al.*, 2002; Heinz *et al.*, 2007)); similarity to other members of the *Betaproteobacteria* was below 90%. This symbiont was provisionally named '*Candidatus* Procabacter EI5'.

Table 1: Amoeba isolates and their symbionts analyzed in this study.

Isolate ATCC number	Source	Growth medium, optimal temperature	16S rRNA GenBank accession no. of symbiont	18S rRNA GenBank accession no. of amoeba host	Highest 16S rRNA sequence similarity to, accession no.	Highest 18S rRNA sequence similarity to, accession no.
Acanthamoeba sp. EI1 PRA-227	Soil, Vienna, Austria	TSY, 20°C	AM408788	AM408796	*Parachlamydia* sp. Hall's coccus (99.5%), AF366365	*Acanthamoeba castellanii* (99.6%), M13435
Acanthamoeba sp. EI2 PRA-226	Soil, Lower Austria, Austria	TSY, 20°C	AM408789	AM408797	*Protochlamydia amoebophila* UWE25 (98.9%), AF083615	*Acanthamoeba castellanii* 4CL (98.9%), AF260724
Acanthamoeba sp. EI3 PRA-225	Rainforest soil, Dominica	TSY, 20°C	AM408790	AM408798	'*Candidatus* Paracaedibacter acanthamoebae' (99.7%), AF132137	*Acanthamoeba* sp. KA/MSS7 (99.6%), AY173015
Acanthamoeba sp. EI4 PRA-224	Garden soil, Vienna, Austria	PYG, 20°C	AM408791	AM408799	'*Candidatus* Amoebophilus asiaticus' TUMSJ-321 (98.3%), AF366581	*Acanthamoeba polyphaga* OX-1 (96.6%), AF019051
Acanthamoeba sp. EI5 PRA-223	Desert sand, Matmata, Tunisia	TSY, 20°C	AM408792	AM408800	'*Candidatus* Procabacter acanthamoebae Page23' (97.3%), AF177425	*Acanthamoeba pustulosa* (98.0%), AF019050
Acanthamoeba sp. EI6 PRA-222	Soil, Schneeberg, Lower Austria, Austria	TSY, 20°C	AM408793	AM408801	*Parachlamydia* sp. UV-7 (98.9%), AJ715410	*Acanthamoeba castellanii* (99.3%), M13435
Acanthamoeba sp. EIDS3 PRA-221	Alkaline lake sediment, Darscho Lacke, Burgenland, Austria	PYG, 30°C	AM408794	AM408802	'*Candidatus* Amoebophilus asiaticus' TUMSJ-321 (99%), AF366581	*Acanthamoeba* sp. MZOR (99.7%), DQ103890
Acanthamoeba sp. 5a2 PRA-228	Lake sediment, Lake Neusiedl, Burgenland, Austria	PYG, 30°C	AM408795	AM408803	'*Candidatus* Amoebophilus asiaticus' TUMSJ-321 (99.3 %), AF366581	*Acanthamoeba royreba* Oak Ridge ATCC30884 (98.8%), U07417

All applied treeing methods used to resolve phylogenetic relationships of the newly identified endosymbionts consistently showed their affiliation with the respective most similar sequences, forming stable monophyletic lineages of symbiotic bacteria with high bootstrap and TREE-PUZZLE support within the *Proteobacteria*, the *Chlamydiae*, and the *Bacteroidetes*, respectively (Fig. 2).



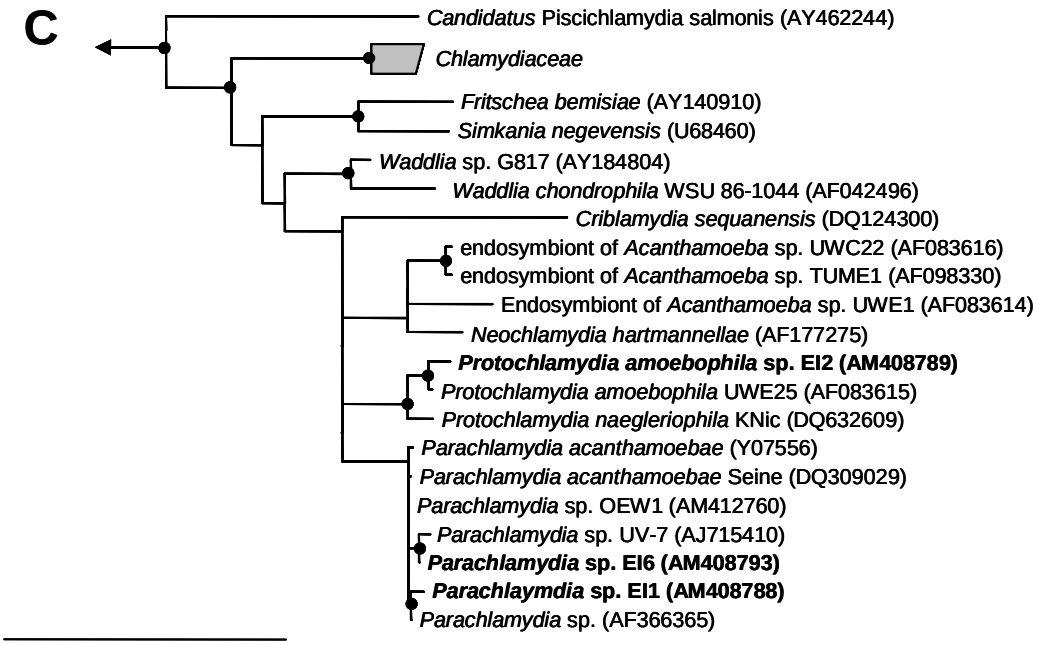


Figure 2. Phylogenetic relationships of *Acanthamoeba* symbionts. 16S rRNA based trees calculated using the TREE-PUZZLE algorithm (HKY nucleotide substitution model; (Strimmer & von Haeseler, 1996) are shown for the proteobacterial symbionts (A), the *Bacteroidetes* symbionts (B) and the chlamydial symbionts (C). A filter considering only positions which are conserved in at least 50% of all *Bacteria* was used for tree calculations. Black dots represent nodes with TREE-PUZZLE support and PHYLIP maximum parsimony bootstrap values (1.000 resamplings; (Felsenstein, 1989) greater than 80%. GenBank accession numbers are given in brackets. Arrows, to outgroups; bars, 10% estimated evolutionary distance.

Subcellular location of bacterial symbionts within their *Acanthamoeba* hosts

In order to demonstrate the intracellular location of the bacterial symbionts within their *Acanthamoeba* hosts, fluorescence *in situ* hybridization (FISH) in combination with confocal laser scanning microscopy was performed. Amoebae were harvested from axenic cultures by centrifugation (4000 x g, 5 min) and washed with 1x Page's saline (Page, 1976). After resuspension in 100 µl 1x Page's saline, 20 µl aliquots of amoebic suspension were incubated on glass slides for 20 min n to allow for attachment of amoebae, and fixed with 20 µl 4% paraformaldehyde for 20 min at room temperature. Hybridization was carried out as described elsewhere (Daims *et al.*, 2005).

Symbiont-specific probes were selected using probeBase ((Kurz & Ewbank, 2007); Supplementary Table 1) and applied for FISH under the recommended conditions. Positive hybridization reactions for all eight endosymbionts with the specific probes Bn9-658, Aph-1180, Proca-438, and CC23a were obtained and confirmed the 16S rRNA based identification and the intracellular location of these symbionts (Fig. 3). Furthermore, the simultaneous hybridization with symbiont-specific probes and the universal bacterial probe set EUB-mix labelled with different dyes showed that all bacteria within the *Acanthamoeba* cells were stained by both probes, demonstrating the presence of only a single symbiont phylotype within the respective *Acanthamoeba* hosts (Fig. 3).

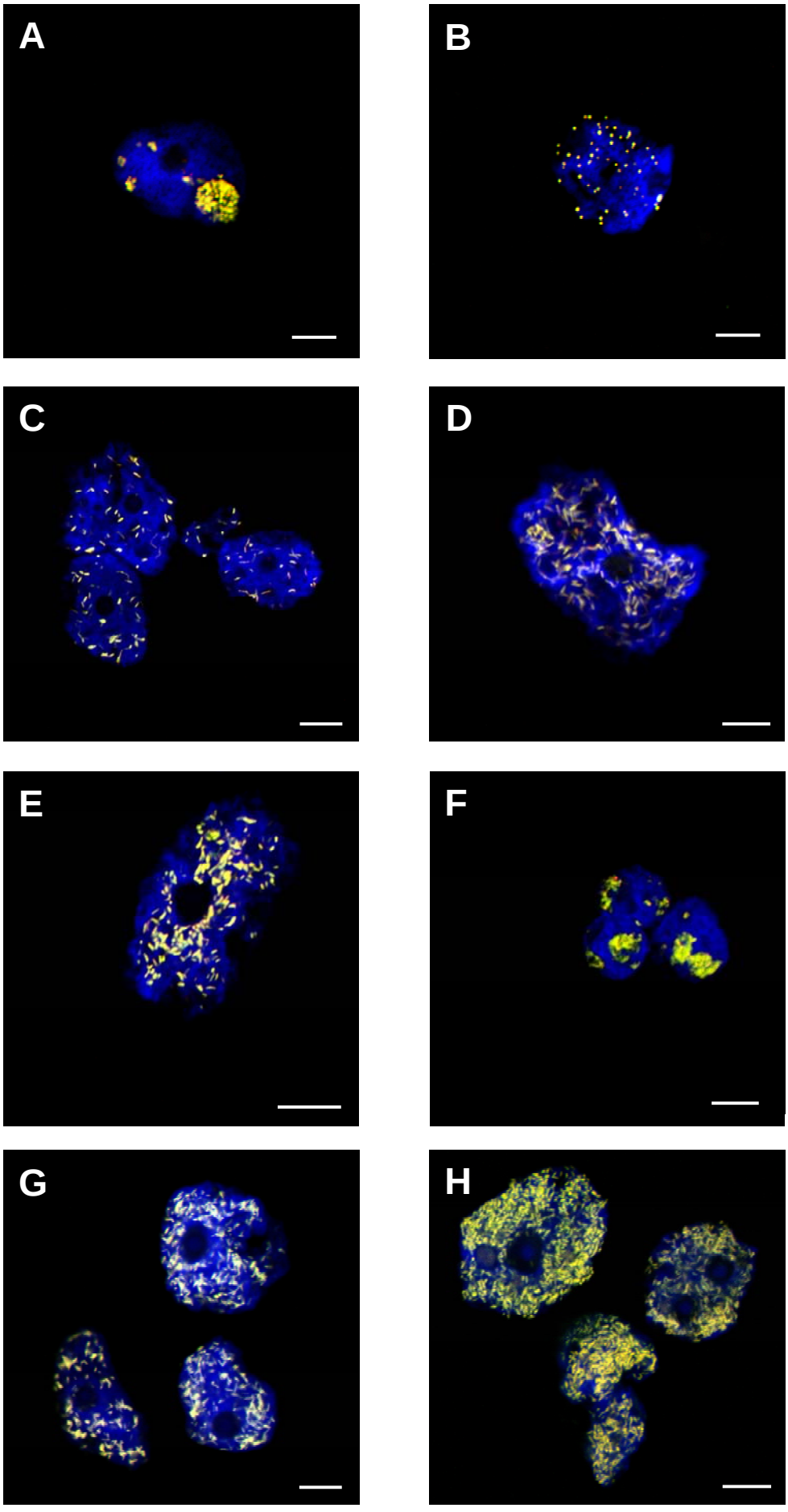

A
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Figure 3. Identification and intracellular localization of *Acanthamoeba* symbionts by fluorescence *in situ* hybridization. Probes EUK516 labelled with Cy5 (and shown in blue), targeting most *Eukarya*, and EUB-Mix labelled with Fluos (green), targeting most *Bacteria*, were used in all experiments in combination with Cy3 labelled symbiont-specific probes (red; Table 2). The combined signal from bacterial and symbiont-specific probes appears yellow. (A) *Parachlamydia* sp. EI1 in *Acanthamoeba* sp. EI1 (probe Bn9-658); (B) *Protochlamydia* sp. EI2 in *Acanthamoeba* sp. EI2 (probe Bn9-658); (C) '*Candidatus* Paracaedibacter EI3' in *Acanthamoeba* sp. EI3 (probe Cc23a); (D) '*Candidatus* Amoebophilus EI4' in *Acanthamoeba* sp. EI4 (probe Aph1180). (E) '*Candidatus* Procabacter EI5' in *Acanthamoeba* sp. EI5 (probe Proca438); (F) *Parachlamydia* EI6 in *Acanthamoeba* sp. EI6 (probe Bn9-658); (G) '*Candidatus* Amoebophilus EIDS3' in *Acanthamoeba* sp. EIDS3 (probe Aph1180); (H) '*Candidatus* Amoebophilus 5a2' in *Acanthamoeba* sp. 5a2 (probe Aph1180). Bars represent 10 µm.

The ultrastructure and intracellular niche of the bacterial symbionts within their amoeba host cells was further investigated by transmission electron microscopy. For this analysis, one representative of each evolutionary lineage was selected (Fig. 4). Amoebae were harvested from axenic cultures and directly fixed with 2% glutaraldehyde in 1 x Page`s amoebic saline for 1 h at room temperature, followed by fixation with 2% osmium tetroxide for 1 h at room temperature and dehydration in an ascending series of acetone. Subsequently, samples were embedded in Spurr resin (Sigma-Aldrich) with polymerisation at 60°C for 8-12 h. Ultra thin sections were stained with 1% uranyl acetate for 4 minutes and 0.3% lead citrate for 2 minutes and examined with a Zeiss CEM 902 transmission electron microscope.

Parachlamydia sp. EI1 showed morphological forms typical of chlamydial developmental stages, consisting of electron-dense elementary bodies and electron-translucent reticulate bodies (Abdelrahman & Belland, 2005; Bradley *et al.*, 1988; Collingro *et al.*, 2005; Fritsche *et al.*, 2000; Greub & Raoult, 2002; Kahane *et al.*, 2002). The diameters of elementary and reticulate bodies were 0.4-0.6 µm and 0.6-0.9 µm, respectively (Fig. 4A). Reticulate but not elementary bodies were observed undergoing binary fission. Furthermore, *Parachlamydia* sp. EI1 resided in large vacuoles resembling the host-derived inclusion characteristic for known chlamydiae (Fields *et al.*, 2002).

'Candidatus Amoebophilus EI4' was rod-shaped (0.3-0.5 µm in diameter and 0.7-1.4 µm in length) and appeared equally spread throughout the host cytoplasm (Fig. 4B). An association of *'Candidatus* Amoebophilus EI4' with ribosome-studded host membranes was not as obvious as for other '*Candidatus* Amoebophilus asiaticus' strains (Cole *et al.*, 2001; Xuan *et al.*, 2007).

'*Candidatus* Paracaedibacter EI3' had a rod-shaped morphology (0.2-0.4 µm in diameter and 0.9-1.4 µm in length). These bacteria seemed to be located directly in the host cell cytoplasm, not enclosed in vacuoles but surrounded by an electron-translucent space indicating a capsule or slime layer similar to that of '*Candidatus* Paracaedibacter acanthamoebae UWC9' and other similar strains (Birtles *et al.*, 2000; Fritsche *et al.*, 1999; Xuan *et al.*, 2007) (Fig. 4C).

The betaproteobacterial '*Candidatus* Procabacter EI5' exhibited rod-shaped morphology (0.3-0.4 µm in diameter and 0.8-1.3 µm in length) and was equally distributed in the host cytoplasm (Fig. 4D). Interestingly, '*Candidatus* Procabacter EI5', similar to another *Procabacter*-related amoeba symbiont described recently ('*Candidatus* Procabacter sp. OEW1'; (Heinz *et al.*, 2007)), was enclosed by a membrane, which contrasts with the original description of its closest relatives, '*Candidatus* Procabacter acanthamoebae' strains Page23, UWC12 and UWE2 that were found directly in the cytoplasm (Beier *et al.*, 2002).

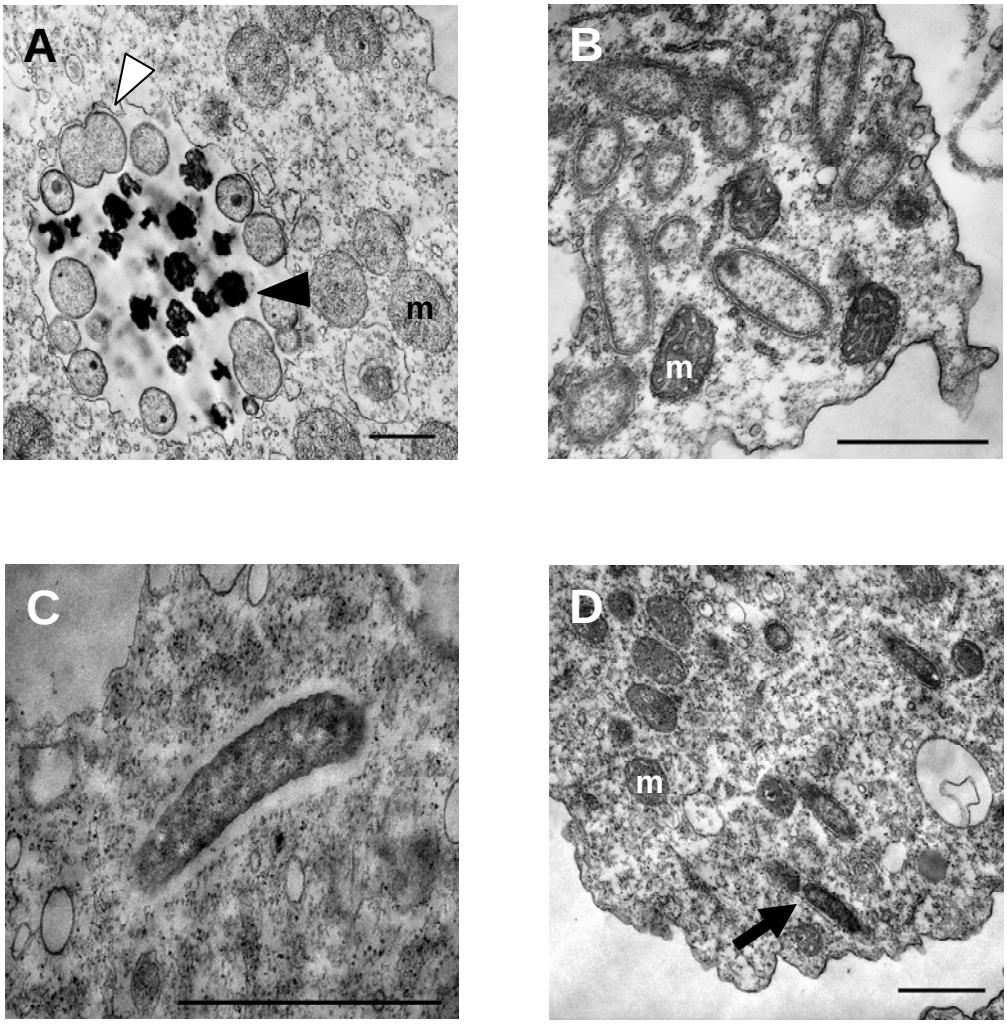

Figure 4. Ultrastructure of symbionts within *Acanthamoeba* host cells. Representatives from each phylogenetic group of symbionts are shown. (A) *Parachlamydia* sp EI1, (B) '*Candidatus* Amoebophilus EI4', (C) '*Candidatus* Paracaedibacter EI3', (D) and '*Candidatus* Procabacter EI5'. Elementary (black arrowhead) and reticulate bodies (white arrowhead) within the chlamydial inclusion can be seen in (A). An electron translucent space, indicative of a capsule or slime layer, surrounding '*Candidatus* Paracaedibacter EI3' is clearly visible in (C). '*Candidatus* Procabacter EI5' (D) is surrounded by a membrane (black arrow). Mitochondria are labelled ("m"). Bars represent 1 µm.

Four evolutionary lineages of *Acanthamoeba* symbionts

In the light of the ubiquity of acanthamoebae and the numerous reported transient associations between facultative intracellular bacteria and amoebae, it was surprising that all symbionts of the new *Acanthamoeba* isolates investigated in this study were related to either of the four known groups of obligate amoeba endosymbionts (Amann *et al.*, 1997; Beier *et al.*, 2002; Birtles *et al.*, 1997; Birtles *et al.*, 2000; Cole *et al.*, 2001; Fritsche *et al.*, 1999; Fritsche *et al.*, 2000; Xuan *et al.*, 2007), Fig. 2). This is even more remarkable as none of the *Acanthamoeba* isolates analyzed here originated from a location sampled previously (Table 2). In fact, for each phylogenetic group of symbionts, amoeba hosts were recovered from different habitats and different locations worldwide. The proteobacterial symbionts, for example, were found in amoebae from America, Europe, Africa, and Asia. This indicates a global distribution of only a small number of phylogenetically distinct groups of amoeba symbionts.

Despite the existence of only a few major evolutionary lineages of amoeba symbionts, there is a considerable diversity within some of these lineages. The alphaproteobacterial and the chlamydial symbionts comprise at least four different genera, respectively (Table 2). In addition, two of the bacterial symbionts identified in this study, '*Candidatus* Amoebophilus EI4' and '*Candidatus* Procabacter EI5', showed a 16S rRNA sequence similarity below the recently proposed thresholds for the discrimination of bacterial species of 98.6 or 98.7 % 16S rRNA similarity (Kalayoglu & Byrne, 2006; Keswani & Whitman, 2001) and thus represent novel species within the tentative genera *Amoebophilus* (at least three species in total) and *Procabacter* (at least four species), respectively (Table 2). This species-level diversity is further supported by differences in ultrastructure and subcellular location observed in this study compared to previous reports (Beier *et al.*, 2002; Cole *et al.*, 2001; Heinz *et al.*, 2007; Xuan *et al.*, 2007).

Table 2: Overview of recognized obligate intracellular symbionts of free-living amoebae

Bacterial lineage	Amoeba symbiont designation	Country of origin	Source habitat	GenBank 16S rRNA accession number	Reference
Alphaproteobacteria	'*Candidatus* Paracaedibacter acanthamoebae UWC9'	USA	Contact lens case	AF132137	(Fritsche *et al.*, 1999)
	'*Candiatus* Paracaedibacter EI3'	Dominica	Rainforest soil	AM408790	This study
	Endosymbiont of *Acanthamoeba* sp. KA/E23	Korea	Human corneal tissue	EF140636	(Xuan *et al.*, 2007)
	Endosymbiont of *Acanthamoeba* sp. KA/E22	Korea	Human corneal tissue	EF140634	
	'*Candidatus* Odyssella thessalonices'	Greece	Water from air condition	AF069496	(Birtles *et al.*, 2000)
	'*Candidatus* Paracaedibacter symbiosus E39'	USA (MN)	Soil	AF132139	(Fritsche *et al.*, 1999)
	Endosymbiont of *Acanthamoeba* sp. TUMK-23	Germany	Activated sludge	AY102614	(Beier *et al.*, 2002)
	Endosymbiont of *Acanthamoeba* sp. KA/E9	Korea	Human corneal tissue	EF140635	(Xuan *et al.*, 2007)
	Caedibacter acanthamoebae HN-3	USA	Nasal swab	AF132138	(Fritsche *et al.*, 1999)
	Endosymbiont of *Acanthamoeba* sp. UWC8	USA	Human corneal tissue	AF069963	(Fritsche *et al.*, 1999)
	Endosymbiont of *Acanthamoeba* sp. UWC36	USA	Human corneal tissue	AF069962	
	Endosymbiont of *Nuclearia pattersoni*	Czech Republic	Gills (roach, *Rutilus rutilus*)	AY364636	(Dykova *et al.*, 2003)
Betaproteobacteria	'*Candidatus* Procabacter acanthamoebae UWC12'	USA	Human corneal tissue	AF177427	(Beier *et al.*, 2002)
	'*Candidatus* Procabacter sp. Page23'	USA (WI)	Freshwater	AF177425	
	'*Candidatus* Procabacter sp. TUMSJ-341'	Malaysia	Lake sediment	AF352386	
	'*Candidatus* Procabacter sp. TUMSJ-226'	Malaysia	Lake sediment	AF352385	
	'*Candidatus* Procabacter sp. UWC6'	USA	Human corneal tissue	AF177426	
	'*Candidatus* Procabacter sp. UWE2'	USA (MN)	Soil	AF177424	
	'*Candidatus* Procabacter EI5'	Tunisia	Desert sand	AM408792	This study
	'*Candidatus* Procabacter sp. OEW1'	Austria	Saline lake sediment	AM412761	(Heinz *et al.*, 2007)

Bacteroidetes	'*Candidatus* Amoebophilus asiaticus TUMSJ-321'	Malaysia	Lake sediment	AF366581	(Cole *et al.*, 2001)
	Endosymbiont of *Acanthamoeba* sp. KA/E21	Korea	Human corneal tissue	EF140637	(Xuan *et al.*, 2007)
	'*Candidatus* Amoebophilus EIDS3'	Austria	Alkaline lake sediment	AM408794	This study
	'*Candidatus* Amoebophilus EI4'	Austria	Soil	AM408791	This study
	'*Candidatus* Amoebophilus 5a2'	Austria	Lake sediment	AM408795	This study
Chlamydiae	*Protochlamydia amoebophila* UWE25	USA (WA)	Soil	AF083615	(Collingro *et al.*, 2005)
	Protochlamydia naegleriophila KNic	Germany	Freshwater aquarium water	DQ632609	(Casson *et al.*, 2008)
	'*Candidatus* Protochlamydia sp. EI2'	Austria	Soil	AM408789	This study
	Endosymbiont of *Acanthamoeba* sp. UWE1	USA (WA)	Soil	AF083614	(Fritsche *et al.*, 2000)
	Parachlamydia acanthamoebae Bn9	Germany	Nasal swab	Y07556	(Amann *et al.*, 1997)
	Parachlamydia acanthamoebae Berg17	Germany	Nasal swab	AM941720	
	Parachlamydia sp. Hall's coccus[1]	USA (VT)	Water, humidifier	AF366365	(Birtles *et al.*, 1997)
	Parachlamydia sp. EI1	Austria	Soil	AM408788	This study
	Parachlamydia sp. EI6	Austria	Soil	AM408793	This study
	Parachlamydia sp. UV-7[1]	Germany	Activated sludge	AJ715410	(Collingro *et al.*, 2005)
	Parachlamydia sp. Seine[1]	France	Freshwater (Seine river)	DQ309029	(McCoy *et al.*, 2006)
	Parachlamydia sp. OEW1	Austria	Saline lake sediment	AM412760	(Heinz *et al.*, 2007)
	Neochlamydia hartmannellae	Germany	Water, water conduit	AF177275	(Fritsche *et al.*, 2000)
	Endosymbiont of *Acanthamoeba* sp. TUME1	Germany	Activated sludge	AF098330	(Fritsche *et al.*, 2000)
	Endosymbiont of *Acanthamoeba* sp. UWC22	USA	Human corneal tissue	AF083616	
	Criblamydia sequanensis[1]	France	Freshwater (Seine river)	DQ124300	(McCoy *et al.*, 2006)

[1] Symbionts were obtained by co-cultivation with *Acanthamoeba* spp.

One possible explanation for the observed limited phylogenetic diversity of bacterial endosymbionts of *Acanthamoeba* species might be a potential bias introduced by the isolation and axenization procedure. The use of non-nutrient agar plates with *E. coli* or *Enterobacter aerogenes* as food source is currently the standard procedure for isolation of free-living amoebae and was used to recover phylogentically diverse amoebae (Finn *et al.*, 2006; Schuster, 2002; Schuster & Visvesvara, 2004). From the eight *Acanthamoeba* isolates analyzed in this study, six belong to *Acanthamoeba* sequence type T4 (Fig. 1), which is the most abundant genotype in the environment and also comprises most of the pathogenic *Acanthamoeba* isolates (Finn *et al.*, 2006; Schuster & Visvesvara, 2004; Walochnik *et al.*, 2000), while two belong to sequence type T2. This suggests that there is considerable phylogenetic diversity within the *Acanthamoeba* isolates obtained with the method applied in this study. However, although unlikely, we cannot exclude that for some unknown reason, amoebae containing certain types of symbionts are selected for by this method. In this context, it seems interesting that the amoeba harbouring '*Candidatus* Procabacter EI5', which is most different from known amoeba symbionts, was recovered from non-nutrient agar plates with *Saccharomyces cerevisiae* instead of *E. coli* as food source. One possibility to isolate free-living amoebae harbouring novel bacterial endosymbionts might therefore be to use alternative food sources during isolation.

Another possibility for the discovery of novel intracellular bacteria has been described recently. Co-cultivation of environmental samples with (symbiont-free) amoebae was successfully used to identify obligate or facultative intracellular bacteria and to grow them in a surrogate *Acanthamoeba* host (Collingro *et al.*, 2005; McCoy *et al.*, 2006; Pagnier *et al.*, 2008). This technique is by far less time-consuming than the isolation and axenization of amoebae using traditional methods. However, the co-cultivation approach bears the disadvantage that the identity of the original host (which does not necessarily have to be an amoeba) remains unknown.

CONCLUSIONS

In concert with previous reports (Amann *et al.*, 1997; Beier *et al.*, 2002; Birtles *et al.*, 2000; Cole *et al.*, 2001; Fritsche *et al.*, 1999; Fritsche *et al.*, 2000; Xuan *et al.*, 2007) this study provides evidence for the existence of only a limited number of phylogenetically different groups of obligate bacterial endosymbionts of *Acanthamoeba* spp., showing a global distribution. This might suggest that adaptation of bacteria to long-term intracellular symbiosis with acanthamoebae has originated only a few times during evolution. The ongoing genome projects of *Parachlamydia acanthamoebae* UV7, '*Candidatus* Amoebophilus asiaticus 5a2', and *Acanthamoeba castellanii* Neff will help to understand

similarities and differences between these symbionts and the interactions with their *Acanthamoeba* hosts, and might illuminate their potential contributions to the role of free-living amoebae as evolutionary training grounds for facultative intracellular bacteria.

Nucleotide sequence accession numbers

18S and 16S rRNA gene sequences of *Acanthamoeba* isolates and their symbionts were deposited at EMBL/DDBJ/GenBank under accession numbers AM408788 to AM408803 (Table 1).

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Supplementary Material

Supplementary Table 1: Primers and oligonucleotide probes used in this study.

Short name	Sequence (5'-3')	Specificity	Target site	Annealing temperature / Formamide concentration	Reference
16S and 18S rDNA targeted primers used for PCR					
616F	AGAGTTTGATYMTGGCTC	most *Bacteria*	8-25[a]	52°C	(Juretschko *et al.*, 1998)
1492R	GGYTACCTTGTTACGACTT	most *Bacteria*	1492-1510[a]	52°C	(Essader *et al.*, 2005)
16S1[c]	CGGATCCTGAGAATTTGATC	*Chlamydiae*	1-18[a]	44°C	(Pudjiatmoko *et al.*, 1997)
16S2[c]	TGTCGACAAAGGAGGTGATCCA	*Chlamydiae*	1528-1549[a]	44°C	
SSU1	AACCTGGTTGATCCTGCCAG	Eukarya	1-17[b]	48°C	(Gast *et al.*, 1994)
SSU2	GATCCTTCTGCAGGTTCACCTAT	Eukarya	2273-2295[b]	48°C	
18SF	GTAGTCATATGCTTGTCTC	Amoebozoa	17-35[b]	48°C	This study
18SR	CGRARACCTTGTTACGAC	Amoebozoa	2256-2273[b]	48°C	
S12.2	GATYAGATACCGTCGTAGTC	Amoebozoa	1220-1239[b]	48°C	(Fahrni *et al.*, 2003)
Aas79F	ACACTTCGGTGTTGCTGG	'*Cand*. Amoebophilus asiaticus'	79-98[a]	50°C	This study
Aas1467R	GTCGCTGATCTAACCCTA	'*Cand*. Amoebophilus asiaticus'	1467-1484[a]	50°C	
16S and 18S rRNA targeted oligonucleotides used for FISH[d]					
EUB338-I[e]	GCTGCCTCCCGTAGGAGT	Most *Bacteria*	338-355[a]	0-70%	(Amann *et al.*, 1990)
EUB338-II[e]	GCAGCCACCCGTAGGTGT	Bacteria not covered by probe EUB338, e.g., many *Planctomycetes*	338-355[a]	0-70%	(Daims *et al.*, 1999)
EUB338-III[e]	GCTGCCACCCGTAGGTGT	Bacteria not covered by probe EUB338, e.g., many *Verrucomicrobia*	338-355[a]	0-70%	
EUK516	ACCAGACTTGCCCTCC	Most Eukarya	502-517[a]	0-70%	(Amann *et al.*, 1990)
Bn9-658	TCCGTTTTCTCCGCCTAC	Subgroup of the *Parachlamydiaceae*	658-675[a]	10%	(Amann *et al.*, 1997)
Aph1180	CTGACCTCATCCCCTCCT	'*Cand*. Amoebophilus asiaticus'	1180-1197[a]	20%	(Cole *et al.*, 2001)
Proca438	CGATTTCCTCCCRGACAA	'*Cand*. Procabacter acanthamoebae'	438-455[a]	20%	(Beier *et al.*, 2002)
CC23a	TTC CAC TTT CCT CTC TCG	*Caedibacter caryophilus* and other *Caedibacter*-related endosymbionts of *Acanthamoeba* spp.	658-675[a]	20%	(Springer *et al.*, 1993)

[a] 16S rRNA position, *E. coli* numbering according to (Brosius *et al.*, 1981)
[b] 18S rRNA position in *A. castellanii* Neff ATCC50373 (U07416)
[c] Primer sequences contain restriction enzyme site for BamH1 and SalI
[d] Further details on the probes used for FISH are available at probeBase (www.microbial-ecology.net/probebase;(Flores *et al.*, 2007)
[e] EUB338, EUB338-II, and EUB338-III were applied simultaneously to target most *Bacteria*

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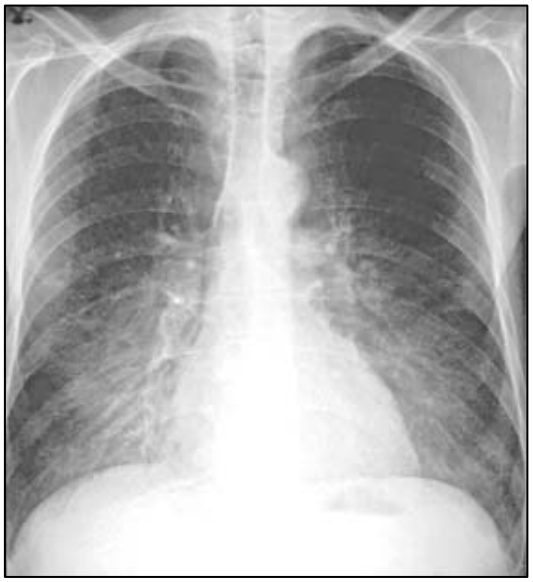
Chapter III

Chlamydia-like bacteria in respiratory samples of community-acquired pneumonia patients



The X-ray shows bilateral interstitial infiltrates which can be caused by viral pneumonia, pneumocystis, mycoplasma, chlamydia, coxiella, and sometimes legionella (www.islamicboard.com).

Chlamydia-like bacteria in respiratory samples of community-acquired pneumonia patients

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M.H., A.C. and S.H. planned the experiments. S.H. developed the PCR assay, accomplished together with A.C. all nested and semi-nested PCR assays, conducted sensitivity experiments and wrote the manuscript. J.W. performed the *Acanthamoeba*-specific PCR.

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ABSTRACT

Chlamydia-like bacteria, obligate intracellular relatives of *Chlamydia trachomatis* and *Chlamydophila pneumoniae*, are widely distributed in nature. Using a two-step nested and semi-nested PCR approach targeting the 16S rRNA gene, we found DNA of *Chlamydia*-like bacteria in respiratory samples from patients with community-acquired pneumonia. Four out of 387 cases (1.03%) were tested positive if only sequences showing less than 99.9% 16S rRNA sequence similarity to known chlamydiae were considered. These included for the first time *Protochlamydia amoebophila*, *Waddlia chondrophila*, and '*Candidatus* Rhabdochlamydia porcellionis'-related sequences. This study extends previous findings suggesting an association of *Chlamydia*-like bacteria with respiratory disease, but a causal link between these microorganisms and respiratory tract infections has yet to be established.

INTRODUCTION

Pneumonia is one of the most frequent infections of humans and animals and the third most common cause of death due to infectious disease worldwide (Welte *et al.*, 2004). Among bacterial pathogens, leading causes of community-acquired pneumonia (CAP) are *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Mycoplasma pneumoniae* and *Chlamydophila pneumoniae*. *C. pneumoniae*, in particular, has been estimated to be responsible for 2-43% of all cases of CAP (Wellinghausen *et al.*, 2006). However, in about 50% of all cases, the causative agent of pneumonia remains unknown (reviewed in (Bartlett *et al.*, 1998). Recently, a number of novel bacteria have been identified that are moderately related to *C. pneumoniae* and that have been proposed to represent emerging pathogens (Friedman *et al.*, 2003; Greub & Raoult, 2002). These obligate intracellular *Chlamydia*-like bacteria (also known as environmental chlamydiae) have been grouped into the novel families *Waddliaceae*, *Parachlamydiaceae*, and *Simkaniaceae* (Everett *et al.*, 1999; Rurangirwa *et al.*, 1999). They are widely distributed in nature and show an extremely broad host range. They live as endosymbionts in free-living amoebae and are able to infect and thrive in insects, crustaceans, reptiles, fish, birds, marsupials, and mammals (reviewed in (Corsaro & Greub, 2006). Additionally, a large number of unidentified chlamydiae exist in various environmental and clinical samples, indicating that chlamydial diversity is still underestimated (Corsaro *et al.*, 2003; Horn *et al.*, 2001). To date, *Chlamydia*-like bacteria have mostly been implicated in human respiratory disease, mainly based on serological and molecular data (reviewed in (Corsaro & Greub, 2006; Friedman *et al.*, 2003). For example, in one study, 2.6% of adult patients hospitalized with CAP (n=308) showed high or rising IgA and/or IgG titers against *Simkania negevensis*, which was taken as evidence for an acute infection (Lieberman *et al.*, 1997). In another study, IgM antibody titers ≥50 against *Parachlamydia* spp. have been observed in 3.7% of CAP patients (n=376), which was considered to represent past infections (Marrie *et al.*, 2001). Two of these patients showed an even higher antibody titer (≥400), indicating an acute infection (Marrie *et al.*, 2001). Additional evidence for a human pathogenic potential of *Chlamydia*-like bacteria might be the documented ability of some *Parachlamydiaceae* to infect and replicate within mammalian cells (Casson & Greub, 2006; Collingro *et al.*, 2005; Greub *et al.*, 2003). However, the actual prevalence of *Chlamydia*-like bacteria in clinical specimens is difficult to assess, as they are not detected by conventional diagnostic procedures. In this study, we investigated respiratory samples from CAP patients for the presence of *Chlamydia*-like bacteria by a novel nested, highly sensitive PCR approach. This work was part of the German medical research network CAPNETZ, which aims to improve current knowledge, diagnostic and therapy of CAP (Welte *et al.*, 2004).

METHODS

Clinical samples

Respiratory samples from 387 CAP patients recruited by CAPNETZ (Welte *et al.*, 2004) were examined. Inclusion criteria encompassed age ≥18, pulmonary infiltration visible in chest X-ray, and at least one of the following symptoms: cough, purulent sputum, pathological sounds on auscultation (Wellinghausen *et al.*, 2006). In total, 493 respiratory samples were analyzed, including primarily sputum (n=383), throat washings (n=101) and bronchoalveolar lavage (BAL, n=24).

DNA purification and PCR assays

DNA extraction was performed at the CAPNETZ central service unit by using the QIAamp DNA-Blood Mini Kit (Qiagen, Hilden, Germany) according to the instructions of the manufacturer (Wellinghausen *et al.*, 2006). For PCR screening we developed and employed a new, highly sensitive nested PCR approach targeting the 16S rRNA gene. Previous studies have shown that PCR screening for *Chlamydia*-like bacteria is extremely susceptible to contaminations (Corsaro & Greub, 2006), possibly due to the ubiquitous occurrence of *Chlamydia*-like bacteria and their amoeba hosts. The assay used in this study tried to minimize this risk by targeting a rather large DNA fragment in the first step of the nested PCR, which should thus be less prone to contamination than PCR targeting shorter and much more stable DNA fragments. This first step of the nested PCR assay amplified the near full-length 16S rRNA gene (~1,530 bp) of most known *Chlamydia*-like bacteria, including the *Parachlamydiaceae*, *Waddliaceae*, and *Simkaniaceae*. The forward primer PCf excluding the *Chlamydiaceae* (Horn *et al.*, 2001) was used in combination with the *Chlamydiales*-specific reverse primer 16S2 (Pudjiatmoko *et al.*, 1997) at an annealing temperature of 56°C (Table 1). Subsequently, a 1:100 dilution of the PCR product was used as template for the second step of the nested PCR assay, which employed the *Chlamydiales*-specific primer set 16SigF2/16SigR2 (modified from (Everett *et al.*, 1999), amplifying ~290 bp fragments, at an annealing temperature of 61°C. The sensitivity of this nested PCR assay was assessed with *Protochlamydia amoebophila* UWE 25 DNA (Collingro *et al.*, 2005). The lowest limit of detection was 10 fg DNA, corresponding to approximately four bacterial cells (data not shown) and demonstrating the high sensitivity of this assay. Samples that tested positive in this first, nested PCR assay were subsequently further analyzed by an additional, semi-nested PCR using the PCR product from the first step of the nested PCR assay (which was not sufficient to be sequenced directly), but primers 16SigF2 and 16S2 in the second step (Table 1). In contrast to the first nested PCR assay, this semi-nested PCR generated a 16S rRNA gene fragment of sufficient length (~1,510 bp) for a detailed phylogenetic analysis.

Positive controls (*P. amoebophila* UWE25 DNA; and negative controls (no DNA added) were included in all PCR reactions. Amplification products were purified by QIAquick PCR Purification Kit (Qiagen, Vienna, Austria) and directly sequenced.

Table 1. PCR primers used in the 16S rRNA-targeted PCR assays

Primer	Sequence (5´-3´)	Position[a]	Reference
PCf[b]	TCAGATTGAATGCTGAC	24	Horn & Wagner, 2001
16S2[bd]	TGTCGACAAAGGAGGTGATCCA	1528	Pudjiatmoko *et al*., 1997
16SigF2[cd]	CRGCGTGGATGAGGCAT	40	mod. from Everett *et al*., 1999
16SigR2[c]	TCAGTCCCARTGTTGGC	309	mod. from Everett *et al*., 1999

[a] target position according to *E. coli* 16S rRNA gene numbering

[b] used in the first step of the nested and the semi-nested PCR assay (length of amplificate ~1,530 bp)

[c] used in the second step of the nested PCR assay (length of amplificate ~290 bp)

[d] used in the second step of the semi-nested PCR assay (length of amplificate ~1,510 bp)

Sequence analysis

The software package ARB (Ludwig *et al.*, 2004) was used to check for chimeric sequences and to perform phylogenetic analysis. Nucleotide sequences were deposited at GenBank/EMBL/DDBJ under accession numbers EU090706 to EU090709.

RESULTS AND DISCUSSION

To study the incidence of *Chlamydia*-like bacteria in CAP patients, 493 respiratory samples from 387 patients were examined using a novel combination of a nested and a semi-nested PCR assay. Of these, 33 samples (6.69%) tested positive in the first, nested PCR assay, but only 15 samples (3.04%) tested positive for the presence of *Chlamydia*-like organisms in both the nested and the semi-nested PCR assay. The difference between the results from those two tests might indicate false positives in the first nested PCR assay (due to short, degraded DNA fragments amplified in the second step of the nested PCR assay, but not targeted by the second step of the semi-nested PCR assay; Table 1). Ambiguous samples were thus excluded from further analysis, although the negative controls included in all PCR assays remained negative. Subsequent comparative sequence analysis of the amplificates from the semi-nested PCR demonstrated that one amplificate was unspecific showing no significant database hit, while 10 sequences were identical or almost identical (99.9 to 100% sequence similarity) among each other and to the 16S rRNA gene of *Parachlamydia acanthamoebae* Berg 17 (n=7) or *P. amoebophila* UWE25 (n=3).

On the one hand, the high 16S rRNA sequence similarity to known *Parachlamydiaceae* might not be very surprising as also all *C. pneumoniae* strains recovered from humans are virtually indistinguishable based on their 16S rRNA sequences (99 to 100% similarity; (Pettersson *et al.*, 1997). On the other hand, however, this could also indicate that these sequences represent PCR contaminations from organisms also handled in our laboratories, despite all possible care taken. To minimize the risk of analyzing false positive data, we thus preferred to exclude all sequences from further analysis that shared ≥99.9% 16S rRNA sequence similarity with known sequences. Phylogenetic sequence analysis of the remaining four sequences allowed us to assign them to the chlamydial families *Parachlamydiaceae* (n=1), and *Waddliaceae* (n=1), and to '*Candidatus* Rhabdochlamydia porcellionis' (n=2), respectively.

Members of the *Parachlamydiaceae* have been suggested previously to be associated with respiratory disease of humans (Corsaro & Greub, 2006). The *Parachlamydiaceae* sequence found in this study (CN823) shows 99.6% similarity to the 16S rRNA of *P. amoebophila* and represents the first *P. amoebophila* sequence from a human specimen.

Currently, the family *Waddliaceae* comprises the two species *W. chondrophila*, isolated from an aborted bovine fetus (Rurangirwa *et al.*, 1999), and *W. malaysiensis*, isolated from urine samples of fruit bats (Chua *et al.*, 2005). *Waddlia*-related sequences have not been amplified from human specimens in a systematic study before, but a recent report described a correlation between seropositivity against *W. chondrophila* and human fetal loss (Baud *et al.*, 2007). The *Waddlia*-like sequence detected in this study (CN761) shared 98.0% and 99.7% nucleotide similarity with *W. chondrophila* strains WSU-85-1044 and 2032/99, respectively, and represents the first *W. chondrophila*-like sequence found in a human respiratory sample.

Two sequences (CN808 and CN554) were related to '*Candidatus* Rhabdochlamydia porcellionis', a recently described symbiont of terrestrial isopods, forming a distinct lineage within the *Chlamydiales*, most closely related to the *Simkaniaceae* (Kostanjsek *et al.*, 2004). 16S rRNA sequence similarity values to '*Candidatus* Rhabdochlamydia porcellionis' were only 89.5% and 90.3%, respectively, and 89.1% and 89.4% to *S. negevensis.* The most similar known sequence was environmental chlamydia clone P-11 (environmental chlamydia lineage VI; (Horn *et al.*, 2001) sharing 90.4% and 93.5% sequence similarity, respectively. To date, only two distantly related 'Candidatus *Rhabdochlamydia* porcellionis'-like sequences (~230 bp) have been detected earlier in human specimens; only one of those originated from a patient with an upper respiratory tract infection (Ossewaarde & Meijer, 1999).

Most chlamydiae live as endosymbionts of free-living amoebae or are able to infect these protozoa. Amoebae are therefore considered to play a key role in the adaptation of environmental bacteria to intracellular life within higher eukaryotes (Collingro *et al.*, 2004). In addition, amoebae are well known as environmental reservoir and vehicle of dispersal for bacterial pathogens such as *Legionella pneumophila* (Molmeret *et al.*, 2005). Although chlamydiae have a broad host range and are able to infect phylogenetically different amoebae, the majority of them can use *Acanthamoeba* spp. as hosts. For this reason, all positive samples were also tested for the presence of amoeba DNA by performing an *Acanthamoeba*-specific PCR assay (Walochnik *et al.*, 2004). However, all samples were negative for *Acanthamoeba* DNA, suggesting either the absence of *Acanthamoeba* spp. in these samples or their presence in a concentration below the detection limit (one amoeba trophozoite ml^{-1}).

The four specimens that tested positive for *Chlamydia*-like DNA originated from four different patients, corresponding to 1.03% of all patients included in this study. Their mean age was 64.5 years (range 56 to 75) and no sex-related differences existed. Only two of the four patients were also positive for other known agents of CAP (Table 2), but all four patients tested negative by three different *C. pneumoniae*-specific PCR assays (Wellinghausen *et al.*, 2006). From two patients specimens from throat washings were also available, but these tested negative in all PCR assays, suggesting that throat washings are less suited for the detection of *Chlamydia*-like bacteria than BAL and sputum. All examined patients recovered from pneumonia after Clarithromycin or Moxifloxacin treatment for 8-19 days (Table 2).

In conclusion, using a two-step nested/semi-nested PCR approach we detected DNA sequences from *Chlamydia*-like bacteria in respiratory samples of CAP in a highly sensitive and specific manner. This PCR assay allowed us to amplify a broad spectrum of *Chlamydia*-like bacteria and to phylogenetically characterize the recovered sequences. The presence of DNA from *Chlamydia*-like bacteria in 1.03% of CAP patients (n=387) adds to a number of recent studies suggesting a possible association of these microorganisms with human disease (Corsaro & Greub, 2006). However, taking into account Frederick's and Relman's revisions of Koch's postulates for sequence-based identification of microbial pathogens (Fredericks & Relman, 1996), current evidence is just a first step towards our understanding of a possible causal link between *Chlamydia*-like bacteria and disease in humans.

Table 2. *Chlamydia*-like sequences detected in CAP patients

Sequence id	Accession no.	Specimens[a]	Highest sequence similarity to (host)	Patient				
				Sex[b]	Age (y)	Other respiratory pathogens	*C. pneumoniae*-PCR	Treatment
CN554	EU090707	BAL	90.3% '*Candidatus* Rhabdochlamydia porcellionis' (*Porcellio scaber* [Crustacea: Isopoda])	M	62	*Haemophilus influenzae* *Bacteroides ureolyticus* *Mycoplasma pneumoniae* (past *C. pneumoniae* infection)	Negative	Clarithromycin (18d)
CN761	EU090708	Sputum	99.7% *Waddlia chondrophila* 2032/99 (cattle)	F	65	None	Negative	Clarithromycin (8d)
CN808	EU090709	Sputum	89.5% '*Candidatus* Rhabdochlamydia porcellionis' (*Porcellio scaber* [Crustacea: Isopoda])	M	56	*Mycoplasma pneumoniae*	Negative	Clarithromycin (14d)
CN823	EU090706	Sputum	99.6% *Protochlamydia amoebophila* UWE25 (*Acanthamoeba* sp.)	F	75	None	Negative	Moxifloxacin (19d)

[a] BAL; Bronchoalveolar lavage
[b] M, male; F, female

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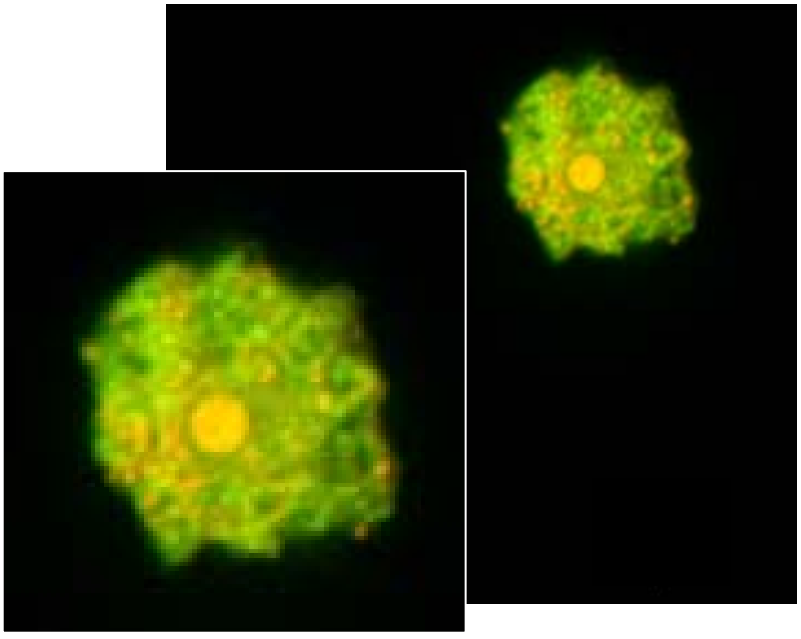
Chapter IV

The developmental cycle of *Protochlamydia amoebophila* in amoebal hosts



The picture shows *Acanthamoeba castellanii* Neff infected with *Protochlamydia amoebophila* after Acridine orange staining. Areas with a high RNA to DNA ratio stain red (RBs and host nucleus), those with a low RNA to DNA ratio stain green (EBs). Bar corresponds to 5 µm.

The developmental cycle of *Protochlamydia amoebophila* in amoebal hosts

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Concept by M.H. and S.H. S.H. developed general infection and real-time PCR assays, accomplished infection and FISH experiments and wrote the manuscript. L.K. performed infection and FISH experiments, developed progeny infection, viability and iron depletion experiments. A.M. made the real-time PCR experiments.

- In preparation -

ABSTRACT

All recognized members of the phylum *Chlamydiae* possess a unique developmental cycle consisting of infectious elementary bodies (EBs) and dividing reticulate bodies (RBs). While the developmental cycle of the medically important *Chlamydiaceae* has been intensively studied, our knowledge about the growth cycle of *Protochlamydia amoebophila* is still scarce, although this amoebal symbiont is the only phylum member outside of the *Chlamydiaceae* for which a genome sequence is available. In this study, the developmental cycle of *P. amoebophila* was characterized using *Acanthamoeba castellanii* Neff as well as *Acanthamoeba* sp. UWC1 as hosts. Infection and intracellular development were monitored by fluorescence *in situ* hybridization, immunofluorescence and quantitative real-time PCR and no host-specific differences were observed. Intracellular bacteria were detected as early as one hour post infection (hpi). Differentiation of EBs to RBs occurred within the first 48 hpi and reached a maximum at 72 hpi. At 96 hpi, RBs re-differentiated to EBs and the developmental cycle became increasingly asynchronous suggesting completion of the productive growth cycle of *P. amoebophila*. Consistent with these findings, infectious progeny were absent before 96 hpi and reached a maximum at 120 hpi. During infection and chlamydial multiplication, lysis of amoeba cells was only very rarely observed, indicating a well-balanced symbiotic interaction and exocytosis as major way for the release of infectious EBs from the host cells. Interestingly, a variation of this growth cycle with abnormally enlarged chlamydial cells, resembling the persistent forms of *Chlamydiaceae,* could be experimentally induced by iron depletion. This observation suggests that the capability to persistently infect eukaryotic cells might be an ancient feature which might have already been present in the last common ancestor of all chlamydiae.

INTRODUCTION

The phylum *Chlamydiae* contains the monophyletic family *Chlamydiaceae* with its well-known clinically relevant members *Chlamydophila pneumoniae* and *Chlamydia trachomatis* and several other more recently discovered deep-branching *Chlamydia*-like lineages including the *Parachlamydiaceae*, *Simkaniaceae* and *Waddliaceae* which contain symbionts of amoebae or insects (Amann *et al.*, 1997; Corsaro *et al.*, 2003; Everett *et al.*, 1999; Kahane *et al.*, 1993; Rurangirwa *et al.*, 1999). All chlamydiae are obligate intracellular bacteria thriving in a wide range of eukaryotic host cells (Horn, 2008) and they can be characterized by a unique biphasic developmental cycle (Abdelrahman & Belland, 2005; Ward, 1988). The developmental cycle involves two morphologically and physiologically distinct developmental forms. Elementary bodies (EBs) of these organisms are spore-like, infectious forms which are believed to be metabolically inactive and reticulate bodies (RBs) are metabolically active, dividing forms (Hatch, 1999). In addition, intermediate bodies (IBs), which are transition stages between RBs and EBs, were described (Hatch, 1999). A new developmental cycle is initiated by an infectious EB after attachment to a host cell. Following internalization through parasite-mediated endocytosis (Byrne & Moulder, 1978), the EB is localized to a phagosome and after the primary differentiation process which involves the commencement of bacterial metabolism and the conversion of the EB to an intracellular replicating RB, replication occurs by binary fission in a specialized non-lysosomal vacuole termed inclusion (Heinzen *et al.*, 1996; Hybiske & Stephens, 2007a; Scidmore *et al.*, 1996; Taraska *et al.*, 1996). At a dedicated time point the RB undergoes a secondary differentiation process back to the EB which is subsequently released back into the environment by exocytosis or host-cell lyses (Hybiske & Stephens, 2007b) and can infect new host cells. Under adverse conditions like antibiotic treatment, nutrient deprivation or immunological responses, a reversible aberrant state of infection has been described which is characterized by viable, non-cultivable and enlarged bacteria (Beatty *et al.*, 1994). Deviation from the typical developmental stages might be used to avoid host immune defence (Mpiga & Ravaoarinoro, 2006), and an association with chronic chlamydial disease is suggested (Hogan *et al.*, 2004).

Characteristics of infection markedly differ between chlamydial species. As described in a number of light- and electron microscopy studies (Hatch, 1999; Matsumoto, 1988; Ward, 1988; Wolf *et al.*, 2000) as well as by gene expression microarrays (Belland *et al.*, 2003; Mäurer *et al.*, 2007; Nicholson *et al.*, 2003), the developmental cycle of pathogenic chlamydiae lasts between 48-72 h (*C. trachomatis*), 72-96 h (*Chlamydia caviae*) and 84-96 h (*C. pneumoniae*).

However, whereas the productive growth cycle of pathogenic chlamydiae is well-documented, knowledge about the developmental cycle of members of the newly described chlamydial families is still sparse and has been derived mainly from two members of the *Parachlamydiaceae* and *Simkaniaceae*. Electron micrograph and immunofluorescence studies of the amoeba-associated symbiont *Parachlamydia acanthamoebae* showed morphologically different developmental stages, resembling *Chlamydiaceae* EBs and RBs (Greub & Raoult, 2002). Furthermore, Greub and coworkers suggested a third developmental stage, the infectious crescent bodies (Greub & Raoult, 2002). After entry of EBs and/or crescent bodies via phagocytosis, bacterial replication took place between 6-8 hours post infection (hpi) within an acidic vacuole and first evidence of host cell lysis was already observed as early as 24-36 hpi (Greub & Raoult, 2002; Greub *et al.*, 2005). In contrast to the fast growing *P. acanthamoebae*, *Simkania negevensis* which is also able to infect and survive in free-living amoebae (Kahane *et al.*, 2001; Michel *et al.*, 2005), revealed some remarkable differences in EB and RB cell morphology, infectivity as well as in the duration of the developmental cycle which takes about 12 to 15 days in mammalian cells. After binary replication, which occurs only between 2-4 days pi, a stable infection is suggested to be established without release of significant amounts of infectious particles from the host cells (Kahane *et al.*, 1999; Kahane *et al.*, 2001; Kahane *et al.*, 2002). Furthermore, an additional member of the *Chlamydia*-like bacteria, *Waddlia chondrophila*, has recently been shown in confocal and electron microscopic studies to grow rapidly within human macrophages inducing lysis already after 36 hpi (Goy *et al.*, 2008).

In the present study, we investigated the intracellular biphasic lifestyle of *Protochlamydia amoebophila* UWE25, a member of the *Parachlamydiaceae* and endosymbiont in free-living amoebae (Collingro *et al.*, 2005; Fritsche *et al.*, 1993). *P. amoebophila* is the first representative among *Chlamydia*-like bacteria for which a complete genome sequence is available (Horn *et al.*, 2004), and this makes it a valuable candidate for detailed biological and physiological investigations. Initial studies demonstrated that *P. amoebophila* shows the two typical morphological stages which are, unlike other chlamydiae (Amann *et al.*, 1997; Horn *et al.*, 2000), surrounded by individual inclusion membranes (Collingro *et al.*, 2005; Fritsche *et al.*, 2000). However, little is known about the duration and dynamics of the developmental cycle of this amoeba symbiont. This study gives a comprehensive description of the four days lasting developmental cycle of this newly identified organism.

MATERIAL AND METHODS

Cultivation and purification of *P. amoebophila*

Acanthamoeba castellanii Neff harbouring *P. amoebophila* was grown at 20°C in 500 cm² culture flasks (Iwaki) as a continuous culture in Trypticase Soy Broth with Yeast Extract (TSY; 30 g/l trypticase soy broth, 10 g/l yeast extract, pH 7.3) under axenic conditions (Visvesvara, 1999). Optimal cell growth was achieved by exchanging medium every 3 to 4 days. For EB purification, cells were harvested by centrifugation (3,214g, 10 min, 4°C), washed once, and resuspended in 500 µl 1 x Page´s amoebic saline (PAS) (Page, 1988). Host cells were disrupted by freezing (-20°C) and thawing (45°C water bath) and subsequent vortexing for 3 min in 1 volume glass beads. Cell debris was removed by centrifugation (300g, 10 min, 4°C), the supernatant was filtered (1.2 µm, Millipore) and centrifuged at 50,000g for 40 min at 4°C to pellet chlamydial cells. The pellet was resuspended in sucrose phosphate glutamic acid buffer (SPG; 750 g/l sucrose, 5.2 g/l KH_2PO_4, 23 g/l $NaHPO_4$*$7H_2O$, 7.5 g glutamic acid) and centrifuged as before. Afterwards, the pellet was resolved in SPG, pulled through a 0.45 x 25 mm syringe (Braun) for several times to dissolve EBs, aliquoted, and stored at -80°C. 10 µl purified EBs were added to 5 ml sterile phosphate-buffered saline (PBS; 130 mM NaCl, 10mM Na_2PO_4; pH 7.2 - 7.4), the suspension was filtered onto a 0.2 µm filter (Millipore), stained with 1 µg ml^{-1} 4', 6-diamidino-2-phenylindole (DAPI, Lactan) for 10 min, and counted by epifluorescence microscopy. Stocks were determined to be free of contamination with *Chlamydia*-like organisms by DNA isolation (DNeasy Blood and Tissue Kit, Qiagen), PCR amplification with the *Chlamydiales*-specific primer set PanF/R (Corsaro *et al.*, 2002) and restriction enzyme digestion (*VspI*; Fermentas GmbH).

Infection assay and fluorescence *in situ* hybridization (FISH) analyses

P. amoebophila EBs were added at a multiplicity of infection (MOI) of 5 to 10 to *A. castellanii* Neff or *Acanthamoeba* sp. UWC1 cells in 6-well plates (Iwaki). After centrifugation at 130g for 15 min, time point 1 hpi was harvested immediately by centrifugation (3,214g, 10 min), washed once, and resuspended in 100 µl 1 x PAS. 20 µl aliquots of amoebic suspension were incubated on glass slides for 20 min and fixed with 10 µl 4% paraformaldehyde (PFA) for 10 min at room temperature (RT). For all other samples, medium containing excess EBs was replaced with fresh medium; cultures were incubated at 20°C, harvested and fixed with 4% PFA at time points 6, 24, 48, 72, 96, 120 hpi as described above. Infection experiments were carried out in biological duplicates in *A. castellanii* Neff as well as in *Acanthamoeba* sp. UWC1. Further extended time points (144, 168, and 192 hpi) were also prepared for FISH from one replicate of *A. castellanii* Neff as well as from one replicate of *Acanthamoeba* sp. UWC1. Uninfected amoebae were used as negative controls. FISH was performed using the

protocol, hybridization and washing buffer described by Daims *et al*. (Daims *et al.*, 2005). Probes EUK516 and Acanth 412a both labelled with Fluos (green), targeting most *Eukarya*, and Cy3 labelled *Chlamydiales*-specific probe Chl523 (red) were used in all experiments. Only the metabolically active chlamydial forms are detected by FISH due to their higher ribosome content. For comparison of the chlamydial developmental stages, samples were simultaneously stained with 0.1 µg ml^{-1} DAPI (blue) for 4 min. Hybridized slides were examined using an epifluorescence microscope (Axioplan 2, Zeiss). Image analysis was performed with the standard software package delivered with the instrument (version 3.2).
For quantification of intracellular bacteria, *A. castellanii* Neff were infected with *P. amoebophila* EBs at a MOI of 10. FISH and DAPI staining was performed as described above at designated time points and EBs (DAPI signals only) as well as RBs (DAPI and FISH signals) were counted in 10-15 randomly collected amoeba cells by epifluorescence microscopy.

Assessment of *P. amoebophila* progeny infectivity

To test for the presence of infectious progeny, *A. castellanii* Neff cells were infected with *P. amoebophila* EBs at a MOI of 10 in 6-well plates as described before. At designated time points (1, 24, 48, 72, 96, 120 hpi) cells were resuspended and transferred to reaction tubes. Uninfected amoebae were used as control and were harvested at time point 120 hpi. Subsequently, the EB progeny in the supernatant was separated from the progeny in attached cells by low speed centrifugation (300g, 10 min, 20°C). The pellet containing the infected amoebae was resuspended in 100 µl SPG and subjected to two freeze (-20°C) and thaw (RT) steps, a ½ volume glass beads was added to the suspension which was subsequently vortexed for 3 min. Amoebal cell debris was removed (300g, 10 min 4°C) and cells in the supernatant were subjected to passaging through an injection needle (0.45 x 25 mm in diameter) followed by another centrifugation step (300g, 10 min, 4°C). The lysates that contained the intracellular bacteria were stored at -80°C. The supernatant containing extracellular bacteria was centrifuged at 20,800g for 30 min, resuspended in 100 µl SPG and also stored at -80°C. Identity of bacteria was controlled by FISH using a *P. amoebophila*-specific probe (E25-454; 5´-GGA TGT TAG CCA GCT CAT-3´ labelled in Cy3).
The numbers of bacteria in the intra- and the extracellular suspensions at each time point and the control were determined by counting of DAPI signals after filtration of suspensions onto a 0.2 µm filter (Millipore). Then, *A. castellanii* Neff cells were infected with the lysate of the attached cells and the supernatant. The infection was carried out in Lab-Tek™ chamber slides (Nunc); the procedure was the same as described earlier. At 12 hpi inclusions were specifically detected by immunofluorescence and DAPI staining. Briefly, cultures were fixed with methanol for 10 min at RT. Fixed cells were incubated with blocking solution (2% bovine

serum albumine in PBS) for 20 min at RT. Blocking solution was replaced by a 1:1000 dilution of primary antibodies (chicken anti-*P. amoebophila* antibody, Eurogentech; and guinea pig anti-Hsp60 antibodies, kindly provided by Daniel D. Rockey, Oregon State University) in blocking solution. After incubation for 1h at RT, cells were washed three times with PBS, and secondary antibodies (donkey anti-chicken and goat anti-guinea pig, respectively, both conjugated to Cy3; Dianova) diluted 1:1000 in blocking solution were added. Incubation was performed for 1h in the dark at RT. Afterwards the cells were washed four times with PBS, DAPI-stained and embedded in Citifluor (Citifluor Ltd).

Counting of amoebal cells and inclusions per visual field using an epifluorescence microscope (x100 magnification) allowed for the calculation of the mean relative infectivity of EB progeny per time point. Control studies were carried out separately under identical conditions using non-infected and infected *A. castellanii* Neff cultures. Each experiment was performed with two biological and one to two technical replicates.

Infectivity titers were determined as follows: Amoebal and intracellular *P. amoebophila* cell counts per visual field were enumerated (30-40 fields and >100 amoebae in total), the numbers of bacteria/amoeba/introduced bacteria and means for each time point including all experiments were determined. The infectivity of EB progeny was expressed as the mean proportion (± SEM) of infectious *P. amoebophila* particles.

Quantitative real-time PCR of *P. amoebophila* and *A. castellanii* Neff

Infected cells were harvested as described before and DNA was isolated from time points 1, 6, 24, 48, 72 96, 120, and 240 hpi using the DNeasy Blood & Tissue Kit (Qiagen). Real-time PCR was used to determine the copy numbers of *P. amoebophila* as well as the copy numbers of infected and non-infected *A. castellanii* Neff cells for all time points during the infection. Primers were designed for selected genes using Primer3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). *P. amoebophila* quantification was performed using the GroEL1-specific primer set EL1-1033F and EL1-1218R (5´-CGCGCTTCACAAATCAAACG-3´ and 5´-GGCTGCAGCGGTAGCTCTTT-3´, respectively) amplifying 185 bp fragments. The *A. castellanii* Neff gene glycerinaldehyde-3-phosphate-dehydrogenase was targeted by the primer set GapDH-F/R (5´-CTGCAACGAGTCGAGCTACA-3´ and 5´-CTTCTGGGTGGCCGTGAT-3´, respectively), creating 176 bp fragments. All reactions were carried out in an I-Cycler (Bio-Rad) using the IQ SYBR green supermix (Bio-Rad) according to the instructions given by the manufacturer. The PCR conditions were 95°C for 5 min, followed by 40 cycles at 95°C for 15 s and 65°C for 30 s. Plasmids carrying the respective cloned genes were used as standards for calibration of the assay and product specificity was controlled using the denaturing protocol of the I-Cycler program (data not shown). Standard curves were performed using total DNA from

uninfected and infected amoebal cells as well as from *P. amoebophila* to measure primer pair efficiency. For the time period of 120 hpi, real-time PCR was performed in triplicates for three biological replicates (*P. amoebophila*) and two biological replicates (*A. castellanii* Neff) and for the extended time period of 240 hpi, one experiment was performed in triplicates for *P. amoebophila* as well as for *A. castellanii* Neff.

Host cell viability experiments

The effect of the intracellular iron chelator deferoxamine mesylate (DAM; Sigma) at different concentrations on the amoeba host cells was determined. *A. castellanii* Neff harbouring asynchronous *P. amoebophila* and uninfected *A. castellanii* Neff cultures grown in non-defined peptone-yeast-glucose-medium (PYG; 20 g/l proteose peptone, 18 g/l glucose, 2 g/l yeast extract, 1 g/l sodium citrate-dihydrate, 980 mg/l $MgSO_4$*7 H_2O, 355 mg/l Na_2HPO_4*7 H_2O, 340 mg/l KH_2PO_4, 20 mg/l $Fe(NH_4)_2(SO_4)_2$* $6H_2O$) (Visvesvara, 1999) at 20°C were harvested as described above. Then, 1 x 10^4 cells were used to inoculate PYG medium without $Fe(NH_4)_2(SO_4)_2$*6 H_2O in a Lab-Tek™ 8-well chambered coverglass system (Nunc). After attachment of the cells, different concentrations (0, 100, 180, 250, 500, 1000 µM final concentration) of freshly prepared DAM solution were added in order to determine the highest DAM concentration that does not affect viability of uninfected or infected amoebae. Afterwards, chambers were incubated for 5 days at 20°C. After 5 days, cells were washed once with PBS, then 150 µl of a 1.5 µM propidium iodide solution (PI; Molecular Probes) were added and cells were incubated in the dark at 20°C for 50 min. The number of total and dead amoebae was counted immediately after the incubation using a CLSM (x40 magnification; 10 randomly chosen fields). Amoebae were considered dead when nuclei or whole cells were stained with PI. Evaluation was done calculating proportions of dead cells/viable cells including all viability experiments. Each experiment was carried out in technical duplicates. Viability experiments for 100, 180 and 500 µM DAM were at least repeated twice, whereas for critical DAM concentrations (0, 250 µM DAM) three biological replicates were conducted so that a total number of 500 or more amoebae per respective concentration were included in the evaluation. Proportions of dead/viable cells allowed for the estimation of the 95% confidence interval (CI) for proportions [$p \pm z \times \sqrt{((p(1-p))/N)}$; p is the proportion, z is the level of confidence = 1,96, N is the sample size]. Significance of differences between DAM exposed (100-1000 µM) and unexposed (0 µM) host cells was determined by calculating *p*-values for unexposed versus DAM treated proportions (two-tailed Fisher's exact test) in combination with relative risk values (proportion exposed/proportion unexposed) and 95% CI for relative risks (Katz's method).

Iron depletion to generate morphological effects on *P. amoebophila*

Iron depletion was induced using the iron chelator DAM at various concentrations. *A. castellanii* Neff harbouring asynchronous *P. amoebophila* and uninfected *A. castellanii* Neff cultures grown in PYG were harvested as described before and cells were seeded in PYG medium without $Fe(NH_4)_2(SO_4)_2$*6 H_2O containing 8-well chambered coverglasses or 24-well dishes (Nunc). For immunofluorescence-based visualization, sterile 12 mm glass cover slips (Roth) were placed in 24-well plates before addition of medium and cells (1 x 10^4 cells in 8-well chambered coverglass system in DAPI experiments; 5 x 10^4 cells for immunofluorescence and FISH experiments in 24-well dishes). After attachment of amoebae (approximately 30 min), freshly prepared DAM solution (25, 50, 100, 180, 250 µM final concentrations) was added. As a control, no DAM was added. In one experiment DAM treated amoebae were infected with *P. amoebophila* EBs at a MOI of 10 to 20 as described above and also incubated at 20°C for 5 and 10 days, respectively. For visualization of phenotypic effects, cells were harvested by resuspension, washed once, resuspended in 20 µl 1 x PAS and transferred to 10-well microscope slides (Marienfeld GmbH). After incubation for 30 min, cells were fixed with 4% PFA for 10 min at RT. For the detection of *P. amoebophila* within infected amoeba cells, FISH and DAPI staining was performed as described above. Probes EUK516 labelled with Fluos (green) and the Cy3 labelled *P. amoebophila*-specific probe E25-454 (red) were used in following experiments. Immunofluorescence was carried out in 24-well dishes as described above.

RESULTS

Infection and FISH analyses

The developmental cycle of *P. amoebophila* was characterized by FISH using rRNA targeted oligonucleotide probes (Daims *et al.*, 2005) in combination with DAPI staining. Two different amoeba strains, *A. castellanii* Neff and *Acanthamoeba* sp. UWC1, were infected with *P. amoebophila* EBs at an estimated MOI of 5 and 10, respectively. The infected cultures were examined by epifluorescence microscopy.

Single DAPI stained cells (indicating *P. amoebophila* EBs) were only observed at 1, 6 and 24 hpi and no or very few signals could be visualized by FISH at early time points (1 and 6 hpi). FISH signals increased about 10-times between 24 hpi and 72 hpi and could be observed until the end of the observation period at 120 hpi (Figure 1). The highly increased number of intracellular bacteria per amoebal cell at late time points did not allow for microscopic quantification (96 and 120 hpi). At 72 hpi only very few DAPI signals for EBs could be detected indicating that 72 hpi is near the metabolic and developmental midpoint. At 96 hpi

an increasing number of DAPI signals was observed. Thus, the developmental cycle becomes increasingly asynchronous as a growing number of RBs convert into EBs suggesting that the productive growth cycle of *P. amoebophila* is completed after approximately 96 hpi. Infectious EBs seem to be released from the host without destruction of the host cells, since no increased host cell lyses could be observed (not even after an extended time up to 8 days) indicating the establishment of a stable and asynchronous infection. No differences in the *P. amoebophila* developmental cycle could be observed for the two *Acanthamoeba* strains used in this experiment.

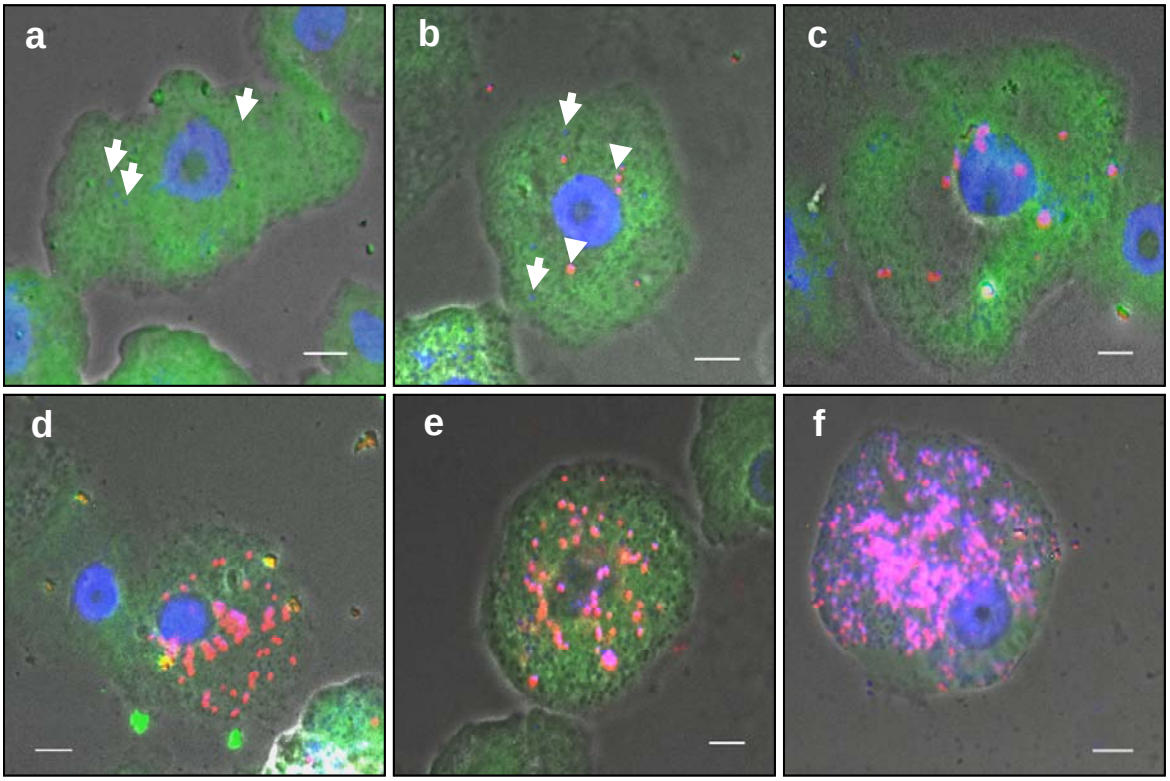

Figure 1. Developmental cycle of *P. amoebophila* within *A. castellanii* Neff. Fluorescence *in situ* hybridization and DAPI staining of infected amoeba cells at various time points after infection (a) 1 hpi, (b) 6 hpi, (c) 24 hpi, (d) 48 hpi, (e) 72 hpi and (f) 96 hpi. Time point 120 hpi was generally very similar to time point 96 hpi and is therefore not shown. Amoeba were stained using probes EUK516 and Acanth 412a labelled with Fluos (green), *P. amoebophila* was stained with the *Chlamydiales*-specific probe Chl523 labelled with Cy3 (red); the nucleic acid stain DAPI fluoresces blue. Cells stained with Cy3 and DAPI are purple. White arrows point to EBs; white arrowheads to RBs. Bars correspond to 10 µm.

Infectivity assay for *P. amoebophila* EB progeny

To demonstrate that the developmental cycle is completed and infectious progeny were produced, *P. amoebophila* harvested from amoeba cells at different time points post infection was added to uninfected amoebae and the amount of infectious chlamydial cells was calculated for the supernatant as well as for the attached amoeba cells from the primary infections. At 48 hpi and 72 hpi infectious particles could be rarely observed in the culture medium; however, the number of intracellular infectious progeny significantly increased at 96 hpi (about 5.7-fold increase) and reached a maximum at 120 hpi (Figure 2). Consistent with this observation, the highest amount of infectious progeny in the culture medium was observed at 96 hpi (3.4-fold increase between infection and 96 hpi) indicating that re-differentiation of RB to EB was finished at this time point. Due to the release of infectious progeny from the host cell into the culture medium, this number decreased significantly when infectious progeny were determined at 120 hpi. These results indicate that the developmental cycle of *P. amoebophila* is completed after 4 days, and that between 48 hpi and 72 hpi the inclusions mainly contain RBs and IBs, whereas EBs are produced within the following 24 h.

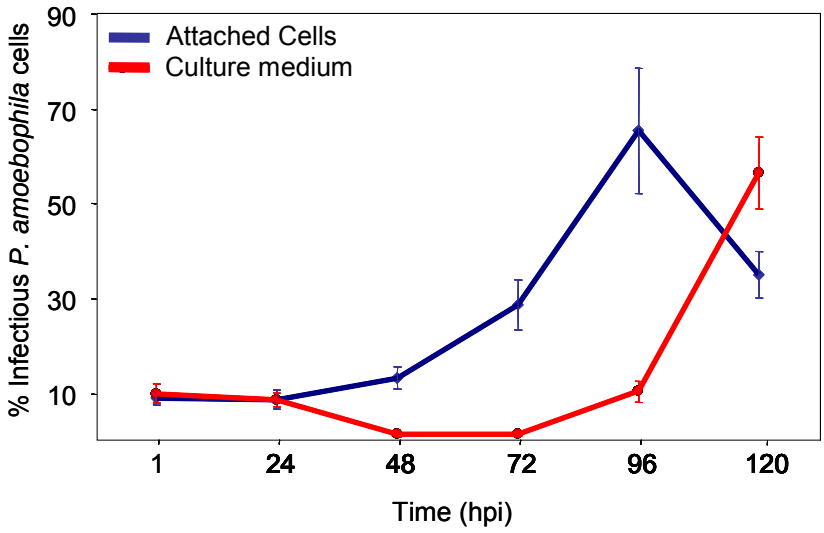

Figure 2. **Infectivity of *P. amoebophila* progeny.** *P. amoebophila* progeny harvested at different time points pi in the supernatant (red line) and in attached amoeba cells (blue line). The progeny infectivity was expressed as the mean proportion (± SEM) of infectious *P. amoebophila* particles.

Quantitative real-time PCR of *P. amoebophila* and *A. castellanii* Neff

Growth curves of *P. amoebophila* and *A. castellanii* Neff were determined by investigating different time points during infection using specific quantitative real-time PCR assays. After a slow decrease of *P. amoebophila* genome equivalents at early time points pi, a remarkable

increase of *P. amoebophila* could be observed from 72 hpi on, which points to high replicative activity of the chlamydial symbionts (Figure 3). The amoeba host DNA copy number remained nearly the same level throughout the whole experiment, indicating to a well-balanced symbiotic growth at later time points. To further investigate the role of host lysis, a prolonged infection experiment was performed (Figure 3, dashed line). The prolonged infection experiment over 240 hpi further confirmed that active lysis does not occur. Not only the chlamydial but also the amoebal cell numbers increased over this time period suggesting a stable symbiotic coexistence. Uninfected host cells, also quantified for all time points, show a similar growth curve as the infected host cells (data not shown).

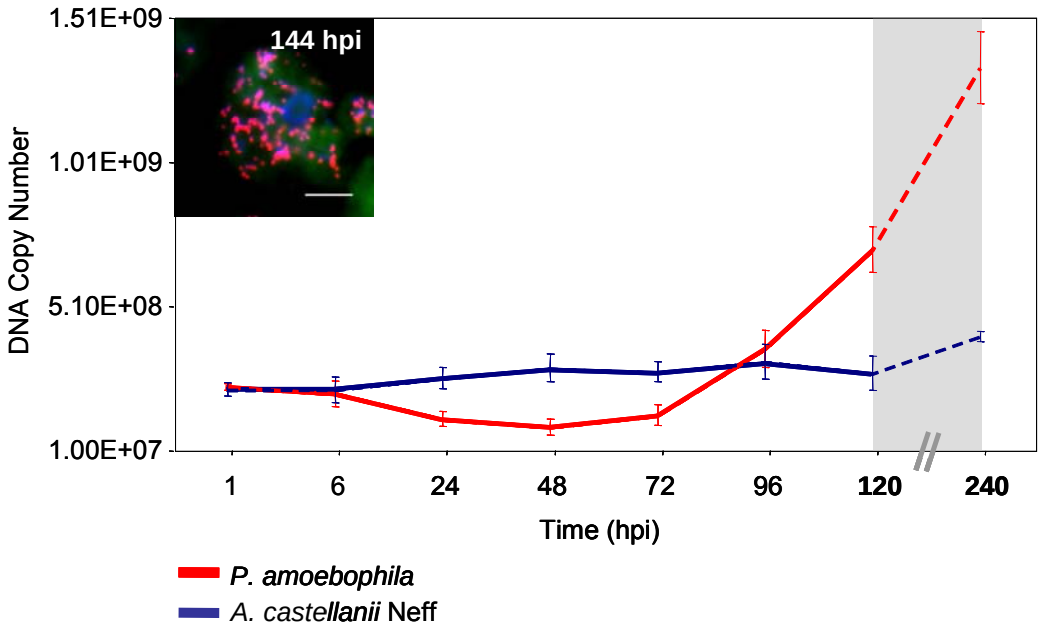

Figure 3. **Growth of *P. amoebophila* and *A. castellanii* Neff.** Relative copy numbers were determined for *P. amoebophila* (red line) and *A. castellanii* Neff (blue line) at different time points pi using quantitative real-time PCR and are shown as means and standard deviations. FISH/DAPI image shows an infected amoeba cell at 144 hpi. Bar represents 10 µm.

Viability of DAM-treated cells

To generate an iron-reduced environment in which the viability of amoeba host cells is not compromised, uninfected and infected host cells were exposed to increasing concentrations of the iron chelating agent DAM. The effect on cell viability was assayed using selective propidium iodide staining of the nuclei of dead cells. After five days of exposure to various DAM concentrations, cell viability of uninfected amoebae significantly decreased at concentrations of >250 µM (p<0.001; Figure 4). No significant influence on host cell viability

was found for tested DAM concentrations lower than 250 µM, implying that morphological changes of chlamydial cells in subsequent iron-depletion experiments were not linked to enhanced stress of the hosts but with iron restriction. Infected amoebae, however, showed higher sensitivity to the presence of DAM. Toxic effects could be observed already at concentrations >180 µM (p<0.001), demonstrating that infected amoebae encounter higher stress due to the combination of reduced iron uptake from the growth medium as well as the presence of intracellular bacteria.

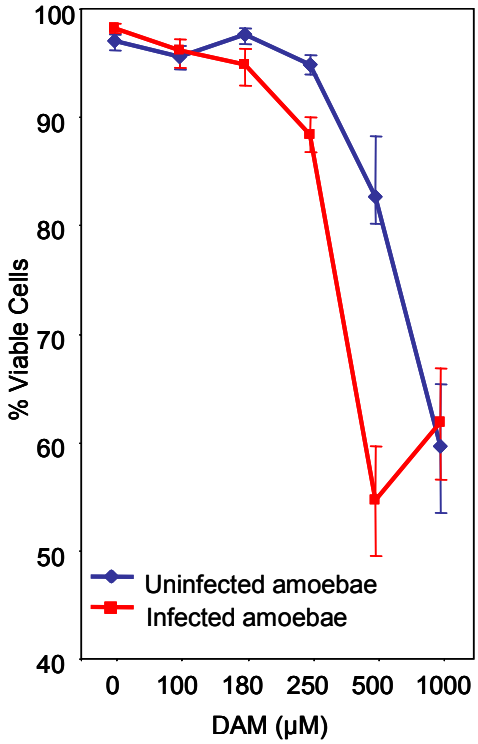

Figure 4. Host cell viability. Toxic effects of various DAM concentrations on uninfected (blue line) and infected (red line) amoebae after five days of iron restriction. Host cell viability was expressed as the percentage of viable cells and corresponding 95% CI for proportions.

Iron depletion to generate morphological effects on *P. amoebophila*

In order to study whether iron restriction show an influence on the morphology of *P. amoebophila*, infected amoeba host cells with and without the presence of the iron chelator DAM were compared. DAPI staining demonstrated an obvious enlargement of some intracellular bacteria (about 5 times the size of normal *P. amoebophila* cells; Figure 5a, 5b). These atypical cells could sporadically be observed in amoebae already at low DAM concentrations (25 µM and 50 µM DAM, respectively). At higher DAM concentrations, the number of amoebae infected with aberrant signals increased slightly but the number of enlarged bacteria remained the same (one to ten per amoebal cell) even at higher DAM concentrations (>100 µM; data not shown). After 5 days of starvation in iron reduced medium (180 µM DAM), approximately 30% host cells contained altered morphological forms compared to the control without DAM addition. In addition to the aberrant bodies, some amoebal cells were also infected with regular-sized bacteria (approximately 1 µm in diameter), but less strongly compared to amoebae without enlarged signals (Figure 5e, 5f).

No differences between asynchronously and synchronously infected amoebae could be observed (data not shown). Immunofluorescence analyses using anti-*P. amoebophila* antibodies (detecting the *P. amoebophila* outer membrane) and anti-Hsp60 antibodies (detecting only *P. amoebophila* RBs) confirmed the presence of atypical chlamydial forms (Figure 5e-h). The signals were up to 5 µm in size, often located close to each other, ring-shaped in the case of anti-*P. amoebophila* (Figure 5g) and evenly and plane in the case of anti-Hsp60 antiserum (Figure 5h). Enlarged signals could also be observed by FISH (using the *P. amoebophila*-specific probe E25-454; data not shown), but interestingly not all aberrant forms detected with DAPI could also be detected with FISH. After 10 days of iron depletion, the relatively low number of abnormal signals in amoebae detected by immunofluorescence and DAPI remained the same, but nearly all amoebae were infected at this time point.

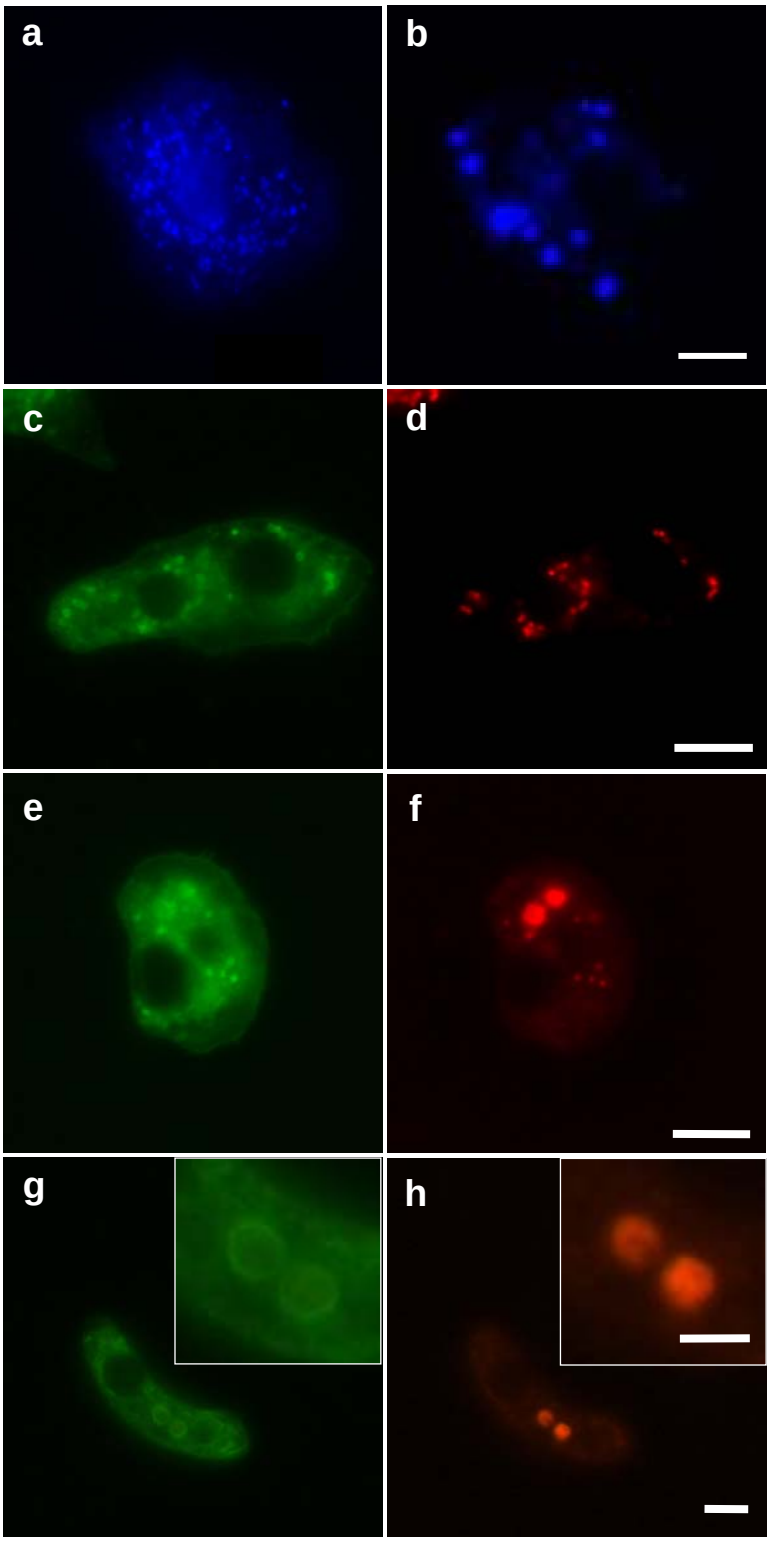

Figure 5. Morphological effects of *P. amoebophila* after iron depletion. DAPI staining of untreated (a) and treated infected amoebae five days after iron depletion [180 µM DAM; (b)]. Immunofluorescence shows *P. amoebophila* labelled with anti-*P. amoebophila* antibodies (c) and anti-Hsp60 antibodies (d), respectively, in the absence of DAM. Panels (e-h) show *P. amoebophila* in the presence of 250 µM DAM 5 days post exposure and post infection.

Segments in (g) and (h) show a magnification of the enlarged ring-shaped signals of the *anti-P. amoebophila* antibodies detecting the *P. amoebophila* outer membrane and the evenly and plane signals of the anti-Hsp60 antibodies. Bars correspond to 10 µm.

DISCUSSION

The developmental cycle of the amoeba-associated *Chlamydia*-like organism *P. amoebophila* was investigated using fluorescence *in situ* hybridization, immunofluorescence and quantitative real-time PCR in two free-living amoeba host strains. The combination of fluorescence *in situ* hybridization and the DNA stain DAPI allowed for discrimination of EBs, which are believed to be inactive exhibiting therefore a lower ribosomal content, and the metabolically active RBs (Poppert *et al.*, 2002). After infection, intracellular EBs have been observed as early as 1 hpi (Figure 1a). In some experiments, FISH signals were also observed at this early time point, thereby suggesting the presence of intermediate forms which still are infectious but resemble physiologically RBs and can therefore be detected by FISH. Primary differentiation of EBs to the replicating RBs occurred within the first 48 hpi as indicated by appearance of FISH signals (Figure 1b-c). Extensive multiplication of *P. amoebophila* occurred between 48 hpi and 120 hpi (Figure 1d-f). EBs were rarely detected at 72 hpi, indicating that this time point is near the metabolic and developmental midpoint but also showing that the infection was not completely synchronous. However, an increasing number of EBs could be observed from 96 hpi on, suggesting that the full reproductive developmental cycle of *P. amoebophila* is finished after 4 days in both *Acanthamoeba* strains used in this study.

Consistent with these observations, few infectious progeny were present inside of the amoeba host cells between 24 hpi and 72 hpi (Figure 2). Re-differentiation of RBs to EBs is indicated by a remarkable increase of infectious particles within the host cells between 72 hpi and 96 hpi. This is further supported by the observation that high amounts of infectious progeny were detected extracellularly from 96 hpi on, demonstrating the release of EB progeny from the host cell after completion of the productive cell cycle. The presence of infectious progeny almost exclusively at later time points strongly suggests that only *P. amoebophila* EBs are infectious and that the infectivity becomes lost soon after infection. This finding is in line with the common perception that EBs represent the infectious stages (Hatch, 1999). The only exception known so far is *S. negevensis* for which both developmental stages have been described to be infectious indicating to a higher extracellular stability of replicative forms (Kahane *et al.*, 2002).

Quantitative real-time PCR demonstrated further, that after a slight decrease in the cell number of *P. amoebophila* during early time points (1 hpi to 24 hpi), chlamydial cell copies increased exponentially between 72 hpi and 120 hpi (Figure 3). The decrease of cell numbers early in infection might either be due to the presence of excess EBs in the culture medium which were not be internalized by the amoebae but detected by PCR or due to the presence of intermediate bodies and/or RBs in the EB suspension used for infection after EB purification. This is most likely because the protocol used for EB purification did not separate clearly intermediate bodies and RBs from EBs. These less stable chlamydial particles might not survive the infection procedure, whereas DNA still could be detected at these time points leading to artificial higher copy numbers. Long-time experiments (up to 8 days) further demonstrated that a synchronous infection starts to become an asynchronous infection after 96 hpi, leading to a stable coexistence without increased host cell lyses between the amoeba host cells and *P. amoebophila* (Figure 3).

By means of these experiments, we conclude that *P. amoebophila* completes its productive developmental cycle at approximately 96 hpi (4 days) which is comparable to the *C. pneumoniae* developmental cycle, as first release of infectious progeny was reported to occur between 84 and 96 hpi (Mäurer *et al.*, 2007; Wolf *et al.*, 2000). Interestingly, other *Chlamydia*-like bacteria exhibit marked differences in the length of their growth cycle as indicated by several studies. First infectious progeny of *P. acanthamoebae* and *W. chondrophila* have been detected as early as 24 hpi and 36 hpi, respectively, leading to apoptosis of infected human macrophages (Goy *et al.*, 2008; Greub *et al.*, 2003c). In contrast to the above described fast completion of the developmental cycle, *S. negevensis* exhibit a significantly longer developmental cycle in mammalian host cells (12 to 15 days) establishing a permanent co-existence of symbiont and host cell without release of significant amounts of EBs or lysis of the host cell (Kahane *et al.*, 2001; Kahane *et al.*, 2002). The third developmental stage, the infectious crescent body, observed by Greub and coworkers in *P. acanthamoebae*, could not be described for *P. amoebophila* in this study (Greub & Raoult, 2002) and future detailed electron microscopic studies will clarify whether this stage is also present in *P. amoebophila*.

Since *Chlamydiaceae* exhibit a sophisticated way to persevere unfavourable conditions in an invulnerable persistent state characterized by morphologically aberrant forms (Beatty *et al.*, 1994; Hogan *et al.*, 2004; Mpiga & Ravaoarinoro, 2006), we examined effects on the morphology of *P. amoebophila* cells exposed to iron restriction. The iron chelator DAM was used to reduce the availability of iron in chlamydia-infected amoeba cultures without visibly affecting the host cells (Figure 4). Interestingly, significant morphological changes could be

observed after five days (Figure 5e-h). Approximately one third of infected amoebae contained clearly enlarged chlamydial cells resembling persistent forms well-known from pathogenic chlamydiae (Beatty *et al.*, 1994; Hogan *et al.*, 2004; Mpiga & Ravaoarinoro, 2006) as well as from *S. negevensis* (Kahane *et al.*, 2007). This long-term association between chlamydiae and their host cells is suggested to be a general stress response conferring flexibility during intracellular growth (Beatty *et al.*, 1994; Harper *et al.*, 2000) and might reflect a possible ancient strategy of *P. amoebophila* to overcome various fast changing environmental conditions. This study reports for the first time altered morphological forms after stress induction of a member of the *Parachlamydiaceae* and the ability to persistently infect amoebae warrants further investigations, in particular considering the possible pathogenic potential of these diverse and widespread bacteria (Baud *et al.*, 2008; Baud *et al.*, 2009; Birtles *et al.*, 1997; Corsaro *et al.*, 2001; Corsaro *et al.*, 2002; Greub *et al.*, 2003a; Greub *et al.*, 2003b; Greub *et al.*, 2006; Marrie *et al.*, 2001).

The genome of *P. amoebophila* is nearly twice the size of known *Chlamydiaceae* genomes (Azuma *et al.*, 2006; Carlson *et al.*, 2005; Horn *et al.*, 2004; Kalman *et al.*, 1999; Read *et al.*, 2000; Read *et al.*, 2003; Shirai *et al.*, 2000; Stephens *et al.*, 1998; Thomson *et al.*, 2005; Thomson *et al.*, 2008) and additional genes might be involved in adaptation strategies of *Chlamydia*-like organisms to a broad range of host cells and for survival and transmission under environmental conditions. Although the course of the *P. amoebophila* developmental cycle is similar to the developmental cycle of pathogenic chlamydiae, *P. amoebophila* EBs have recently been shown to be metabolically active outside of their host cells and remain infectious for at least three weeks (see chapter III). These findings contrast to the inactive *Chlamydiaceae* EBs which survive extracellularly just long enough until re-infection. Only *C. pneumoniae* koala Type I EBs remained viable for up to 28 days at ambient temperature in laboratory and maintained infectivity for cell culture after exposure on eukalyptus leaves for 3 days (Rush & Timms, 1996). *S. negevensis* RBs were suggested to be also infectious and laboratory experiments indicate that this *Chlamydia*-like organism is more resilient to various temperatures and osmotic shock (Kahane *et al.*, 2002; Kahane *et al.*, 2004). All together, *Chlamydia*-like bacteria might have retained ancient features reflecting the role of the environment in the bacterial transmission which were lost or reduced in *Chlamydiaceae* and might explain their huge diversity and ecological success.

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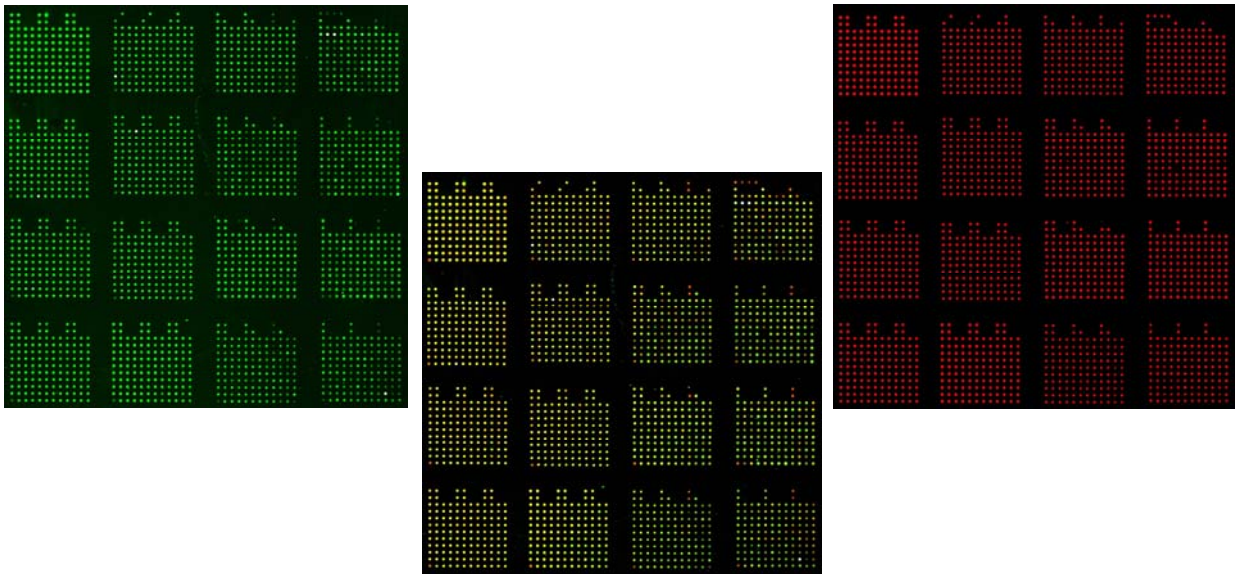
Chapter V

First insights into the gene expression profile of *Protochlamydia amoebophila* during infection



The images show a segment of the *Protochlamydia amoebophila* microarray after poly-T spacer hybridization. Left panel, Cy3 labelling (green); right panel Cy5 labelling (red); middle panel overlay (yellow).

First Insights into the Gene Expression Profile of *Protochlamydia amoebophila* during Infection

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M.H., M.W. and S.H. planned the experiments. S.H. designed and printed the oligonucleotides, developed the whole genome microarray (including optimization of DNA, RNA extraction, labeling procedures and hybridization), analyzed the gene expression and wrote the manuscript. A.M. optimized labeling procedures and hybridization.

Work in Progress – Preliminary Results

ABSTRACT

All members of the phylum *Chlamydia* reside exclusively within eukaryotic host cells and exhibit a unique biphasic life cycle consisting of infectious elementary bodies (EBs) and non-infectious, replicating reticulate bodies (RBs). Besides the well-characterized pathogenic bacteria of the family *Chlamydiaceae* an increasing diversity of non-pathogenic *Chlamydia*-like bacteria have been found in the environment inhabiting a great number of different host cells. The amoeba symbiont *Protochlamydia amoebophila* UWE25 is the best characterized *Chlamydia*-like organism and its complete genome has been sequenced. In this study, a whole genome oligonucleotide microarray was designed and applied in order to analyze the global gene expression profile of *P. amoebophila* during asynchronous intracellular growth and to reveal new insights into the interaction with its amoeba host. We found that 61% of the genes in the *P. amoebophila* genome are transcribed during infection including 52% of the 1,093 genes present in the *P. amoebophila* genome but absent from all other chlamydial genomes. More specifically, the gene expression profile shows that all representative transcripts involved in major metabolic reactions were expressed. In addition, the genes of several specific and general amino acid transporters were strongly transcribed reflecting the incompleteness of the respective biosynthetic pathways in the genome of the chlamydial symbiont. Furthermore, according to its transcriptome *P. amoebophila* imports from the host cell cytosol some of the few amino acids for which prototrophy was predicted *in silico*. In addition, the microarray data indicate direct host cell manipulation by the symbiont as all genes encoding the type three secretion system and many predicted genes encoding inclusion proteins were found to be transcribed. Additionally, many genes annotated as plant and cyanobacterial homologues showed activity and the identification of the functions of these proteins will be an interesting topic for further investigations. More generally, the developed gene expression microarray has been proven suitable for initial transcriptomic studies of *P. amoebophila* and can be used in future to decipher gene expression patterns linked with the different stages of the developmental cycle or environmental stresses.

INTRODUCTION

The obligate intracellular *Chlamydiae* are extremely successful bacterial pathogens involved in severe diseases. *Chlamydia trachomatis* causes trachoma and is the most frequently sexually transmitted bacterial pathogen worldwide (WHO, 2001; WHO, 2008) and *Chlamydophila pneumoniae* is a widespread respiratory pathogen and is estimated to be involved in 2 to 43% of community-acquired pneumonia cases (Wellinghausen *et al.*, 2006). The host range of these pathogenic chlamydiae covers mostly higher eukaryotes such as mammals, birds, marsupials, amphibians and reptiles (Horn, 2008). In the last years, an amazing diversity of newly identified *Chlamydia*-like bacteria was discovered which thrive in phylogenetically diverse host groups such as fish, insects, crustaceans, molluscs and protozoa (Horn, 2008). So far, the majority of *Chlamydia*-like bacteria were found to inhabit free-living amoeba of the genus *Acanthamoeba* (Amann *et al.*, 1997; Collingro *et al.*, 2005a; Fritsche *et al.*, 2000; Horn *et al.*, 2000). These symbionts include *Protochlamydia amoebophila* UWE25 which is the first representative of this chlamydial group for which a complete genome is available (Collingro *et al.*, 2005b; Horn *et al.*, 2004).

Characteristic for all chlamydiae is the complex biphasic developmental cycle, during which they develop and grow within a specialized host-derived intracellular vacuole, called inclusion (Abdelrahman & Belland, 2005). The chlamydial developmental cycle starts with the entry of an infectious elementary body (EB) into the host cell and differentiation of the EB to the metabolically active and replicating reticulate body (RB). At a strain-dependent dedicated time point, the RB transforms back into the spore-like EB and after release from the host the EB initiates a new infection cycle (Abdelrahman & Belland, 2005; Moulder, 1991; Ward, 1988). As EBs and RBs are morphologically different (Ward, 1988), the developmental cycle of several pathogenic but also non-pathogenic members of the *Chlamydiae* could be well-described by electron microscopy (Greub & Raoult, 2002; Kahane *et al.*, 2001; Kahane *et al.*, 2002; Matsumoto, 1988; Miyashita *et al.*, 1993; Ward, 1988). However, the regulation mechanisms that trigger interconversion of the morphologically distinct forms are of great interest and have to be investigated on the molecular level. The identification of temporally regulated proteins implicates a thoroughly ordered system of developmental regulation and indicates that the chlamydial developmental cycle strongly relies on the accurate coordination of gene expression (Hackstadt *et al.*, 1991; Hatch *et al.*, 1986; Perara *et al.*, 1992).

As the obligate intracellular growth aggravates the study of the genetically inaccessible chlamydiae, whole genome microarrays represent a valuable tool to obtain information about

their biology including their complex interaction with their host cell. The availability of 12 complete genome sequences of pathogenic chlamydial species (Azuma *et al.*, 2006; Carlson *et al.*, 2005; Kalman *et al.*, 1999; Read *et al.*, 2000; Read *et al.*, 2003; Shirai *et al.*, 2000; Stephens *et al.*, 1998; Thomson *et al.*, 2005; Thomson *et al.*, 2008) has provided a great opportunity to study the coordinated expression of temporally regulated genes by the use of microarrays. Based on transcriptomic data of *C. trachomatis* and *C. pneumoniae* their genes were classified into three major groups according to their temporal expression pattern. Early cycle genes like ribosomal genes and genes involved in transcription, transport and energy compound acquisition are expressed within 12 hours post infection (hpi) and gene products initiate bacterial metabolism. Mid cycle genes showed an expression peak at 18 hpi and are particularly involved in RB growth and replication, cell envelope biogenesis, type III secretion, energy metabolism as well as DNA condensation. Late cycle genes show a greater abundance after 36 hpi, and identified late cycle gene products participate in the secondary differentiation (RB-to-EB), however, most transcripts of late genes encode *Chlamydia*-specific proteins of undetermined functions (Belland *et al.*, 2003; Mahony, 2002; Mäurer *et al.*, 2007; Nicholson *et al.*, 2003; Shaw *et al.*, 2000). Moreover, a comparison of EB transcriptome and EB proteome data recently revealed that genes expressed in the late cycle did not contribute equally to EB mRNA and EB proteins, possibly reflecting carryover mRNA. Therefore, a further differentiation and classification in late genes (mainly associated with EB proteins) and tardy genes (mainly coding for EB mRNA) has been suggested (Mäurer *et al.*, 2007).

In contrast to the well-characterized pathogenic chlamydiae, our understanding of the biology of the novel chlamydiae is far less profound and is largely based on *in silico* analysis of the genome sequence of *P. amoebophila.* Comparative genomics predicted that this organism is, like its pathogenic counterparts, strongly dependent on its host because it is incapable to synthesize many amino acids, nucleotides and NAD^+ and must thus import them from the host cell cytosol. In the meantime, some of these predictions were experimentally confirmed for *P. amoebophila* by Raman microspectroscopic analysis of amino acid uptake (see chapter VI) and heterologous expression and characterization of its five nucleotide transporter genes in *E. coli* (Haferkamp *et al.*, 2004; Haferkamp *et al.*, 2006; Schmitz-Esser *et al.*, 2004). On the other hand, the genome of *P. amoebophila* is much larger than those of the pathogenic chlamydiae and *P. amoebophila* has maintained several pathways like the tricarboxylic acid cycle (TCA cycle) which are no longer complete in the pathogenic chamydiae. Thus, *P. amoebophila* has been considered as living fossil which has retained several ancient features of the last chlamydial ancestor (Horn *et al.*, 2004), but it remains to be demonstrated that the respective genes which are absent in the pathogenic chlamydiae

are actually expressed. In this study, a DNA microarray for global gene expression analysis of *P. amoebophila* was developed and successfully applied during asynchronous infection. The transcriptome data demonstrate that at least 61% of the genes in the *P. amoebophila* genome, including 52% of those genes which have no homologues in pathogenic chlamydiae, are transcribed during infection of an amoebal host cell. Furthermore, microarray analyses provided novel insights into the complex interplay between symbiont and host.

MATERIAL AND METHODS

Design and synthesis of oligonucleotide probes

Oligonucleotide probes with a length between 45 and 55 bases were designed using the program OligoWiz 2.0 (http://www.cbs.dtu.dk/services/OligoWiz; Nielsen *et al.*, 2003). The program utilizes a total score (including sub-scores for cross-hybridization, melting temperature, low-complexity, folding, and position within the query sequence) between 0.0 (not suited) and 1.0 (well-suited) for probe selection. Sequences exhibiting <75% nucleotide identity and homology stretches below 15 contiguous bases to the corresponding aligned regions of any BLAST hit sequences were selected as potential probes. Oligonucleotide probes targeting positions close to the starting point of reverse transcriptase (3´-end of RNA) or in the middle of the transcript were preferred.

A 20 dATP spacer (A-spacer) was added to the 5´-end of each oligonucleotide to increase the on-chip accessibility of spotted probes to target DNA (Shchepinov *et al.*, 1997; Southern *et al.*, 1999). All oligonucleotides were synthesized with a C6-amino linker modification at the 5´-end by Microsynth (Microsynth AG) in 384-well microtiter plates (Genetix Ltd). Desalted oligonucleotides were adjusted to a concentration of 100 µM in 50% dimethyl sulfoxide (DMSO) to prevent evaporation during storage and printing (Hegde *et al.*, 2000). For each probe, information about oligonucleotide sequence, melting temperature, sequence location, oligonucleotide parameter scores and plate and microarray position is summarized in Table S1.

Microarray printing and post-array processing of slides

5´-amino modified oligonucleotide probes obtained from Microsynth were printed onto silylated amine-aldehyde glass slides (VSS-25C, CEL Associates) using a *Bio*Robotics *Micro*Grid 610/TAS system and 16 MicroSpot 2500 split pins (Zinsser Analytic GmbH). The number of prints per source visit was set to a maximum of 80 spots. Pre-spotting of 20 spots after source visit was performed, to avoid printing excess material from the external surface of the pin onto the glass slide. After pre-spotting the average spot diameter was about 150

µm and spot centres were 300 µm apart. The relative humidity during spotting was set to 50% within the spotting compartment. After spotting of each oligonucleotide, a washing procedure was included and repeated six times, to minimize carry-over effects. For carry-over control, 588 spots were printed with printing buffer only. Spotted microarrays were allowed to rest for one day at 100% humidity to increase covalent coupling between aminated 5´-ends of oligonucleotides to the aldehyde group-coated glass slides. Subsequently, active aldehyde groups on the slide surface were deactivated, and salt deposits and unbound DNA was washed off by soaking slides twice in 0.2% sodium dodecyl sulfate (SDS) for 2 min and twice in double-distilled water for 2 min. After air drying for 5 min, the slides were incubated in freshly prepared sodium borohydride solution [0.6 g $NaBH_4$ in 200 ml phosphate-buffered saline (PBS) and 60 ml of absolute ethanol] for 5 min to convert reactive aldehyde groups into non-reactive alcohol counterparts in order to reduce non-specific attachment of molecules to the microarray surface during hybridization (Schena, 2003). In the next step, slides were rinsed in ice-cold absolute ethanol and subsequently washed two times in 0.2% SDS for 1 min and two times in double-distilled water for 1 min. Finally, slides were dried by centrifugation (240g, 2 min) and stored in the dark at room temperature. All washing and inactivation steps were carried out at room temperature (RT) and under constant manual agitation of the slides in respective solution.

Spotting quality assessment

To assess the spotting quality, spotting failures and the covalent linkage of the printed oligonucleotides to the glass slide, the first and the last slide of a spotting series was hybridized with poly-dTTP spacer probes (12 nucleotides) which target the A-spacer of the printed oligonucleotides. Per hybridization, 1 pmol μl^{-1} poly-dTTP probe was resuspended in 400 µl of hybridization buffer [5x SSC (20x SSC; 3M sodium chloride, 0.3M sodium citrate, pH 7.0), 0.02% SDS, 0.1% *n*-lauryl sarcosine (Sigma); 0.1% blocking reagent, (Roche)], applied to the spotted slides using sealed coverslips (HybriWell Sealing System; GRACE Bio Labs) and incubated at 30°C for 1 h under constant shaking at 400 rpm (ThermoTWISTER Comfort, QUANTIFOIL Instruments GmbH). After hybridization, slides were rinsed two times in ice-cold double-distilled water for 2 min and dried by centrifugation. Slides series were only used for transcriptome analyses if these test slides showed similar-sized and uniform hybridization signals for all printed oligonucleotides (Figure 1).

Cultivation and purification of *P. amoebophila*

P. amoebophila was grown in *Acanthamoeba castellanii* Neff at 20°C in 500 cm² culture flasks (Iwaki) as an asynchronous culture in Trypticase Soy Broth with Yeast Extract (TSY;

30 g/l trypticase soy broth, 10 g/l yeast extract, pH 7.3) (Visvesvara, 1999) under axenic conditions. Medium was exchanged every 3 to 4 days to achieve optimal cell growth.
For EB purification, amoebal cells were harvested by centrifugation (3,214g, 10 min, 4°C), washed once, and resuspended in 500 µl 1 x Page´s amoebic saline (PAS; (Page, 1988). Then, host cells were disrupted by a freezing (-20°C for approximately 20 min) and thawing (45°C water bath for approximately 3-4 min) and subsequently by vortexing for 3 min after addition of 1 volume glass beads. Cell debris was removed by centrifugation (300g, 10 min, 4°C), the supernatant was filtered (1.2 µm, Millipore) and centrifuged at 50,000g for 40 min at 4°C to pellet chlamydial cells. The pellet was resuspended in sucrose phosphate glutamic acid buffer (SPG; 750 g/l sucrose, 5.2 g/l KH_2PO_4, 23 g/l $NaHPO_4*7H_2O$, 7.5 g glutamic acid) and centrifuged as before. Afterwards, the pellet was resuspended in SPG, pulled through a 0.45 x 0.25 mm syringe (Braun) for several times to disintegrate clumped EBs, aliquoted, and stored at -80°C. Stocks were determined to be free of contamination with other *Chlamydia*-like organisms by DNA isolation (DNeasy Blood and Tissue Kit, Qiagen), PCR amplification with the *Chlamydiales*-specific primer set PanF/R (Corsaro *et al.*, 2002) and restriction enzyme digestion (*VspI*; MBI Fermentas).

Genomic DNA isolation of *P. amoebophila*

For genomic DNA isolation, infected amoebal cells were harvested by centrifugation (3,200g, 5 min, 20°C), washed once in 500 µl 1 x PAS and centrifuged again as before. DNA was isolated according to the protocol described in (Zhou *et al.*, 1996). Briefly, the pellet was resuspended in 250 µl TE buffer (10mM Tris-HCl pH 7.5, 1mM EDTA), mixed with 675 µl DNA extraction buffer including proteinase K (200 µg ml^{-1} final concentration) and incubated for 30 min at 37°C. After addition of 75 µl 20% SDS the suspension was incubated at 65°C for 2 h with gentle inversions every 20 min. Then, an equal volume of chloroform/isoamylalcohol (24:1, vol/vol; Roth) was added and after centrifugation (10,600g, 10 min, RT), the aqueous phase was transferred into a new microcentrifuge tube. Nucleic acids were allowed to precipitate after addition of 0.6 vol isopropanol at RT for 1 h. Subsequently DNA was pelleted by centrifugation at 16,000g for 20 min at RT, washed with ice-cold 70% ethanol and centrifuged again for 5 min at maximum speed. Finally, nucleic acids were resuspended in double-distilled water, the amount of isolated DNA was determined spectrophotometrically by measuring the optical density at 260nm using a Nanodrop Photospectrometer (Thermo Scientific) and subsequently the DNA was fragmented by sonication for 40 s with 50% power and 10% cycle (Bandelin Sonopuls HD 2070, MS72) aliquoted and stored at -20 °C. Fragmented DNA size was checked on a 1% agarose gel [1 g agarose in 100 ml 1x TBE buffer (10xTBE buffer; 108g Tris base, 55g boric acid, 20 µl 0.5 M EDTA pH 8.0 in 1 l water)].

RNA isolation of *P. amoebophila*

Total RNA was isolated from *Acanthamoeba castellanii* Neff infected with *P. amoebophila* grown at 20°C in 500 cm² culture flasks as described above. Cells were harvested by centrifugation (3,200g, 5 min, RT), and the pellet was immediately resuspended in 1.5 ml TRIzol (Invitrogen) to stabilize the mRNA pool. The suspension was transferred to a bead beater tube containing zirconium beads (Bio 101 Savant) and host and chlamydial cells were subsequently disrupted by homogenizing for 10 s at speed 4.5 (Beadbeater Bio 101 Savant). After centrifugation (13,300g, 5 min, RT), the supernatant was transferred to a clean microcentrifuge tube and nucleic acids were extracted by addition of 0.2 ml chloroform per ml supernatant, subsequent vigorous shaking by hand for 15 sec followed by an incubation for 5 min at RT and another centrifugation step at 12,000g for 15 min at 4°C. Then, the aqueous phase containing extracted RNA was precipitated by addition of 0.5 ml isopropyl alcohol per ml supernatant, 0.12 ml 5 M ammonium acetate and 5 µl glycogen (20 mg ml^{-1}) and incubation for 15 min at -20°C. Afterwards, the RNA was pelleted at 20,800g for 15 min at 4°C, washed and carefully mixed with 1.5 ml 75% ethanol, pelleted again (7,000g, 5 min, 4°C) and air dried for 5-10 min. Subsequently, the RNA was dissolved in RNase-free water, eventually remaining DNA was digested by adding 1U DNase (Sigma) per 2 µg RNA for 1 h at RT, and subsequently the reaction was stopped by another precipitation step in 1/10 volume 3M sodium acetate (pH 5.2), 1/100 volume glycogen, 3 volume absolute ethanol at -20°C over night. The next day, the RNA was pelleted and washed as described before, resolved in RNase-free water and the RNA concentration was determined using a Nanodrop Photospectrometer. The A_{260}/A_{280} ratio was measured for all samples and should be close to 2.0 ensuring high purity of RNA. RNA quality was furthermore checked on a 1% agarose gel [1 g agarose in 100 ml 1x TAE buffer (50x TAE buffer; 242 g Tris base, 57.1 ml glacial acetic acid, 100 ml 0.5 M Na_2 EDTA pH 8.0 in 1 l water)] and RNA was subsequently stored at -80°C in the presence of RNase inhibitor (40U $µl^{-1}$; Fermentas). All solutions used during RNA extraction were prepared with double-distilled water treated with 0.1% diethylpyrocarbonate (DEPC; Sigma) to remove RNases.

Labelling of genomic DNA

Genomic DNA can be used in microarray experiments for normalization of RNA hybridization data as well as for slide quality control purposes. Genomic DNA was random primed and labelled with Cy3 or Cy5 fluorophores by using the DecaLabel DNA Labelling Kit (Fermentas) according to the manufacturer´s instructions with some modifications. Briefly, per reaction (final volume 45 µl) 2 µg fragmented DNA and 10 µl decanucleotides in reaction buffer were mixed, incubated at 95°C for 10 min and immediately placed on ice. After addition of 1 µl dNTP mix (containing 2 mM dCTP, 5mM dATP, dTTP, dGTP each, Fermentas; dNTP mix

was prepared according to the microarray hybridization protocol of Mersinias *et al.*, http://www.surrey.ac.uk/SBMS/Fgenomics), 2 µl 1 mM Cy-dCTP (Amersham Biosciences) and 0.8 µl Klenow fragment (exo$^-$, 50U µl^{-1}; New England Biolabs), the labelling reaction mixture was incubated at 37°C for 90 min. To complete the labelling reaction, another 4 µl of dNTP mix were added to the reaction mix and incubated at 37°C for 60 min. Unincorporated desoxynucleotides and decanucleotides were removed using the QIAquick Nucleotide Removal Kit (Qiagen) and purified genomic DNA was eluted by using double-distilled water. Finally, purified labelled genomic DNA was vacuum-dried in a Speed Vac (Eppendorf concentrator 5301) and stored in the dark at -80°C.

Reverse transcription and indirect labelling of total RNA

Target preparation for the microarray experiments was performed by reverse transcription of 20 µg total RNA per reaction in the presence of aminoallyl-dUTP (aa-dUTP) with the CyScribe Post Labelling Kit (Amersham Biosciences) according to the manufacturer's instructions with one modification. 2 µl of random primers were added to the primer annealing reaction mix instead of 1 µl. To calculate cDNA yield and incorporation rates for cyanine-dNTPs (Cy-dNTP), absorbance of cDNA at 260 nm and of the fluorophore at wavelength 550 nm (Cy3) and 650 nm (Cy5), respectively, were determined using a Nanodrop Photospectrometer. Frequency of incorporation (FOI) was calculated using the following formula: FOI = pmol incorporated dye x 324.5 (average molar mass of a deoxynucleotide base) / ng of cDNA in the sample (http://www.promega.com/pnotes /86/11217_02/11217_02.pdf). The results were expressed as the number of Cy-dNTP incorporated per 1,000 nucleotides of cDNA. For successful hybridizations, dye incorporation of approximately 20-50 Cy-dNTP per 1,000 nucleotides of cDNA is generally recommended (http://www.biology.ualberta.ca/facilities/microarray/uploads/documents/Microarray/Pronto_cdna_microarray_reagent_system.pdf). Labelled samples were immediately hybridized to the microarray or vacuum-dried and stored until hybridization at -80°C.

Total RNA labelling was additionally performed using a two-step labelling procedure. Here, for each reaction 20 µg of total RNA were primed with 1 µl random nonamers (Amersham Biosciences) in a final volume of 11 µl and incubated at 65°C for 10 min. After cooling the reaction for 5 min at RT and further 5 min on ice, 4 µl 5x First Strand Buffer (Invitrogen), 2 µl 0.1 M dithiothreitol (DTT; Invitrogen), 2 µl aminoallyl-dNTP mix [containing 6 mM dATP, dCTP, dGTP each, 0.8 mM dTTP (Fermentas) and 5 mM aa-dUTP (Sigma)] and 1.5 µl SuperScript II reverse transcriptase (200U µl^{-1}; Invitrogen) were added, mixed and incubated at 42°C for 2 h. After generation of aa-cDNA, remaining RNA was hydrolyzed applying 5 µl 2.5 M NaOH during incubation at 37°C for 15 min. The reaction mix was neutralized by adding 10 µl of 2 M Hepes (pH 7; Roth) and purified from unincorporated aa-dUTPs and free

amines by precipitation at -20°C overnight after addition of 6 µl 3 M sodium acetate and 150 µl absolute ethanol. The next day, aa-cDNA was centrifuged at 18,000g for 30 min at 4°C, washed in 70% ethanol, centrifuged again for 10 min and air-dried for about 10 min. aa-cDNA was than resuspended in 16 µl 0.1 M sodium bicarbonate buffer (pH 9), transferred into one tube Cy3 or Cy5 esters (Amersham Biosciences) and incubated for 2 h in the dark at RT. Afterwards, 7.5 µl 4 M hydroxylamine (Sigma) were added to each coupling reaction and the mixture was incubated at RT in the dark for 15 min. Finally, after addition of 35 µl 100 mM sodium acetate (pH 5.2) to each reaction, uncoupled dye was removed using the QIAgen PCR Purification Kit (Qiagen).

Prehybridization of slides

Before hybridization, slides were treated by addition of blocking reagent to inactivate non-specific binding sites in order to reduce background in following hybridizations. Prehybridization took place immediately prior to hybridization in 5x SSC, 0.1% SDS and 1% bovine serum albumin (BSA) for at least 2 hours at 42°C (Hegde *et al.*, 2000). Prehybridized slides were washed two times in double-distilled water for 2 min at RT, then in isopropanol for further 2 min at RT, and quickly dried by centrifugation.

Hybridization on microarrays and stringency optimization

To determine optimal hybridization and wash conditions for the *P. amoebophila* microarray experiments, 20 µg total RNA were labelled using the CyScribe Post Labelling Kit as described above. Labelled targets were then hybridized in 400 µl of hybridization buffer [5x SSC, 0.1% SDS, 0.1% *n*-lauryl sarcosine, 0.1% blocking reagent, 50 µg ml^{-1} salmon sperm DNA (Eppendorf AG)] containing 0.5 pmol of the Cy-labelled control oligonucleotide (CONT-COMP) to slides from the same printing run at increasing stringency [10%, 20%, 30%, 35% and 40% deionized formamide (Roth) in the hybridization buffers]. After denaturation at 95°C for 10 min, the hybridization solution was immediately applied to the spotted slides using sealed coverslips.

Following 16 hours of incubation at 42°C, the slides were subjected to different wash regimes. Regime 1 included three serial washes, first in 2xSSC, 0.1% SDS at 42°C, then in 0.1xSSC, 0.1% SDS at 20°C (room temperature) and finally in 0.1xSSC at 20°C. Washregime 1 was also modified by omitting the first low-stringency wash buffer to increase stringency and consisted therefore of washes in 0.1x SSC, 0.1% SDS at 42°C and 0.1x SSC at 20°C. After each completed wash regime, slides were briefly rinsed in ice-cold double-distilled water, quickly dried by centrifugation and signal-to-noise ratios were determined by microarray scanning.

In addition, slides hybridized at 35% formamide were not only washed by using regime 1 but were also treated by applying wash regimes 2 and 3. Regime 2 was performed as regime 1 but all wash buffers were at 42°C to increase stringency. Regime 3 was performed at 45°C using wash buffers containing 1xSSC, 0.1% SDS/0.4xSSC, 0.1% SDS/0.4x SSC. For all experiments, slides were kept in each washing buffer for 5 min under constant manual agitation, were briefly rinsed in ice-cold double-distilled water, quickly air-dried and stored in the dark until scanning.

The stringency of each hybridization buffer and of each wash was calculated using the following formula for determining the melting temperature (T_m) (Lathe, 1985): T_m = 81.5°C + 16.6 log[Na^+] + 0.41(%GC) – 0.63(%formamide) – (500/length). [Na^+] is the sodium concentration (0.39 M for 2x SSC); %GC is the percentage of guanine and cytosine in the DNA (35.8% for *P. amoebophila*); % formamide is the volume percentage of formamide in the solution (0-40%) in these experiments; and length is the length of the DNA probe that is being hybridized (50 bp). Stringency can then be calculated by subtracting the wash temperature from the calculated melting temperature, as follows: $\Delta T = T_m - T_{wash}$. As ΔT is decreased, the stringency increases (Korkola *et al.*, 2003). Table 1 shows the wash conditions and calculated stringencies for each of the conditions used.

Slide scanning, signal quantification and data analysis

Gene expression was visualised by scanning of hybridized slides using a GenePix 4100 instrument (Axon Instruments Inc.). Initial microarray data analysis was carried out using the GenePix Pro 5.0 software (Axon Instruments Inc.). After calculating the mean intensity of the signal within the spot and of the local background area, the signal-to-noise ratio (SNR) was computed for each spot to discriminate true signals from noise using the following formula: SNR = (signal mean – background mean)/ (background standard deviation). A commonly accepted criterion for the minimum fluorescence signal (threshold) that can be accurately quantified is SNR≥3 (Verdnik, 2002; Franke-Whittle *et al.*, 2006; He *et al.*, 2005a; Tiquia *et al.*, 2004; Wei *et al.*, 2006) and this threshold was also used in this study. For further analyses, microarray data were transferred to Microsoft Excel and SPSS version 14.0 (SPSS Inc).

Preparation of 16S rRNA for internal control purposes

To examine the sensitivity of the microarray, internal controls were used to identify the minimum concentration of transcripts which can be detected above the threshold. As internal controls 16S rRNA from four phylogenetically distinct bacterial organisms were produced by *in vitro* transcription and specific probes targeting signature regions of these 16S rRNA

molecules were included in the microarray. Clones from *Desulfotomaculum thermoacetoxidans* DSM 5813 (*Firmicutes*), *Thermodesulfovibrio islandicus* DSM 12570 (*Nitrospira*), *Desulfovibrio profundus* DSM 11384 (*Deltaproteobacteria*) and *Thermodesulfobacterium thermophilum* DSM 1276 (*Thermodesulfobacteria*) were used for PCR amplification. Primers T3-BACT8F (5´-AAT TAA CCC TCA CTA AAG GG AGA GTT TGA TYM TGG CTC-3´) and 630R (5´-CAK AAA GGA GGT GAT CC-3´) were used creating approximately 1,600 bp fragments. The PCR conditions were as follows: initial denaturation at 94°C for 3 min, 35 amplification cycles at 94°C for 30 sec, 57°C for 30 sec, 72°C for 90 sec and final elongation at 72°C for 7 min. After purification using the QIAquick Gel Extraction Kit (Qiagen), 0.5-1 µg purified PCR product was transcribed into RNA after addition of 6 µl 5x T3 RNA polymerase buffer, 3 µl 10 mM dNTP mix, 0.5 µl RNase inhibitor (40U μl^{-1}) and T3 RNA polymerase (20U μl^{-1}) in a final volume of 30 µl during incubation at 37°C for 4 hours. Subsequently, DNA was digested after addition of 3 µl DNase I buffer and 3 µl RNase-free DNase I (1U μl^{-1}) during incubation at 37°C for 15 min. The enzymatic reaction was stopped by addition of 3 µl 25 mM EDTA and RNA was allowed to precipitate overnight at -20°C after addition of 10 µl 5 M NaCl and 300 µl ice-cold absolute ethanol. The next day, RNA was centrifuged for 30 min at 20,800g at 4°C, washed once with ice-cold 70% ethanol and resuspended in RNAse-free water. RNA concentration was quantified and RNA was stored at -80°C after addition of 0.5 µl RNase inhibitor. The integrity of transcript RNA was determined on a 1% agarose gel. All used solutions and enzymes in this experiment were from Fermentas.

Separation of bacterial RNA from mixed total RNA samples

Microarray analyses of prokaryotic organisms living exclusively inside eukaryotic host cells are complicated by the fact that the extracted total RNA does not only contain bacterial but also (potentially large amounts of) eukaryotic total RNA which can cause high background and decreasing signal intensities in hybridization. To avoid these problems, removal of eukaryotic ribosomal and polyadenylated RNA as well as bacterial ribosomal RNA was performed using the MICROB*Enrich* Kit (Ambion) according to the manufacturer´s instructions. After quality examination of enriched RNA on a 1% agarose gel, enriched bacterial RNA was labelled using both labelling protocols and hybridized to the microarray as described above.

RESULTS

Oligonucleotide design and microarray setup

A whole genome microarray was constructed representing 100% of the putative coding sequences (CDSs) of the *P. amoebophila* genome (Horn *et al.*, 2004). In total, 2,031 predicted CDSs were identified, with a mean length of 980 bp (minimum 140 bp, maximum 9,546 bp). 17% of all predicted genes are smaller than 300 bp and 4.8% are more than 2,600 bp in size. For each putative gene as well as for some positive, negative and internal controls a specific probe was designed using the public domain program OligoWiz (Nielsen *et al.*, 2003). The analysis of the designed probes showed, that 87% achieved a total score of ≥0.95 (optimal score is 1) and were considered as well-suited oligonucleotide probes. Probes below this theoretically determined threshold were blasted manually against the genome of *P. amoebophila* to check for specificity and were, if they showed cross-hybridization, omitted and new designed.

Oligonucleotide probes (mean theoretically predicted melting temperature 74.2°C ± 7°C) were spotted in triplicates in different locations on a single slide. Several nonsense probes (NONSENSE and a probe for the 18S rRNA of *Acanthamoeba* sp. UWC1) were also immobilized in triplicates on the microarray for hybridization control purposes. In addition, another nonsense probe (CONT) was spotted at the beginning and the end of most subarrays which served as positive control in hybridizations and as landmarks in the microarray readout. During hybridization, a labelled oligonucleotide fully complementary to this probe was added for hybridization efficiency control (Loy *et al.*, 2005). Probes for four internal controls, derived from the phylogenetically distinct bacteria *Desulfotomaculum thermoacetoxidans* DSM 5813 (*Firmicutes*), *Thermodesulfovibrio islandicus* DSM 12570 (*Nitrospira*), *Desulfovibrio profundus* DSM 11384 (*Deltaproteobacteria*) and *Thermodesulfobacterium thermophilum* DSM 1276 (*Thermodesulfobacteria*) were printed six times each on two different positions onto the microarray for hybridization sensitivity experiments. These probes showed no cross-hybridization to sample RNA and thus were used in experiments without spiked RNA as additional negative controls. Including a probe for the *folA* gene encoding dihydrofolate reductase (a gene found on a contig of *P. amoebophila* which could not be correctly assembled so far), several negative and positive controls, finally, the microarray was composed of 6,720 spots in total (Figure 1).

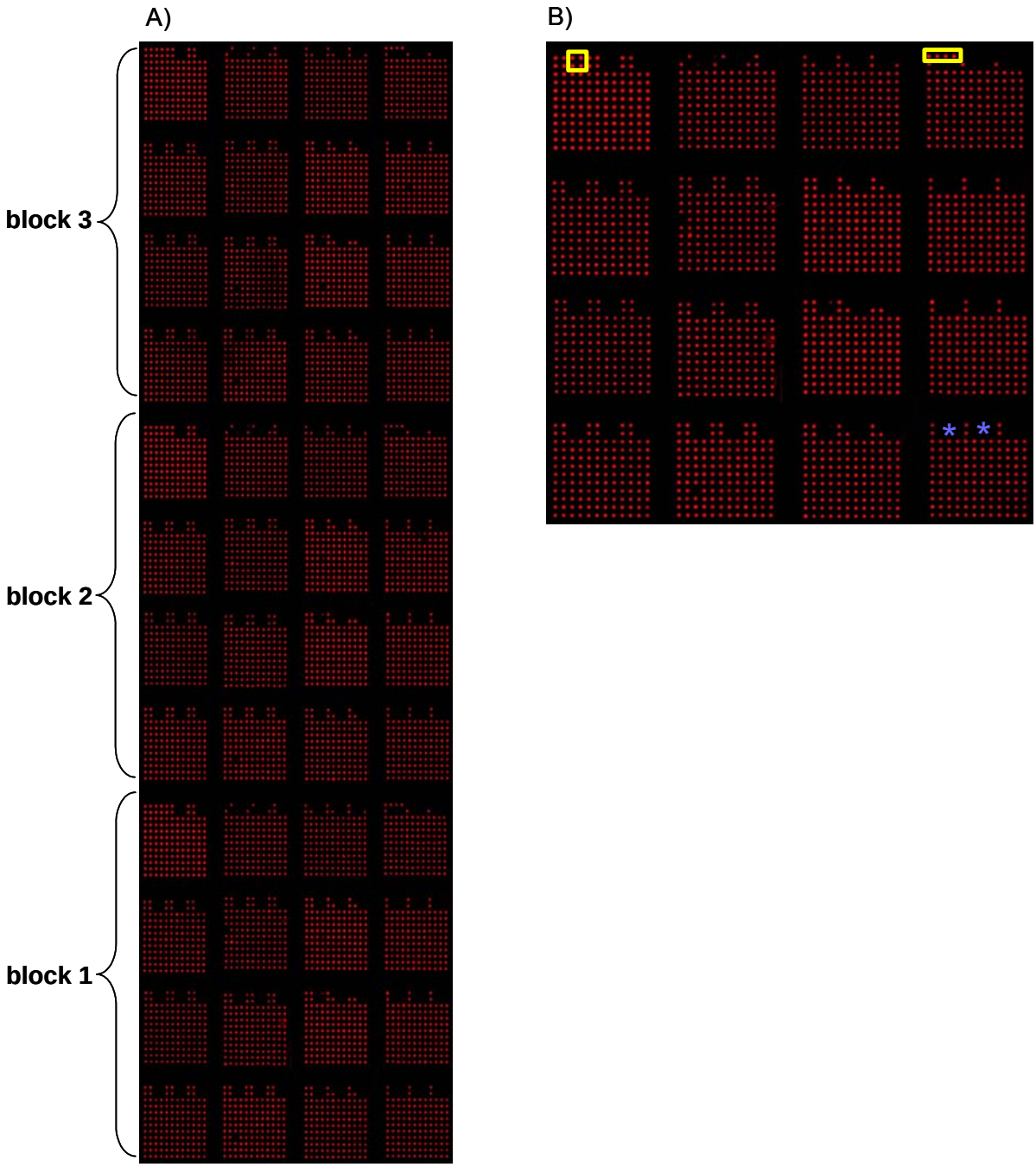

Figure 1. The *P. amoebophila* microarray after hybridization with a spacer probe to check for spotting quality. A) The whole genome microarray of *P. amoebophila* consists of three replicated blocks/metagrids; each block is composed of 16 subgrids printed by one pin-tool (16 pins) and contains probes targeting all 2,031 *P. amoebophila* CDSs as well as several positive and negative control probes. In total, the microarray is composed of 6,270 spots. B) The positions of the negative controls are indicated in yellow, some blank spots (produced by spotting printing buffer only) are indicated in blue.

Optimizing stringency

Hybridization temperature and washing conditions can have profound effects on hybridization results. Therefore, a well-balanced hybridization evaluation between intensity and specificity is required, so that the signal is maximized and cross-hybridization is minimized. In this study, stringency was adjusted by varying the formamide concentration in the hybridization buffer, in combination with different stringency levels during microarray washes, which can be achieved either by decreasing the ionic strength or increasing the washing temperature (Wildsmith & Elcock, 2001).

Suitable hybridization and wash conditions were determined by calculating the total number of genes detected above the signal threshold (SNR≥3) as well as by non-specific binding of labelled targets to several negative controls. At lower formamide concentrations (10-30%) in combination with wash regime 1, 52-78% genes showed a signal above the threshold. However, in all these hybridizations non-specific binding to the negative controls on the array could be recorded. In the presence of 40% formamide all negative controls could be discriminated, but the percentage of detected signals decreased significantly to 18%. The highly stringent, modified wash regime 1 did not improve the hybridization, as specific signals were removed indicated by a generally low percentage of genes detected (7-41%). In addition, surprisingly, some negative controls showed evidence of non-specific binding.

Because of the low number of signals at 40% formamide and the low level of signal intensity, further hybridization experiments in the presence of 35% formamide were performed and washes were again varied to obtain different specific stringencies. 52% genes and 2 out of 5 negative controls were above the threshold when the slides were washed with wash regime 1 and 56% genes and 3 out of 5 negative controls were detected after wash regime 3. The best result could be obtained using wash regime 2, leading to 62% genes detected and no non-specific binding to negative controls.

Therefore, all further experiments were performed using 35% formamide in the hybridization buffer, and wash regime 2 (2xSSC, 0.1% SDS/0.1xSSC, 0.1% SDS/0.1xSSC) at 42°C. The information about hybridization and wash conditions, melting temperature, stringency, specificity and percentage of genes detected is summarized in Table 1.

Table 1. Summary of hybridization, washing conditions, melting temperature, specificity and detected genes after hybridization.

Hybridization Buffer			Washing Buffer					
(% FA)	Hybridization Temperature (°C)	Calculated [a]T_m (°C)	Wash Regimes	Washing Temperature (°C)	Calculated [a]T_m (°C)	[b]ΔT (°C)	Specificity	Detected Genes [%]
10	42	79	**1)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 20 20	79 57 57	37 37 37	3/5	78
20	42	73	**1)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 20 20	79 57 57	37 37 37	3/5	69
30	42	67	**1)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 20 20	79 57 57	37 37 37	3/5	67
40	42	61	**1)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 20 20	79 57 57	37 37 37	0/5	18
10	42	79	**1 mod.)** 0.1xSSC, 0.1% SDS 0.1xSSC	42 20	57 57	15 37	1/5	33
20	42	73	**1 mod.)** 0.1xSSC, 0.1% SDS 0.1xSSC	42 20	57 57	15 37	1/5	41
30	42	67	**1 mod.)** 0.1xSSC, 0.1% SDS 0.1xSSC	42 20	57 57	15 37	1/5	33
40	42	61	**1 mod.)** 0.1xSSC, 0.1% SDS 0.1xSSC	42 20	57 57	15 37	0/5	7
35	42	64	**1)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 20 20	79 57 57	37 37 37	2/5	52
35	42	64	**2)** 2xSSC, 0.1% SDS, 0.1xSSC, 0.1% SDS 0.1xSSC	42 42 42	79 57 57	37 15 15	0/5	62
35	42	64	**3)** 1xSSC, 0.1% SDS 0.4xSSC, 0.1% SDS 0.4x SSC	45 45 45	74 67 67	29 22 22	3/5	56

SSC, standard saline citrate; SDS, sodium dodecyl sulfate; T_m, melting temperature; ΔT, stringency.
[a]$Tm = T_m = 81.5°C + 16.6 \log[Na^+] + 0.41(\%GC) – 0.63(\%formamide) – (500/length)$; [b]$\Delta T = T_m – T_{wash}$

Evaluation of *P. amoebophila* genomic DNA hybridization

For determining the overall hybridization signal distribution, coverage of genes and reproducibility of labelling and hybridization, genomic DNA was obtained from infected amoebal cells, fragmented to improve labelling efficiency, labelled and hybridized to the array. Fragmentation of isolated high molecular weight DNA using a sonicator resulted in nucleic acid fragments mainly ranging between 500 bp and 1,500 bp, which were considered to be suitable for subsequent labelling. As labelled genomic DNA comprised of labelled as well as unlabelled sense and antisense strands, the optimal amount of genomic DNA for hybridization could not be measured spectrophotometrically but was experimentally determined.

The number of detected genes was always ≥99%, when 2 µg fragmented genomic DNA was used in one labelling reaction and hybridized to the microarray. A decreasing number of genes were detected when less genomic DNA was used (92.4% - 1 µg, 73.6% - 0.2 µg). In general, each single oligonucleotide probe on the array was able to give a signal above the threshold, all negative controls were below the threshold and small background values were obtained. Cross-over effects could be observed only in 0.2-3.4% analyzed spots containing only printing buffer (n=588).

Biased incorporation of fluorophores during labelling was checked by performing a self-self hybridization of equal amounts of genomic DNA labelled with Cy5 and Cy3 fluorophores (Figure 2). Comparing the signal-to-noise values of Cy3 and Cy5, a high linear correlation level was obtained [correlation coefficient (r) >0.92], although the fluorescence signal intensity of Cy5 was about five times higher (Figure 2a). Analysis of the signal ratios generated from the hybridization signals of the three replicates of oligonucleotide spots on a single array revealed reproducible signals above the background level with r >0.85-0.95 indicating homogeneous sample hybridization to the microarrays (Figure 2b). Correlation values between two replicate arrays produced from the same genomic DNA pool (technical replicates) were in a range of r >0.83-0.95, biological replicates show a lower correlation (r = 0.65; Figure 2c).

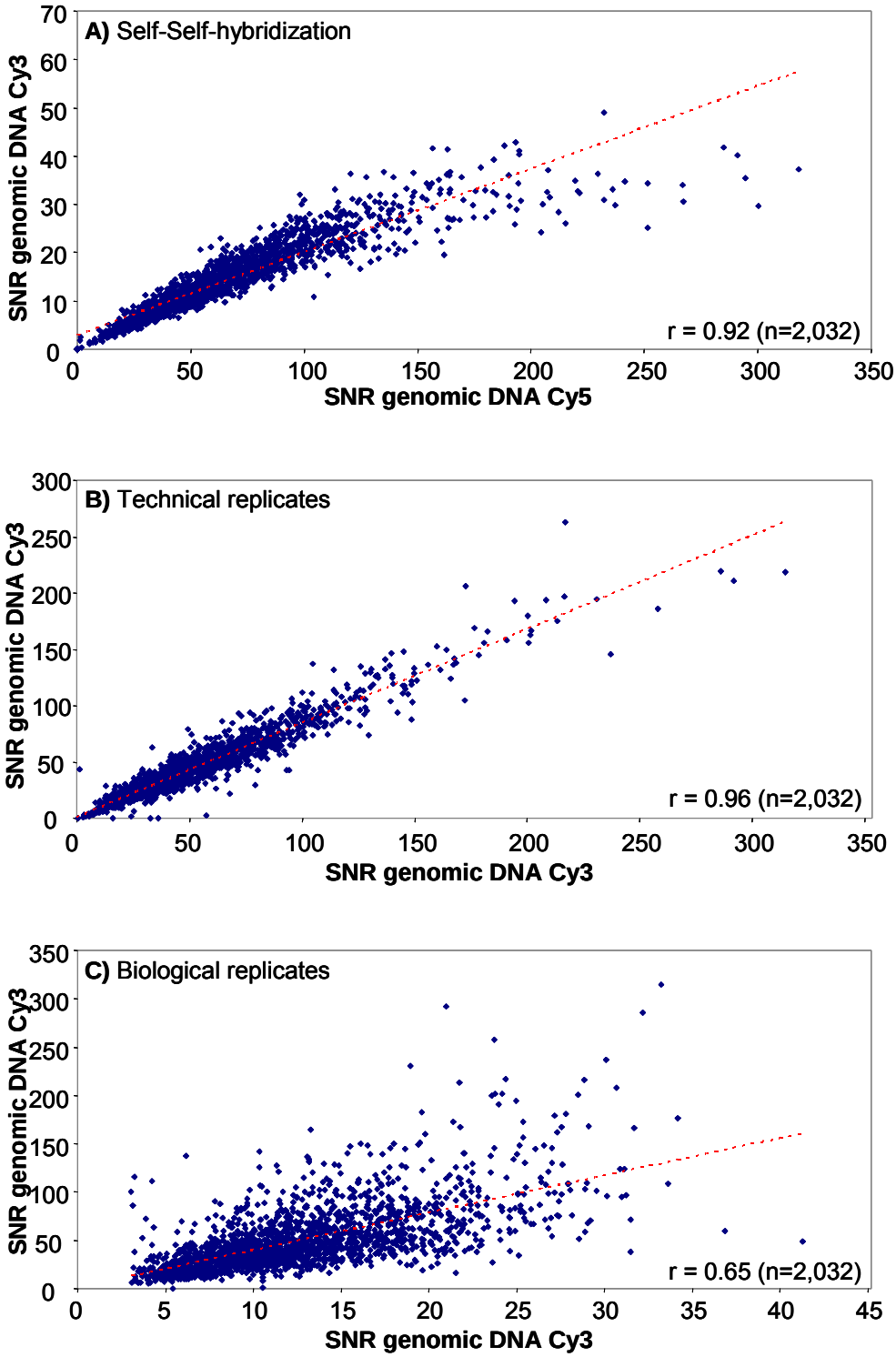

Figure 2. Reproducibility of labelling and hybridization of genomic DNA. Scatter plots of genomic DNA hybridization intensities are shown in panel A) for self-versus-self hybridization, in panel B) for technical replicates, and in panel C) for biological replicates. Correlation coefficients (r) for the two channels are shown in each plot. The total number of plotted signals includes the 2,031 *P. amoebophila* genes as well as the gene for *folA* which was found on the not assigned contig.

Evaluation of *P. amoebophila* cDNA hybridization

To examine any biased incorporation of Cy3 or Cy5 fluorophores used for labelling of *P. amoebophila* RNA, equal amounts of the same batch of total RNA was labelled using the CyScribe Post Labelling Kit.

After hybridization to the same microarray, signal intensities were analyzed and showed a highly similar and obviously unbiased incorporation of both fluorophores during cDNA generation with r >0.95-0.98 (Figure 3a). Additional analysis of the signal ratios generated from technical replicates revealed highly reproducible signals above the background levels (r >0.84-0.90) indicating uniform sample hybridization to the microarrays (Figure 3b). Biological replicates resulted in correlations r >0.83-0.86 when RNA labelled with CyScribe was applied to the array (Figure 3c). Comparison of both labelling methods used in this study showed an even higher correlation level for biological replicates with r >0.89.

The number of genes which could reproducibly detected after hybridization of total *P. amoebophila* RNA generated from asynchronously infected amoeba cultures was generally between 52% and 63% (Cy3 56-59%; Cy5 52-63%). In order to investigate expressed genes of intracellular growing *P. amoebophila*, the mean signal ratio of each single gene from eleven microarray hybridizations derived from three biological replicates were calculated and further analyzed. In total, 33 data points were analyzed per predicted gene.

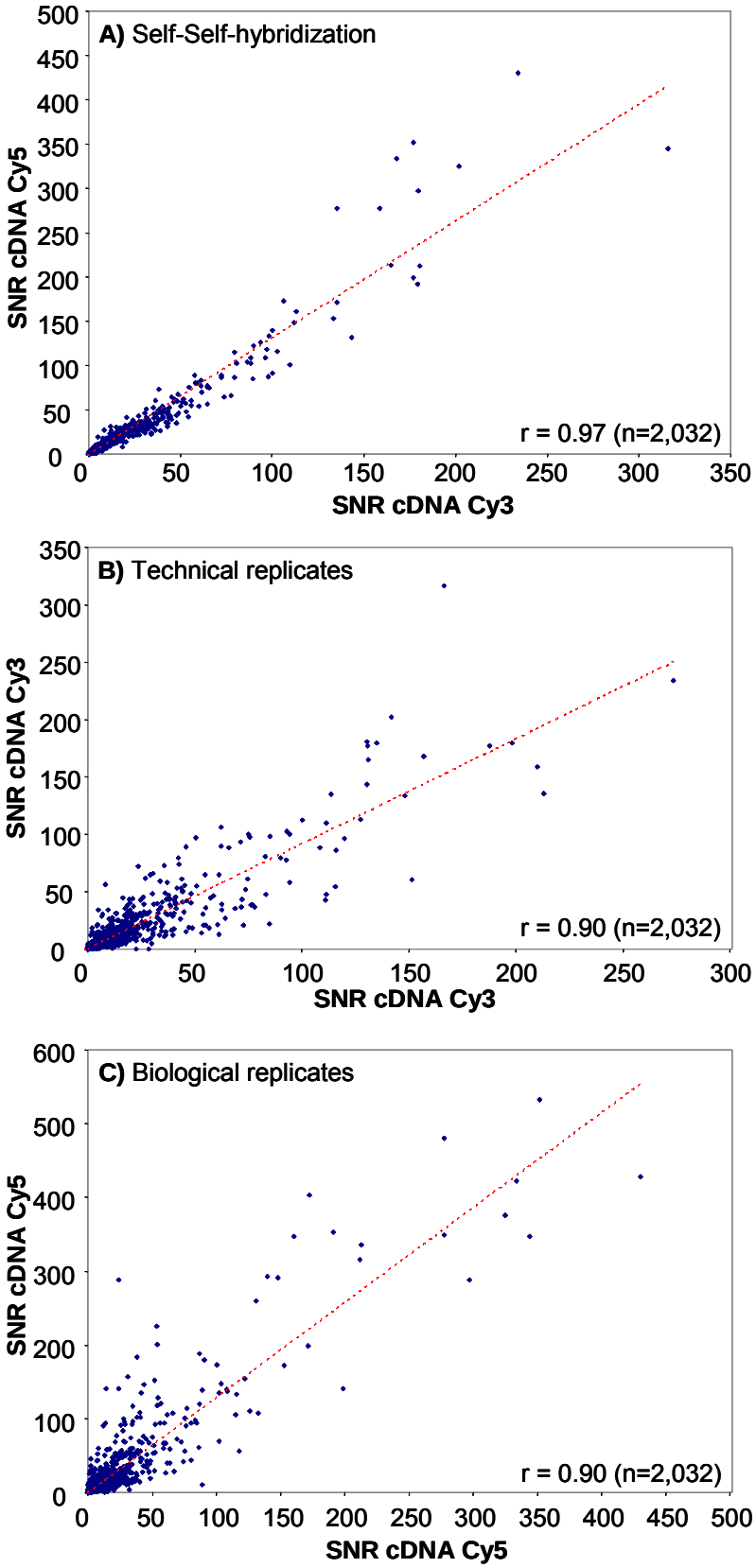

Figure 3. Reproducibility of labelling and hybridization of cDNA. Scatter plots of cDNA hybridization intensities are shown in panel A) for self-versus-self hybridization, in panel B) for technical replicates, and in panel C) for biological replicates. Correlation coefficients (r) for

the two channels are shown in each plot. The total number of plotted signals includes the 2,031 *P. amoebophila*-genes as well as the gene for *folA* which was found on the not assigned contig.

Determination of the sensitivity detection limit

Internal controls were implemented to evaluate the detection limit of the microarray hybridizations. *In vitro*-transcribed control 16S rRNA from four phylogenetically distinct bacterial species was generated and different concentrations (5, 10, 25, 50, 100, 500 pg) of *Desulfotomaculum thermoacetoxidans* (Dth) transcripts were spiked into total RNA prior to cDNA synthesis. A signal was observed exclusively for the highest applied control transcript concentration (500 pg). No signals were detected when labelled cDNA was prepared from total RNA lacking these spiked prokaryotic transcripts.

Separation of bacterial RNA from mixed samples

Obligate intracellular bacteria can not be grown outside of their host cells, hampering the purification of high concentrations of bacterial mRNA needed as target for microarray analysis. Therefore, enrichment of bacterial mRNA was carried out using the MICROB*Enrich* Kit which selectively removes eukaryotic total RNA and also bacterial ribosomal RNA (>90% removal of total RNA) (Figure 4).

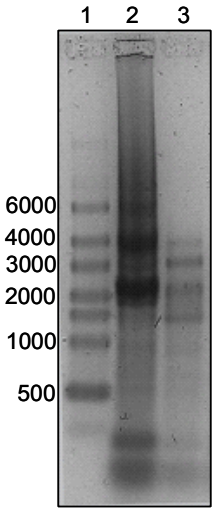

Figure 4. RNA before and after enrichment with MICROB*Enrich*. Total RNA (eukaryotic and bacterial total RNA mixture) was subjected to the MICROB*Enrich* procedure. RNA sample was analyzed by denaturing agarose electrophoresis. Lane 1, molecular weight marker; lane 2, total RNA; lane 3, enriched bacterial mRNA.

CyScribe labelling of 3 µg enriched mRNA resulted in very high FOI values of 228 and 140 and few signals (13% and 7%, respectively). No improvement in signal intensity or sensitivity of hybridization could be obtained by an alternative labelling method with increased starting material of enriched bacterial mRNA (5 µg – 18% detected genes and 10 µg – 14% detected genes, respectively), although the incorporation of fluorophores into cDNA was near the optimum (FOI 41 and 49) (Table 2).

Table 2. Labelling efficiency and number of genes detected after hybridization

Labelling method	Enriched bacterial mRNA [µg]	Incorporation of CyDye per sample [pmol]	FOI	CyDye	[%] Genes Detected
CyScribe	3	208	228	Cy3	13
CyScribe	3	176	140	Cy3	7
Labelling II	5	115	41	Cy5	18
Labelling II	10	199	49	Cy5	14

Exploring transcriptional activity of *P. amoebophila* during intracellular growth

To explore the global gene expression profile of *P. amoebophila* during intracellular growth, total RNA from *P. amoebophila* grown in *A. castellanii* Neff was extracted, labelled with either Cy3 or Cy5 fluorophors, hybridized to the microarray and signal ratios were determined. Of the 2,032 CDSs (including *folA*) identified previously in *P. amoebophila*, a mean of 61% (n=1,234) showed a hybridization signal above SNR≥3, including 52% of the 1,093 *P. amoebophila*-specific genes. For the remaining 39% (n=798) of the predicted genes the hybridization signal was either absent or below the threshold (Figure 5). A complete list of expressed and not expressed genes can be found in Table S3.

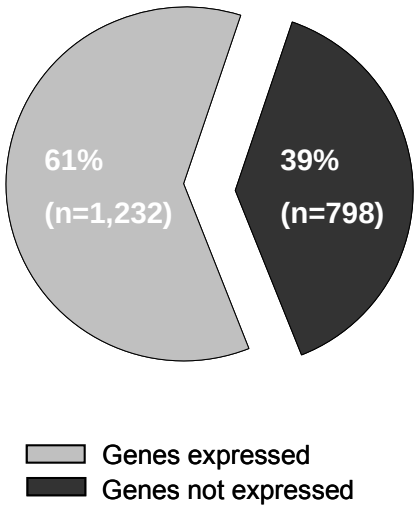

Figure 5. Expressed and not expressed genes during intracellular growth. The mean proportion of genes which gave a signal above the threshold (light grey) and of genes without signal in any hybridization (dark grey) is depicted in the circle diagram.

47% (n=580) of transcribed genes show homology to functionally characterized proteins, 29% (n=359) are annotated as conserved hypothetical and hypothetical genes, and 24% (n=295) of the expressed CDSs have no homology to any publicly available sequence (unknown genes). The analysis of genes without signals showed, that 27% (n=216) are

functionally characterized CDSs, 32% (n=255) are conserved hypothetical or hypothetical CDSs, and 41% (n=327) are unknown genes (Figure 6). Within CDSs classified as unknown genes, predicted genes which were not transcribed in any hybridization were almost 2-times higher compared to expressed genes.

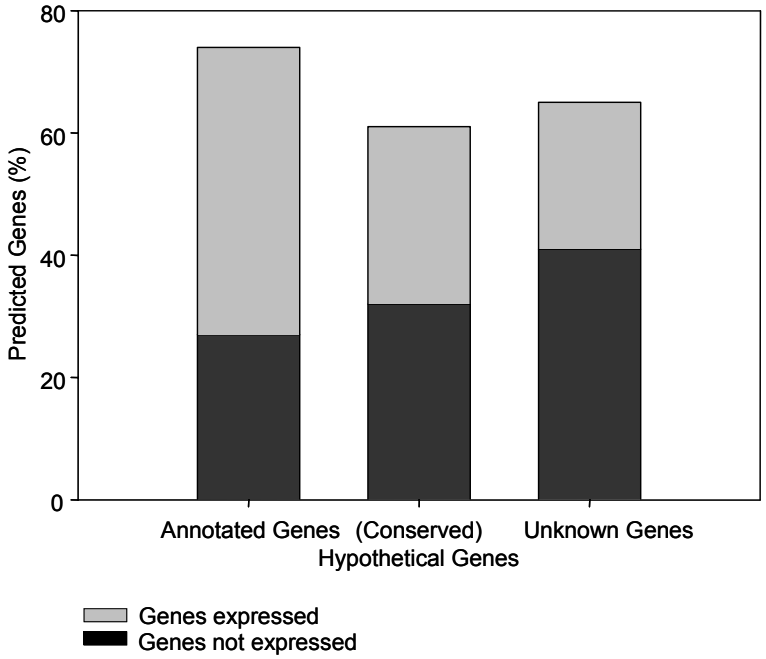

Figure 6. Classification of expressed and not expressed genes. Each bar, representing the functional assignment of the sequences, is divided in the proportion of genes which gave a signal above the threshold (light grey) and in genes without signal in any hybridization (dark grey).

Additionally, small sequences (<500 bp; n=344) were conspicuous abundant among unknown genes without signal (31%, n=243) compared to longer sequences (7%, n=43, CDSs up to 1000 bp and 5%, n=41, sequences >1000 bp) (Figure 7).

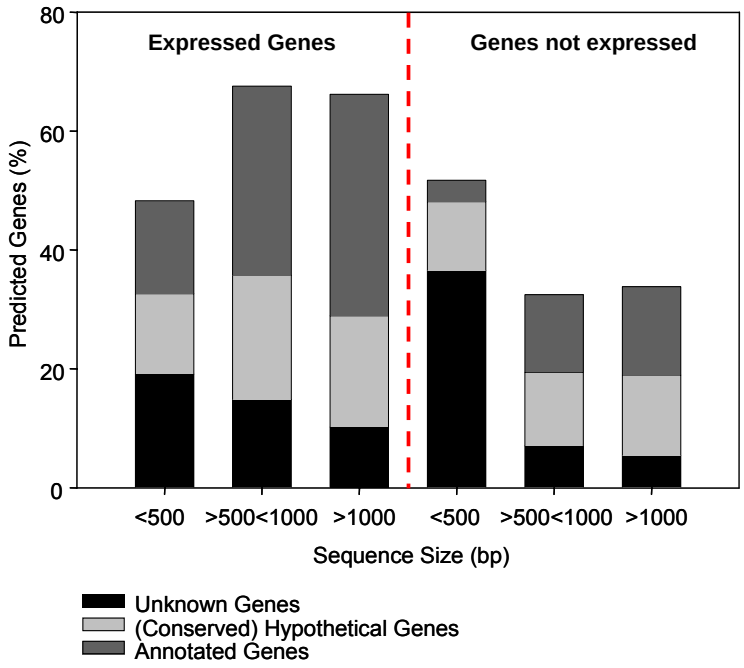

Figure 7. Analysis of CDSs according to gene size, annotation and expression. The percentages of expressed genes (left panel) or not expressed genes (right panel) in any hybridization were shown. Each bar, representing the size of the sequences, is divided into annotated CDSs (grey), conserved hypothetical and hypothetical CDSs (light grey), and unknown CDSs (dark grey).

According to the Similarity Matrix of Proteins (SIMAP) database which provides a pre-calculated sequence similarity matrix for all proteins deposited at major public sequence databases (Rattei *et al.*, 2008), no homology to any other protein could be obtained for 13% of genes which were predicted to encode small proteins (n=264; average size 96 amino acids; E value: 0.0). Among these sequences, 64% (n=169; average size 239 bp; 79 amino acids) were not transcribed in any hybridization indicating a potentially wrong annotation (Table S2).

Expressed genes involved in metabolism

Based on *in silico* genome analyses *P. amoeobophila* was shown to be largely dependent on its host and has to acquire amino acids, nucleotides and NAD^+ from the amoeba cytosol. This is reflected in several truncated biosynthetic pathways and reduced metabolic reactions

(Horn *et al.*, 2004). Here we used the genome-wide transcriptional pattern to assess the physiological state of intracellular growing *P. amoebophila*.

Figure 8 shows a comparison of the 61% experimentally verified gene transcripts to the number of annotated genes. This analysis is based on the classification of proteins in different functional categories using the MIPS FunCat (http://mips.gsf.de/genre/proj/uwe25/Search/Catalogs/searchCatfirstFun.html). Only 74% (n=1,166) of the genes predicted to be involved in 14 different functional categories were found to be transcribed. In all investigated categories, *P. amoebphila* did not utilize its complete gene set during intracellular growth. Between 1-3% difference could be determined for genes involved in transcription, cellular transport, cycle processing, cell rescue, defence and virulence, protein fate, interaction with cellular environment, biogenesis of cellular components, subcellular localization, unknown and other genes. 5% of genes involved in metabolism and 6% of genes involved in protein binding and cofactor requirement were not expressed under the applied condition although they are encoded in the genome. Almost all genes involved in energy production and protein synthesis could be detected by microarray analyses.

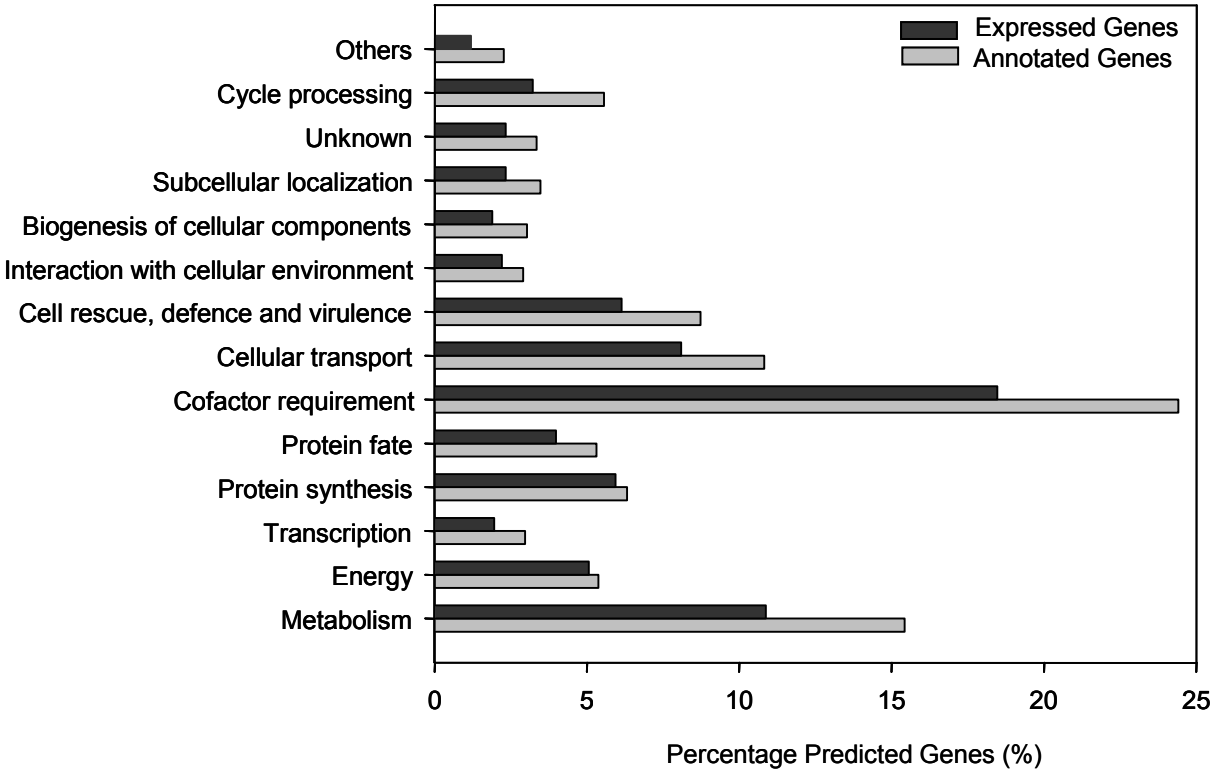

Figure 8. Comparison of annotated and expressed genes. Annotated (n=1,581) and experimentally determined gene products (n=1,166) were classified into 14 functional categories based on the MIPS FunCat.

In detail, *P. amoebophila* was shown to encode all enzymes involved in the TCA cycle and analyses of the microarray hybridizations demonstrated that all genes needed in the chemical conversion of molecules to produce energy were transcribed except of one (pc1843; similar to succinate dehydrogenase cytochrome b558) which was marginally lower than the threshold (Table S4). Similarly, all genes needed for the pentose phosphate pathway were expressed, except of pc1302 (similar to UDP-glucose 4 epimerase), and the whole gene set included in oxidative phosphorylation showed clear signals above the threshold, again except of one gene [pc1667; similar to H^+-transporting two-sector ATPase (epsilon chain, *atpC*)]. All enzymes participating in the conversion of glucose into pyruvate during glycolysis were expressed (Table S4).

According to the genome analysis, *P. amoebophila* encodes several enzymes for the synthesis of six amino acids (glutamate, serine, glycine, aspartate, proline and glutamine). However, the transcriptional pattern obtained in this study demonstrated only synthesis of three of them, namely serine produced directly from pyruvate (pc0878; *sdaB*), glycine converted from serine (pc0444; *glyA*), as well as proline transformed from glutamate (pc1132; *proC*; Table S5). The remaining essential amino acids might be imported via general and specific amino acid transporters across the inclusion membrane. Consistent with this finding, gene expression for specific transporters for glutamate (pc1785, *gltT*), tyrosine and tryptophan (pc0589; *tyrP*), alanine (pc0622, pc1598, pc1656, pc1657; *dagA, cycA*), and methionine (pc0453, *yaeC, metQ*; pc0454, *yaeE, metI*) could be shown. In addition, transcripts for general amino acid transporters which most likely deliver the remaining required amino acids to the intracellular bacteria were detected (di-/oligopeptide transporter and the neutral amino acid transporter AaaT (pc0103, pc1502, pc1504-pc1506 and pc1734, respectively) (Table S6). In summary, during growth of *P. amoebophila* in amoebae, 12 of 20 essential amino acids were either synthesized by the symbionts themselves or could most likely be uptaken by one of the many specific or general amino acid transporters (Table 3). Aminoacyl-tRNAs were produced from all amino acids under the investigated situation except of cysteine which is just below the threshold.

Table 3. Summary of predicted amino acid biosynthetic pathways and amino acid transporters

Amino acid	Properties of the side chain	Genome prediction	Microarray analyses*	Genome encoded transporter	Microarray Analyses*
Glycine (Gly)	nonpolar, aliphatic R groups	+	+	alanine/glycine transporter (DagA) neutral aa transporter (AaaT)	+
Serine (Ser)	polar, uncharged R groups	+	+	amino acid transporter	-
Glutamine (Gln)	polar, uncharged R groups	+	-	glutamine transporter (FliY, GlnQ)	-
Proline (Pro)	polar, uncharged R groups	+	+	prolin transporter (PutB)	-
Glutamate (Glutamic acid, Glu)	negatively, charged R groups	+	-	glutamate transporter (GltT)	+
Aspartate (Aspartic acid; Asp)	negatively charged Rgroups	+	-	amino acid transporter	-
Threonine (Thr)	polar, uncharged R groups	-	-	amino acid transporter	-
Cysteine (Cys)	polar, uncharged R groups	-	-	amino acid transporter	-
Valine (Val)	nonpolar, aliphatic R groups	-	-	neutral aa transporter (AaaT) branched aa transporter (BraB)	+ -
Leucine (Leu)	nonpolar, aliphatic R groups	-	-	neutral aa transporter (AaaT) branched aa transporter (BraB)	+ -
Isoleucine (Ile)	nonpolar, aliphatic R groups	-	-	neutral aa transporter (AaaT) branched aa transporter (BraB)	+ -
Lysine (Lys)	positively charged R groups	-	-	cationic amino acid transporter	-
Arginine (Arg)	positively charged R groups	-	-	cationic amino acid transporter	-
Phenylalanine (Phe)	aromatic R groups	-	-	neutral aa transporter (AaaT) tyrosine/tryotophan transporter	+ +
Tyrosine (Tyr)	aromatic R groups	-	-	tyrosine/tryotophan transporters (tyrP 1-4)	+
Trypthophan (Trp)	aromatic R groups	-	-	tyrosine/tryotophan transporters (tyrP 1-4)	+
Methionine (Met)	nonpolar, aliphatic R groups	-	-	methionine transporter (MetINQ) neutral aa transporter (AaaT)	+ +
Alanine (Ala)	nonpolar, aliphatic R groups	-	-	alanine/glycine transporter (DagA) neutral aa transporter (AaaT)	+ +
Histidine (His)	positively charged R groups	-	-	cationic amino acid transporter	-
Asparagine (Asn)	polar, uncharged R groups	-	-	amino acid transporter	-

* Expressed according to Microarray analyses

Genes involved in virulence and other selected genes

Like many pathogenic bacteria, *P. amoebophila* possesses a TTSS. The microarray data showed that all predicted TTSS genes were transcribed suggesting that it is probably used to manipulate the amoeba cell during infection (Table S7). A remarkable finding in the genome of *P. amoebophila* was the presence of a complete gene set encoding a type four secretion system (TFSS) that is missing in all pathogenic chlamydial species. From the 12 predicted *P. amoebophila* genes belonging to the TFSS, 10 genes were always below the signal threshold. mRNA expression was detectable only for two predicted TFSS genes (pc1432; *traW* and pc1441; *traD*, respectively) indicating that translocation of molecules via the TFSS might not occur during infection (Table S7).

Furthermore, 65% (n=23) of genes encoding putative Inc proteins, which are likely to be involved in modifying the inclusion membrane of *P. amoebophila* (E. Heinz, unpublished), were transcribed (Table S7). *P. amoebophila* exhibits in its genome a remarkably high number of plant and cyanobacterial gene homologues and the majority of these genes (plant genes; 74%; n=88 and cyanobacterial genes; 61%, n=104) were also transcribed in asynchronous culture (Tables S8 and S9, respectively).

DISCUSSION

Specificity of the *P. amoebophila* oligonucleotide microarray

During hybridization, target molecules bind to immobilized single-stranded oligonucleotide probes by hydrogen bond formation between the bases of complementary nucleic acid sequences. As gene expression measurements can be hampered by cross-hybridization, multiple criteria such as sequence composition, degree of homology, hybridization temperature, pH and salt concentration have to be considered during probe design and hybridization (Schena, 2003).

For 50-mer oligonucleotides, Kane *et al*. suggested that an oligonucleotide probe showing >75% identity and/or complementary sequence stretches of >15 contiguous bases to any “non-target” transcript will contribute to the overall signal intensity (Kane *et al.*, 2000). Additionally, as demonstrated in further studies, oligonucleotide specificity was also affected by free energy (He *et al.*, 2005a; Liebich *et al.*, 2006). Thermal energy increases the rate of diffusion and melts secondary structures in the target molecules. Increased hybridization temperature therefore supports the formation of the probe/target hybrids. As a rule of thumb, hybridization can start at a hybridization temperature 5-15°C below the mean melting temperature of the oligonucleotides used (Ehrenreich, 2006; Schena, 2003). The optimum hybridization temperature of the oligonucleotides depends basically on the G+C content of

the organism and can be adjusted by including formamide into the hybridization buffer avoiding degradation of target due to high hybridization temperature. Addition of 1% formamide lowers the melting temperature of the probe/target duplex of about 0.65°C (Hutton, 1977; Sadhu *et al.*, 1984). In this study, best hybridization results were obtained when incubations were carried out at 42°C in the presence of 35% formamide. The relatively low formamide concentration needed in the *P. amoebophila* microarray hybridization assays can be explained by the AT-rich genome of *P. amoebophila* (35.8% CG content; Horn *et al.*, 2004). Because of only two hydrogen bonds, AT-rich oligonucleotides show weaker hybridization affinity producing therefore also much weaker fluorescence signals than sequences composed of mainly GC base pairs (Schena, 2003).

Following hybridization, slides were washed to remove imperfect hybrids originating from unspecific probe/target duplexes. Several different post-hybridization washes - stringent conditions were adjusted by temperature and by including different amounts of salt - were tested and showed that low-stringency wash conditions did not prevent unspecific binding and high-stringency wash conditions decreased significantly signal intensities. A well-balanced wash condition for the *P. amoebophila* microarray was found to include an initial low-stringency wash, followed by two high-stringency washes at the end of the washing procedure. Similar conditions have also been described for 50-mer microarray experiments (Talaat *et al.*, 2002; Talaat *et al.*, 2004).

The discrimination of negative control probes for hybridization specificity control purposes gives only an impression of the minimal stringency conditions during hybridization and washes, and expression of interesting genes should be further verified by quantitative real-time PCR to avoid misinterpretation of microarray hybridization patterns caused by non-specific binding (Chuaqui *et al.*, 2002). However, another possibility to optimize specificity would be the discrimination of *P. amoebophila* probes with the lowest scores for cross-hybridization similar to the commonly used strategy for the Affimetrix GeneChip system (Affimetrix) or PhyloChip hybridizations where discrimination between perfectly matched as well as mismatched sequences as internal controls ensure maximum gene specificity of the probes (Chou *et al.*, 2004; Ehrenreich, 2006; He *et al.*, 2005a; Lockhart *et al.*, 1996; Loy *et al.*, 2002; Relogio *et al.*, 2002). Deng *et al*. recently demonstrated for 50-mer oligonucleotide probes that mismatch probes with three to five evenly distributed mismatched nucleotides could be differentiated (Deng *et al.*, 2008).

Sensitivity of the *P. amoebophila* microarray

Considering the small fraction of bacterial target mRNA, acquisition of accurate signals from the complex mixture of bacterial and eukaryotic total RNA is challenging and hence high sensitivity of the microarray is crucial. The sensitivity of the *P. amoebophila* microarray was determined in only one preliminary experiment (without replicates) by spiking different concentrations of 16S rRNA transcripts of an unrelated bacterial species to the labelling reactions. Signal detection limit was estimated to be approximately at a concentration of 500 pg. Previous studies have demonstrated that the sensitivity of a single 50-mer oligonucleotide probe per gene is not only comparable to those obtained with PCR amplicon arrays (Kane *et al.*, 2000; Rhee *et al.*, 2004; Tiquia *et al.*, 2004) but can provide significantly better sensitivity than those with 25- to 30-mer in complex mixtures of RNA (He *et al.*, 2005b; Relogio *et al.*, 2002). Both probe types could reproducibly detect approximately 10 mRNA copies per cell (Kane *et al.*, 2000). The detection limit of a 50-mer probe is ranging from approximately 5 – 10 ng for genomic DNA from pure culture and approximately 8 ng for 16S rRNA (Tiquia *et al.*, 2004) to approximately 50 - 100 ng for genomic DNA from mixed bacterial samples (He *et al.*, 2005b; Rhee *et al.*, 2004; Tiquia *et al.*, 2004),. However, the 16S rRNA is highly prone to form stable secondary structures, and a detection limit determined with rRNA as target is therefore hard to interpret. The suitability of these probe/target mixtures for sensitivity tests in a gene expression system has to be reconsidered. Unfortunately, no additional sensitivity tests could be included in this study because of ample labelling problems starting at this time point.

Reproducibility of the *P. amoebophila* microarray hybridizations

The reliability and precision with which the abundance of RNA species could be quantified depends essentially on the selection of the optimal normalization strategy (Conway & Schoolnik, 2003). For the *P. amoebophila* microarray, a normalization procedure based on comparison of gene expression levels to signals generated from genomic DNA was planned, most similar to the genomic normalization procedure described in Talaat *et al*, 2002. Genomic DNA represents a constant copy number of a given amount of DNA, thus representing coverage of all genes with uniform and highly reproducible signals between hybridizations and was found to be reliable as a universal standard for expression measurements (Gadgil *et al.*, 2005; Pollack *et al.*, 1999; Talaat *et al.*, 2002; Weil *et al.*, 2002; Williams *et al.*, 2004).

To test the stability and reproducibility of the *P. amoebophila* microarray and the applied hybridization protocol, performance and quality of replicate hybridizations using genomic DNA as well as RNA samples was assessed using scatter plots and correlation

determination, and both sample types successfully met the correlation criteria suggested in literature (Hovatta, 2005). Although high correlation levels of directly measured ratios were obtained for both nucleic acid samples, genomic DNA labelled with Cy5 exhibited 5-times higher signal intensities than labelled with Cy3. Dye artefacts are a well known problem in microarray experiments, however, generally Cy5 results in lower signals because of higher background levels on glass surfaces and higher sensitivity to photobleaching than Cy3 (Smyth *et al.*, 2003; van Hal *et al.*, 2000).

Interestingly, signals generated from genomic DNA samples were approximately 4-times higher than signals obtained from RNA samples. This observation contrasts to a previous report where most RNA samples were found to generate higher signals than genomic DNA samples because of the presence of multiple transcripts per gene (Talaat *et al.*, 2002). The low signals obtained from *P. amoebophila* RNA strongly indicate too low concentrations or fast degradation of bacterial targets within the bacterial/amoebal RNA mixture. However in all hybridizations, genomic DNA was shown to generate true signals for >99% of the predicted *P. amoebophila* genes and absence of signals could be attributed to a failure in oligonucleotide deposition onto slides during the printing run.

P. amoebophila gene expression

For a better understanding of the physiology of *P. amoebophila* during intracellular growth, total RNA extracted simultaneously from *P. amoebophila* and the amoeba host was used to explore the global gene expression profile of the amoeba symbiont. This type of study addresses the question whether specific genes or pathways are expressed and at what level these genes are transcribed (Rhodius *et al.*, 2002; Wei *et al.*, 2001). As genes are usually only transcribed when their function is required, a substantially lower number of expressed genes (between 53% and 63% putative chlamydial genes) compared to genomic DNA was detected. The proportion of transcribed genes is comparable to those reported for *Mycobacterium tuberculosis* (between 45% and 70%, using RNA extracted from logarithmic and stationary cultures) (Talaat *et al.*, 2002), *Nitrosomonas europaea* in full ammonia medium (75% expressed genes) (Wei *et al.*, 2006), *Pseudomonas aeruginosa* growing in regular medium (40% expressed genes) (Guina *et al.*, 2003) and *E. coli* growing in LB medium (65% expressed genes) (Corbin *et al.*, 2003). Missing signals can be caused by either sample degradation, sensitivity failures of low abundant RNA species, not expressed genes, varying life styles of the organisms, differences in methodology among laboratories or simply by a wrong functional assignment of putative genes during gene annotation. 169 unknown genes were found in this study which might present a potential false assignment. These genes were neither found to be homolog to any other protein in public sequence databases nor could expression be observed in any hybridization (Table S2).

As existing knowledge on metabolic activity of *P. amoebophila* is almost exclusively based on genome sequence data, the obtained RNA expression profile of *P. amoebophila* provides a simple but useful reflection of the transcriptional activity of the amoeba symbiont during infection of host cells. Transcriptome analyses show, that 61% of the *in silico* predicted *P. amoebophila* genes are transcribed *in vivo* and that the majority of enzyme transcripts are predicted to be involved in metabolism, protein synthesis, molecule uptake and host-cell manipulation (Figures 5 and 8). Interestingly, more than half of *P. amoebophila*-specific genes, which are absent in the genomes of pathogenic chlamydiae, are expressed. This finding indicates that these genes, which lack a functional annotation in most cases, might be of importance for adaptation and survival within the amoebal host cell.

In detail, the expression pattern of *P. amoebophila* allows the conclusion, that the intracellular bacteria gain energy and NADPH by independent oxidation of metabolites during glycolysis, during the citrate cycle as well as during phosphate pentose pathway and oxidative phosphorylation indicating a partially autonomous life style within their host cells (Table S4). Almost all genes available for energy production are expressed when compared to the gene equipment for energy production in the genome (Figure 8).

However, the obligate intracellular lifestyle of *P. amoebophila* is also reflected in many reduced central metabolic and biosynthetic pathways (Horn *et al.*, 2004) and the bacteria acquire nutrients and metabolites via a number of transporters from their host cells. We found only enzymes expressed for the synthesis of three amino acids (serine, glycine and proline) which can easily be synthesized from intermediates of glycolysis (Table S5). According to the genome, three further amino acids can be synthesized; namely aspartate, glutamine and glutamate (Table 3). Despite of the key role of glutamate in the cellular metabolism, this amino acid is obviously not produced directly from 2-oxoglutarate but might be very effectively imported via general and specific amino acid transporters (Table S6). Furthermore, the expression of all required aminoacyl-tRNA synthetases for the production of the essential aminoacyl-tRNAs could be observed with the exception of cysteine which is marginally under the threshold.

To compensate for the inability to synthesize *de novo* essential compounds like DNA and RNA nucleotides and also the electron carrier NAD^+, *P. amoebophila* employs five highly specific nucleotide transport proteins (NTT1-NTT5) (Haferkamp *et al.*, 2004; Haferkamp *et al.*, 2006; Schmitz-Esser *et al.*, 2004), and consistent with previous reports (Schmitz-Esser *et al.*, 2004) expression of all five transporters could be shown during intracellular growth of *P. amoebophila* (Table S6)

Expression of all genes participating in the production of the TTSS suggested that this unique bacterial mechanism is used by the intracellular bacteria to translocate effector proteins into the eukaryotic host cells as described earlier (Hueck, 1998; Table S7). Two proteins which are homolog to type three secreted proteins of pathogenic chlamydiae (Subtil *et al.*, 2005) have previously been shown to be expressed in *P. amoebophila* by a specific reverse transcription PCR and furthermore they could be detected by immunofluorescence within the inclusion and in the amoeba nucleus, respectively (I. Kolarov, unpublished). However, in this study only one of the two TTSS substrates (pc0374) was shown to be expressed indicating a lower detection limit of the microarray analysis when directly compared to a specific reverse transcription PCR amplification method.

Translocation via the TTSS could also be observed for Inc proteins which are incorporated into the inclusion membrane and may act as porins or transporters for the uptake of nutrients in pathogenic chlamydiae (Hackstadt *et al.*, 1997; Rockey *et al.*, 2002). In a previous study, 24 genes encoding putative Inc proteins have been identified in the *P. amoebophila* genome and temporal expression analysis of four selected Inc candidates (pc0156, pc0399, pc0530, and pc1111) revealed expression during early and mid cycle (E. Heinz, unpublished). The microarray data showed the expression of most predicted *inc* genes (65%) including three of the four above described putative Incs. pc0156, however, marginally failed to achieve the given threshold of the microarray. As specific functions remained largely unknown so far, the involvement of these proteins in modifying the inclusion membrane represents an interesting topic for further analysis (Table S7).

In contrast to the conspicuous expression of transcripts involved in type three secretion, expression of the TFSS components may be not required during intracellular growth (Table S7). The TFSS may have played an important role in contribution of genes from an environmental chlamydia to *Plantae* (Brinkman *et al.*, 2002; Christie & Vogel, 2000; Huang & Gogarten, 2007; Moustafa *et al.*, 2008). This secretion system has been postulated to provide a mechanism by which environmental chlamydiae DNA could integrate into the host genome (Christie & Vogel, 2000), bacterial effector proteins could be secreted into the amoebal host cell (Horn *et al.*, 2004) and/or could play a role in conjugative DNA transfer (Greub *et al.*, 2004). However, activity of the TFSS might not be necessary under the investigated condition.

Although no specific functions could yet be assigned to the remarkably high number of plant and cyanobacterial homologues in *P. amoebophila* (Horn *et al.*, 2004), the microarray analysis revealed that the majority of these genes were shown to be expressed during

growth of intracellular bacteria indicating that they might have functions necessary for intracellular life (Table S8 and S9).

Evaluation of the *P. amoebophila* microarray – issues and troubleshooting

Unfortunately, co-hybridization experiments where genomic DNA and RNA samples compete to hybridize to the same oligonucleotide probe in order to compare relative gene expression levels could not yet be realized because of substantial technical issues associated with generating reproducibly sufficient signals from bacterial RNA. Despite huge efforts to optimize sample and hybridization protocols, measurement of gene expression was accompanied by main challenges including the following:

i) Sample preparation. The identification of gene expression profiles during host-microbe interaction is technically demanding, and the most important factor for a successful application of microarray technology is the extraction of adequate quantities of intact bacterial RNA (Mangan *et al.*, 2002). In this study, low abundance of bacteria during infection resulted in low bacterial RNA templates for microarray experiments. Improvement of infection to increase the number of bacteria is needed but difficult to accomplish because of labor-intensive extended volumes of cultures. Additionally, required synchronization of infection for exact measurements of gene expression is demanding and can not be assured under such conditions. The use of linear amplification techniques like GenomiPhi (Amersham) or MessageAmp (Ambion) might overcome limiting amounts of target RNA as described in several successful microarray studies including some sophisticated host-pathogen arrays (Francois *et al.*, 2007; Garzoni *et al.*, 2007; Renesto *et al.*, 2008) and application should be considered in future gene expression experiments.

ii) Appropriate labelling of bacterial RNA samples. One of the big challenges in prokaryotic expression analysis is the specific labelling of bacterial mRNA. Considering that only 3-5% of total RNA is mRNA, the rest being mainly rRNA and tRNA (Alberts, 1994; Ehrenreich, 2006; Talaat *et al.*, 2000), the already small fraction of bacterial mRNA decreases again substantially in the mixture of bacterial and eukaryotic total RNA and the amount of host RNA far exceeds that of bacterial RNA. Audia *et al*. recently demonstrated for *Rickettsia prowazekii* that in a total RNA extraction of rickettsia-infected host cells, the rickettsial RNA makes up less than 10% of the total RNA (Audia *et al.*, 2008). Bacterial RNA (in contrast to eukaryotic RNA) lacks polyadenylation for specific priming and therefore only total RNA (prokaryotic and eukaryotic total RNA) can be labelled by random priming. In this study, the large amount of non-target RNA most likely contributed to a high background and

low signals during hybridization and resulted in a low sensitivity and in turn in missing low abundant mRNA populations during gene expression profiling.

For the *P. amoebophila* microarray, the application of a commercially available two-step random labelling kit (CyScribe) was preferred to minimize variability during the labelling procedure and increase sensitivity (Mangan *et al.*, 2002; Schroeder *et al.*, 2002). This labelling kit performed well at first but stopped working suddenly without explainable reasons. Changing to another labelling method was time-consuming but finally resulted in reasonable performance. Unfortunately, the new labelling procedure caused a loss of signals because of higher unspecific binding compared to the CyScribe labelling method. Low specific hybridization signals of total RNA before purification is well-known and has previously been reported in several studies (Audia *et al.*, 2008; Garzoni *et al.*, 2007; Mäurer *et al.*, 2007; Nicholson *et al.*, 2003; Renesto *et al.*, 2008), therefore purification of bacterial RNA from the eukaryotic host RNA was carried out using capture oligonucleotides and magnetic beads (MICROB*Enrich*). Subsequently, enriched bacterial mRNA was selectively labelled. Although significant amounts of host RNA could be removed (Figure 4), the application of this method was unfortunately not successful as the number of genes which could be detected was not increased after hybridization (Table 2).

iii) High background intensities caused by non-specific attachment of nucleic acids to the microarray surface during hybridization. Several described and recommended methods to reduce background in microarray hybridizations were applied without mentionable success. For instance, prolonged incubation experiments were performed to enhance blocking during post array processing, during prehybridization as well as during the actual hybridization experiments. In the latter, also different concentrations of blocking reagent were applied. Additionally, several commercially available hybridization solutions [SlideHyb Glass Array Hybridization Buffer #1 (Ambion), PerfectHyb Plus (Sigma)] and various concentrations of labelled RNA samples were tested but failed to improve the hybridization.

In conclusion, the developed *P. amoebophila* gene expression microarray was suitable for first insights into the physiology of these obligate intracellular bacteria and how they might interact with their amoebal host cell. However, accurate interpretation of the microarray data is difficult in the absence of any normalization method particularly in terms of different transcript levels. Low target concentration and contaminating host cell material substantially complicated the experiments. Labelling optimization, mRNA enrichment and background blocking did not improve signal intensities so far, suggesting a cautious sample preparation

as well as the application of amplification techniques to increase target concentration in future gene expression experiments.

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Table S1. Oligonucleotide probes used for microarray hybridization

Pin	Plate	Position	ORF	Description	Gene name	ORF length	Oligo position	Oligo sequence 5´- 3´	Tm	Oligo length	Total score	Cross-hybr	Δ Tm	Folding	Oligo position	Low-complexity	Oligo search
1	1	A01	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
1	1	E01	**pc0001**	unknown protein	-	216	pc0001_25-69	CTTAAAACTTGCGCTGTCTCTTCATTAAGCTCATGGCTTTTGTTG	74	45	0,96	1	0,972	0,999	0,916	0,76	mid
1	1	I01	**pc0002**	unknown protein	-	285	pc0002_83-131	TGATGGGGTTGATTATTACAGAATGCCATGTAAAACCAGACGTTTTACT	74,2	49	0,973	1	0,999	0,967	0,939	0,836	mid
1	1	M01	**pc0003**	hypothetical protein	-	2970	pc0003_1558-1611	TTTAGAGAGTATTTCCAAGAAGTTTACGATGCAGATATGCAAGAAGTGTTGACA	74,2	54	0,973	1	0,995	1	0,928	0,821	mid
1	1	A05	**pc0004**	hypothetical protein	-	1413	pc0004_1133-1187	TAGGAAGTATCGGACGTGGAAATCTTGTTAATGACGATTTTGCAGATTATATAGA	74,2	55	0,984	1	0,999	1	0,999	0,824	random
1	1	E05	**pc0005**	conserved hypothetical protein	-	2397	pc0005_1139-1185	GACTTCCAGATTTCCGTTCTTACCAATTAGAAGTTGTCACTCCAGGA	74,2	47	0,979	1	0,998	1	0,94	0,857	mid
1	1	I05	**pc0006**	unknown protein	-	213	pc0006_51-96	TTTTTACTCACCTCCCATGGCTCAAAGCTACCAAAATGCATTTAAT	74,2	46	0,976	1	0,991	1	0,975	0,801	random
1	1	M05	**pc0007**	conserved hypothetical protein	-	1704	pc0007_896-946	TTGAGATTCCTCTCGACTCTTACATTCAAGTTGCTAGTCCTAAACAAATGC	74,1	51	0,976	1	0,989	1	0,957	0,83	mid
1	1	A09	**pc0008**	similar to exodeoxyribonuclease V gamma chain	**recC**	3588	pc0008_1808-1857	AATTAATGGAGAGGTGGATTCGATTGTTGCATTCTTTACGAGATGATTTA	74,2	50	0,979	1	0,998	1	0,987	0,79	mid
1	1	E09	**pc0009**	similar to exodeoxyribonuclease V beta chain	**recB**	3501	pc0009_1806-1852	AGCTGTTCTTCATCCGCAAAACATAGGGACTCTTAGGACACTGTTAG	74,2	47	0,98	1	0,998	1	0,946	0,862	mid
1	1	I09	**pc0010**	similar to exodeoxyribonuclease V alpha chain recD	**recD**	1869	pc0010_920-964	CAGCGGATTTGATTATTGTAGATGAAAGTTCGATGATCGATGTCA	74,3	45	0,972	1	0,994	1	0,984	0,732	mid
1	1	M09	**pc0011**	unknown protein	-	195	pc0011_34-88	ATGTATGTATATGGTTTTTCTTTGATGTTGTGGGCTATCTTTTTTGATAAACGCC	74,5	55	0,96	1	0,978	1	0,973	0,664	random
1	1	A13	**pc0012**	unknown protein	-	1983	pc0012_938-982	TTGGATTTTATAGGGTGGGAATCATGTCTGATATGCGAAATGGTT	74,3	45	0,974	1	0,989	1	0,945	0,822	mid
1	1	E13	**pc0013**	similar to substrate-binding protein of aliphatic sulfonate ABC transporter	**ssuA**	1095	pc0013_531-575	TAACTTATTTGGGGGACAGGTCACGGTTATTCCAATGGAAAATGT	74,7	45	0,969	1	0,954	1	0,982	0,818	mid
1	1	I13	**pc0014**	strongly similar to ATP-binding component of ABC transporters	**ssuB**	792	pc0014_385-429	TTGGTTGGCCTAGATAAGTTTGCTTACGCACACACACATGAATTA	74,2	45	0,984	1	0,999	1	0,988	0,848	mid
1	1	M13	**pc0015**	similar to integral membrane components of the ABC transporters	**ssuC**	777	pc0015_457-501	GCACGCACATTAGGATCTCAAGGCTTTCACACTTGGTTTAAAGTA	74,2	45	0,973	1	0,998	1	0,932	0,811	mid
1	1	A17	**pc0016**	similar to bifunctional protein UDP-N-acetylglucosamine pyrophosphorylases, Glucosamine-1-phosphate N-acetyltransferase	**glmU**	1332	pc0016_614-667	CGGGCTTATACGACGTATGGAAACAACGGGGTATTGAATACATTAATATTATCT	74,2	54	0,975	1	0,998	0,981	0,947	0,833	mid
1	1	E17	**pc0017**	similar to ADP-heptose--lipopolysaccharide heptosyltransferase II	**rfaF;waaF**	1050	pc0017_540-587	GATTTCTCATAGGGTTGAACCTCAAGATCTAATCATTGGCATCAATCC	74,5	48	0,974	1	0,975	0,984	0,986	0,833	mid
1	1	I17	**pc0018**	hypothetical protein	-	1623	pc0018_679-728	CAAATCCAAATTCCAGACTTGAATCAAAGTAAAAAAGAGCTTGAGGAGTG	74,2	50	0,952	1	0,994	1	0,866	0,677	mid
1	1	M17	**pc0019**	strongly similar to Holliday junction endodeoxyribonuclease	**ruvC**	507	pc0019_235-279	GTTCAAAGTGCTATGAAATTGGGAATGGCAAGAGGTGTTATCATG	74,3	45	0,976	1	0,991	1	0,98	0,795	mid
1	1	A21	**pc0020**	strongly similar to Holliday junction DNA helicase	**ruvA**	606	pc0020_224-278	TAATGAATGTTACAGGTATTGGTCCTAAGATGGCTTTAAGCTTAATCGGACATCT	74,2	55	0,974	1	0,998	1	0,92	0,834	mid
1	1	E21	**pc0021**	strongly similar to endonuclease III (UV endonuclease)	**nth**	642	pc0021_237-284	TATTATCCATTCATGTGGACTCGGATTTCGTAAAGCGACAAATATCTG	74,3	48	0,975	1	0,996	1	0,915	0,858	mid
1	1	I21	**pc0022**	strongly similar to GTP-binding protein in thiophene and furan oxidation	**thdF;trmE**	1377	pc0022_695-744	GATGCCCAAATGTAGGTAAGTCTTCTTTGATGAACGCTCTGCTAGATAAG	74,3	50	0,983	1	0,997	1	0,995	0,827	mid
1	1	M21	**pc0023**	similar to phosphatidylserine decarboxylase proenzyme	**psdD**	918	pc0023_458-503	TAGCTCAGAAATATCAGGGAGGAAGTATGGTGATTGTCCGACTTTG	74,3	46	0,987	1	0,997	1	0,998	0,865	mid
1	2	A01	**pc0024**	strongly similar to proteins related to alkyl hydroperoxide reductase (AhpC) and thiol specific antioxidant (TSA)	**ahpC**	558	pc0024_269-313	AAACCATTGCACATGATTATGATGTGTTAATTCCTCATGAAGGCA	74,3	45	0,979	1	0,995	1	0,989	0,801	mid
1	2	E01	**pc0025**	conserved hypothetical protein	-	633	pc0025_272-316	GTTCGGATGGTTTGCCTTGTTGGCTTACTATTCAACCTGTTAAAG	74	45	0,967	1	0,98	0,967	0,954	0,808	mid
1	2	I01	**pc0026**	conserved hypothetical protein	-	4536	pc0026_2237-2285	AAAGTGGTAAACTCGCAACAGTTATTAAACCTGATGGCAAACAAATTCA	74,3	49	0,975	1	0,996	1	0,968	0,784	mid
1	2	M01	**pc0027**	similar to ribosomal protein L11 methyltransferase	**prmA**	795	pc0027_388-434	CAAAGTGTCATCGATATTGGAAGTGGAAGTGGTGTTTTGACTTTAGC	74,3	47	0,982	1	0,997	1	0,989	0,821	mid
1	2	A05	**pc0028**	unknown protein	-	363	pc0028_168-216	TAATAACAATCAACGTTCCAATCAAAATAGCGTCAAAGGAATTTCGATG	74,3	49	0,971	1	0,997	1	0,994	0,696	random
1	2	E05	**pc0029**	conserved hypothetical protein	-	252	pc0029_4-50	CCCCATTACGATTATTGCTGTACAAGCTGTGGCTATCAAGAAGAAGT	74,3	47	0,971	1	0,997	1	0,998	0,695	random
1	2	I05	**pc0030**	strongly similar to 60 kDa chaperonin (GroEL)	**groEL, hsp60**	1674	pc0030_872-925	ATATTGCCATTTTGACAGGAGGAAAAGTCGTTTCAGAAGAAGTAGGTCTAAAAT	74,2	54	0,971	1	0,999	1	0,966	0,731	mid
1	2	M05	**pc0031**	strongly similar to chaperonin groES	**groES, cpn10**	348	pc0031_41-93	GGAGAATAGACATGACAACTAAGACTAAAATTAAACCTTTGGGAGATCGCGTT	74,1	53	0,977	1	0,987	1	0,998	0,785	random
1	2	A09	**pc0032**	conserved hypothetical protein	-	1236	pc0032_660-707	CATGAAAGGGTGGAAAAGAGAGATGACATTTAATGAGACAGGACTCAT	74,2	48	0,978	1	0,999	1	0,959	0,817	mid
1	2	E09	**pc0033**	similar to bifunctional protein (proline dehydrogenase and delta-1-pyrroline-5-carboxylate dehydrogenase)	**putA, poaA**	3648	pc0033_1854-1900	AACATTGATTGAAGCAGATATAGAAGTTTCCGAAGCGATCGATTTTG	74,2	47	0,972	1	0,992	1	0,971	0,761	mid
1	2	I09	**pc0034**	strongly similar to ATP-dependent DNA helicase	**mutD, uvrD, recL**	2286	pc0034_1185-1230	TGAAGACTACTTGCTTTATCGTGGAATACCCTATGTCATTGTGGGG	74,4	46	0,98	1	0,985	1	0,959	0,878	mid
1	2	M09	**pc0035**	conserved hypothetical protein	-	300	pc0035_32-84	AACAATTAATAGAACTAAGGTATCGCTTTCACCCTAATTATTGGGGCAGAGGA	74,2	53	0,967	1	0,999	1	0,881	0,815	mid
1	2	A13	**pc0036**	unknown protein	-	582	pc0036_322-366	GGTCTACGTGGAATAGGCTATGATGCGACTGATCGTTCAACATAT	74,3	45	0,986	1	0,998	1	0,97	0,898	mid
1	2	E13	**pc0037**	similar to metalloprotease	-	942	pc0037_34-83	TATTCTTCTAATCCACCACGACGACCTTATTCAAATCCTAATAGCATGGA	74,2	50	0,92	1	0,995	1	0,562	0,755	mid
1	2	I13	**pc0038**	conserved hypothetical protein	-	2862	pc0038_1412-1461	GGTCGCTTACAAATCTGGTCAATCTTCAAACGCTTGATTTGAATAATAAC	74,2	50	0,972	1	0,997	0,994	0,98	0,743	mid
1	2	M13	**pc0039**	unknown protein	-	348	pc0039_13-57	AATACGTCTATATTACACATTACCGTTCCTGCTTGGGCAGCTGCT	74,1	45	0,987	1	0,989	1	0,997	0,889	random
1	2	A17	**pc0040**	hypothetical protein	-	3423	pc0040_1693-	GGACATGCTTTTTTTTTCCTCGGTAGATTTCCTAAGGCACTTGAG	74,2	45	0,965	1	0,997	0,979	0,98	0,682	mid

						1737											
1	2	E17	**pc0041**	hypothetical protein	-	3432	pc0041_1766-1813	AAATAAGCGATAGTCTAACAGTAAAAGCAAGCCGCCTCAATGGCTTAG	74,2	48	0,979	1	0,997	1	0,951	0,852	mid
1	2	I17	**pc0042**	hypothetical protein	-	3438	pc0042_1695-1741	AAATGTAGCACGAGCTTTTTATTACTTCGGTGAATTCGATGAAGCAA	74,2	47	0,972	1	0,999	1	0,975	0,732	mid
1	2	M17	**pc0043**	unknown protein	-	1329	pc0043_997-1041	AGTTTAAGAGAGGTTCGAACGCATTCTATCCACGCCGAAGAAAAA	75,7	45	0,938	1	0,852	1	0,997	0,749	random
1	2	A21	**pc0044**	hypothetical protein	-	3429	pc0044_829-874	TCAATCATGAAAATTCATGAACAACTTTCAAGCTGGAATCGACTTC	74,3	46	0,856	1	0,993	0,974	0,114	0,739	mid
1	2	E21	**pc0045**	hypothetical protein	-	3462	pc0045_939-983	AAAAGCACTGCGAATAGTGAAAACATTAGGCACCCCCTATGAAAT	74,4	45	0,878	1	0,984	1	0,207	0,833	mid
1	2	I21	**pc0046**	hypothetical protein	-	3282	pc0046_1623-1669	TGGTTTAGTTGAAGCGTGTTTGGAGGCTAAAGAACATATTAAAGCGA	74,2	47	0,978	1	0,993	1	0,981	0,8	mid
1	2	M21	**pc0047**	unknown protein	-	306	pc0047_17-61	TTTTTTTAGCAAAGAATAAGCGACGCGATAAGAATGGCTTCTGTC	73,8	45	0,73	0,456	0,951	0,974	0,863	0,729	mid 2.Wahl
1	3	A01	**pc0048**	hypothetical protein	-	1596	pc0048_40-94	TTCTCCAATCCAGCTACCTACTACTATGAATCGAATAACTGTTTAAAGTTCTCTG	72	55	0,827	1	0,774	1	0,241	0,829	mid
1	3	E01	**pc0049**	unknown protein	-	858	pc0049_104-157	CTCTTACTTCCGAGAATAAAATTTCTGTCATAGCCAAGAATATGCTTCCTGTTG	74,3	54	0,927	1	0,996	1	0,674	0,675	mid
1	3	I01	**pc0050**	unknown protein	-	1053	pc0050_439-486	CCTGTGAGTGGACCTTATACTATGCGAGAAAATTTAGCCTCTCCTCAA	74,3	48	0,966	1	0,991	1	0,911	0,781	mid
1	3	M01	**pc0051**	hypothetical protein	-	3456	pc0051_1725-1771	TTTGGGAGAAATTTACTTCCTCGCTAGTATGTTTGATGAGGCACTTG	74,3	47	0,979	1	0,995	1	0,996	0,784	mid
1	3	A05	**pc0052**	hypothetical protein	-	1140	pc0052_573-617	TCTTTCGAAAATACAGATGACATTGCCACTTGGATTATTCCTTCTCA	74,4	45	0,622	0,08	0,987	1	0,998	0,822	mid
1	3	E05	**pc0053**	hypothetical protein	-	2127	pc0053_1085-1135	TTGGTGCCCTTGCAGAAGTTTATACTCACATAGGTAATAATGAAGAGGTGA	74,3	51	0,648	0,15	0,99	1	0,98	0,828	mid
1	3	I05	**pc0054**	hypothetical protein	-	2916	pc0054_1175-1224	TTTTAAATATGGCGAATGTTTGGGGTGAACTTGGTAAGTTTGATAAGACA	74,3	50	0,939	1	0,996	1	0,716	0,746	mid
1	3	M05	**pc0055**	unknown protein	-	510	pc0055_5-59	ATGTAAAGTCAATTGAATCTAGTACTTTTTTTCTACTACCCTCCTCCTTTTTCCCA	72,3	55	0,891	1	0,808	0,988	0,749	0,725	mid
1	3	A09	**pc0056**	unknown protein	-	1350	pc0056_950-1004	TGCAAAGCCTAGAGGAATTATCTAAAGACGATGCTCATAAGGATTATATTCAAGA	73,6	55	0,832	0,709	0,933	0,881	0,994	0,767	mid
1	3	E09	**pc0057**	hypothetical protein	-	3435	pc0057_1730-1779	TCGCTGAAGCGATTATATGTTATAAAAAAGCGAATAAGATTGATGACCCA	74,3	50	0,973	1	0,993	1	0,989	0,74	mid
1	3	I09	**pc0058**	hypothetical protein	-	3042	pc0058_841-885	GCCCAACAACATCAGCTAGCCGAAGAGGACTATAAAAAAGCTCTT	74,2	45	0,877	1	0,994	1	0,319	0,635	mid
1	3	M09	**pc0059**	hypothetical protein	-	3444	pc0059_1801-1855	AAAAACAGCCTCCTTGTCCTAGGTATATGTTATAGTTTTCTGGGAAACAAAGAGC	74,1	55	0,641	0,15	0,987	0,993	0,922	0,857	mid
1	3	A13	**pc0060**	similarity to extracellular metalloproteinase	-	855	pc0060_489-536	TGACCTAAGCACAGAACCTGAGCCATTTAAACCTGCAAGTACGTATAC	74,2	48	0,979	1	0,995	1	0,94	0,864	mid
1	3	E13	**pc0061**	hypothetical protein	-	663	pc0061_9-54	GCGTTTTACATTGACTGCAGAGGCTATTAATCTATCCGAGCGTTTT	74,2	46	0,98	1	0,992	1	0,996	0,805	5´preference
1	3	I13	**pc0062**	unknown protein	-	711	pc0062_341-392	TCAAAACGCAAAGCAATTTAAAACCAGCTACAATTGAGAGTATTGATCATTT	74,2	52	0,966	1	0,997	0,97	0,985	0,698	mid
1	3	M13	**pc0063**	hypothetical protein	-	888	pc0063_524-575	AATATCGTGAAGGAAAAGCAGATGATTTAGCGATAACTGAAAGTTCTGTTGA	74,3	52	0,967	1	0,996	1	0,921	0,766	mid
1	3	A17	**pc0064**	unknown protein	-	1584	pc0064_995-1047	TCTCAGTGTTCGCAAAAACATGTTGGGTAGATTATTTACTTCATGAGGTAAAA	74,3	53	0,942	1	0,993	0,994	0,798	0,677	mid
1	3	E17	**pc0065**	hypothetical protein	-	549	pc0065_133-179	ATGGAAAGCGCTATTTTTCCTTGTGTAAAACGCTATTTTCACGAAAA	74,2	47	0,962	1	0,997	0,916	0,993	0,722	random
1	3	I17	**pc0066**	conserved hypothetical protein	-	909	pc0066_378-422	CAGCTTTCCACGTCAATTCAATTACCCTTCAGAAGGTCATATCAG	74,1	45	0,969	1	0,984	1	0,922	0,813	mid
1	3	M17	**pc0067**	hypothetical protein	-	1173	pc0067_578-622	AATCTCGCGTTCGATTAATTACAGACACAGGTCTAACCCCTTCTG	74,2	45	0,986	1	0,999	1	0,99	0,866	mid
1	3	A21	**pc0068**	hypothetical protein	-	183	pc0068_46-98	CTCATGCTTGTGCATTTAGTCTTTTTAAACGGAGTAAAAGAAAACCTGCGTAT	74,7	53	0,954	1	0,951	1	0,953	0,699	mid
1	3	E21	**pc0069**	strongly similar to aspartate transaminase	**aspC**	1221	pc0069_687-732	TTTAGAACTCGATGCACAACCTATTCGGTACTTTGCTAGTGAAGGC	74	46	0,976	1	0,98	1	0,925	0,895	mid
1	3	I21	**pc0070**	unknown protein	-	240	pc0070_54-107	GAAATTGGAAAGTCATACATGGGGAAAAATAACTTTCGCTTATGATTTTTATGG	74,2	54	0,967	1	0,996	0,975	0,989	0,697	random
1	3	M21	**pc0071**	similar to DNA topoisomerase I	**topA, top1**	2604	pc0071_1213-1264	GATACTGTTTCAGCTGATATTTTAGCTGGTGAAGGAATTTTACTCAGAGCGA	74,2	52	0,965	1	0,995	1	0,91	0,756	mid
1	4	A01	**pc0072**	similar to protein required for chromosomal DNA transformation	**dprA**	1092	pc0072_642-691	ACGAAATCGTTTAGTGAGTGGAATGAGTTTAGGCACACTGTTGATAGAAG	74,2	50	0,971	1	0,994	1	0,905	0,838	mid
1	4	E01	**pc0073**	similar to 3-dehydroquinate synthase	**aroB**	1059	pc0073_585-639	TTGGTCCCTTATAGAACAAAGAGATGAAGGATTACTCGAGATTATCATTCAACAA	74,2	55	0,963	1	0,999	0,909	0,946	0,799	mid
1	4	I01	**pc0074**	unknown protein	-	246	pc0074_60-109	AGCCAGAACAAAGAGAGCTATAGCTGATATCACCAAAGCTAACTCATCGT	74,1	50	0,981	1	0,985	0,998	0,989	0,853	random
1	4	M01	**pc0075**	unknown protein	-	246	pc0075_74-118	GCAATTATAACAGCTCGCTCGCGTTAGAAGATGTTCACGAATATG	74,3	45	0,983	1	0,997	1	0,983	0,844	random
1	4	A05	**pc0076**	unknown protein	-	753	pc0076_279-326	GCTATTAGCTATTATGGCTCGCCATCCTGAACTCCATGCTAAATATGA	74,3	48	0,973	1	0,998	1	0,901	0,845	mid
1	4	E05	**pc0077**	similarity to chromosome partitioning protein	**parB**	783	pc0077_388-441	TCAACAGTGGCTAATTATCTTCGTTTATTGACTTTGCCTATGACAATTCAAACT	74,2	54	0,977	1	0,992	0,99	0,995	0,789	mid
1	4	I05	**pc0078**	similar to copper-transporting ATPase	**copA, zntA**	2190	pc0078_1095-1139	CTCTGTTCTAGTGATTGCATGCCCTTGTGTTTTAGGATTAGCCAC	74,1	45	0,981	1	0,986	1	0,999	0,832	mid
1	4	M05	**pc0079**	strongly similar to UDP-glucuronat epimerase	-	984	pc0079_446-493	TCTCTTTAGAAGATCGTACCGATCAACAAGCAAGCTTATACGGAGTGA	74,2	48	0,976	1	0,999	1	0,953	0,809	mid
1	4	A09	**pc0080**	unknown protein	-	225	pc0080_45-93	TCGATTCGATATATGTCAATACGGAAATTCACCAAGAGGAAAAGTCTTG	74,3	49	0,981	1	0,995	1	0,986	0,821	random
1	4	E09	**pc0081**	unknown protein	-	651	pc0081_388-433	TTTTACGGTCGTTTTGCTGACGAACAATATGTAGGTTTGATTTCGT	74,3	46	0,976	1	0,997	1	0,939	0,831	mid
1	4	I09	**pc0082**	conserved hypothetical protein	-	1500	pc0082_794-842	TAAGAGCTGGAAGTGGTATGGTACATCTGTTATATCCTGAAGACATGCG	74,2	49	0,983	1	0,997	1	0,957	0,884	mid
1	4	M09	**pc0083**	stongly similar to NAD(P)H-dependent glycerol-3-phosphate	**gpsA**	1002	pc0083_483-	CCAAGAGATTTGTGAAACATTTATGACCCCTACTTTTCGAGTCTATCCTAACA	74,2	53	0,981	1	0,999	1	0,981	0,825	mid

				dehydrogenase			535										
1	4	A13	**pc0084**	unknown protein	-	669	pc0084_220-271	ATCATTACTTCAGATAAAAAACTGGCAAAGTTAGCCCGAAATAAACAGGCTC	74,4	52	0,957	1	0,986	1	0,884	0,728	mid
1	4	E13	**pc0085**	conserved hypothetical protein	-	600	pc0085_153-200	TATTTCTAAAGCGGAACATGCAGCTAAACACCTCAATAGATGGGTTCT	74,2	48	0,98	1	0,997	1	0,992	0,805	random
1	4	I13	**pc0086**	conserved hypothetical protein	-	2172	pc0086_1150-1197	AAAAAACGTGCATTAGTTTATGTTAAAGAACAAAGATCGGATTGGCCC	74,3	48	0,972	1	0,997	1	0,937	0,795	mid
1	4	M13	**pc0087**	unknown protein	-	441	pc0087_70-115	AAATCTAGTCCTTTAACCGAGTTGGATCAATTCGACCCCGATAAAA	74,2	46	0,962	1	0,992	1	0,849	0,818	mid
1	4	A17	**pc0088**	hypothetical protein	-	1194	pc0088_533-578	AAGAGGCGGCGGAGTTAACACTCAATGAGCAACAGATATCCTATAT	74,2	46	0,981	1	0,999	1	0,935	0,887	mid
1	4	E17	**pc0089**	similar to A/G-specific adenine glycosylase, mutY	**mutY**	1060	pc0089_528-574	TTGGATATCTTCTGAGGCTTTAATTGAATTGGGAGCGACAATTTGTA	74,2	47	0,976	1	0,998	1	0,997	0,747	mid
1	4	I17	**pc0090**	unknown protein	-	198	pc0090_31-76	AGTCAGCTCTGTTGCGATAATGGCTTCATGGACTTGAACATTAGTA	74,2	46	0,98	1	0,991	1	0,985	0,823	5´preference
1	4	M17	**pc0091**	similar to bacterioferritin comigratory protein (BCP)	**bcp**	489	pc0091_107-152	TATATTTTTATCCCAAAGATGATACCCCTGGCTGTACGTTGCAAGC	74,3	46	0,97	1	0,996	1	0,947	0,755	5´preference
1	4	A21	**pc0092**	strongly similar to porphobilinogen synthase (delta-aminolevulinic acid dehydratase, (ALAD)), hemB	**hemB**	1035	pc0092_567-612	AATTGGCTATATTCGACACGCTCTTGATCAAGAAGGTTATCAGCAA	74,3	46	0,976	1	0,998	1	0,951	0,817	mid
1	4	E21	**pc0093**	hypothetical protein	-	2163	pc0093_1141-1195	GATGCAGTCCCAGCACTTATTCAAGAATATCACTTTAACATGGAGTATATCAGAC	74	55	0,969	1	0,974	1	0,942	0,814	mid
1	4	I21	**pc0094**	similar to Na(+)/H(+) antiporter	**napA**	1233	pc0094_592-646	ATTGCTGCTAAGTTGATATCGCAAATCGTTAAATATTATGACGTTAAAAGTGCAA	74,3	55	0,976	1	0,998	1	0,974	0,784	mid
1	4	M21	**pc0095**	similar to component of alpha subunit of Na+-translocating NADH-quinone reductase (NQR)	**nqrA, nqr1**	1401	pc0095_737-788	CTCCTCAAGATGTTATTTGGACCTTAGATGTACATACTGTTGTTGCAATTGG	74,2	52	0,975	1	0,999	1	0,965	0,779	mid
1	5	A01	**pc0096**	strongly similar to ATP binding protein, component of oligopeptide permease, oppF	**oppF**	825	pc0096_450-494	GAATAGGTACCCTCACGAATTTTCAGGAGGTCAGCAACAACGTAT	74,2	45	0,979	1	0,994	1	0,963	0,834	mid
1	5	E01	**pc0097**	strongly similar to ATP binding protein, component of oligopeptide permease, oppD	**oppD**	1026	pc0097_545-592	CAGATGAGCCAACGACAGCTTTAGATGTCACTATTCAAGCACAAGTAT	74,3	48	0,979	1	0,998	1	0,969	0,823	mid
1	5	I01	**pc0098**	conserved hypothetical protein	-	732	pc0098_324-372	CCAAGATAGTATCGCGGATACTGTTGAAGATATCGCAGTAGTCGCTACT	74,1	49	0,967	1	0,988	0,937	0,957	0,822	mid
1	5	M01	**pc0099**	conserved hypothetical protein	-	1416	pc0099_653-706	TTGGCTTGATGGGTTCTTTCGTTAGTTATTTATTAGTACGCCGAATTCCTATTA	74,2	54	0,974	1	0,999	1	0,944	0,795	mid
1	5	A05	**pc0100**	unknown protein	-	579	pc0100_236-285	ATAAGGGATCTCAAGCAAGCCCTAAAGGTGATATCTATTTGTGCTATGGA	74,3	50	0,974	1	0,995	1	0,945	0,811	mid
1	5	E05	**pc0101**	similar to oligopeptide transport system permease protein, oppC	**oppC**	1764	pc0101_815-861	GTCAAACAAGCTCTCTCGATCACTTACCTTCTTGGCAAACATGTAAA	74,3	47	0,974	1	0,998	1	0,932	0,814	mid
1	5	I05	**pc0102**	similar to dipeptide transport system permease protein, dppB	**dppB**	1497	pc0102_739-783	ACATTGCGTAATGATTCAAGTAAGCCTGTTCTTACCGAAGTCACG	74,2	45	0,981	1	0,994	0,975	0,989	0,862	mid
1	5	M05	**pc0103**	similar to substrate binding proteins, component of oligopeptide permease, oppA	**oppA**	2148	pc0103_1087-1132	CCTGATTATTTTAATGCTTATGCTGCCCTAACCGAAGCGCTAGAAT	74,2	46	0,967	1	0,998	0,974	0,988	0,696	mid
1	5	A09	**pc0104**	hypothetical protein	-	693	pc0104_383-427	TTTTTACAGTGATGTTACCTTGCGGTCAAACCCTCGTTGTTTTTT	74,4	45	0,967	1	0,979	0,982	0,965	0,772	mid
1	5	E09	**pc0105**	unknown protein	-	210	pc0105_66-111	GATTTATGTCACCTATGTAGCTTTTACACGCCTTTCAGGTTCAGCG	74,1	46	0,972	1	0,988	0,94	0,96	0,873	mid
1	5	I09	**pc0106**	strongly similar to glycogen phosphorylase	**glgP**	2604	pc0106_1318-1363	GCCATTGTAGGCTCGCATAAAGTCAATGGAGTAGCAAAACTTCATA	74,3	46	0,982	1	0,991	1	0,985	0,844	mid
1	5	M09	**pc0107**	unknown protein	-	2052	pc0107_882-935	ATGCCCCACAATTACTCTATTTACCTACATGCAGCATTTACAACTAGTAGCTCA	74,1	54	0,963	1	0,991	1	0,855	0,83	mid
1	5	A13	**pc0108**	similar to amino acid ABC transporter, periplasmic amino acid-binding protein	**fliY**	837	pc0108_438-482	GAAAGGTTGGAATGAAAAAGCGATCAAGCTCATCGGTATACAATC	74,2	45	0,979	1	0,999	1	0,981	0,803	mid
1	5	E13	**pc0109**	strongly similar to glucose-1-phosphate adenylyltransferase	**glgC**	1419	pc0109_674-719	AAAAGCCGCAAGATAACGATTTATTACAACAATTGCGAAGTCCATC	74,3	46	0,975	1	0,99	1	0,964	0,806	mid
1	5	I13	**pc0110**	conserved hypothetical protein	-	768	pc0110_379-426	CCAGGAATCAGTTTTAATGAGTGGATTGATTTTAAGGATTTTGCGTGT	74,2	48	0,969	1	0,998	1	0,994	0,678	mid
1	5	M13	**pc0111**	similar to ribonucleoside triphosphate reductase	**nrdD**	2013	pc0111_971-1015	GATCTGAACCTGGTATTATTAACGCCGCAGAAGCTGAAAGAAGAG	74	45	0,973	1	0,979	1	0,964	0,81	mid
1	5	A17	**pc0112**	unknown protein	-	213	pc0112_116-168	AAATCCCTCAAAAGTTGCTAATTACTTCGCTATCAAGACTTTCAAATCATCTT	73	53	0,943	1	0,879	1	0,992	0,734	mid
1	5	E17	**pc0113**	hypothetical protein	-	984	pc0113_587-635	CCTATTTAGGAACCAATAAGTGGTTTGATTTATTGCGGGCAAGACTTTC	74,4	49	0,966	1	0,984	1	0,906	0,801	mid
1	5	I17	**pc0114**	similar to batE protein	**batE**	756	pc0114_202-255	GCGATTGCTGATACTTACTTCCAACTCGAAGAATATCCTTGGTCTATTTTGTAC	74,3	54	0,961	1	0,998	1	0,823	0,834	mid
1	5	M17	**pc0115**	hypothetical protein	-	378	pc0115_1-45	ATGACAGATCCTCAACCTTCTGTAGATGAACGAATCCTTCTCGCT	74,7	45	0,972	1	0,948	0,997	0,995	0,856	random
1	5	A21	**pc0116**	unknown protein	-	1773	pc0116_896-943	CTTTTAATGGAGCATTGGGTGTCGTTGATGTTAAAATCAAAATGAGAA	74,2	48	0,97	1	0,996	1	0,992	0,69	mid
1	5	E21	**pc0117**	unknown protein	-	1677	pc0117_802-848	AATTGGGAAAATGTTCAGAATCACCTCCAATTTTCAGAGGATTCTCT	74,2	47	0,967	1	0,996	0,996	0,962	0,704	mid
1	5	I21	**pc0118**	unknown protein	-	1071	pc0118_405-457	ATCCCTTTATGCTTTTACCTCTACTTTAACTCCTATGGTCCCTTCAACAAACG	74,3	53	0,961	1	0,997	1	0,869	0,766	mid
1	5	M21	**pc0119**	similar to batA protein	**batA**	1089	pc0119_677-725	TTTTAACTGATGGGTTCCAAGATCCTAATCGATTGGATTATGGTAATCG	74,3	49	0,965	1	0,997	1	0,869	0,812	mid
1	6	A01	**pc0120**	similar to protein involved in cell wall biosynthesis, morphogenesis and cell division	**cicA**	618	pc0120_340-385	AGCGCATCTATTGACCTTTATTTACGTCCTTGGGCAGAAAGATATG	74,1	46	0,975	1	0,986	1	0,97	0,803	mid
1	6	E01	**pc0121**	conserved hypothetical protein	-	2658	pc0121_1353-1404	AGACTTTGCCAAACGTCAGCTTATTCTTATGACAAGAGAATGGTATATGCAT	74,2	52	0,982	1	0,998	1	0,977	0,846	mid
1	6	I01	**pc0122**	unknown protein	-	201	pc0122_55-99	GCGGGAGGCTCTGCTTGCTATATTTGTGGGGTTTCTTATTTTATC	74,8	45	0,953	1	0,946	1	0,953	0,704	mid
1	6	M01	**pc0123**	strongly similar to glucose-1-phosphate thymidylyltransferase (dTDP-glucose synthase), rfbA	**rfbA, rmlA**	888	pc0123_531-575	TAATCAAGTCGTAGACATAGCTCATGGCTTAAAACCCTCTGCACG	74,3	45	0,976	1	0,996	1	0,914	0,874	mid
1	6	A05	**pc0124**	strongly similar to dTDP-4-dehydrorhamnose 3,5-epimerase,	**rfbC, rmlC**	555	pc0124_238-	TATGATGTGGCTGTTGATATTCGTCCTGAATCTCCTACATTTGGAC	74,2	46	0,981	1	0,997	1	0,959	0,853	mid

				rfbC			283										
1	6	E05	**pc0125**	similar to dTDP-4-keto-L-rhamnose reductase, (TDP-rhamnose synthetase), rfbD	**rfbD, rmlD**	885	pc0125_408-452	ACTCTTAGATGAATTTGATCGCTCTTGTGTCATTCGCACATCTTG	74,3	45	0,974	1	0,993	1	0,964	0,78	mid
1	6	I05	**pc0126**	strongly similar to dTDP-glucose 4,6-dehydratase, rfbB	**rfbB, rmlB**	1059	pc0126_492-540	ATCTGACCATCTTGTTCGCGCTTATCATCATACCTATCATTTATCCACT	74,2	49	0,978	1	0,997	1	0,961	0,824	mid
1	6	M05	**pc0127**	similar to multidrug resistance membrane translocase protein, emrB	**emrB**	1542	pc0127_687-733	AAACTCTTTGACTATTCGTGTCCTTATCGTGACTTGCGTAATCGCTT	74,2	47	0,971	1	0,993	1	0,915	0,826	mid
1	6	A09	**pc0128**	strongly similar to multidrug resistance protein, emrA	**emrA**	1200	pc0128_570-615	CATTGCTGCTATAGGCTCAACATCATTGGAGAATCATCCCAATATT	74,3	46	0,977	1	0,989	1	0,969	0,825	mid
1	6	E09	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
2	1	B01	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
2	1	F01	**pc0129**	unknown protein	**-**	882	pc0129_356-401	GAAAAGATCTCTGGAATGGGGTTCTTCTTTCCACATTAGAAGGACA	74,3	46	0,964	1	0,993	0,987	0,914	0,762	mid
2	1	J01	**pc0130**	unknown protein	**-**	450	pc0130_84-128	TTTAGATTTCTATCATTATCAGCGCTTGAACTGCTCCCTTCCAGC	74,2	45	0,983	1	0,999	1	0,996	0,825	random
2	1	N01	**pc0131**	similar to ribosomal large subunit pseudouridine synthase (pseudouridylate synthase), rluA	**rluA**	732	pc0131_417-462	ATATTTCGTTCATGAAACCGAAGATGAAACCTATGGTCGTCTAGCC	74,3	46	0,979	1	0,994	0,998	0,95	0,864	mid
2	1	B05	**pc0132**	similar to 30S ribosomal protein S20	**rpsT**	291	pc0132_97-151	TACAAATCACGTGTTCGAACAGCTGTACGTTCTTTTCAAGAGTCTTTAGTAAAAG	74,2	55	0,975	1	0,996	1	0,951	0,806	mid
2	1	F05	**pc0133**	similar to acylase and diesterase	**-**	1686	pc0133_887-938	TAAAGGGAGAAGTAAATGAAGTTGAATCTCTACCGCCCGTCCTTTATTATGT	74,2	52	0,975	1	0,997	1	0,957	0,795	mid
2	1	J05	**pc0134**	conserved hypothetical protein	**-**	744	pc0134_408-456	AGCCATGATTGTGAATCGTACGAAAGTAGCGGAGGAAGAAGTTAAGTAT	74,2	49	0,983	1	0,996	1	0,965	0,869	mid
2	1	N05	**pc0135**	conserved hypothetical protein	**-**	3465	pc0135_1740-1784	GACGGGAAGCTTTGTCAAAATTCAGTCAGTTGTCAAAGAAATGAC	74,3	45	0,967	1	0,989	1	0,994	0,672	mid
2	1	B09	**pc0136**	strongly similar to 30S ribosomal protein S2	**rpsB**	819	pc0136_471-515	ACGATCTATGCGTAAACCACCTGGATTAGTCATTGTTGTTGATCC	74,1	45	0,972	1	0,99	1	0,94	0,808	mid
2	1	F09	**pc0137**	similar to elongation factor Ts (EF-Ts)	**tsf**	975	pc0137_562-608	ACTCTACAGAAAAGCCCAGAGCGTTCATTTGGTATTTATTCGCATTT	74,2	47	0,972	1	0,998	0,988	0,927	0,814	mid
2	1	J09	**pc0138**	conserved hypothetical protein	**-**	1077	pc0138_616-662	TTAACTGGTGCTAGTGGACCAGCTTTTGGCAATAATTATGTTTTTGC	74,2	47	0,97	1	0,999	1	0,924	0,779	mid
2	1	N09	**pc0139**	similar to methyl-directed mismatch repair (MMR) protein, mutL	**mutL**	1959	pc0139_903-947	TATTTTACATCTCCGCCTTCCAGGCTCACTTTTTGACGTTAATGT	74,1	45	0,973	1	0,988	1	0,922	0,853	mid
2	1	B13	**pc0140**	similar to poly A polymerase	**pcnB**	1239	pc0140_603-654	GATGGCTATGTATCCATGTTTTGATCAGGCTATTGTAGAGATGCATAGATTG	74,2	52	0,98	1	0,999	0,99	0,982	0,828	mid
2	1	F13	**pc0141**	conserved hypothetical protein	**-**	750	pc0141_391-445	AACGGAATTTATTTACTCCCTACCAGTTGCGATCCTTACAATGAAAAAGTTTTAA	74,2	55	0,967	1	0,993	1	0,985	0,681	mid
2	1	J13	**pc0142**	hypothetical protein	**-**	1065	pc0142_572-619	AAGCTTATGCGGTAGCTAAAGTACCTGTCATTTCAGTTAGTGCCGCTA	74,2	48	0,976	1	0,998	1	0,962	0,792	mid
2	1	N13	**pc0143**	strongly similar to phosphopyruvate hydratase (enolase)	**eno**	1305	pc0143_679-727	GAAAAAGCTGGTTATCAACCTGGTAAACAAGTGGTTCTAGCAATGGATT	74,2	49	0,978	1	0,998	0,982	0,975	0,821	mid
2	1	B17	**pc0144**	conserved hypothetical protein	**-**	396	pc0144_9-57	TACAATTTATACAATCGTTTTATTTGGAGAGGCTGAACGCGGAGAGTTT	74,2	49	0,979	1	0,996	1	0,996	0,783	5´preference
2	1	F17	**pc0145**	conserved hypothetical protein	**-**	747	pc0145_265-318	TTATCAGCGCCCTTATATGCTATTATGGAAGGTCTATTCTTAGGAGGAATTTCA	74,2	54	0,98	1	0,992	1	0,99	0,812	random
2	1	J17	**pc0146**	similar to preprotein translocase SecA	**secA**	3063	pc0146_1584-1629	CGATGTTTTAGAAATACCTACGCATCGAGCTAATCGACGTGTTGAT	74,3	46	0,969	1	0,995	0,988	0,949	0,762	mid
2	1	N17	**pc0147**	unknown protein	**-**	225	pc0147_62-116	CTTTTGAAAAAAACATTCTCAATGACATTCCTATTGAGGATATAGATTCCATTGA	73,3	55	0,794	0,691	0,903	0,877	0,948	0,585	mid
2	1	B21	**pc0148**	similar to aspartyl/asparaginyl beta-hydroxylase (= peptide-aspartate beta-dioxygenase)	**aspH**	612	pc0148_318-363	AAAACATTTCCCTAGCATTAATTTCGTCGCTCTTTCAAGGCTTCAT	74,3	46	0,976	1	0,994	1	0,989	0,773	mid
2	1	F21	**pc0149**	similar to arsenical pump membrane protein	**arsAB**	1260	pc0149_618-668	CGAAAAGGTGAAATCTTGGATTCCTTCGTTATTGTTAGTGATTTTGATTGT	74,2	51	0,976	1	0,999	0,994	0,987	0,762	mid
2	1	J21	**pc0150**	hypothetical protein	**-**	474	pc0150_222-268	GACCGAATTAGCTGAAGGATCGTTTGTTACGATAGAAATGTCTTGGA	74,3	47	0,981	1	0,992	1	0,984	0,838	mid
2	1	N21	**pc0151**	strongly similar to dihydrolipoamide dehydrogenase	**lpdA**	1410	pc0151_767-812	ATTACGTTGCTGACTGTTGTTTAGTCGCAGTAGGTCGTTCTCTCAA	74,3	46	0,979	1	0,993	1	0,939	0,872	mid
2	2	B01	**pc0152**	strongly similar to lipoate synthetase	**lipA**	972	pc0152_434-487	AGGTCATTGAGGCGATTAGGCAAACTAATGAAGATGTAACTATTGAGGTCTTAA	74,2	54	0,98	1	0,999	1	0,947	0,856	mid
2	2	F01	**pc0153**	unknown protein	**-**	921	pc0153_459-512	TCCTGGCTATGGATTGCTACCCTCTTTGATAGTTAAATGTTTAGGTAAAATTGG	74,3	54	0,976	1	0,994	1	0,997	0,757	mid
2	2	J01	**pc0154**	conserved hypothetical protein	**-**	900	pc0154_444-495	TCAATATAACCTTGGAGTCATATATGACAATGGGCAGGGTATTACACAATCA	74,3	52	0,635	0,101	0,998	0,984	0,993	0,875	mid
2	2	N01	**pc0155**	conserved hypothetical protein	**-**	1647	pc0155_860-904	ATCGTACGCATCAAAGTTACGCCCAGTTTTTAGAAACAATGCAAT	74,3	45	0,972	1	0,989	1	0,965	0,776	mid
2	2	B05	**pc0156**	hypothetical protein	**-**	903	pc0156_464-514	AAATATTAGCCTATCAATCTTCTCCCTCTCGCCTACGTCGTTTTTTAGGAC	74,2	51	0,981	1	0,998	1	0,989	0,809	mid
2	2	F05	**pc0157**	unknown protein	**-**	204	pc0157_100-154	TTTGGCAATTCTTCTTCACATTTTTCAGTTGTGGTTTCTTCCAATATAGATAAAA	74,2	55	0,953	1	0,994	0,968	0,997	0,553	mid
2	2	J05	**pc0158**	unknown protein	**-**	1791	pc0158_932-979	AACACTGTGGATGGGCGTTAATAGATGAGTTAGTGCATGCCTATACTC	74,2	48	0,985	1	0,998	1	0,965	0,895	mid
2	2	N05	**pc0159**	hypothetical protein	**-**	1179	pc0159_586-632	CTTTTAGAACGTTTGACCCCACAAGGACATTTATTGCTTGTTGAAAG	74,2	47	0,977	1	0,998	1	0,995	0,756	mid
2	2	B09	**pc0160**	similar to ribosomal large chain pseudouridine synthase B	**yjbC**	705	pc0160_436-482	CATGAACATCTGATTGCTATTGCCAATGGAACTCTTGTAGAAGGAGT	74,3	47	0,971	1	0,998	1	0,918	0,809	mid
2	2	F09	**pc0161**	similar to phosphoglycerate mutase	**pgmA**	681	pc0161_264-316	ATGGGCAAGTATTTATAGTTCCGAATCTCAATCTCAGACAATACCTGTCATTC	74,3	53	0,974	1	0,992	1	0,922	0,846	mid
2	2	J09	**pc0162**	similar to iron-sulfur cofactor synthesis protein/cysteine desulfurase nifS	**nifS**	1182	pc0162_596-640	ATTTTATGACGTTTAATGGAGATCAGCTTCATGCTCCCAAAGGAA	74,2	45	0,983	1	0,997	1	0,996	0,826	mid
2	2	N09	**pc0163**	similar to iron-sulfur cluster assembly protein nifU	**-**	792	pc0163_449-493	CTCTTGCTTCTAGCTATGTGGCTTCTCCGACTCCTTTGGATATTG	74,3	45	0,977	1	0,996	1	0,948	0,832	mid
2	2	B13	**pc0164**	unknown protein	**-**	465	pc0164_292-	TTTACAAATACCCTTATGAGTTCATTGAGAGATCTCGGCCATGCAT	74,2	46	0,974	1	0,994	1	0,942	0,817	mid

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2	2	F13	**pc0165**	similar to biotin-[acetyl-CoA-carboxylase] ligase/biotin repressor (bifunctional)	**birA**	681	pc0165_290-344	TGTTAGAGCAAAAACGGTATATGATTAACGGCATAGGACTAAACGTTAATATGCC	74,3	55	0,979	1	0,994	1	0,948	0,858	mid
2	2	J13	**pc0166**	strongly similar to cell shape (rod)-determining protein	**rodA**	1137	pc0166_568-612	ATTAAAGCAATGACAATTTGCGGAGGACTGGGATTATGTCTTGTT	74,1	45	0,978	1	0,987	1	0,998	0,793	mid
2	2	N13	**pc0167**	unknown protein	**-**	486	pc0167_132-185	ACGATGGCATATTATTCAAGAGTCAATAGATTTCATTCGAGCTGTACAAATTGT	74,2	54	0,968	1	0,998	1	0,935	0,746	5´preference
2	2	B17	**pc0168**	similar to tyrosine/tryptophan transport protein	**tyrP_1**	1191	pc0168_668-712	TGATTGGAAGCGCCATTCCTTTAGTGATTTATTTAGCTTGGGAAT	74,3	45	0,963	1	0,997	1	0,929	0,705	mid
2	2	F17	**pc0169**	similar to tyrosine/tryptophan transport protein	**tyrP_1**	1200	pc0169_603-653	TCCTACCCTGACTGACTATTTGAAACGAGATGTCAAGCAAATTAGAAATGT	74,1	51	0,974	1	0,99	0,998	0,998	0,747	mid
2	2	J17	**pc0170**	similar to tryptophanyl-tRNA synthetase (=tryptophan-tRNA ligase)	**trpS**	1062	pc0170_544-596	CCTGAAGTGTTATTAAGTCAAACTCCTACTCTTGTGGGAACAGATGGTAAAGG	74,2	53	0,982	1	0,998	1	0,988	0,822	mid
2	2	N17	**pc0171**	similar to O-linked N-acetylglucosamine transferase	**-**	2481	pc0171_1350-1395	GGCTGTTGAAAGATTTCAAAGAGCGCTAGAAGTCGATCCAGATAAT	74,2	46	0,962	1	0,999	1	0,892	0,739	mid
2	2	B21	**pc0172**	similar to O-linked N-acetylglucosamine transferase	**-**	3414	pc0172_1571-1624	CGTCGACAAACCTAGATGTGGTATTGTTTTATGCGGAAATATTACAACAGATAG	74,3	54	0,963	1	0,996	1	0,863	0,802	mid
2	2	F21	**pc0173**	similar to O-linked N-acetylglucosamine transferase	**-**	3591	pc0173_1820-1874	AATATAAAAGGATGATCAATTTAGGCATACCTCTTTCTAGAGAAAGCCGAGCAAA	74,2	55	0,973	1	0,995	1	0,977	0,754	mid
2	2	J21	**pc0174**	strongly similar to Helicase subunit B of the DNA excision repair complex (excinuclease ABC)	**uvrB**	2022	pc0174_1007-1052	TACTTGTTATTGATGAATCTCACCAAACACTTCCTCAGGTCCATGC	74,4	46	0,972	1	0,982	0,958	0,995	0,812	mid
2	2	N21	**pc0175**	hyopthetical protein	**-**	1074	pc0175_623-667	AAATTATTGGATATGGACATTCCATTGGAGCAGGAGTTCAAGCAG	74,5	45	0,964	1	0,97	1	0,915	0,807	mid
2	3	B01	**pc0176**	similar to ATP-dependent DNA helicase dinG	**dinG, yoaA**	2262	pc0176_1079-1124	AGAAACTACGCATTTTGAACGAACATATGAACCACACAAAGTGGAA	74,2	46	0,976	1	0,997	1	0,947	0,819	mid
2	3	F01	**pc0177**	strongly similar to transcription initiation factor sigma 70	**sigA, rpoD**	1665	pc0177_761-808	AAAAGGAAATTCAGGAACTTACACCTCGTGCGGAAAGAAATAAGTTTG	74,3	48	0,968	1	0,997	0,993	0,927	0,768	mid
2	3	J01	**pc0178**	hypothetical protein	**-**	867	pc0178_350-394	AATTAAGCAAACGGAATCACGATTATCAGAAAATGGGATGGTCTG	74,3	45	0,98	1	0,998	1	0,988	0,803	random
2	3	N01	**pc0179**	hypothetical protein	**-**	871	pc0179_541-594	ATGGCAGATAAGTGTCCGCAGTTATATGTTTGGACTCATTATTATGAAGAAGAA	74,2	54	0,968	1	0,995	1	0,895	0,807	mid
2	3	B05	**pc0180**	hypothetical protein	**-**	1131	pc0180_658-702	TTTATTGGTTCTTTGCTTTGTTGGGCGATGTTGAGCTTAGTATCC	74,3	45	0,971	1	0,995	1	0,908	0,827	mid
2	3	F05	**pc0181**	strongly similar to ABC transporter ATP-binding protein wzt	**wzt**	1257	pc0181_652-698	GTGAGTCACAGTGTGAGTTCTGTGCTTTCTCTATGCAATAAAGGAGC	74,1	47	0,981	1	0,989	1	0,978	0,856	mid
2	3	J05	**pc0182**	strongly similar to ABC transporter protein wzm	**wzm**	834	pc0182_318-368	AGTGAATAATGCAGCAATGATTTCCAAGGTCTATTTTCCTCGTATGATTCT	74,3	51	0,968	1	0,998	1	0,9	0,799	mid
2	3	N05	**pc0183**	unknown protein	**-**	186	pc0183_113-167	GTTGCACACTATTCTCTCCCTTGTTATGTTCTTACAATATAGAAAACAATTTCAA	71,7	55	0,91	1	0,743	1	0,981	0,769	mid
2	3	B09	**pc0184**	hypothetical protein	**-**	1308	pc0184_747-793	TAACTCCAATGGACCATTTATTGAAGACTTCGATGATTTTCCCACTC	74,2	47	0,969	1	0,999	1	0,908	0,791	mid
2	3	F09	**pc0185**	unknown protein	**-**	1365	pc0185_689-741	CAGGTAATCGTATTTCTCTCCTTGCCCATTTGATCTGTTTTTTTAGGTAAACTC	74,2	53	0,974	1	0,995	1	0,995	0,734	mid
2	3	J09	**pc0186**	similar to polysaccharide export protein wza	**wza**	1050	pc0186_448-495	AATAGACTTTCCAGAAAAGTTGAACTCACAGGAGCTGTAGCCACTCCT	74,2	48	0,974	1	0,993	1	0,922	0,84	mid
2	3	N09	**pc0187**	similar to Tyrosine-protein kinase	**wzc**	2946	pc0187_1470-1521	TGTGTATGAAAAGATTTTACAAACTCGATTAACTCATCAGCAAAGTTCGTCG	74,5	52	0,972	1	0,978	1	0,996	0,76	mid
2	3	B13	**pc0188**	hypothetical protein	**-**	849	pc0188_203-253	ATGTCGGATTTTGCCAAGGTAATAATATCGGCTTGTCTTATATCCCTAGTG	74,3	51	0,967	1	0,993	0,972	0,899	0,843	5´preference
2	3	F13	**pc0189**	strongly similar to ABC transporter protein sufB	**sufB**	1446	pc0189_735-780	TAATCAACTTCATGCCGCTGTCGTTGAACTAATAGCCCTTGATAAC	74,3	46	0,984	1	0,994	1	0,989	0,859	mid
2	3	J13	**pc0190**	strongly similar to ABC transporter ATP-binding protein sufC	**sufC**	765	pc0190_328-372	GAGGGGAAATCAGAACTGACAACGGCTGAATTTGAAAGGTTACTA	74,2	45	0,973	1	0,999	0,999	0,945	0,787	mid
2	3	N13	**pc0191**	similar to sufD	**sufD, ynhC**	1353	pc0191_708-753	AGATCAAGCATATGTTCACTACACGCAAATTTTGAATGAGGAGCAC	74,3	46	0,973	1	0,996	0,993	0,969	0,774	mid
2	3	B17	**pc0192**	strongly similar to SufS L-cysteine desulfurase/L-selenocysteine lyase	**sufS, nifS, csdB**	1233	pc0192_921-970	TTATGAACATACCCTGTTAGAGTATGCGACCAAGAAATTGATGCAGATTC	74,3	50	0,98	1	0,995	0,987	0,998	0,816	random
2	3	F17	**pc0193**	conserved hypothetical protein		936	pc0193_510-563	AATTTTACATTATCGAAATTCTCAGTGGGAAATAGCACGTCTAGGAGCCTTATC	74,2	54	0,979	1	0,996	1	0,959	0,837	mid
2	3	J17	**pc0194**	unknown protein	**-**	1206	pc0194_765-819	AAAATTTATTGGTCTGGGGTTAAAGAGTGAAGGAATAACAGAAAAAGAGCTTGAG	74,1	55	0,944	1	0,989	0,971	0,839	0,686	mid
2	3	N17	**pc0195**	similar to metalloendopeptidase	**npr**	813	pc0195_455-503	GTACGAGTCAAAATGATTGGCAAATTGGTAATTTGCGTAACTTAAGCAA	74,2	49	0,964	1	0,999	0,957	0,952	0,733	mid
2	3	B21	**pc0196**	similar to glycerophosphoryl diester phosphodiesterase	**glpQ;ugpQ**	891	pc0196_404-458	TGAAGTCTTTACCTACTGAGACTCTAATCAAAGCCCTAATACGAGCAATTTCTGA	74,1	55	0,971	1	0,983	1	0,957	0,795	mid
2	3	F21	**pc0197**	unknown protein	**-**	216	pc0197_12-56	ACACTGCGGATCAGAATTTTCGCTGTTTAGAGCGTGGCAAACAAG	78,8	45	0,603	0,38	0,546	0,92	0,903	0,838	mid 2.Wahl
2	3	J21	**pc0198**	similar to F-box protein	**ppaB**	990	pc0198_466-520	TATTTAGAGCTCACAGTTGTGAGTGCATTATTAAACCAGACTTCTCAGTTAACGG	74,2	55	0,639	0,13	0,999	1	0,97	0,807	mid
2	3	N21	**pc0199**	similar to F-box protein	**ppaA**	1014	pc0199_480-525	TCTGAAAAGGTGTGATAATCTCACGGACATTGGATTAGCTCATTTG	74,2	46	0,623	0,097	0,998	1	0,972	0,77	mid
2	4	B01	**pc0200**	similar to type III secretion inner membrane protein SctT	**yscT, sctT**	843	pc0200_394-438	AATCAATCCTCCCCTTTGGGAACACTTTTTAACCTCGTTTTGATT	74,3	45	0,967	1	0,99	1	0,971	0,705	mid
2	4	F01	**pc0201**	strongly similar to type III secretion inner membrane protein SctS	**sctS**	237	pc0201_77-125	TAGTGAGTATGTTTTTTGGAATTATTGTGGCTATCTTTCAGGCTGCCAC	74,3	49	0,974	1	0,997	1	0,962	0,773	5´preference
2	4	J01	**pc0202**	similar to type III secretion inner membrane protein SctR	**yscR, sctR; fliP**	972	pc0202_530-574	AAACTGCTATCAATCAACCAAACGTACCCGAATCTTTTCTTTCCC	74,2	45	0,975	1	0,999	1	0,957	0,785	mid
2	4	N01	**pc0203**	similar to type III secretion protein SctL	**yscL, sctL**	672	pc0203_361-413	TTAGATATTGTAGCAAATAATTTAAAAGCCGTTACCCAACACAAACACGCAAC	74,2	53	0,969	1	0,995	1	0,976	0,708	mid

2	4	B05	**pc0204**	hypothetical protein	**-**	846	pc0204_357-402	TGAGCGTCTCCCCTATGATTATCTCCCTGAGACAGATTTATCAGAG	74,1	46	0,974	1	0,989	1	0,933	0,844	mid
2	4	F05	**pc0205**	similar to type III secretion protein SctJ	**yscJ, sctJ**	1014	pc0205_540-593	TGTTTTAGATGATCCTAATGCCCACCTAATTACACGTATAAAGCGTTTAGTTGC	74,3	54	0,98	1	0,996	1	0,968	0,842	mid
2	4	J05	**pc0206**	strong similarity to 30S ribosomal protein S10	**rs10**	336	pc0206_54-99	ACTGAAAGGTTATGATCAACGTCTGCTAGATCGTTCAACAGGTGAC	74,2	46	0,987	1	0,993	1	0,999	0,873	random
2	4	N05	**pc0207**	strongly similar to translation elongation factor EF-G	**fusA**	2088	pc0207_972-1018	TGATCCTTATGTCGGCCGTTTAACTTACATTCGTATTTACAGCGGTA	74,3	47	0,976	1	0,991	1	0,927	0,867	mid
2	4	B09	**pc0208**	strong similarity to 30S ribosomal protein S7	**rpsG; rs7**	474	pc0208_241-285	ATTGGGGGAGCCACATATCAAGTACCTATCGAAATTCCTGCTAAC	74,3	45	0,988	1	0,996	1	0,997	0,886	mid
2	4	F09	**pc0209**	strong similarity to 30S ribosomal protein S12	**rs12**	381	pc0209_134-178	CAAACTCTGCTTTACGTAAAGTAGCATGGGTACGCCTTTCTACCG	74,1	45	0,978	1	0,984	1	0,934	0,893	5´preference
2	4	J09	**pc0210**	conserved hypothetical protein	**-**	705	pc0210_370-414	GAAATTTCTCAAGGTTATGTTTTGCGCACACATGAAGAATATGCC	74,2	45	0,976	1	0,991	1	0,984	0,782	mid
2	4	N09	**pc0211**	conserved hypothetical protein	**-**	732	pc0211_342-386	AGAACTTTCAGCCAGACAGGATAAGCAACTAGCATGCTATTTCCG	74,4	45	0,98	1	0,985	0,995	0,975	0,865	mid
2	4	B13	**pc0212**	unknown protein	**-**	186	pc0212_4-58	GAAAACACAAGTTATTATTGTTACAAATCGCGTAGCATAGGAAAAGTTATTCGCC	74,2	55	0,971	1	0,998	1	0,91	0,815	mid
2	4	F13	**pc0213**	unknown protein	**-**	216	pc0213_17-65	TAAGCAACTTAATTGGGTTAAACAGCATCCAGTCTCTAGGGGTTTTCAC	74,2	49	0,984	1	0,999	1	0,992	0,834	5´preference
2	4	J13	**pc0214**	similar to carboxy-terminal (= tail-specific) proteinase	**tsp**	2016	pc0214_1047-1095	AAACAATAATCGAGTTGATGTTAGCGAAGAAACTTTTGGCAATGGAATT	74,2	49	0,97	1	0,996	1	0,962	0,74	mid
2	4	N13	**pc0215**	unknown protein	**-**	183	pc0215_1-45	ATGAGTGAAATAAAGAAGAATGGCCAGAACTGGAATCGAACCAGC	75,4	45	0,949	1	0,888	1	0,985	0,775	random
2	4	B17	**pc0216**	unknown protein	**-**	183	pc0216_18-72	AGAAAACGAAGTTTACCCTAATTATCGTTTGAAATCAATCAGAAAAAAACTTTCA	72,8	55	0,901	1	0,855	0,811	0,975	0,629	random
2	4	F17	**pc0217**	strong similarity to 50S ribosomal protein L21	**rplU**	345	pc0217_44-88	AAGAAGGAGACATCATTGATGTAGAACTGCTCAATACCGACCCAG	74,2	45	0,987	1	0,998	1	0,998	0,866	random
2	4	J17	**pc0218**	strongly similar to 50S ribosomal protein L27	**r(p)l27**	252	pc0218_88-132	GTTGTTAGAGCTGGAAGCATTCTTGTTAGACAACGCGGTACAAAA	74,2	45	0,98	1	0,998	0,983	0,978	0,839	random
2	4	N17	**pc0219**	strong similarity to GTP binding protein	**yhbZ;obg**	1014	pc0219_517-570	ACTTTGATTTCCTCATTAGCAGGATTAAGAGTGAAAGTAGCAGCCTATCCTTTT	73,9	54	0,972	1	0,968	1	0,991	0,797	mid
2	4	B21	**pc0220**	hypothetical protein	**-**	750	pc0220_308-356	TCCAAGCTCTAGCTCGACGTCAAGGAGCTTTAACTATAGATGAACTTCA	74,3	49	0,965	1	0,991	1	0,932	0,739	mid
2	4	F21	**pc0221**	strongly similar to transcription termination factor Rho	**rho**	1386	pc0221_732-777	AATTGTACTAATCGTTTTGCTTATCGATGAACGCCCCGAAGAAGTA	74,2	46	0,978	1	0,994	1	0,962	0,824	mid
2	4	J21	**pc0222**	similar to Dephospho-CoA kinase	**yacE**	612	pc0222_328-373	CAGTTTCCTTTCTTCATTGCGGAAGTTCCCCTCTTATATGAAAGTG	74,2	46	0,978	1	0,991	1	0,979	0,819	mid
2	4	N21	**pc0223**	strongly similar to DNA polymerase I	**polA**	2676	pc0223_1320-1365	ATTAATCGGGAAAGGAAAAAACCAGCTTAACATGAAGAATGTGGCT	74,2	46	0,972	1	0,995	1	0,981	0,734	mid
2	5	B01	**pc0224**	similar to proteinase IV	**sohB**	1038	pc0224_518-565	GAAGTGTGGGCGTTATTGCCCCTACATTTATGAATGTCACAAAATTAT	74,4	48	0,976	1	0,983	1	0,998	0,786	mid
2	5	F01	**pc0225**	conserved hypothetical protein	**-**	1950	pc0225_974-1024	TTATTAACTCAGATCTAGCCAATCAAAAGTGGGTTGTTGCTTCTTTGTCTG	74,3	51	0,98	1	0,997	1	0,998	0,794	mid
2	5	J01	**pc0226**	similar to sulfite reductase (NADPH) flavoprotein	**yvgR, cysJ, sirA**	1155	pc0226_689-734	TTAGATTACCTGAAGATTTACACGCTCCTCTTGTCATGGTTGGACC	74,2	46	0,971	1	0,996	1	0,89	0,852	mid
2	5	N01	**pc0227**	similar to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECDP-synthase)	**ipsF, ygbB**	480	pc0227_92-136	ATGATGCCCCAGGTTTTAATGCTAATTCTGATGGAGATGTCGTAT	74,2	45	0,979	1	0,991	1	0,994	0,799	random
2	5	B05	**pc0228**	hypotetical protein	**-**	1089	pc0228_523-570	CAATCGACTCTAACACCAGCTACATTGAATTTTTGTGAAAAGGAATGG	74,3	48	0,97	1	0,993	1	0,977	0,72	mid
2	5	F05	**pc0229**	similar to UDP-N-acetylglucosamine 1-carboxyvinyl transferase (= UDP-N-acetylglucosamine enolpyruvyl transferase)	**murA, murZ**	1398	pc0229_685-730	TTTTATGAAGTCGAACACACAGTTATTCCAGATCGAATTGAGGCAG	74,2	46	0,982	1	0,998	1	0,985	0,825	mid
2	5	J05	**pc0230**	simlar to L-lysine 2,3-aminomutase	**yodO, kamA, yjeK**	1044	pc0230_582-628	TCATCTTAAGCGAATTCGTTTCCATACACGTTTTCCAATTGGTATTC	74,3	47	0,971	1	0,998	0,97	0,941	0,81	mid
2	5	N05	**pc0231**	strong similarity to arginyl-tRNA synthetase (=arginine-tRNA-ligase)	**argS**	1755	pc0231_781-831	ATCATAGATCGAGGTGAATCGTTTTACAATCCTTTTTTACCAAACATCGTC	74,3	51	0,963	1	0,997	0,994	0,902	0,754	mid
2	5	B09	**pc0232**	similar to endopeptidase Clp ATP-binding chain B (heat shock protein)	**clpB**	1125	pc0232_575-627	CTCTATTTCTACATATATTTGACGAAGGTTATTTTACGAGTGGTGTCGGCGAA	74,3	53	0,981	1	0,997	1	0,989	0,815	mid
2	5	F09	**pc0233**	conserved hypothetical protein	**-**	735	pc0233_353-397	AATGTCCAGAAAATACTGAAAGGATTGGCGGTTTGAGAGTCAAAC	74,2	45	0,981	1	0,999	1	0,985	0,812	mid
2	5	J09	**pc0234**	conserved hypothetical protein	**yjeE**	441	pc0234_60-104	TAATTTTGGTTTAACATTGCCCGCCAACTCTGTCATCTGTTTTTT	74,3	45	0,968	1	0,994	1	0,971	0,711	5´preference
2	5	N09	**pc0235**	conserved hypothetical protein	**-**	621	pc0235_359-412	TGGATATTAGACGCATTCCTAATGAAGAAGACATTCAATTTTTAGAGTGGGTTC	74,3	54	0,962	1	0,989	1	0,953	0,68	mid
2	5	B13	**pc0236**	similar to DNA polymerase III epsilon chain	**dnaQ_2**	750	pc0236_375-422	AATGGCCCGACTTTATGGAGAAAGCCCTGTTAATTCTCTTGAATATTT	74,3	48	0,978	1	0,997	1	0,999	0,763	mid
2	5	F13	**pc0237**	conserved hypothetical protein	**-**	900	pc0237_389-434	TTGTTTGTGGTTGTCGAGATTTAGGGGAAGCTTTAAGAAGAATTGG	74,2	46	0,97	1	0,999	1	0,938	0,759	mid
2	5	J13	**pc0238**	similar to glutamine amidotransferase	**hisH**	594	pc0238_324-369	GCGGCAAGTCGATTCTTTTCAAGTGGATGTGTCTGTTTATTTAAAA	74,3	46	0,966	1	0,997	1	0,974	0,671	mid
2	5	N13	**pc0239**	strongly similar to 3-phosphoglycerate kinase	**pgk**	1209	pc0239_589-634	TGTGCAGTGTTAGGAGGTGCAAAAATTTCCACAAAGTTTAAAGTCA	74,2	46	0,97	1	0,998	1	0,983	0,699	mid
2	5	B17	**pc0240**	strongly similar to ADP/ATP translocase	**ntt_3**	1611	pc0240_741-794	TCGTTGGATGAATGTAGAAGTCTTAACCGATAAACGTTTTTATGATCCTTCTTC	74,3	54	0,972	1	0,992	1	0,934	0,805	mid
2	5	F17	**pc0241**	strongly similar to ADP/ATP translocase	**ntt_2**	1551	pc0241_917-966	ATTCGTCAGCCCTTGATTATAATCGCTATATGAATAACATGACATCAGCA	74,2	50	0,968	1	0,999	1	0,86	0,85	mid
2	5	J17	**pc0242**	similar to Phosphatidylglycerophosphate synthase (= CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase)	**pgsA**	426	pc0242_224-269	CATTTCGATTTCGCTCTATCTGGTCTGGTAAAGTGACAACAGCTTT	74,3	46	0,979	1	0,995	1	0,99	0,799	mid
2	5	N17	**pc0243**	hypothetical protein	**-**	1146	pc0243_593-646	GAGTCATGGTCTATCTCACACAACCTTTTAGCATCGGAGAACTCATTAATATTC	74,2	54	0,98	1	0,997	1	0,981	0,811	mid
2	5	B21	**pc0244**	strongly similar to glutamate-tRNA ligase (= glutamyl-tRNA synthetase)	**gltX**	1509	pc0244_670-714	ATCTTGCTATATGAATCCTTTGGATGGACTCCTCCAACGTTCTTG	74,3	45	0,972	1	0,995	0,987	0,915	0,846	mid
2	5	F21	**pc0245**	unknown protein	**-**	366	pc0245_71-115	CAGGCTACATTCCAGGCATAGGAACAGTCTCTGCTTATGTCAGAG	74,7	45	0,98	1	0,956	1	0,999	0,907	random
2	5	J21	**pc0246**	similar to carboxy-terminal (= tail-specific) proteinase	**tsp**	1962	pc0246_882-	AGAACATACTCCCGTTATTTTGACAGTCATTCGAGAAACGACAAGTACTG	74,1	50	0,972	1	0,991	1	0,9	0,858	mid

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2	5	N21	**pc0247**	strongly similar to lysine-rich histone-specific protease	**euo**	420	pc0247_287-331	AAATTTATTACGCGACTCGTATTGGTTTGCTGAAAGCAGAGCGAA	75.5	45	0,972	1	0,998	1	0,941	0,783	testchip
2	6	B01	**pc0248**	similar to RNA methyl transferase	**-**	1305	pc0248_769-815	TTTCGGTTTACTCCTCAAGCCTTCATACAAAATCATCCTGAACAAAG	74,2	47	0,966	1	0,998	1	0,885	0,791	mid
2	6	F01	**pc0249**	similar to ssDNA-specific exonuclease	**recJ**	1785	pc0249_873-922	TACCATAGCCTCAAAAATTGCACCTCGTTTAAACAGTTTAGGACGTATTG	74,2	50	0,976	1	0,994	1	0,979	0,786	mid
2	6	J01	**pc0250**	ADP/ATP translocase	**ntt_1**	1542	pc0250_1155-1201	TGCCTTAGGAACTACTCCACTATTCTTAGCTGTCATCTTTGGTGCGG	75.5	47	0,987	1	0,998	1	0,994	0,869	testchip
2	6	N01	**pc0251**	similar to fusion protein export proteins SecD/SecF	**secDF**	4533	pc0251_2298-2350	AGATATTTGGAACGAAGCCGTTGTAACAAATCGTAGAGATATAGAAAGCATCA	74,3	53	0,98	1	0,998	1	0,97	0,83	mid
2	6	B05	**pc0252**	unknown protein	**-**	444	pc0252_104-149	AAATAGGACATGATCATTTTAAGTCTCAGCAGGGAACGATTTGGGT	74,1	46	0,981	1	0,989	1	0,997	0,826	random
2	6	F05	**pc0253**	conserved hypothetical protein	**-**	498	pc0253_186-231	TAATAGCAGTAATCCTCAAGAAGTTACTCCAAAACCCCGTGCTGCT	74,2	46	0,976	1	0,993	1	0,936	0,852	mid
2	6	J05	**pc0254**	conserved hypothetical protein	**-**	861	pc0254_429-474	AAAATCTCATTTAACAGGGGCCTTATTGGTAACGACACCACAAGAA	74,3	46	0,981	1	0,997	1	0,997	0,803	mid
2	6	N05	**pc0255**	hypothetical protein	**-**	324	pc0255_146-195	CGAATTGTCGGGATAAAAACAAGGGGAATAGATTGTTGAATCTTACAAGT	74,2	50	0,97	1	0,998	0,952	0,988	0,759	random
2	6	B09	**pc0256**	similar to ABC transporter periplasmic substrate-binding protein ytgA	**ytgA**	1011	pc0256_491-535	AAGATCCTTTACATGCCGACCTATTTCGTAAAAACGCCAATGAAT	74,2	45	0,972	1	0,993	1	0,984	0,738	mid
2	6	F09	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
3	1	C01	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
3	1	G01	**pc0257**	similar to ABC transporter ATP-binding protein ytgB	**ytgB**	843	pc0257_428-477	ATATTGTAGGAATGAGCGCCTATGCAGATCGTCAAATTAGTCAATTATCG	74,4	50	0,982	1	0,984	0,999	0,995	0,852	mid
3	1	K01	**pc0258**	similar to ABC transporter permease ytgC	**ytgC**	1353	pc0258_788-837	ATTTACTTGCAAGTTATTATCCTTCTTCACGTCTCGTGTTACCAACAGGC	74,2	50	0,971	1	0,998	1	0,89	0,844	mid
3	1	O01	**pc0259**	similar to ABC transporter permease ytgD	**ytgD**	1011	pc0259_463-507	TTAATTCGAGATGCTCATATAGGGACAGAAGCGGTCATGGGTAAT	74,2	45	0,982	1	0,996	1	0,956	0,877	mid
3	1	C05	**pc0260**	strongly similar to 1-deoxy-D-xylulose 5-phosphate reductoisomerase	**dxr**	1155	pc0260_581-625	ATCATCCAACTTGGAGTATGGGGCCTAAAGTCACAATTGATTCAT	74,3	45	0,979	1	0,992	1	0,997	0,796	mid
3	1	G05	**pc0261**	conserved hypothetical protein	**-**	1962	pc0261_879-928	TCGTATCCCTAGAATTCGTGTGGAAGAACTTAAGCTGGATTCAGAAGTAA	74,2	50	0,971	1	0,997	1	0,897	0,839	mid
3	1	K05	**pc0262**	hypothetical protein	**-**	1710	pc0262_843-888	ACTGATTTCATTAATGTTTGTGATGTCTCGTGATGGAGAAATGCCT	74,1	46	0,975	1	0,983	1	0,987	0,792	mid
3	1	O05	**pc0263**	unknown protein	**-**	285	pc0263_55-99	GAAATAACCCCCTTATCACCCAATAGTTTCCCAAAAACCCCTTTC	74,3	45	0,628	0,09	0,992	1	0,999	0,832	random
3	1	C09	**pc0264**	hypothetical protein	**-**	5418	pc0264_4010-4061	TGAATGATCCTAAGTTCGCCTCTGTTAACCTCTCTAATCAGAAAATAAGTGA	73,1	52	0,786	1	0,889	1	-0,3	0,823	mid
3	1	G09	**pc0265**	conserved hypothetical protein	**-**	327	pc0265_240-287	CATGAAAAGGAATAAGATCCTCAAAGATTTGGCCAAAAGAGGAAAAAC	74	48	0,61	0,13	0,978	0,943	0,925	0,693	mid
3	1	K09	**pc0266**	similar to nitrogen regulatory IIA protein (enzyme IIA-ntr) (phosphotransferase enzyme II, A component)	**ptsN;rpoP**	720	pc0266_372-422	TGAAGTCATGACTGAATTATTATTAGACCGTGAAAATATGATGCCTACCGC	74,3	51	0,978	1	0,993	1	0,989	0,798	mid
3	1	O09	**pc0267**	similar to nitrogen regulatory IIA protein (enzyme IIA-ntr) (phosphotransferase enzyme II, A component)	**ptsN;rpoP**	339	pc0267_76-123	GCTGCTATTCCACATGCTAAACTCCCTTCCTATGATCGGTTTTTTTATT	74,1	48	0,971	1	0,99	0,971	0,999	0,757	random
3	1	C13	**pc0268**	strongly similar to Deoxyuridine 5'-triphosphate nucleotidohydrolase	**dut**	453	pc0268_206-255	GCCCGAGAAGTGGTTTAGCATTGAAACATCAAGTGACAGTTTTAAATACT	74,2	50	0,975	1	0,999	1	0,979	0,761	mid
3	1	G13	**pc0269**	strongly similar to acetyl-CoA carboxylase, carboxyltransferase beta chain	**accD**	918	pc0269_548-592	CACTTGCCAAGTTACATGAAGCGCGTATCCCCTATATTTCTGTTT	74,2	45	0,972	1	0,999	1	0,912	0,821	mid
3	1	K13	**pc0270**	strongly similar to superoxide dismutase (Mn) precursor	**sodM**	627	pc0270_338-388	CTTTACAAACCCTAATTGAACAATTAAGTGCGAAAGCAATCGCTATTCAAG	74,2	51	0,976	1	0,996	1	0,977	0,78	mid
3	1	O13	**pc0271**	conserved hypothetical protein	**-**	654	pc0271_232-276	TCTAAAACTTCGATAGCTGTTGGTCAAGTCTCGGGATCTCATTTG	74	45	0,968	1	0,979	1	0,904	0,846	mid
3	1	C17	**pc0272**	similar to Porphobilinogen deaminase	**hemC;gmc**	702	pc0272_321-365	CATTTGTCTAACAAAAGGTGTCGACTGCAGTGATGTCTTGGTCTT	74,3	45	0,981	1	0,99	1	0,969	0,867	mid
3	1	G17	**pc0273**	strongly similar to DNA repair	**sms**	1371	pc0273_690-739	TGTGGATACGGTTCTTTACTTTGAAGGTGATAAACAACACCATTATCGAA	74,2	50	0,98	1	0,998	0,988	0,996	0,81	mid
3	1	K17	**pc0274**	similar to Ribonuclease III	**rnc**	729	pc0274_347-392	AAGGAGAACGCATGAATGATGGAAGAGGTAGAGAATCTATTTTGGC	74,2	46	0,977	1	0,993	1	0,982	0,791	mid
3	1	O17	**pc0275**	unknown protein	**-**	675	pc0275_323-371	AACAAACTCTAAGTTTAGAATCGATTAGTGGCGTAAGTGGCGTCCTTTG	74,3	49	0,982	1	0,998	1	0,984	0,833	mid
3	1	C21	**pc0276**	conserved hypothetical protein	**-**	666	pc0276_357-404	TCATAAAGCTGATTATCAAGGATTTTGCATGGCGAAACCTACTCAGTA	74,2	48	0,977	1	0,998	1	0,977	0,791	mid
3	1	G21	**pc0277**	unknown protein	**-**	1218	pc0277_594-639	TCCTGATACCGCAACAAATGCACCAATTCATAAGAAATATGTTGTC	74,2	46	0,978	1	0,994	1	0,984	0,795	mid
3	1	K21	**pc0278**	hypothetical protein	**-**	1038	pc0278_473-526	ATGATAACGTGAGTCCTAAAGCTTTTGATAGCCGTGTTAAGTTGTTTTTAGCAG	74,3	54	0,965	1	0,994	1	0,953	0,699	mid
3	1	O21	**pc0279**	hypothetical protein	**-**	1518	pc0279_662-706	TACTAGATCATGCTATATTAGGGGCGGCTCCTACGGATGACTTGA	74,2	45	0,976	1	0,999	0,998	0,902	0,887	mid
3	2	C01	**pc0280**	unknown protein	**-**	639	pc0280_365-409	AAAAAACGCATTTTCGAACAGAAGATAGCCATCCTTTGTGTGATT	74,2	45	0,976	1	0,992	1	0,956	0,822	mid
3	2	G01	**pc0281**	strongly similar to glycine cleavage system T protein	**gcvT**	1035	pc0281_466-514	TCGATCCAAGAACTAGATCAACCTTTGATTCTTTCGCGTACAGGTTATA	74,2	49	0,978	1	0,996	1	0,948	0,847	mid
3	2	K01	**pc0282**	strongly similar to glycine cleavage system H protein	**gcvH;gcsH**	369	pc0282_129-177	AAAAGTTACTGCTGGACAGGAGGTGGTGGTTTTAGAGTCTACTAAAGCG	74,2	49	0,981	1	0,996	1	0,943	0,879	mid
3	2	O01	**pc0283**	strongly similar to glycine dehydrogenase P protein subunit 1	**gcvP1**	1341	pc0283_690-740	TCAAGGAGCCTTAACAATTCTTTGTGCAAATCCTATTTCTTATGGACTGTT	74,2	51	0,976	1	0,995	1	0,982	0,773	mid
3	2	C05	**pc0284**	strongly similar to glycine dehydrogenase (decarboxylating) P protein subunit 2	**gcvP2**	1443	pc0284_684-728	AATTGTTCATAAAGTTGGTGGTTTTCTGTATTACGATGGGGCCAA	74,2	45	0,976	1	0,997	1	0,961	0,804	mid

3	2	G05	**pc0285**	unknown protein	-	387	pc0285_6-56	TTTAAATATGGGTCAATGGATAGGCGTTTTATTAGGGCTTATTGTCATTGC	74,3	51	0,976	1	0,991	0,991	0,998	0,779	5´preference
3	2	K05	**pc0286**	strongly similar to alkylated DNA repair protein	**alkB**	669	pc0286_428-473	AAGATGAAGACGATTTGGATTCACCTATTGTTTCTGTTTCACTCGG	74,2	46	0,97	1	0,997	1	0,908	0,815	mid
3	2	O05	**pc0287**	similar to cadmium-transporting ATPase	**cadA**	1926	pc0287_925-970	TTAATCAAAGGAGGAAAATATCTCGAAGCTATGGGGCAAGTGAATG	74,1	46	0,973	1	0,989	1	0,961	0,794	mid
3	2	C09	**pc0288**	strongly similar to cation efflux system membrane protein A	**czcA**	3216	pc0288_1771-1816	AGAGATCTAGCCATGCATGTTATGCGTATTCCAAGCACCTCATTAT	74,2	46	0,969	1	0,999	1	0,838	0,888	mid
3	2	G09	**pc0289**	similar to cation efflux system membrane protein B	**czcB**	1143	pc0289_552-606	TGAGCCTAACTTGAGACTCTACTCTATACGCTCTCCTATCGATGGAACAGTAATC	74,2	55	0,987	1	0,997	1	0,979	0,901	mid
3	2	K09	**pc0290**	similar to cation efflux system membrane protein C	**czcC**	1155	pc0290_586-632	TTTGACCTCGAAATGCCGAAAGAACTTCAAACTTACATTGAAGATCT	74,2	47	0,978	1	0,996	1	0,993	0,782	mid
3	2	O09	**pc0291**	unknown protein	-	186	pc0291_114-168	TTTAACGAATTTGGAGAACATCTATCCTCTCTATTTATTCAACCCGAGTTTTCAA	74,2	55	0,978	1	0,999	1	0,98	0,787	mid
3	2	C13	**pc0292**	unknown protein	-	201	pc0292_14-59	ATTTCTTCTTGTGTAAGCTCTTTGCCAGCTTTAAATGCTTGTGCAA	74,2	46	0,973	1	0,999	1	0,994	0,715	5´preference
3	2	G13	**pc0293**	unknown protein	-	432	pc0293_128-178	TGTTAAAGTTAGTCACTATTTCCCAACCTATCTTCGAAATTTGCCGTGCTA	74,4	51	0,969	1	0,986	1	0,911	0,824	mid
3	2	K13	**pc0294**	unknown protein	-	804	pc0294_456-506	AGCAGATTTACTTCCTTCGCCAAAGGAATATGCGAATTACTTTCTTAATCA	74,3	51	0,966	1	0,989	0,971	0,947	0,778	mid
3	2	O13	**pc0295**	conserved hypothetical protein	-	348	pc0295_66-117	ATGGCATATTCCAAAGTTTTAAGGCAAAAAGCACTCAACTATTTAGAAACTGG	74,2	52	0,605	0,06	0,997	0,985	0,891	0,872	mid
3	2	C17	**pc0296**	unknown protein	-	387	pc0296_12-63	CAATTCTTGTGATTCTAGCACTATTGTTGAGCCTTGCTACACTTGTAAACGT	74,2	52	0,981	1	0,997	1	0,995	0,808	5´preference
3	2	G17	**pc0297**	unknown protein	-	762	pc0297_462-512	GATAGACCTCTTTATAAGTCATGTGCCTGAAACGAAGTTGGAAAATTTTCG	74,2	51	0,966	1	0,995	1	0,92	0,755	mid
3	2	K17	**pc0298**	strongly similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain E	**nqrE**	744	pc0298_360-407	CCTTTATATGTCGCTTGGACTCTATCTTCCTCTCATTGCAGTCAATTG	74,2	48	0,985	1	0,997	1	0,987	0,866	mid
3	2	O17	**pc0299**	strongly similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain D	**nqrD**	636	pc0299_314-364	TTGTTGGATTAATTATTACAAATTGCATTGTGATGGGAAGAACAGAAGGAA	74,3	51	0,971	1	0,991	0,987	0,995	0,735	mid
3	2	C21	**pc0300**	similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain C	**nqrC**	933	pc0300_385-439	GACGAATCTCAATATGTGGCTCAATACCGTAAAACAGGATACTATAGACAACCAT	74,2	55	0,976	1	0,999	1	0,917	0,861	mid
3	2	G21	**pc0301**	similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain B	**nqrB**	1530	pc0301_873-917	GAAAGAAGTCGGACAACATCAAGCCACTTTAACACAACTCGAATC	74,3	45	0,969	1	0,989	1	0,893	0,84	mid
3	2	K21	**pc0302**	unknown protein	-	477	pc0302_95-140	TTTATCCTCACATCTGGCTTTTAGTGGAAGCATTACCCGAACTTTC	74,3	46	0,979	1	0,993	1	0,953	0,859	5´preference
3	2	O21	**pc0303**	unknown protein	-	5115	pc0303_2586-2639	GCATTCTGAATCTTGTTTAACTCTCTCTGATATTCAAGGGACATTACTCATTGG	74,2	54	0,979	1	0,999	1	0,973	0,808	mid
3	3	C01	**pc0304**	unknown protein	-	978	pc0304_543-596	TCAACGTAAAGGGGAGACACTTGGTAATCATCTAACGAGTTTATTAGAACAAGG	74,4	54	0,971	1	0,982	1	0,947	0,805	mid
3	3	G01	**pc0305**	similar to competence-related protein comF	**comF**	726	pc0305_354-400	ATTAAAGTGGCCATTGCCTGATATCGTAATCCCTGTTCCTATGTCTT	74,2	47	0,979	1	0,991	1	0,99	0,805	mid
3	3	K01	**pc0306**	similar to divalent cation transport protein	**corA**	1134	pc0306_545-591	AAGGTAACATTCGCATACGCAAACAAAAGGCAGATTATTTGGCTTAT	74,2	47	0,976	1	0,996	1	0,977	0,783	mid
3	3	O01	**pc0307**	similar to replication initiation protein dnaA	**dnaA**	1386	pc0307_774-826	AATTGTTATCACAAGTGATAAACCTCCTTCTCTTTTAAAGCTTTCGGAACGAA	74,2	53	0,963	1	0,999	1	0,92	0,705	mid
3	3	C05	**pc0308**	hypothetical protein		1173	pc0308_598-647	GGAATGGTGACAACTAATGACCCTGGCCTTTATCATCGTTTACTTTTATT	74,2	50	0,976	1	0,997	0,998	0,99	0,762	mid
3	3	G05	**pc0309**	conserved hypothetical protein	-	396	pc0309_31-83	GGCTGGACTGAAGAACACATTGAAGATTTACGTTATACGGGTTACTCTTATGT	74,2	53	0,986	1	0,996	1	0,996	0,863	random
3	3	K05	**pc0310**	hypothetical protein	-	450	pc0310_174-219	AATTGTACCTATTCAAACTCCTTGGGCTTACTTTTTTCCCCCACCT	74,1	46	0,97	1	0,984	1	0,948	0,786	mid
3	3	O05	**pc0311**	strongly similar to S-adenosyl-methyltransferase	**mraW;yabC**	951	pc0311_404-449	GTAAGCTAACTGCCGCTGATATTGTCAATACCTGGTCAGAACATGA	74,2	46	0,975	1	0,999	1	0,927	0,832	mid
3	3	C09	**pc0312**	conserved hypothetical protein	-	294	pc0312_220-265	TTTGGACATCTGAAATACCCTCCCTTAACCGATGTTCTATTGATCC	74,2	46	0,977	1	0,999	1	0,928	0,848	mid
3	3	G09	**pc0313**	similar to penicillin-binding protein 2 (transglycolase/transpeptidase)	**pbp2**	2031	pc0313_931-976	ATTGAACATACGAAAGTGAAAGCTGTAACAGATGCAAATGAGCCTG	74,2	46	0,973	1	0,999	1	0,914	0,831	mid
3	3	K09	**pc0314**	similar to UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	**murE**	1479	pc0314_716-760	CAATTGTGAATATTGACGATCCATGGTGCGAACAAATAGTCAAAG	74,3	45	0,98	1	0,998	1	0,976	0,825	mid
3	3	O09	**pc0315**	similar to N-acetylmuramoyl-L-alanine amidase	**amiA, cwlC**	843	pc0315_394-438	TTTGTCAGCGTCCATTATAACTCAGCTCCTAGTAGCGAAGCTCAA	74,3	45	0,985	1	0,997	0,988	0,971	0,899	mid
3	3	C13	**pc0316**	hypothetical protein	-	891	pc0316_498-552	TGACGAGTATATTATTGAGTCTGTCCCATTAAATGAAACTGTTACTCATTGGTCG	74,4	55	0,971	1	0,984	1	0,949	0,796	mid
3	3	G13	**pc0317**	strongly similar to phosphogluconate dehydrogenase (decarboxylating)	**pgd**	1455	pc0317_783-827	AAAAGGCACAGGAAAATGGACAGTGATTAATGCATTGGATTTAGG	74,2	45	0,971	1	0,997	1	0,945	0,773	mid
3	3	K13	**pc0318**	similar to 1-acylglycerol-3-phosphate O-acyltransferase	**plsC**	633	pc0318_241-292	GCTCATCCCACTAAAGACCTACATTCCTTTCGAGTCTTACAACAACTTCTTT	74,3	52	0,973	1	0,994	1	0,923	0,825	mid
3	3	O13	**pc0319**	strongly similar to cytidylate kinase	**cmk**	687	pc0319_245-291	TCTCCAAGCTTATTCGCGGAAAAGAAGTCACTTCATCTGTTTCTAAA	74,3	47	0,964	1	0,995	1	0,9	0,764	mid
3	3	C17	**pc0320**	similar to phosphatidate cytidylyltransferase	**cdsA**	939	pc0320_430-476	CCCTTAGGTAATATTGCTGTCAACCTATTCGGAATTGGCTATGTCGT	74,2	47	0,982	1	0,999	1	0,959	0,862	mid
3	3	G17	**pc0321**	strongly similar to undecaprenyl pyrophosphate synthetase	**uppS**	777	pc0321_473-520	GTTCTCGCAATGAACTACAACGGGCTTTTACGAGGATATTAGATGAAG	74,2	48	0,976	1	0,997	1	0,917	0,864	mid
3	3	K17	**pc0322**	strongly similar to GTP-binding protein lepA	**lepA**	1809	pc0322_933-980	ATTTGAAGGGCTCAGAGATGCATTAGGTAAGCTTCAATTGAATGATTC	74,2	48	0,976	1	0,996	1	0,973	0,781	mid
3	3	O17	**pc0323**	unknown protein	-	1056	pc0323_401-446	AAAAAACTAGTCCCATCATTGCCATCGAAGAGAAGAATGAAGCAAT	74,3	46	0,963	1	0,998	1	0,872	0,78	mid
3	3	C21	**pc0324**	hypothetical protein	-	2196	pc0324_1065-1110	TAATAGTGCCGAAGGCACAAACGTTGTTATTGAAACCTACTACCCA	74,2	46	0,983	1	0,998	1	0,966	0,866	mid
3	3	G21	**pc0325**	conserved hypothetical protein	-	297	pc0325_157-207	CAAACCAATAAACGTAATATCAATCCCGATGCCAAACTTGGTAAAGTATTG	74,3	51	0,981	1	0,998	1	0,993	0,81	mid
3	3	K21	**pc0326**	conserved hypothetical protein	**ykuE, yael**	966	pc0326_451-498	AAAGGGTTTGGACGTTTATTGAGTTCTATTCGCTTAACAGGAAAGGTG	74,2	48	0,981	1	0,998	1	0,967	0,839	mid

3	3	O21	**pc0327**	similar to 4-diphosphocytidyl-2C-methyl-D-erythritol synthase	**ispD**	693	pc0327_383-429	CTGCTGTATTGGGTGTACGAGTAAAAGCGACGATTAAGATTTGTGAA	74,2	47	0,975	1	0,995	1	0,965	0,793	mid
3	4	C01	**pc0328**	similar to tRNA pseudouridylate synthase I	**truA**	774	pc0328_355-401	AAAGTGATGGACCCTTTTCAACGTTTATATAGCTGGCATTTCCAAAG	74,2	47	0,967	1	0,999	1	0,967	0,692	mid
3	4	G01	**pc0329**	hypothetical protein	**-**	684	pc0329_346-398	CGGTGTGTCGTTACTCATTCTGCTTTTCAACTTATTAAAACTATTCGAGAACA	74,2	53	0,976	1	0,998	1	0,997	0,742	mid
3	4	K01	**pc0330**	unknown protein	**-**	927	pc0330_498-545	TAAACGAGTTGTAATTACATGTGGTCATTGCTGCCCTGATCATAATGT	74,2	48	0,984	1	0,999	1	0,966	0,88	mid
3	4	O01	**pc0331**	hypothetical protein	**-**	369	pc0331_6-52	CCCTATTGGTATGCAGCTCGCGTGGATTACTGTCTCGAATATTAATA	74,3	47	0,985	1	0,992	1	0,996	0,868	random
3	4	C05	**pc0332**	hypothetical protein	**-**	987	pc0332_500-545	TTTCTCAAATTACTTTACCCGATGAACGTCACTTGCGTTTATGCTC	74,3	46	0,983	1	0,998	1	0,994	0,832	mid
3	4	G05	**pc0333**	conserved hypothetical protein	**-**	261	pc0333_160-214	CTTCTGGACAAAAGAGGAGAAATCACAGGAATTGTTTTTATTGATTCTATATCGA	73,9	55	0,59	0,054	0,969	1	0,972	0,677	mid
3	4	K05	**pc0334**	hypothetical protein	**ppaA**	1851	pc0334_1785-1835	CTTTTTACGTAGAGGACAGTGGGGTTTGCCTACATTGATAAGAAAACACTC	74,3	51	0,874	1	0,994	1	0,142	0,854	mid
3	4	O05	**pc0335**	hypothetical protein	**ppaA**	1929	pc0335_922-972	GCACTTAATTTTTCAAAGAATGCTCATTTGACTGATGCTCAACTCTTAACG	74,5	51	0,613	0,13	0,976	1	0,956	0,607	mid
3	4	C09	**pc0336**	hypothetical protein	**ppa**	1809	pc0336_199-243	TTTTGGGGGCGAAAGGAGATTGTTATTTCTAAAAGAACTCGCACT	74,9	45	0,69	0,331	0,929	1	0,935	0,749	mid
3	4	G09	**pc0337**	hypothetical protein	**-**	444	pc0337_200-245	CTGTCCCTCTCACAGATAAAGCTATGCGCCAAGTCGTAGGTTATAA	74,1	46	0,975	1	0,981	1	0,977	0,816	mid
3	4	K09	**pc0338**	hypothetical protein	**-**	636	pc0338_240-288	AACACCTGATATGTATGCTTCAATTGATAAAGCGATTGCAAGACTTGAA	74,2	49	0,966	1	0,994	1	0,921	0,76	mid
3	4	O09	**pc0339**	hypothetical protein	**-**	1077	pc0339_482-527	TGGGAGAACCTTTTGATAATTATGATACTGTCATGCATGCATTTCG	74,2	46	0,972	1	0,999	1	0,942	0,777	mid
3	4	C13	**pc0340**	hypothetical protein	**-**	696	pc0340_422-471	TAAAACTACTAAAGCATGAAGGAATTTTAGCCCATCCTTTGGTCTGCAGT	74,2	50	0,974	1	0,997	0,958	0,999	0,779	random
3	4	G13	**pc0341**	conserved hypothetical protein	**-**	801	pc0341_405-449	AATTCGTCGCACATTTCAATTCACTAAGCGAATTCCTCAAGATTT	74,2	45	0,977	1	0,999	0,97	0,997	0,794	mid
3	4	K13	**pc0342**	unknown protein	**-**	186	pc0342_43-89	ATTAAGTCGGTACTGCGTCTAAAGAATGACTTCGCCACATTGAGAAT	74,2	47	0,978	1	0,993	0,999	0,953	0,848	random
3	4	O13	**pc0343**	unknown protein	**-**	978	pc0343_550-597	CAATTAGCTAATGTTGTCAACGAACTTTGGAAGGACTGGAAACATTTG	74,3	48	0,974	1	0,997	0,993	0,94	0,82	mid
3	4	C17	**pc0344**	hypothetical protein	**-**	1608	pc0344_825-872	AATTAGAATTCAGCAACTTCCCTTAGCACTTTTTGGTATCGCTATCGC	74,2	48	0,98	1	0,997	1	0,98	0,819	mid
3	4	G17	**pc0345**	strongly similar to endonuclease IV	**nfo**	849	pc0345_424-469	TTACGTTTACTTCTTGAAGCTACTGCGGGACAAGGTACTTCTGTCG	74,2	46	0,987	1	0,996	1	0,998	0,868	mid
3	4	K17	**pc0346**	strongly similar to asparagine-tRNA ligase	**asnS**	1404	pc0346_681-726	TTATACATTTGGTCCAACATTTCGGGCAGAAAATTCCAATACTTCC	74,2	46	0,979	1	0,996	1	0,978	0,811	mid
3	4	O17	**pc0347**	similar to glutamyl tRNA reductase	**hemA**	1023	pc0347_609-654	GACGATTTGCAATCGTTCAGAAATTCGCTCCAAAGAATTAGCTATT	74,2	46	0,964	1	0,997	1	0,904	0,75	mid
3	4	C21	**pc0348**	conserved hypothetical protein	**-**	1851	pc0348_1015-1065	ACAACTGACGAAATTGCTTTAATAGGGAAAACAGGAACTTCTTTTTCTGCT	74,2	51	0,958	1	0,998	0,999	0,911	0,674	mid
3	4	G21	**pc0349**	conserved hypothetical protein	**-**	1029	pc0349_585-632	ATCCTTACCTATAACAGATGAGCGAATGACTCGTTTCTGGATCACCTT	74,2	48	0,978	1	0,995	1	0,931	0,872	mid
3	4	K21	**pc0350**	similar to DNA gyrase (topoisomerase) chain B	**gyrB**	1821	pc0350_915-966	CTTTGAATCGCAGACTAAAAATAAGCTAGGTAATAACGAATTACGCGCTCCT	74,2	52	0,981	1	0,999	1	0,997	0,793	mid
3	4	O21	**pc0351**	similar to DNA gyrase (topoisomerase) chain A	**gyrA**	1902	pc0351_896-942	TCAAAGACAATTATCCCTGGGAAACAGATGTCGATTCTATCTTACGG	74,3	47	0,979	1	0,998	1	0,944	0,855	mid
3	5	C01	**pc0352**	hypothetical protein	**-**	624	pc0352_372-422	ACATAGTTTGCGATCCATTCTTGTTAAACTTCAAACAAAAGGGTTAACGAG	74,2	51	0,97	1	0,995	1	0,941	0,772	mid
3	5	G01	**pc0353**	unknown protein	**-**	267	pc0353_87-132	TGGAACATTAAAGTCTAGTTCGGAAGTCAAAAGTTTGGCTGCCTTC	74,5	46	0,969	1	0,971	1	0,988	0,756	random
3	5	K01	**pc0354**	unknown protein	**-**	306	pc0354_57-101	ATTGCTCCAGATTTCAGAACCAGTTCGCAACTTATTCATTCAAGA	74,2	45	0,973	1	0,995	1	0,999	0,722	random
3	5	O01	**pc0355**	strongly similar to 23S RNA-specific pseudouridine synthase D	**rluD**	957	pc0355_380-425	AGAAGTTACCGCTTTTACCAGACACTATACGTCCTGGCATTGTTCA	74,3	46	0,975	1	0,996	1	0,9	0,88	mid
3	5	C05	**pc0356**	strongly similar to D-tyrosyl-tRNA(Tyr) deacylase	**dtd**	456	pc0356_48-94	TGATAACCTGTTTAGTGCAATTGGCCCTGGCTTAATGTTATTGCTAG	74,2	47	0,985	1	0,999	1	0,993	0,843	random
3	5	G05	**pc0357**	conserved hypothetical protein	**-**	249	pc0357_40-85	GATCATCCAGACAAGGTAAAGATTAATGAAATCGGCGGTACACAAA	74,2	46	0,982	1	0,998	1	0,995	0,814	random
3	5	K05	**pc0358**	unknown protein	**-**	2658	pc0358_1329-1376	TGTTAATCTAAGAAGCGACATCGATGAAATACGTCACAAAATGCAGAG	74,3	48	0,984	1	0,995	1	0,999	0,841	mid
3	5	O05	**pc0359**	unknown protein	**-**	405	pc0359_68-120	TTATTTACGGTAAATTATTCCATATCAATGCAGAATTGACAGCCACCATCTTT	74,2	53	0,976	1	0,993	1	0,967	0,799	5´preference
3	5	C09	**pc0360**	unknown protein	**-**	234	pc0360_62-116	TGAATTTTTTGAATTTAAATTTTATACTACTTGCTAAAGTTGATTTTAACTATGA	66,7	55	0,549	0,491	0,246	1	0,982	0,397	random
3	5	G09	**pc0361**	similar to multifunctional folic acid synthesis protein	**folK**	516	pc0361_307-354	AATATCATTTATTCTGATGAAGCATTGCAAATTCCTCATCCACATTGG	74,3	48	0,968	1	0,993	1	0,952	0,741	mid
3	5	K09	**pc0362**	strongly similar to 2-dehydro-3-deoxyphosphooctonate aldolase (KDO synthetase)	**kdsA**	828	pc0362_419-465	TTTTAGCTCCTTGGGATATGGAAAATGTCATCAGAAAAATGGAATCC	74,3	47	0,973	1	0,989	1	0,996	0,737	mid
3	5	O09	**pc0363**	unknown protein	**-**	633	pc0363_311-355	TTACGGAAGTAACTTGCCAATGTCAAGAACAATTGGATGCTTGTT	74,3	45	0,978	1	0,996	1	0,994	0,782	mid
3	5	C13	**pc0364**	unknown protein	**-**	1524	pc0364_772-816	GATTTTAGTGCTGATGAATTAGTGTGGGATCAATCTTCGCAACGT	74,3	45	0,979	1	0,997	1	0,991	0,791	mid
3	5	G13	**pc0365**	conserved hypothetical protein	**-**	741	pc0365_414-459	AAATGCTGCTACTTTATCAGGAGGAGAAAGACGTCGAGTGGAGATT	74,3	46	0,979	1	0,997	1	0,958	0,835	mid
3	5	K13	**pc0366**	strongly similar to nucleoside-diphosphate kinase	**ndk**	729	pc0366_428-480	TGACAAAAGATCAAGCAAGTAAATTCTACGCTATTCATAAGGATCGACCTTTC	74,2	53	0,971	1	0,994	1	0,938	0,785	mid
3	5	O13	**pc0367**	strongly similar to p-aminobenzoate synthase	**pabA**	579	pc0367_277-327	GTTGTCAAAGCCGCTTATCCTATGCATGGTAAAAGTAGTTTCATCTACCAT	74,3	51	0,982	1	0,995	1	0,986	0,841	mid
3	5	C17	**pc0368**	strongly similar to nucleoside-diphosphate kinase	**ndk**	432	pc0368_23-68	CTATCATTAAGCCTGACGCAGTAGGTAACAATCACATTGGCGAAAT	74,2	46	0,985	1	0,999	0,995	0,993	0,853	random
3	5	G17	**pc0369**	similar to phenylalanine-tRNA ligase beta chain	**pheT**	2409	pc0369_1245-1290	TCGAATAAATCAGATATTGGGGACAACGCTTAGTCGAGGAGAAGTT	74,2	46	0,977	1	0,998	0,999	0,961	0,809	mid

3	5	K17	**pc0370**	hypothetical protein	**-**	966	pc0370_481-526	CAAATAGAATCTTCTGTGCAAGATGGGTTTGGTAAGCGAATAGTGC	74,2	46	0,984	1	0,993	1	0,997	0,844	mid
3	5	O17	**pc0371**	similar to ferredoxin [2Fe-2S] IV	**fdxC**	276	pc0371_70-117	GCTTATCAATTGAATTGTTCTCTTCCTTTCCGTTTTGGTTGTACCAAA	74,2	48	0,978	1	0,999	1	0,996	0,764	random
3	5	C21	**pc0372**	unknown protein	**-**	552	pc0372_245-298	AACTTAACAAAGGATCCACACAAATTCAGTGTTTATTACGTAATCAAGAAGGCC	74,2	54	0,979	1	0,995	1	0,968	0,826	mid
3	5	G21	**pc0373**	conserved hypothetical protein	**-**	228	pc0373_101-152	AGTTAGTTTACGTTGATAGCTTGCTTAAATCTGTTGGATTTCCTCACGGTCT	74,2	52	0,98	1	0,994	1	0,986	0,819	mid
3	5	K21	**pc0374**	unknown protein	**-**	213	pc0374_116-160	GATTAGTTGGCTTCGCAGGTGGTCTTGAAACAGTCAAAGTTACAG	74,3	45	0,985	1	0,993	1	0,992	0,866	mid
3	5	O21	**pc0375**	similar to rapA, a bacterial member of the swi/snf helicase family	**rapA**	2682	pc0375_1356-1400	TAACTATGGATTCCATGGAATTTTAGCAGACGAAATGGGACTTGG	74,2	45	0,974	1	0,998	1	0,986	0,744	mid
3	6	C01	**pc0376**	hypothetical protein	**-**	819	pc0376_373-421	TTTTCTTATTGTCATAAACCTTTTGAATGTCCGTCTGGTCGCTTTACAC	74,2	49	0,976	1	0,995	1	0,962	0,801	mid
3	6	G01	**pc0377**	unknown protein	**-**	258	pc0377_64-111	GTTATTTATCTCCTGTTCCTTTTGTCAGATAGTGCGGACATTGACACC	74,1	48	0,975	1	0,983	1	0,992	0,785	random
3	6	K01	**pc0378**	conserved hypothetical protein	**-**	963	pc0378_517-568	GAACAAACTCCTATTATGATGTATTGTACAGGGGGCATTCGATGTGAACTAT	74,2	52	0,982	1	0,995	1	0,966	0,867	mid
3	6	O01	**pc0379**	strongly similar to thioredoxin	**trxA**	321	pc0379_109-161	ATAGCTCCAATTGTTGAACAATTATCTACTACGCTACAGGGGAAAGCAAAAGT	74,2	53	0,97	1	0,996	1	0,947	0,754	mid
3	6	C05	**pc0380**	unknown protein	**-**	222	pc0380_54-108	TTCACATTCTACCCTAACAAAGGGTAAAAATGACCTTTTGAGAGTTTTAGTCGTT	73,9	55	0,846	0,709	0,965	0,946	0,979	0,763	random
3	6	G05	**pc0381**	similar to glutathione-regulated potassium-efflux system protein	**kefC**	1680	pc0381_720-764	ATTCATGATAGCAGTCGCTTCAGCACTAGTTTTTGGAACATCGAT	74,2	45	0,967	1	0,997	1	0,879	0,813	mid
3	6	K05	**pc0382**	conserved hypothetical protein	**-**	451	pc0382_37-90	AATGCTGGTAATATTGTAAGAACTTGTGCCGTTACTGGAACAGATTTAATGATG	74,2	54	0,981	1	0,995	1	0,993	0,82	random
3	6	O05	**pc0383**	similar to mip (macrophage infectivity potentiator, fkbp-type peptidyl-prolyl cis-trans isomerase)	**mip**	873	pc0383_463-515	GTCGTTGAACCTCACTCTTCTCCAAAAATTCATTATACAGGAAAATACCAAGA	74,3	53	0,973	1	0,997	1	0,975	0,752	mid
3	6	C09	**pc0384**	strongly similar to aspartate-tRNA ligase	**aspS**	1800	pc0384_891-935	CGATCTTCGCTTTGGTATGAAACTGCACAATTTAAATCATCTTGC	74,2	45	0,973	1	0,996	1	0,99	0,732	mid
3	6	G09	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
4	1	D01	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
4	1	H01	**pc0385**	strongly similar to histidine-tRNA ligase	**hisS**	1275	pc0385_655-700	CAAGACAAACAAATTGTTGCTGACGCTCCCTCAATTCTAGATTTTC	74,4	46	0,969	1	0,982	0,985	0,984	0,751	mid
4	1	L01	**pc0386**	unknown protein	**-**	2472	pc0386_1192-1241	AAACAAGGAACTCTCACTCGACTAGCTACTCTTTCAACCGATCCTAATCA	74,2	50	0,98	1	0,998	1	0,955	0,849	mid
4	1	P01	**pc0387**	strongly similar to regulatory protein uhpC	**uhpC, glpT**	1383	pc0387_662-711	AAAAATACCGTAATGATTATGTGGATAAAGCTGAGGCAGACAAAGAGGCT	74,2	50	0,979	1	0,999	1	0,969	0,819	mid
4	1	D05	**pc0388**	unknown protein	**-**	483	pc0388_215-265	TGGCTCGCAAATATGAAGTAGGAACCCAAGCATCAGACAGTATCTATAATA	74,2	51	0,983	1	0,998	1	0,973	0,86	mid
4	1	H05	**pc0389**	similar to DNA polymerase III, alpha chain	**dnaE**	3759	pc0389_1862-1907	TGAAGACACTGACTGCTATCCAGATTTGTGTAAATGCTGTGAAAGC	74,2	46	0,985	1	0,998	1	0,981	0,872	mid
4	1	L05	**pc0390**	hypothetical protein	**-**	1407	pc0390_760-809	GAAAGGTATGTTCAAAGAATTAAGGATATGTATGCCAAAGGTTTGTGCGA	74,3	50	0,975	1	0,998	1	0,944	0,81	mid
4	1	P05	**pc0391**	hypothetical protein	**-**	558	pc0391_306-354	TACTGAAACTCGCTTAAATGCTGTTGCAGAAGTGATTATTACGGAAGCT	74,2	49	0,975	1	0,998	1	0,974	0,772	mid
4	1	D09	**pc0392**	similar to rsbW, negative regulator of sigma-B activity (switch protein/serine kinase)	**rsbW**	423	pc0392_114-164	TGTTGCAGCTGAAGAAGCTCTTGTAAATATTATTCACTATGGATATCCCGA	74,3	51	0,964	1	0,997	1	0,901	0,756	mid
4	1	H09	**pc0393**	hypothetical protein	**-**	498	pc0393_269-319	ATGATTATATCGTATGGATTGTTCCTGATCAGCTAGATGATTTACCCGTCA	74,2	51	0,982	1	0,995	1	0,981	0,848	mid
4	1	L09	**pc0394**	similar to serine-type D-Ala-D-Ala carboxypeptidase (penicillin binding protein)	**dac**	1371	pc0394_624-675	ACATCAAACAACGGCTTACGATTTAGCTCTAATAACCAAAGAAGCTTTGAAA	74,2	52	0,969	1	0,999	1	0,937	0,753	mid
4	1	P09	**pc0395**	similar to dimethyladenosine transferase	**ksgA**	771	pc0395_380-424	AAGTCGCTAGGCGTATGACAGCTTTACCTGGCCAATCTGATTATA	74,2	45	0,985	1	0,998	1	0,993	0,856	mid
4	1	D13	**pc0396**	hypothetical protein	**-**	1128	pc0396_489-533	AATTGTTCAAGGTGATATCCTTTTAAAGCGTATGATCGGTGCCAG	74,2	45	0,971	1	0,999	1	0,924	0,787	mid
4	1	H13	**pc0397**	similar to 16S rRNA m5C967 SAM-dependent methyltransferase	**rsmB, fmu, fmv, sun**	1134	pc0397_535-580	AAAGAAGGCTTGTTCGAAGTACAGGACGAAGGAAGTCAACTATTGG	74,2	46	0,98	1	0,999	0,966	0,967	0,874	mid
4	1	L13	**pc0398**	similar to D-alanine--D-alanine ligase	**ddlA**	2397	pc0398_1215-1269	TGGAAAAAATGACTTAATCTGGCAACTACCTTATGCTTATACACTGGATCATACA	73,9	55	0,97	1	0,968	1	0,985	0,787	mid
4	1	P13	**pc0399**	similar to eucaryotic myosin heavy chain	**zip**	2523	pc0399_1269-1323	GAAAAATCGACTTACCAAGTTTTCAGCAGATATGTTGGAAATGTTAAAGGGTAAA	74,3	55	0,976	1	0,997	0,993	0,994	0,759	mid
4	1	D17	**pc0400**	similar to apolipoprotein N-acyltransferase	**cutE**	1590	pc0400_823-874	CCTTTAATATCTCCTTATGCTTCATTTTTATCGTCCGATCGAGGAAATCAAT	74,2	52	0,971	1	0,999	1	0,973	0,718	mid
4	1	H17	**pc0401**	similar to UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	**envA, lpxC**	879	pc0401_464-514	TGGCTTTACCCTTCGATGGTTATCGTATTAGCTACACTTTGAGTTATCCAG	74,3	51	0,984	1	0,997	0,996	0,977	0,869	mid
4	1	L17	**pc0402**	strongly similar to myristoyl-acyl carrier dehydratase	**fabZ**	465	pc0402_47-91	TCATCAATATTTTACCCCACCGTTATCCTTTTCTGCTTGTCGATC	74,3	45	0,975	1	0,998	1	0,977	0,76	5´preference
4	1	P17	**pc0403**	strongly similar to acyl-(acyl-carrier-protein)-UDP-N-acetylglucosamine o-acyltransferase	**lpxA**	849	pc0403_422-469	CAGGACATGTAATTGTGGAAGATTATGCTGTGATTGGAGGTATGACTC	74,3	48	0,986	1	0,996	1	0,997	0,859	mid
4	1	D21	**pc0404**	strongly similar to methionyl-tRNA formyltransferase	**fmt**	957	pc0404_459-503	CAAAAAAGTGTCAGTGCAAATCACTTCGGAAATGACTTATGGTGA	74,4	45	0,979	1	0,986	1	0,979	0,837	mid
4	1	H21	**pc0405**	hypothetical protein	**-**	828	pc0405_427-479	TTGAAAGTAACAGTCTTAGCTTCTCAAGATGGGTGCCCTTTTAGAGTTATCCT	74,2	53	0,982	1	0,999	1	0,988	0,822	mid
4	1	L21	**pc0406**	unknown protein	**-**	186	pc0406_28-82	TCTTTCTTACATACATGTGCTAAGTGTTTTTTGAATCGATATATTGCCTTAAGGA	72,5	55	0,929	1	0,829	1	0,97	0,755	random
4	1	P21	**pc0407**	unknown protein	**-**	186	pc0407_2-53	TGAAAAAGGCTGATCATTACTCCAAGCAAACTAACGGTAGTAAAACATACCA	74,3	52	0,973	1	0,992	1	0,985	0,749	random
4	2	D01	**pc0408**	unknown protein	**-**	1005	pc0408_451-502	TTAGCACTGCAGAATCGTTTGCAAGAACCTATAGCTGATTTAACAAGTAGCT	74,3	52	0,974	1	0,995	1	0,947	0,809	mid
4	2	H01	**pc0409**	unknown protein	**-**	897	pc0409_447-491	AGTTGTTGCGTTTCAAACTGTTTCTAGATTAGGTGCTGCAATTGG	74,2	45	0,98	1	0,994	1	0,997	0,804	mid
4	2	L01	**pc0410**	unknown protein	**-**	1083	pc0410_791-837	TGCCTGGACAGAGTCTAGATACTTGGGTACGAGGGGGTCTATGTATA	74,3	47	0,984	1	0,993	0,956	0,999	0,903	random

4	2	P01	**pc0411**	unknown protein	**-**	558	pc0411_251-302	CTGATTTAAGCAGTTTTAAACCTAATCAACTTTTGCGTGATGGACAAGTGAT	74,2	52	0,967	1	0,999	1	0,971	0,686	mid
4	2	D05	**pc0412**	strongly similar to 50S ribosomal protein L3	**rplC**	708	pc0412_362-406	ATACTTTTAATGGTATCGAATTCGTTGATGCGACAGCGATCTCAA	74,2	45	0,978	1	0,996	1	0,993	0,784	mid
4	2	H05	**pc0413**	similar to 50S ribosomal protein L4	**rplD**	591	pc0413_21-66	TGCACTTAGAGCAAATGCTAGACAGTGGTCAGCTAGTACCAAAACG	74,5	46	0,983	1	0,976	1	0,99	0,894	5´preference
4	2	L05	**pc0414**	strongly similar to 50S ribosomal protein L23	**rplW**	336	pc0414_42-86	TGTGACTGAAAAGTCTATGGTGCTTCAACAGTTGAAAACTGCAGA	74,3	45	0,981	1	0,997	1	0,999	0,802	random
4	2	P05	**pc0415**	strongly similar to 50S ribosomal protein L2	**rplB**	846	pc0415_425-475	TGCCACTTGGTTCTGTTATACATAATATTGAATTATACCCTGGAAAAGGCG	74,2	51	0,983	1	0,997	1	0,999	0,826	mid
4	2	D09	**pc0416**	strongly similar to 30S ribosomal protein S19	**rpsS**	264	pc0416_111-161	TTCAATGATTACACCTGATATGGTCGGACATACGTTTGAAGTACATAATGG	74,3	51	0,985	1	0,993	1	0,978	0,885	mid
4	2	H09	**pc0417**	strongly similar to 50S ribosomal protein L22	**rplV**	336	pc0417_14-61	AAGCAATAAGCAAATATATACGCATCAGTCCTCGCAAAGCTCGTTTAG	74,2	48	0,983	1	0,996	1	0,998	0,824	random
4	2	L09	**pc0418**	strongly similar to 30S ribosomal protein S3	**rpsC**	645	pc0418_416-460	AATCATCGATTGATGCTGGTGCATTCGGTATTAAAGTTCAGTTGT	74,3	45	0,968	1	0,989	0,987	0,907	0,834	mid
4	2	P09	**pc0419**	strongly similar to 50S ribosomal protein L3	**rplP**	420	pc0419_214-263	GATAAACCAATTACAAAGAAACCTGCCGAAGTGAGAATGGGTAAAGGTAA	74,2	50	0,981	1	0,998	1	0,997	0,803	mid
4	2	D13	**pc0420**	similar to 50S ribosomal protein L29	**rpmC**	222	pc0420_136-185	AAACATACTCGCAAAGATATCGCTCGCTTGTTAACAGTGATTACAGAGAA	74,2	50	0,985	1	0,998	1	0,976	0,878	mid
4	2	H13	**pc0421**	strongly similar to 30S ribosomal protein S17	**rpsQ**	246	pc0421_80-128	TGAAAGTTGAGCGTACTTTTGCTCATCCTCAGTATGGTAAAATTGTCAC	74,2	49	0,975	1	0,997	0,972	0,979	0,806	random
4	2	L13	**pc0422**	strongly similar to 50S ribosomal protein L14	**rplN**	369	pc0422_63-107	CTTTAAAGTATTAGGTGGATCAAAGCGTCGTTATGCCCATGTTGG	74,3	45	0,984	1	0,994	1	0,998	0,844	random
4	2	P13	**pc0423**	strongly similar to 50S ribosomal protein L24	**rplX**	351	pc0423_69-123	CAGCCGAGGTCAGATAGGAACTGTACAATCATGTAAGGGTGATAGAGTAATAGTT	74,2	55	0,99	1	0,998	1	0,999	0,901	random
4	2	D17	**pc0424**	strongly similar to 50S ribosomal protein L5	**rplE**	558	pc0424_298-345	ATTGACCGTTTTGTTAACATCGTTTGTCCTCGTATTCGTGACTTTAGA	74,2	48	0,983	1	0,999	1	0,982	0,846	mid
4	2	H17	**pc0425**	strongly similar to 30S ribosomal protein S8	**rpsH**	402	pc0425_46-90	AATGGTACAAAAGCTCAACATCGCTATGTCGATGTAAACTGGAGC	74,3	45	0,976	1	0,998	0,982	0,978	0,803	5´preference
4	2	L17	**pc0426**	strongly similar to 50S ribosomal protein L6	**rplF**	549	pc0426_197-244	TTCACGGCCTTTACCGTACTCTTATCCATAATATGGTAGTTGGGACAA	74,3	48	0,979	1	0,997	1	0,921	0,894	mid
4	2	P17	**pc0427**	strongly similar to 50S ribosomal protein L18	**rplR**	372	pc0427_29-73	AACTACGTGTTAAACGTGCCGTTAGAGTTCGTAAGCATCTTCGTG	74,1	45	0,98	1	0,989	0,938	0,997	0,9	random
4	2	D21	**pc0428**	strongly similar to 30S ribosomal protein S5	**rpsE**	504	pc0428_249-293	AACTGAAGGTACAACCATTCCTCACGAAGTAACTGTTCAATGGGA	74,2	45	0,985	1	0,994	1	0,996	0,86	mid
4	2	H21	**pc0429**	strongly similar to 50S ribosomal protein L15	**rplO**	453	pc0429_9-58	TTTAAATACACTCAAAGATTCTACGCGTAAACGTAAACCTCGCAAACGAG	74,2	50	0,985	1	0,998	1	0,992	0,854	random
4	2	L21	**pc0430**	similar to preprotein translocase SecY	**secY**	1482	pc0430_742-786	GCAATGGGATTAATTTTCCAACAACTTAATCTGGACTCGCAAGAA	74,3	45	0,976	1	0,994	1	1	0,754	mid
4	2	P21	**pc0431**	strongly similar to 30S ribosomal protein S13	**rpsM**	369	pc0431_112-158	GGTTTAGATCCAAACATGCGTGCTCATAAACTTACCCAAGATGACTT	74,2	47	0,978	1	0,998	1	0,945	0,838	5´preference
4	3	D01	**pc0432**	strongly similar to 30S ribosomal protein S11	**rpsK**	408	pc0432_89-139	AAGCTACCTTTAACAATACCATTATTGCGATTACTGATCCATCAGGTCGAG	74,3	51	0,982	1	0,994	1	0,998	0,825	random
4	3	H01	**pc0433**	similar to DNA-directed RNA polymerase alpha chain	**rpoA**	1116	pc0433_599-645	TCGAGAATACACGGGTAGGTCAAGATACTGATTTTGATCGACTCATC	74,3	47	0,978	1	0,997	0,989	0,96	0,841	mid
4	3	L01	**pc0434**	strongly similar to 50S ribosomal protein L17	**rplQ**	429	pc0434_6-50	ACACCTCAATCAAACATGTAAGCTCAATCGAACCACGTCTCATAG	74,1	45	0,983	1	0,989	1	0,993	0,859	random
4	3	P01	**pc0435**	strongly similar to Glyceraldehyde 3-P dehydrogenase A	**gapA**	1020	pc0435_520-564	TTAATGACCACTATACATGCTGTCACAGCTTCTCAACCAACCGTT	74,2	45	0,988	1	0,997	1	0,989	0,891	random
4	3	D05	**pc0436**	unknown protein	**-**	351	pc0436_185-232	AAATAGGAATTCGCAATCACCCTTCGCATTTGTTTCATCAATTATCTA	74,2	48	0,977	1	0,999	1	0,981	0,774	random
4	3	H05	**pc0437**	hypothetical protein	**-**	1131	pc0437_705-757	AACTGAAGAGGAACAGTATAAGCCTCATGACAAGGTTCAAGAACTCCTAAATG	74,3	53	0,963	1	0,996	1	0,862	0,805	mid
4	3	L05	**pc0438**	unknown protein	**-**	1992	pc0438_1017-1063	TTTAAGCTTAGATTCTGACGGTTTGGCATATAGCCTACAACCAGGCT	74,2	47	0,986	1	0,999	1	0,98	0,882	mid
4	3	P05	**pc0439**	unknown protein	**-**	195	pc0439_50-104	TTTGCACTTTAATTGATCCGAGGAATGATTATATAGAGTTTACTTCCAACAACGT	73,8	55	0,961	1	0,952	1	0,951	0,774	mid
4	3	D09	**pc0440**	unknown protein	**-**	759	pc0440_425-476	TGTTCTTTCAAATAAACTGGTGTTATATGGGAGGTGTTGCATATGGGTATCT	74,2	52	0,976	1	0,999	1	0,956	0,802	mid
4	3	H09	**pc0441**	conserved hypothetical protein	**-**	1167	pc0441_574-622	AAAACTTACTATTCCAACGAAGCTTTAAATCCCCGTCCAAAAAGAGGTC	74,3	49	0,974	1	0,992	1	0,989	0,749	mid
4	3	L09	**pc0442**	similar to diaminopimelate epimerase	**dapF**	810	pc0442_404-454	ATTATGTGCACTCATTAAATACAGGGGTTCCACACATTATCTTATTCGCTG	74,2	51	0,982	1	0,994	0,997	0,998	0,824	mid
4	3	P09	**pc0443**	strongly similar to ATP-dependent Clp protease proteolytic subunit	**clpP**	621	pc0443_144-189	AATTATTCGCAAGCTTTGGTATCTCGAATTAACAGATCCTGGCAAA	74,3	46	0,98	1	0,996	1	0,99	0,802	random
4	3	D13	**pc0444**	strongly similar to glycine hydroxymethyltransferase	**glyA**	1476	pc0444_728-775	TTGCAGATAGTGTAGGAGCTACTTTGATGGTAGATATGGCCCACTTTG	74,2	48	0,989	1	0,999	1	0,989	0,896	mid
4	3	H13	**pc0445**	unknown protein	**-**	441	pc0445_222-267	TAACAATCAACTGTACATTCGAGGTAATGGAGCGAACCTAACCTGG	74,4	46	0,986	1	0,986	1	1	0,882	mid
4	3	L13	**pc0446**	conserved hypothetical protein	**-**	771	pc0446_361-413	GAAGAAGATATGCTTAAGAGTTTGAAAGAGGGTGCAGAAGAAACAGCTGTTAA	74,2	53	0,972	1	0,996	1	0,974	0,74	mid
4	3	P13	**pc0447**	conserved hypothetical protein	**-**	285	pc0447_11-56	AATATGCTCTTGTCGGTCTTGCTTCAGATAGGGTTTGTCACTGTTT	74,1	46	0,984	1	0,986	1	0,999	0,864	random
4	3	D17	**pc0448**	unknown protein	**-**	675	pc0448_208-262	TTTCAAATACTTAAGCCTCTATTCAATCCTACATTCTCTCTTATTCCAGCAACGC	74,3	55	0,962	1	0,998	1	0,869	0,776	mid
4	3	H17	**pc0449**	strongly similar to GTP cyclohydrolase I	**folE**	675	pc0449_340-386	CACTTTGTTCCCATGTCAGGTTTTGCTTATGTTGCCTATATCCCTAC	74,3	47	0,982	1	0,996	1	0,999	0,814	mid
4	3	L17	**pc0450**	similar to tRNA (Guanosine-2'-O-)-methyltransferase	**trmH**	741	pc0450_294-347	GTCAGCTCATAACGTGGGAAGTATTATCAGAACAGTAGAAGCTTTCTCCTTAGG	74,2	54	0,975	1	0,998	1	0,922	0,845	mid
4	3	P17	**pc0451**	conserved hypothetical protein	**-**	1587	pc0451_815-859	GAACTCGTGCAAGCCAGGTACAATCTCGTCTAAGAGAAATTGAAC	73,9	45	0,973	1	0,968	1	0,98	0,82	mid
4	3	D21	**pc0452**	hypothetical protein	**-**	1317	pc0452_718-764	AATTTACGCTACGCTTTTTACCTTGCACAAACATACAAAGATGCTGG	74,2	47	0,976	1	0,999	1	0,942	0,827	mid
4	3	H21	**pc0453**	similar to ABC transporter substrate binding protein yaeC	**yaeC, metQ**	807	pc0453_381-434	GAAAAATGGCCTTACTTTAGCTATTCCTAGTGACCCCTCTAATCAAGCTAGAGC	74,2	54	0,977	1	0,995	1	0,976	0,798	mid
4	3	L21	**pc0454**	strongly similar to ABC transporter permease yaeE	**yaeE, metI**	621	pc0454_387-438	ACTTGGAATGACTACAACAATTATTAATCTCGTAGGCTATAGCGCAATGGCT	74,3	52	0,973	1	0,998	1	0,925	0,82	mid
4	3	P21	**pc0455**	strongly similar to ABC transporter ATP-binding protein abc	**abc**	1026	pc0455_502-547	CTTTTATGTGATGAGCCAACATCTGCCTTAGATCCAAAAACTACGC	74,2	46	0,981	1	0,993	1	0,988	0,828	mid

4	4	D01	**pc0456**	unknown protein	**-**	1485	pc0456_655-700	CTAGGTGCGACAACGACCTCATTTTTGGAAAATCCTCAAGTAAAAT	74,2	46	0,963	1	0,998	1	0,911	0,726	mid
4	4	H01	**pc0457**	unknown protein	**-**	198	pc0457_57-107	AAGATACGATACCAACGAATTTGCAATTCGATTAAACAACAGGTCAAAGTT	74,3	51	0,966	1	0,99	1	0,957	0,711	mid
4	4	L01	**pc0458**	similar to XerC Protein	**xerC**	990	pc0458_506-551	TTTATAGTTCAGGTCTGCGAGTGAGCGAACTTGTTTCCTTAGATCG	74,3	46	0,986	1	0,991	1	0,99	0,881	mid
4	4	P01	**pc0459**	similar to binuclear zinc phosphodiesterase	**elaC**	921	pc0459_414-465	TTTACAACACGGTATAGAAAATATCGGTTGGCGTATTACAGAAGCAGATACG	74,2	52	0,976	1	0,997	1	0,952	0,812	mid
4	4	D05	**pc0460**	similar to glpG protein	**glpG**	1176	pc0460_640-685	AAAAATAGAGTTGAAAACGCATTAAAAGGGGATTTAGCTCCCCCCT	74,2	46	0,969	1	0,999	1	0,949	0,739	mid
4	4	H05	**pc0461**	strongly similar to ADP-heptose synthase	**rfaE**	513	pc0461_201-250	TGTCGCACTAAATAGTGATGAATCCATTAAGCGCTATAAAAACCCAAATC	74,1	50	0,972	1	0,987	1	0,943	0,816	mid
4	4	L05	**pc0462**	similar to endopeptidase (ATP-dependent serine protease) La	**lon**	2508	pc0462_1107-1161	TGGTGTGGGTAAATTAGCTAAAGGTGTTCGAGGTAGTATTATTTGTTTAGTTGGC	74,2	55	0,961	1	0,994	1	0,852	0,797	mid
4	4	P05	**pc0463**	unknown protein	**-**	2139	pc0463_1069-1119	TTTAAGTATTATTTACCATTGGATCATGGGTTATCAGAGTGGGTGAAAGCC	74	51	0,976	1	0,975	1	0,998	0,812	mid
4	4	D09	**pc0464**	unknown protein	**-**	2229	pc0464_987-1038	GCAAATAGGACATCAGATAGACACATTAAATAGTCAGCTGGTCAAAAAGGCT	74,1	52	0,962	1	0,987	0,989	0,871	0,814	mid
4	4	H09	**pc0465**	similar to deoxyguanosinetriphosphate triphosphohydrolase (dGTPase)	**dgt**	1149	pc0465_612-662	GAATATCATGCCAGGTACTTTAGAGGGATGTTTAGTCAAGCTTTGCGATAC	74,2	51	0,981	1	0,999	1	0,964	0,85	mid
4	4	L09	**pc0466**	hypothetical protein	**-**	669	pc0466_333-377	AATTGGAGGTGCTTATGTACGCAAAGGCATATTAACTGATCAGGG	74,2	45	0,987	1	0,999	1	0,997	0,864	mid
4	4	P09	**pc0467**	strongly similar to 30S ribosomal protein S21	**rpsU**	183	pc0467_46-90	CTCCGTGCCTTGAAGAAACGTCTCGATAAAGAAGGAGTTATGAAG	74,2	45	0,973	1	0,996	1	0,953	0,778	mid
4	4	D13	**pc0468**	strongly similar to heat shock protein dnaJ	**dnaJ**	1161	pc0468_461-508	CTAACTACGCAAATTGTAATGTTTGCAATGGTAAAGGCTCCTCCTCAT	74,2	48	0,968	1	0,998	1	0,879	0,829	mid
4	4	H13	**pc0469**	conserved hypothetical protein		780	pc0469_475-529	TGTGATTACTTATATCTTGAATCTAACCATCAACCTTCTATGGTACATGCCTCCC	74,2	55	0,976	1	0,998	1	0,916	0,866	mid
4	4	L13	**pc0470**	similar to multifunctional cell division protein ftsK	**ftsK**	2628	pc0470_1264-1308	GGAATAGAGGCAAAGGTTGGTCAAATTAATTGTGGCCCAACTATC	74,4	45	0,97	1	0,987	1	0,949	0,78	mid
4	4	P13	**pc0471**	similar to bacitracin resistance protein (probable undecaprenol kinase)	**bacA**	774	pc0471_416-460	TTGGATTATTTCAAGCCGTGGCAGTTTTACCAGGTATTTCTCGTA	74,3	45	0,977	1	0,99	1	0,972	0,811	mid
4	4	D17	**pc0472**	hypothetical protein		1554	pc0472_827-875	TAGCTATCTACTTTACCTTTCTAGGCTTCAACGCCTCTGTTGTTCGAGC	74,2	49	0,98	1	0,996	1	0,951	0,858	mid
4	4	H17	**pc0473**	hypothetical protein	**-**	807	pc0473_449-495	TTCTGCAAATACATAACGGATTTGCCAAGTTAACAGATACGGGAATC	74,2	47	0,976	1	0,999	1	0,956	0,807	mid
4	4	L17	**pc0474**	strongly similar to HPr(Ser) kinase/phosphatase	**hprK;ptsK**	948	pc0474_402-448	TCCTAGTGTTAGTTGTCATGGGTCTCTTGTTGAGGTATTTGGAGTGG	74,3	47	0,976	1	0,993	1	0,927	0,864	mid
4	4	P17	**pc0475**	similar to phosphocarrier protein hpr (histidine-containing phosphocarrier protein of the PTS)	**ptsH**	267	pc0475_3-52	GAAACTCGTTTGTAAAGTACAAGTAAAAAATCGCATGGGTCTTCATACGC	74,1	50	0,977	1	0,989	1	0,998	0,781	random
4	4	D21	**pc0476**	similar to phosphoenolpyruvate-protein phosphotransferase (PTS enzyme I)	**ptsI**	1779	pc0476_1514-1564	GTGGAGAAATCGCCTCTGATCCTCGTTTTATTCCTTTATTACTAGGACTTG	74,3	51	0,981	1	0,997	1	0,999	0,802	random
4	4	H21	**pc0477**	hypothetical protein	**-**	297	pc0477_80-124	AAAATCTTGAAGTGGTAGGTGTCGCAGGAAGTGGTTTAGTGACAA	74,2	45	0,977	1	0,998	1	0,931	0,855	mid
4	4	L21	**pc0478**	strongly similar to DNA-directed DNA polymerase III subunits gamma/tau dnaX	**dnaX, dnaX, dnaZX**	1569	pc0478_757-806	GAATTAGATTTAGCGGGTAAGGAAGGCAATTTCGTAAAGGCTTTTGAAAT	74,2	50	0,969	1	0,999	1	0,971	0,702	mid
4	4	P21	**pc0479**	hypothetical protein	**-**	1410	pc0479_642-687	CTCGAATTTAGTAAAGGCTTTAAGAGCCCCACATGTACGTGGAAGA	74,3	46	0,976	1	0,997	1	0,936	0,835	mid
4	5	D01	**pc0480**	conserved hypothetical protein	**-**	1518	pc0480_918-966	TCTAGATGAACTTCCTGAATTTTCACGCACTGTTCTCGAGGTATTAAGG	74,3	49	0,962	1	0,993	1	0,842	0,831	mid
4	5	H01	**pc0481**	hypothetical protein	**-**	684	pc0481_352-406	CTTCACTATATTAGTCTCATGAGCTTAACATTTGAAATGGCGAATTTGGATTTTG	74,2	55	0,97	1	0,999	0,945	0,991	0,765	mid
4	5	L01	**pc0482**	conserved hypothetical protein	**-**	1296	pc0482_560-610	GCCAAGAGAAACGAAAAGAAGACGTTTATCGCTTATTAGCCAATACAGAAT	74,2	51	0,966	1	0,998	1	0,911	0,763	mid
4	5	P01	**pc0483**	conserved hypothetical protein	**-**	702	pc0483_367-411	GAAATGCTGGATAAAATCGGTGCAATTGCGAAAATTATAGGAACA	74,3	45	0,973	1	0,989	1	0,985	0,76	mid
4	5	D05	**pc0484**	similiar to phosphate starvation-inducible protein (phoH)	**phoH, psiH**	1302	pc0484_643-689	AAGACAAATCAATTGTGGGGTATTAAACCTCGTAACGTTGAACAACG	74,3	47	0,981	1	0,996	1	0,991	0,816	mid
4	5	H05	**pc0485**	similar to ATP/ADP translocase (AATP1) precursor (Arabidopsis thaliana)	**ntt_4**	1296	pc0485_759-805	AGATTATTCTGGTACTACATTTCCGAATGATGTGATTGCACAAACGC	74,2	47	0,972	1	0,998	1	0,89	0,86	mid
4	5	L05	**pc0486**	hypothetical protein	**-**	501	pc0486_327-373	ATCCAAAAACGAAGGAGAAGGGAAACGAGCTATACGAGTTTATCCAT	74,2	47	0,973	1	0,999	0,996	0,925	0,819	mid
4	5	P05	**pc0487**	similar to mutT protein	**mutT**	459	pc0487_245-292	AAAGTAAGCATTATGTCACCCTTTTTGTGTTTGTCAACGAGTTTGAGG	74,1	48	0,979	1	0,985	0,998	0,986	0,838	mid
4	5	D09	**pc0488**	conserved hypothetical protein	**-**	321	pc0488_60-106	TAAACATTACACACAAGAACAAGTCGATGTGTGGGCTCCTGAATTAA	74,2	47	0,978	1	0,995	0,964	0,999	0,821	random
4	5	H09	**pc0489**	conserved hypothetical protein	**-**	1023	pc0489_528-574	AAGATCAGAACACTGGCCTGTCAGCGAACATAAAATACAGAGCTATG	74,3	47	0,984	1	0,995	1	0,985	0,862	mid
4	5	L09	**pc0490**	conserved hypothetical protein	**-**	630	pc0490_309-359	AAATCTAGTCGGTCTTTCAACACAAGTTCCTGGTCGAATCATCTTTTTAAC	74,2	51	0,98	1	0,998	1	0,993	0,799	mid
4	5	P09	**pc0491**	unknown protein	**-**	276	pc0491_125-171	CAAAAAGAGTGCAGCGAGAAGTTCATCGAGAAATGGAAAAAATAGAG	74,3	47	0,967	1	0,995	1	0,986	0,673	mid
4	5	D13	**pc0492**	unknown protein	**-**	345	pc0492_9-53	CTCTCTTACCTTTCTTTCCATTGCAAGATACAACCCCTTTTTCGC	74,2	45	0,981	1	0,997	1	0,997	0,807	random
4	5	H13	**pc0493**	unknown protein	**-**	204	pc0493_24-68	CGGTCCAGTTTCAGACTATCGGGCTACCAAGACTGTTAGGTCTTA	74,4	45	0,977	1	0,98	1	0,921	0,921	mid
4	5	L13	**pc0494**	similar to isoleucyl-tRNA synthetase	**ileS, ilvS**	3117	pc0494_1550-1594	GTTGGTTTGAATCAGGTTCCATGCCTTATGCTCAGAATCACTATC	74,1	45	0,979	1	0,99	1	0,99	0,814	mid
4	5	P13	**pc0495**	conserved hypothetical protein	**-**	225	pc0495_97-145	GAAGGGACGGTCATTATTTTATCGGAAGAAACCTACCAGAACCTACTTG	74,3	49	0,969	1	0,989	1	0,927	0,798	random
4	5	D17	**pc0496**	similar to signal peptidase I	**lepB**	1965	pc0496_957-1007	CAACATCGCCATCGCAAGATTATTGACAAAAGATCAGATAGAAAAGTTTAC	74,2	51	0,972	1	0,998	1	0,973	0,738	mid
4	5	H17	**pc0497**	hypothetical protein	**-**	738	pc0497_399-443	ATTATCTCCTATTCCTCAAGAAGCCCGTAAAAAAATCGGACCCAA	74,2	45	0,97	1	0,999	1	0,971	0,711	mid
4	5	L17	**pc0498**	unknown protein	**-**	327	pc0498_157-	AATGAAGTAGTGACAGGGCAAGAATATATGATTGCAGATTGGTCAGCTTA	74,2	50	0,981	1	0,995	0,972	0,992	0,862	mid

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4	5	P17	**pc0499**	unknown protein	-	330	pc0499_71-115	GTTTGTTTTGGGATATCTCTCTTTCCATTGGCCCATTAGAGCTTC	74,2	45	0,969	1	0,999	1	0,905	0,797	mid
4	5	D21	**pc0500**	conserved hypothetical protein	-	279	pc0500_119-164	CCGATAAAGGCCAAGCAAATACAGAACTCATTCGTTTTCTCTCTTC	74,3	46	0,976	1	0,998	1	0,978	0,775	mid
4	5	H21	**pc0501**	conserved hypothetical protein	-	1560	pc0501_771-819	AAGCTATACTGCAACAGCTTGGTATCACAAAAAACTTCCTCCTGACTTG	74,2	49	0,978	1	0,999	0,997	0,99	0,777	mid
4	5	L21	**pc0502**	conserved hypothetical protein	-	234	pc0502_37-90	TTGTTTACCACAACCATACTTAATCATGAGAGGTCAAAAATGGATGTAACTGAA	74,2	54	0,605	0,042	0,997	0,977	0,992	0,814	rand 2.Wahl
4	5	P21	**pc0503**	similarity to DNA-3-methyladenine glycosylase II	**alkA**	414	pc0503_103-154	GCTTTAGGGTTTAGCCAACATAAAAGTGGAACTTTGATATTGATTGCTTCAA	74,3	52	0,971	1	0,991	1	0,949	0,776	5´preference
4	6	D01	**pc0504**	unknown protein	-	201	pc0504_23-74	GGAATGGTAAAACAGGCCACATAGACTGCAAAATTATATCCAAATATGTCAA	74,2	52	0,979	1	0,998	1	0,984	0,795	random
4	6	H01	**pc0505**	conserved hypothetical protein	-	357	pc0505_206-256	TCGAAGAATTGGATGAAAACCAAGTAGCCTTAGAACCTATTTTGAAAGCTC	74,4	51	0,968	1	0,982	1	0,968	0,74	random
4	6	L01	**pc0506**	unknown protein	-	249	pc0506_108-152	GGATGGAGAAAAGCTGAGCCTGGAAAACGATATTTATCGACACTA	74,1	45	0,972	1	0,988	1	0,953	0,79	random
4	6	P01	**pc0507**	unknown protein	-	351	pc0507_7-57	GGGATGAACGATATCATTTTAAGCGCAGGACTAGCAGTAGACTATAACCAG	74,2	51	0,987	1	0,998	1	0,997	0,863	random
4	6	D05	**pc0508**	unknown protein	-	378	pc0508_80-134	CCTTTTCCATTTCTCTTATACGCTTCTCTATTTTCAGTAGCGATTCTCAATCCTT	74,3	55	0,976	1	0,995	0,988	0,999	0,771	random
4	6	H05	**pc0509**	unknown protein	-	189	pc0509_72-117	CGAAAGTTCTCAAGACAATTTTGTGAAAAGGCTACATGTTGAGTCG	74,1	46	0,964	1	0,981	1	0,895	0,808	random
4	6	L05	**pc0510**	unknown protein	-	624	pc0510_176-225	AGTGGAGAAAGCTGGCTTGTTGGACTGACTCTACCATAGAAGAGTTAAAA	74,2	50	0,979	1	0,994	1	0,991	0,804	random
4	6	P05	**pc0511**	unknown protein	-	198	pc0511_71-115	ACTTCATATATGGGGCAGCCTATGACTCCTTTCGGGTCGATGACT	76,9	45	0,912	1	0,731	1	0,923	0,913	random
4	6	D09	**pc0512**	similar to antibiotic resistance protein	-	339	pc0512_191-237	TTTTCCACAATTGCGATCTGTGCAATGCAGATTTTTCTAGTAGTACC	74,3	47	0,976	1	0,997	0,988	0,964	0,812	random
4	6	H09	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
5	1	A02	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
5	1	E02	**pc0513**	unknown protein	-	270	pc0513_99-148	AGAGAAATCACAACTATTGAAGGTGCAGTCAGTGAAGGAATGCTTTTCTA	74,2	50	0,979	1	0,994	0,997	0,984	0,81	random
5	1	I02	**pc0514**	conserved hypothetical protein	-	1626	pc0514_689-733	GCTACGGAGGCAGCTATGACTTCTATCTTACAGAGCAGGAAAGGA	74,2	45	0,984	1	0,997	1	0,967	0,876	random
5	1	M02	**pc0515**	unknown protein	-	213	pc0515_47-92	CGATTCAAGCCAAGCTTTGGATTACGACTCTAATGAATTTCATCAG	74,2	46	0,973	1	0,999	1	0,977	0,735	random
5	1	A06	**pc0516**	hypothetical protein	-	600	pc0516_280-325	GAAATTCCGCGAGAACATTGGATTGCTATACCACATACTACTTCCA	74,3	46	0,987	1	0,998	1	0,998	0,862	random
5	1	E06	**pc0517**	conserved hypothetical protein	-	849	pc0517_384-429	GAGGGATAAGATTCAGATCGATGTAGGCATAGGAGACGTAGTCACG	74,2	46	0,989	1	0,995	1	0,991	0,905	random
5	1	I06	**pc0518**	strongly similar to DNA-6-O-methylguanine[protein]-L-cysteine S-methyltransferase	**ada**	375	pc0518_76-125	GTAGATACTTCGACTGCTCGCCGTCAGTTTAAGAAAAGATTTGGTATGAC	74,2	50	0,976	1	0,998	0,988	0,963	0,813	5´preference
5	1	M06	**pc0519**	strongly similar to streptogramin A acetyltransferase	**vatB, satG**	639	pc0519_304-348	GAAAGCGCTTTCAATGTTTACGACTTACCAGTCAAGGGAGACATT	74,3	45	0,985	1	0,997	1	0,983	0,868	mid
5	1	A10	**pc0520**	conserved hypothetical protein	-	219	pc0520_107-159	TCTATGATGTCAATGGCAGAAATGGGCGTATTATTAAAATACTTTGTCTTGTG	74,2	53	0,976	1	0,999	1	0,996	0,746	mid
5	1	E10	**pc0521**	unknown protein	-	225	pc0521_124-168	AGTAATCTTGAATGGCTTTCCATTGAAATATGTGGTACACGGCAG	73,9	45	0,972	1	0,967	1	0,989	0,802	mid
5	1	I10	**pc0522**	unknown protein	-	981	pc0522_515-567	GTGAGATTGATGTTGTTACCTATTGTTTACCTCTTGCGTATTATCCTGAAGCA	74,2	53	0,98	1	0,999	1	0,977	0,811	mid
5	1	M10	**pc0523**	unknown protein	-	216	pc0523_57-102	TATTGACCAAGCTAACTCTTCGCCATCTTTGTGGACTATTCCTGAG	74,3	46	0,98	1	0,994	1	0,948	0,867	mid
5	1	A14	**pc0524**	unknown protein	-	195	pc0524_5-53	CAGATCATCGCTCTTATAAATCGTTGGTCGTAGGTTCTAATCTCATTCG	74,2	49	0,831	0,636	0,999	0,991	0,907	0,849	mid 2.Wahl
5	1	E14	**pc0525**	unknown protein	-	186	pc0525_56-103	AAGTTTTACTCATTCTTCTGACATTCTTAAGGTCGAAACCAGCATCCG	74,3	48	0,975	1	0,995	1	0,929	0,844	random
5	1	I14	**pc0526**	conserved hypothetical protein	-	213	pc0526_74-118	TTACTCCTATATCTTAGAAGCAAGCCAGATGGTCCGGTTTATTTGGG	74,2	45	0,974	1	0,995	1	0,967	0,775	mid
5	1	M14	**pc0527**	unknown protein	-	291	pc0527_39-92	AAAAACTCATCTCGCGGCAGCCATTGCCAAGCTTAAACGATTTAG	74,3	54	0,589	0,028	0,998	1	0,892	0,807	mid 2.Wahl
5	1	A18	**pc0528**	conserved hypothetical protein	-	723	pc0528_375-419	CTTCTCGTTGGATACGTGTGACAGAGAAGTCATGCGTTATATTGC	74,3	45	0,982	1	0,99	0,979	0,987	0,882	mid
5	1	E18	**pc0529**	unknown protein	-	237	pc0529_23-77	CAGTAGTAAAAGCTGTCCAAGAGATTGAATACATAAATAAGCTACTCGCGTCAGA	73,7	55	0,967	1	0,949	1	0,995	0,787	random
5	1	I18	**pc0530**	unknown protein	-	756	pc0530_401-450	CAGTCGCTAAAACAAGGACTTTAGATGGTCGAAATGTTGTCATTATCAAA	74,2	50	0,976	1	0,997	1	0,978	0,781	mid
5	1	M18	**pc0531**	similar to chloramphenicol 3-O phosphotransferase	**cpt**	279	pc0531_52-98	AAATTGAGTCAAACCCTTAAAGAAATTGTCCTCCCGCTTGCTAAGAT	74,2	47	0,975	1	0,999	1	0,998	0,732	random
5	1	A22	**pc0532**	unknown protein	-	678	pc0532_328-373	ATGAAAGCTATCTATAATATGAGAAGAGCGGCAGCAACCGCAAATC	74,3	46	0,983	1	0,995	1	0,988	0,841	mid
5	1	E22	**pc0533**	unknown protein	-	201	pc0533_60-114	AAGGTTGTCTTATTGCGACAAATTAAGAATAATAACAAATGACTGCTTTGGCTTT	74	55	0,968	1	0,978	0,998	0,958	0,77	mid
5	1	I22	**pc0534**	unknown protein	-	468	pc0534_268-312	AATTTCGGAGTTTGGACAGGGGGTTCTTTGTATCCAAAAACATTA	74,3	45	0,966	1	0,997	0,926	0,967	0,789	mid
5	1	M22	**pc0535**	unknown protein	-	234	pc0535_89-143	GCGAAATATTAGAATTAAAAGGGTGGCCACTCTGTATAACAGATAATAAAGTGCG	73,8	55	0,963	1	0,96	0,988	0,971	0,761	mid
5	2	A02	**pc0536**	unknown protein	-	1245	pc0536_677-725	TAAATCAGTTGGGAATTCGTGATGGGGATCAATGTACTTTTGTTGATAT	74,3	49	0,974	1	0,995	1	0,947	0,802	mid
5	2	E02	**pc0537**	hypothetical protein	-	1593	pc0537_765-813	TGATCCCCATTATTTAGGCGACATCCCTTCCGTTTTATATCATTATTCT	74,2	49	0,977	1	0,998	1	0,967	0,796	mid
5	2	I02	**pc0538**	similar to RTX-toxin, partial length	**rtxA**	1089	pc0538_499-553	TTCTTAGTTGGATACGGTATGAACATGCTTGTATTCAATTATTCACAAACAGGTC	74,2	55	0,977	1	0,994	1	0,953	0,832	mid
5	2	M02	**pc0539**	unknown protein	-	240	pc0539_106-159	AAACGATCAAGCTTTTTAGATGATCGAGCAATACCTATCACTAATTATCCTCGA	74,1	54	0,961	1	0,989	0,955	0,94	0,754	random
5	2	A06	**pc0540**	hypothetical protein	-	309	pc0540_60-104	GACCCATCCTCAACTTCCCCATTTTCGAATAGACAAACACTTATG	74,3	45	0,971	1	0,994	1	0,904	0,831	mid
5	2	E06	**pc0541**	similar to Peptide deformylase	**def, fms**	471	pc0541_192-236	AATTCTTAGCATGAGTGAAGAAACGCAAACCTTTTCAGAGGGATG	74,3	45	0,976	1	0,992	1	0,955	0,826	mid
5	2	I06	**pc0542**	conserved hypothetical protein	-	432	pc0542_233-286	AAGTAAATTATCTGTTACCTGTTTCAACTAAGTTTGAGGCGGAATGTGAAATGC	74,3	54	0,98	1	0,997	1	0,984	0,81	mid
5	2	M06	**pc0543**	strongly similar to oxidoreductase MocA family	**mocA**	1032	pc0543_497-551	TGAAATCACTAGCAACTTCTGAAAAATATGGTTTAGCTCGCTATGTTGTCTATCA	74,2	55	0,978	1	0,999	1	0,98	0,785	mid
5	2	A10	**pc0544**	similarity to nasA protein	**nasA**	1224	pc0544_617-661	ATAAACGCGTCATTTGGTGTTGTCTATTTGCAGGTCTAATGGTTG	74,4	45	0,984	1	0,988	1	0,996	0,863	mid
5	2	E10	**pc0545**	unknown protein	-	918	pc0545_436-	TTATCCGATCTTTCATTTCAAGCATTATTTATTACTCCCACTTACGGGAAATG	74,3	53	0,972	1	0,991	1	0,976	0,756	mid

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5	2	I10	**pc0546**	similar to methionine aminopeptidase	**map**	897	pc0546_461-505	GGCATGGGTTAGGGCCTCATAAAATTCACACTTCGCCTATAATAC	74,2	45	0,981	1	0,992	1	0,989	0,826	mid
5	2	M10	**pc0547**	unknown protein	**-**	198	pc0547_43-89	TTTATCACGGAATTTATCACGGAGCTCAAAAAAATCATGAAACAGCT	74,2	47	0,963	1	0,997	1	0,968	0,646	random
5	2	A14	**pc0548**	similar to peptide chain release factor 2	**rf-2, prfB**	357	pc0548_70-115	TTTCGCTCAAGTGGAAGTGGAGGACAACATATTAATGTTACCAACA	74,2	46	0,987	1	0,998	1	0,999	0,862	random
5	2	E14	**pc0549**	conserved hypothetical protein	**-**	756	pc0549_393-444	GAGTTTATTAAGTGGTTTTCTACTTGGGCAATTGACAGGTTGTAGTGGTGTC	74,2	52	0,982	1	0,998	1	0,986	0,833	mid
5	2	I14	**pc0550**	similar to multidrug-efflux transport protein acrA	**acrA;mexA**	1188	pc0550_568-615	CCAGTTTCAGGTCAAGTAGGACAAGCTAATTACAGAGAGGGAGCTCTC	74,2	48	0,985	1	0,998	1	0,973	0,882	mid
5	2	M14	**pc0551**	strongly similar to multidrug-efflux transport protein, acrB	**acrB;mexB**	3114	pc0551_1557-1607	TACAAATGGTTATATGCATATTACCAAATGGATTTTAAATCATGCCTGGGC	74,3	51	0,974	1	0,998	1	0,999	0,719	mid
5	2	A18	**pc0552**	similar to outer membrane protein, componenet of multidrug efflux systems	**oprK**	1470	pc0552_675-719	GTCTGAGTTAGAAGTTAAGCAAGCAGCTGCTGAAGTGGATGAAGC	74,3	45	0,97	1	0,992	0,999	0,939	0,783	mid
5	2	E18	**pc0553**	hypothetical protein	**-**	738	pc0553_381-428	TAAACTAGGTTATCAAACCGCTTTGCTCTCAAACGTTCGTATGAATCA	74,1	48	0,982	1	0,99	1	0,989	0,85	mid
5	2	I18	**pc0554**	conserved hypothetical protein	**-**	2073	pc0554_1023-1070	AAAACAAGATGGGCACTATGTGAATGTCATTAGCTTAAAAAACGGTCC	74,2	48	0,978	1	0,997	1	0,985	0,789	mid
5	2	M18	**pc0555**	similar to dTDP-glucose 4,6-dehydratase, rfbB	**rfbB, rmlB**	918	pc0555_466-511	GTCCTTCGAATCAGTAATCCTTACGGAACTCTTCTGGAACCTGAAC	74,2	46	0,985	1	0,992	1	0,994	0,867	mid
5	2	A22	**pc0556**	unknown protein	**-**	183	pc0556_47-93	GTTTGTTTCTAATTCAAGTTTTTATTTTGGCATTCGTGCAGCGACAT	74,3	47	0,957	1	0,996	1	0,941	0,622	random
5	2	E22	**pc0557**	unknown protein	**-**	216	pc0557_26-74	TGTTAGTTAATATTTGTGGCGTCGAAGAGTGGACTTTTGTTTTTGATGC	74,7	49	0,963	1	0,956	1	0,989	0,735	random
5	2	I22	**pc0558**	unknown protein	**-**	270	pc0558_105-159	ATTTGTACTTGTGAAAATTAGTCCCTTAGTACAAAATCGATTTGATTCCCAATCA	73,7	55	0,955	1	0,946	1	0,969	0,703	mid
5	2	M22	**pc0559**	similar to NADH-ubiquinone oxidoreductase chain A	**nuoA, nuo1**	363	pc0559_158-203	TTTTGGAAAAGCGTTTCCCTCTTCGGCACTATTTAGTCGCTCTAAT	75,2	46	0,949	1	0,901	0,967	0,996	0,772	random
5	3	A02	**pc0560**	strongly similar to NADH-ubiquinone oxidoreductase chain B	**nuoB, nuo2**	495	pc0560_24-69	AAAAACACCGTTTCTCATTGCCCCACTAGAAAAACTAGTCAATTGG	74,1	46	0,98	1	0,99	1	0,989	0,825	5´preference
5	3	E02	**pc0561**	similar to NADH-ubiquinone oxidoreductase chain C/D	**nuoC, nuoCD, nuo3nuo4**	525	pc0561_294-343	GACTGTTACAGATTTGTGGGAAGGAGCGAACTGGTATGAGAGAGAATTAT	74,3	50	0,977	1	0,994	1	0,97	0,803	mid
5	3	I02	**pc0562**	similar to NADH-ubiquinone oxidoreductase chain C/D	**nuoD, nuoCD, nuo3nuo4**	1209	pc0562_617-662	TTTGGTGTAAACGCTTACAAGGTGTTGCTGTCATTGATCAAGAAAT	74,2	46	0,98	1	0,999	1	0,989	0,794	mid
5	3	M02	**pc0563**	similar to NADH-ubiquinone oxidoreductase chain E	**nuoE, nuo5**	480	pc0563_212-256	TTTCTTGCATGTTAAGAGGCGCTGATGGATTTCTAGCGAGATTAT	74,4	45	0,978	1	0,988	1	0,971	0,831	mid
5	3	A06	**pc0564**	strongly similar to NADH-ubiquinone oxidoreductase chain F	**nuoF, nuo6**	1299	pc0564_654-701	TCACATTGTGAATCGTGGAGTTGAATGGTATCAAAGTATTGGTAAACC	74,1	48	0,972	1	0,981	1	0,997	0,752	mid
5	3	E06	**pc0565**	similar to NADH-ubiquinone oxidoreductase chain G	**nuoG, nuo7**	2322	pc0565_1277-1326	CGCCAGGAAAAGAACTAGAGAATTGGGATGAGAACTTACCTCTTATTGAC	74,2	50	0,968	1	0,999	1	0,885	0,82	mid
5	3	I06	**pc0566**	strongly similar to NADH-ubiquinone oxidoreductase chain H	**nuoH, nuo8**	978	pc0566_462-506	TCAAATGATCAGTTACGAAATTCCAATGGGGCTTTCTTTGCTAAC	74,3	45	0,975	1	0,994	1	0,972	0,781	mid
5	3	M06	**pc0567**	strongly similar to NADH-ubiquinone oxidoreductase chain I	**nuoI, nuo9**	432	pc0567_71-115	TACCAGCCAGGTCTCGAGGTAGGCATTATTTAACAAAATGGAATG	74,2	45	0,976	1	0,997	1	0,996	0,748	random
5	3	A10	**pc0568**	similar to NADH-ubiquinone oxidoreductase chain J	**nuoJ, nuo10**	513	pc0568_239-290	AAGATGCCCATAATCAAATTCACCAATTTGTAGCTCAAAGTAAATCTTCGAT	74,2	52	0,972	1	0,999	1	0,982	0,725	mid
5	3	E10	**pc0569**	similar to NADH-ubiquinone oxidoreductase chain K	**nuoK, nuo11**	300	pc0569_16-60	AGCCTTTTTATTAGTATGGCCATGTTTACCTTTGGCATCATTGGC	74,3	45	0,972	1	0,995	1	0,993	0,714	5´preference
5	3	I10	**pc0570**	similar to NADH-ubiquinone oxidoreductase chain L	**nuoL, nuo12**	1887	pc0570_982-1027	GCTTACTATGCAGCAATGTTTCACTTGACTATTCACGCATTTGTGA	74,2	46	0,974	1	0,999	0,947	0,963	0,843	mid
5	3	M10	**pc0571**	similar to NADH-ubiquinone oxidoreductase chain M	**nuoM, nuo13**	1446	pc0571_709-753	TTATCGGGGTTGTTGTCTAAAGCAGGTATTTATGGGATTATCCGC	74,3	45	0,982	1	0,997	1	0,985	0,831	mid
5	3	A14	**pc0572**	similar to NADH-ubiquinone oxidoreductase chain N	**nuoN, nuo14**	1443	pc0572_740-784	CATTTATGGCTGTAGGGACTAAGGTAGGGGTTTTTGCTGCTTTTG	74,3	45	0,981	1	0,99	1	0,983	0,839	mid
5	3	E14	**pc0573**	conserved hypothetical protein	**-**	855	pc0573_394-439	AATAAGTTACAAACGGAAGGACAATTAGCAGGGGTTTTAGCCCATG	74,2	46	0,978	1	0,995	1	0,965	0,823	mid
5	3	I14	**pc0574**	unknown protein	**-**	207	pc0574_57-105	ATTTATGTCAACTGCTTACGCTGAAAATGAAAATGTCAATCCTACGTCC	74,3	49	0,974	1	0,998	1	0,963	0,77	random
5	3	M14	**pc0575**	conserved hypothetical protein	**-**	1029	pc0575_537-587	TGGTAATTGGGCTCTTCGGTTAAGAGGATATCACATTTCTACTCATATTGG	74,3	51	0,983	1	0,996	1	0,979	0,859	mid
5	3	A18	**pc0576**	unknown protein	**-**	963	pc0576_424-469	AACCGTCTTTTAGCCTCTGAATCTAATTTACGGCCTATCAATCCGA	74,3	46	0,974	1	0,997	1	0,941	0,808	mid
5	3	E18	**pc0577**	unknown protein	**-**	606	pc0577_112-158	GTAATGATGGGCCATGCTTGTAGTGAAATGTTCCGATTTATTGAAAT	74,2	47	0,956	1	0,999	1	0,808	0,797	mid
5	3	I18	**pc0578**	unknown protein	**-**	1029	pc0578_297-350	TTCTCTGATCTCAAGAGTTAGCTCAATGATTTCAATGGTTTCAGTATTTTCTCC	74,2	54	0,95	1	0,995	1	0,781	0,781	mid
5	3	M18	**pc0579**	unknown protein	**-**	606	pc0579_148-198	ATTTTTGGAAGAGTCGAAGGAAAATTAAACCAACAAATTACTCGTCTCACG	74,7	51	0,727	0,447	0,954	1	0,844	0,719	mid
5	3	A22	**pc0580**	unknown protein	**-**	1005	pc0580_576-621	GGCGCAAAATTTCAGTTCAATTTGTCCTAAGCGTAGCTACGATTTA	74,4	46	0,948	1	0,986	0,928	0,928	0,669	mid
5	3	E22	**pc0581**	conserved hypothetical protein	**-**	2223	pc0581_1131-1175	GATTACAAGAGAAACAAGAACCCACGAATTTCCAGGAGCTTTTCA	74,3	45	0,976	1	0,995	1	0,981	0,782	mid
5	3	I22	**pc0582**	conserved hypothetical protein	**-**	873	pc0582_389-434	TTTCTAATTTCACGCCTATTCATTACGATTGTGCTCATGAAGAGCA	74,2	46	0,973	1	0,998	1	0,951	0,783	mid
5	3	M22	**pc0583**	similar to protein kinase C inhibitor 1	**PCKI 1**	339	pc0583_150-197	ACAGTCTATCCAACAAGAAGATCTTGAACTCGTGAGCGAAATCGTAGT	74,2	48	0,98	1	0,993	0,995	0,98	0,839	mid
5	4	A02	**pc0584**	conserved hypothetical protein	**-**	570	pc0584_296-341	CTTACATTCAACAATGGGTCATTGTCGGTCTTGAAGCTCATATTTG	74,3	46	0,98	1	0,997	1	0,99	0,801	mid
5	4	E02	**pc0585**	hypothetical protein	**-**	1743	pc0585_847-896	TATCAAGCAATGGGCTTGCTTAAGTCGAAAGAGCAAAATGATAGTGTTAT	74,3	50	0,975	1	0,995	0,992	0,974	0,784	mid
5	4	I02	**pc0586**	hypothetical protein	**-**	1674	pc0586_815-859	GCCATCGACAAGCTTCTTCCAAACCTCCTGTTAGACTTGTTTTAG	74,1	45	0,968	1	0,991	0,973	0,977	0,75	mid
5	4	M02	**pc0587**	hypothetical protein	**-**	1194	pc0587_573-619	TATGCTAAAACTTATGACCGAACACAATTGTGTGACAGCAGATCCTC	74,2	47	0,981	1	0,993	1	0,975	0,846	mid

5	4	A06	**pc0588**	similar to ATP-binding cassette protein, nasD	**nasD**	741	pc0588_278-326	TTTCTGAGCTTGGACCTAAATCTATCAACCTGCAAGAAGTCAAAGAAGA	74,3	49	0,966	1	0,997	1	0,906	0,765	mid
5	4	E06	**pc0589**	similar to aromatic amino acid-specific transport protein	**tyrP**	1284	pc0589_643-687	AGGAATGCGATAGCATTACGTTGGGCTATTATTGGAGGAACAACT	74,4	45	0,976	1	0,981	1	1	0,793	mid
5	4	I06	**pc0590**	hypothetical protein	**-**	480	pc0590_196-241	CAAGTAGGGGCTGCTGTTCGTAAAATTCATCAAGACTGTTCTCAAT	74,2	46	0,981	1	0,999	1	0,999	0,797	random
5	4	M06	**pc0591**	similar to heat shock protein 70 (chaperone protein dnaK)	**dnaK, grpF, groP, seg**	1836	pc0591_924-978	CGAAATGACAATCCTTGGGAGAGGAAGTAAGTTAATAGGGAATACTCTTACAACA	74,3	55	0,984	1	0,997	1	0,995	0,838	mid
5	4	A10	**pc0592**	hypothetical protein	**-**	441	pc0592_230-275	TAATTTCCGCGGGGTTAGCTGCCTTACTTGTAAAGGTCTATAGTGG	74,3	46	0,987	1	0,996	1	0,992	0,884	mid
5	4	E10	**pc0593**	unknown protein	**-**	1593	pc0593_915-962	CTCTAAAGAACAATTGAAAGAACTTCAAAGCGCAAAAAATGAGTTGGC	74,3	48	0,953	1	0,998	1	0,883	0,652	mid
5	4	I10	**pc0594**	strongly similar to translation initiation factor IF-1	**infA**	270	pc0594_58-111	AAAGAAGATACAATTAAGATTGAAGGAAGCGTCGAAGAATTGCTCCCTAATATG	74,2	54	0,978	1	0,999	0,988	0,996	0,781	random
5	4	M10	**pc0595**	strongly similar to translation elongation factor Tu (EF-Tu)	**tufA**	1186	pc0595_596-640	CTGTTCCAACACCTCAACGTGAGACAGATAAGCCTTTCTTAATGC	74,3	45	0,983	1	0,989	1	0,998	0,849	mid
5	4	A14	**pc0596**	unknown protein	**-**	192	pc0596_9-63	ATCAATCGTTATTAAAACGATAAAGCAGTCAAAAAGTGTGATTTTTTACAAACAA	72,3	55	0,881	1	0,802	0,829	0,912	0,629	mid 2.Wahl
5	4	E14	**pc0597**	similar to preprotein translocase SecE	**secE**	288	pc0597_68-112	TAGAAAGCTCTTTTACGGTTAAAAAGGCACGTAATTTTGTCGCCG	74,3	45	0,966	1	0,994	1	0,923	0,754	mid
5	4	I14	**pc0598**	similar to transcription antitermination factor NusG	**nusG**	204	pc0598_44-88	AAAAAGTCAAAAAAGCGTTGGAAGAGCATCTCGAGTTAAAAGGGA	74,2	45	0,972	1	0,998	1	0,972	0,741	random
5	4	M14	**pc0599**	strongly similar to transcription antitermination factor NusG	**nusG**	375	pc0599_82-126	GATTTTCTAGGTGGAGATAAACCAACGCCTCTGACAGATTTCGAA	74,3	45	0,983	1	0,991	1	0,999	0,844	random
5	4	A18	**pc0600**	strongly similar to 50S ribosomal protein L11	**rplK**	429	pc0600_151-202	GGGGATGTACTTCCTACACTCATCACTGTGTATCATGATAAGTCGTTTTCAT	74,4	52	0,973	1	0,987	1	0,936	0,829	mid
5	4	E18	**pc0601**	strongly similar to 50S ribosomal protein L1	**rplA**	711	pc0601_347-391	CAACACCTGACATGATGCGAGAAGTGGGTAAGTTAGGTAAGGTTC	74,2	45	0,987	1	0,998	0,983	0,99	0,904	mid
5	4	I18	**pc0602**	similar to 50S ribosomal protein L10	**rplJ;rl10**	546	pc0602_306-351	AATTATCCAAGTCCTCGGTGGACGTTTTGATGGACAGATTTATAGC	74,3	46	0,973	1	0,998	0,935	0,968	0,848	mid
5	4	M18	**pc0603**	strongly similar to 50S ribosomal protein L7/L12	**rplL;rl7**	390	pc0603_72-116	CAAGACTCTACTCGAAGATAAATGGGGTGTTAAAGCTGCAGCTCC	74,2	45	0,983	1	0,998	1	0,998	0,818	random
5	4	A22	**pc0604**	strongly similar to DNA-directed RNA polymerase, beta chain	**rpoB**	3765	pc0604_1895-1939	AACGTCAGGGAGTTCCTCTTCTCAAACCTACTGCTCCAATTGTAG	74,2	45	0,985	1	0,997	1	0,988	0,863	mid
5	4	E22	**pc0605**	strongly similar to DNA-directed RNA polymerase, beta' chain	**rpoC;tabB**	4167	pc0605_2007-2056	TGCTGTAGTCAGAAAACAGTACGAAGATGGTATCATAACTGAAGGGGAAC	74,2	50	0,978	1	0,994	1	0,923	0,883	mid
5	4	I22	**pc0606**	strongly similar to peptidoglycan-associated lipoprotein precursor (pal)	**pal**	468	pc0606_189-233	ACTTGGTATAGCTGGAGGAGGCGTAACTGGAGGAATTATTGGAAA	74,2	45	0,976	1	0,992	1	0,954	0,826	mid
5	4	M22	**pc0607**	hypothetical protein	**-**	2163	pc0607_1083-1128	AGAGCTTCCTACCCTGTCAGTAAACTTTAAGCCTTTCCCTTTGCAA	74,2	46	0,981	1	0,997	1	1	0,798	mid
5	5	A02	**pc0608**	unknown protein	**-**	183	pc0608_33-82	ATTTCGGCAAGAAGTAGCAAGCTATTTGATGCAAAAATTTGGAGTAAAAG	74,2	50	0,934	1	0,994	0,839	0,94	0,612	mid
5	5	E02	**pc0609**	hypothetical protein	**-**	1686	pc0609_929-976	AAAGTGCGGTTCTTACAAACTTCTTAGACCACTCAAATCCTCAATTGC	74,3	48	0,973	1	0,996	1	0,915	0,839	mid
5	5	I02	**pc0610**	strongly similar to septum formation protein	**maf**	585	pc0610_281-325	AACTTGCTGGCCATTGGCATTCCGTTTATACAGGAGTTAACGTAT	74,8	45	0,969	1	0,942	1	0,987	0,845	mid
5	5	M02	**pc0611**	unknown protein	**-**	297	pc0611_48-101	AGGAGAAATTGCAATACATCTTCAACAAACGTCTCAAGAAAATAGACAAAAGTG	74,3	54	0,973	1	0,997	1	0,999	0,714	random
5	5	A06	**pc0612**	unknown protein	**-**	258	pc0612_69-120	TTTACTTCATCAACCTCTTGAATCTGACGAAACGTTGATACAAGATAGTCGT	74,1	52	0,981	1	0,987	0,998	0,991	0,848	random
5	5	E06	**pc0613**	unknown protein	**-**	201	pc0613_32-76	TTGACATTAAATTGGTTGATAAATGGTTGGCGGAAATTGAAGACA	74,3	45	0,966	1	0,996	1	0,979	0,67	random
5	5	I06	**pc0614**	unknown protein	**-**	309	pc0614_95-147	AATTGACAAAAGGATTGAATCTCATTGAATTGCAAGTCATCACTCTAATTGAT	74,2	53	0,97	1	0,997	0,987	0,998	0,705	random
5	5	M06	**pc0615**	unknown protein	**-**	1380	pc0615_762-810	TAAACATAAGCTTCGCCCTCTTCTTCCGTTGAGATTTACAAAACCATTA	74,2	49	0,97	1	0,997	1	0,929	0,782	mid
5	5	A10	**pc0616**	similar to 60 kDa cysteine-rich outer membrane protein	**omcB**	1677	pc0616_1262-1310	ATGTCACTAACTGTGAAGGTTGCAACTCTAGCTGCGAATTTGGTACAAA	75.5	49	0,988	1	0,998	1	0,993	0,881	**-7.2**
5	5	E10	**pc0617**	similar to 9 kDa cysteine-rich outer membrane protein	**omcA**	270	pc0617_123-174	ATTAGTATTGTCTTTATCTAGCTGCTGTTTCGATCGTAACCCAAGCTGTGAG	74,1	52	0,982	1	0,987	1	0,987	0,861	mid
5	5	I10	**pc0618**	conserved hypothetical protein	**-**	840	pc0618_386-430	GTTTTGCAGTTAATGAAGTCGTTATTCACCGTGCTCAGAATCCAT	74,2	45	0,981	1	0,998	1	0,965	0,844	mid
5	5	M10	**pc0619**	similar to 1-deoxy-D-xylulose 5-phosphate synthase	**dxs**	1908	pc0619_1068-1113	AACTTTTCCTGAACGCTGTATTGATGTGGGTATTGCTGAATCTCAT	74,4	46	0,967	1	0,988	1	0,887	0,831	mid
5	5	A14	**pc0620**	similar to exodeoxyribonuclease VII, small chain	**xseB**	279	pc0620_5-55	ATAATCCATCTGATCAAGAACCTACTGCTAGCTTTGAAACAGCTTTATGCC	74,2	51	0,981	1	0,996	1	0,999	0,804	random
5	5	E14	**pc0621**	similar to exodeoxyribonuclease VII, large chain	**xseA**	1449	pc0621_678-722	AGATCATTGCATCGCTGATTATGTTGCAGATATTAGAGCTCCCAC	74,4	45	0,977	1	0,981	1	0,953	0,87	mid
5	5	I14	**pc0622**	similar to D-alanine/glycine transport protein, sodium-dependent	**dagA**	1380	pc0622_782-826	AAGCTATCTCTACAGGATTTGATCGGGGAGTTTTTGCAACTGATG	74,3	45	0,968	1	0,992	1	0,909	0,806	mid
5	5	M14	**pc0623**	strongly similar to endonuclease V (deoxyinosine 3'endonuclease)	**nfi**	708	pc0623_359-411	GAATATCTCATCCTCGAAGGTTAGGTATTGCGAGTCATATTGGAGTGTTAGTC	74,2	53	0,988	1	0,999	1	0,996	0,872	mid
5	5	A18	**pc0624**	unknown protein	**-**	192	pc0624_1-55	TTGCTAATTATTGATCCAAACTTTGAGGAATCAAAACAACCTCCTGAAATATACC	74,3	55	0,847	0,709	0,993	1	0,904	0,717	mid 2.Wahl
5	5	E18	**pc0625**	hypothetical protein	**-**	492	pc0625_238-287	TCCTTGTTTCAATCGTTGGCAAATATTGGAGAGGCTTTAGAATATAAAGC	74,2	50	0,975	1	0,995	1	0,991	0,747	mid
5	5	I18	**pc0626**	conserved hypothetical protein	**-**	675	pc0626_374-420	TTGCTCCTAAATCTGGTAGTGAGCTGAGAGATGATATTGTCGAAGGA	74,3	47	0,98	1	0,997	1	0,965	0,835	mid
5	5	M18	**pc0627**	unknown protein	**-**	354	pc0627_56-104	CAGCTTTATTATTAGCACCGAAGTCGGGTAATCAACTCATTAAGGATGC	74,2	49	0,981	1	0,999	1	0,999	0,799	random
5	5	A22	**pc0628**	unknown protein	**-**	618	pc0628_398-451	TAGCTGTTTGCTTTGCTTGTCCTATCCTTCTTCAACTTTTCTATCAATCTTTTC	74,2	54	0,964	1	0,999	1	0,912	0,728	mid
5	5	E22	**pc0629**	unknown protein	**-**	231	pc0629_87-141	TTCAATTTGTAAAAGTGGGATTGATAGTGGGATGTTTCAATTTACAGAGTTTTTT	73,7	55	0,821	0,673	0,943	1	0,97	0,64	mid 2.Wahl
5	5	I22	**pc0630**	similar to Thermostable carboxypeptidase 1	**-**	1521	pc0630_860-905	GAACACCCCTAGGAGATGCTTGTTCATTAGGAATTCATGAAAGTCA	74,3	46	0,97	1	0,998	1	0,902	0,813	mid
5	5	M22	**pc0631**	similar to alanine racemase	**alr**	2526	pc0631_1145-1198	AAATTGGTAAGACGATCTCTAAAGCACACCTTCGACATTTGTTATTATTTGGTC	74,3	54	0,966	1	0,997	0,995	0,881	0,808	mid
5	6	A02	**pc0632**	conserved hypothetical protein	**-**	201	pc0632_64-109	GGCAAGCTAACCGATAATGATTTGACAGAAATCAATGGACAAAGAG	74,2	46	0,968	1	0,994	0,992	0,944	0,761	random
5	6	E02	**pc0633**	similar to acriflavin resistance protein D	**acrD**	3078	pc0633_1636-1686	CGATCAGAATTCGTTCCACTAGAAGATCAAAGTGAATTTTTCATCAATGTT	74,3	51	0,961	1	0,993	1	0,904	0,724	mid
5	6	I02	**pc0634**	hypothetical protein	**-**	813	pc0634_425-	AAGAGTTGCGAAGAGTCAAAAAGCACCTTGCAGAAACAATCATTA	74,2	45	0,972	1	0,995	1	0,983	0,732	mid

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5	6	M02	**pc0635**	similar to outer membrane protein TolC	**tolC**	1269	pc0635_569-619	ATTCCATGGAAGCTAAACTTAACACGAAATTAGCGACTGAAAGGCTTAATC	74,2	51	0,974	1	0,994	1	0,933	0,828	mid
5	6	A06	**pc0636**	hypothetical protein	**-**	1083	pc0636_619-671	GATCATCTTTTAAGACAGCCTAACGGCGAACTATTACAACAACAGGCATATAG	74,2	53	0,973	1	0,997	1	0,924	0,824	mid
5	6	E06	**pc0637**	conserved hypothetical protein	**-**	1152	pc0637_612-660	AGCCACGTTGTTAACAACAACATCTCTCAATCAAGAGAACACTTTTGAT	74,3	49	0,975	1	0,996	1	0,965	0,788	mid
5	6	I06	**pc0638**	unknown protein	**-**	336	pc0638_142-193	ATCAAAGAACTGGAATCCGTATTTAAGGATGAGCCTTTATCATCTAATCACG	74,1	52	0,978	1	0,99	1	0,994	0,798	random
5	6	M06	**pc0639**	conserved hypothetical protein	**-**	1377	pc0639_721-769	TTTTTAGGCCGAGTGTCTCCTTTACTAGGTCAGATCGTTAAAGGTCCTT	74,2	49	0,982	1	0,995	1	0,969	0,859	mid
5	6	A10	**pc0640**	strongly similar to cell division protein FtsH	**ftsH;hflB**	2751	pc0640_1380-1425	TTTATGCATTGGACCTCCAGGAACAGGTAAAACATTGATAGCAAAG	74,2	46	0,982	1	0,995	1	0,997	0,823	mid
5	6	E10	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
6	1	B02	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
6	1	F02	**pc0641**	hypothetical protein	**-**	747	pc0641_395-439	TAAAAATGAATTATGCTCTTCCCATTCCCGAATTTGTCATCGAAC	74,1	45	0,968	1	0,983	1	0,98	0,727	mid
6	1	J02	**pc0642**	similar to beta-1,4-galactosyltransferase	**cps**	810	pc0642_364-415	GCTGATCATCTCGTCTTTTCAACACTTTTAGAGGTTTATGAGTTTCCTTCTG	74,2	52	0,974	1	0,998	1	0,958	0,783	mid
6	1	N02	**pc0643**	strongly similar to polyribonucleotide nucleotidyltransferase	**pnp**	2109	pc0643_1046-1090	TTACAAGAGGTGAAACACAAGCATTAGCTGTATGTACATTGGGCG	74,1	45	0,984	1	0,987	1	0,99	0,877	mid
6	1	B06	**pc0644**	strongly similar to 30S ribosomal protein S15	**rpsO;rs15**	270	pc0644_40-85	AAGTTCCAATTACATGAAAAAGATACAGGGTCAGCAGACGTCCAAA	74,3	46	0,98	1	0,994	1	0,998	0,798	random
6	1	F06	**pc0645**	conserved hypothetical protein	**-**	276	pc0645_35-85	CAGAGCTTAAAACTGGGCAGTTGTTTATTATGGATCATGCTACTTTTCACA	74,5	51	0,594	0,032	0,975	1	0,983	0,781	5´preference
6	1	J06	**pc0646**	conserved hypothetical protein	**-**	369	pc0646_30-84	AGCATTCAACTATTTAGAAACTGGACATTCTGCAGAAGAAGTCAGACAAGTTTTT	74,2	55	0,605	0,05	0,998	1	0,986	0,75	5´preference
6	1	N06	**pc0647**	unknown protein	**-**	684	pc0647_368-417	CTGTCAGTCAGTTTGGGGCACTTAAAACGTACTTATTCGCTGTTTTAAAC	74,3	50	0,979	1	0,996	1	0,975	0,812	mid
6	1	B10	**pc0648**	conserved hypothetical protein	**-**	501	pc0648_95-140	AAGTTCCTGTGGGAGCAGTCCTTGTCAAAGATAAACACATTATTGC	74,2	46	0,982	1	0,995	1	0,994	0,821	random
6	1	F10	**pc0649**	conserved hypothetical protein	**-**	258	pc0649_85-129	ATCATTCCATTTTTGACAACGGACGATATTTTGCAGCCTAATGAT	74,4	45	0,965	1	0,983	1	0,984	0,681	random
6	1	J10	**pc0650**	unknown protein	**-**	1188	pc0650_544-596	CCAGATAATGGTAATTGTCTATTCAGTGCTATCGCCATAGGAATAAAGCTCAC	74,3	53	0,978	1	0,998	1	0,949	0,835	mid
6	1	N10	**pc0651**	similar to 50S ribosomal protein L31	**rpmE;rl31**	354	pc0651_46-90	GATTCTGCTTCTGGACATCGCTTTGTATGTGGGTCAACTTTAAAG	74,1	45	0,976	1	0,986	1	0,978	0,811	5´preference
6	1	B14	**pc0652**	strongly similar to translation releasing factor RF-1	**prfA**	1080	pc0652_507-558	GAATGTTTATCGTTTTATGCAATATGAAGCTGGAACTCATCGTGTACAAAGA	74,3	52	0,978	1	0,996	1	0,966	0,814	mid
6	1	F14	**pc0653**	similar to HemK protein	**hemK**	840	pc0653_406-455	CAATTACATGTCATTTCGAGTGATTTATCTTCTGCCGCATTATCATTAGC	74,2	50	0,981	1	0,999	1	0,985	0,818	mid
6	1	J14	**pc0654**	strongly similar to signal recognition particle chain ffh	**ffh**	1365	pc0654_668-713	TTTTAAATCCAGGTGAGATACTTTTCGTTGCTAATGCGACAACTGG	74,2	46	0,979	1	0,999	1	0,984	0,793	mid
6	1	N14	**pc0655**	similar to 30S ribosomal protein S16	**rpsP;rs16**	321	pc0655_58-102	TTAGTTGTGACCGATGCTCGTTCACCAAGAGATGGAAAGTATGTC	75,2	45	0,959	1	0,9	1	0,972	0,88	5´preference
6	1	B18	**pc0656**	strongly similar to tRNA (guanine N-1)-methyltransferase	**trmD**	669	pc0656_324-374	ATGTGGTCACTATGAAGGAATAGATCAGCGCGTTTTAGATGAAGAAGTAGA	74,2	51	0,981	1	0,999	1	0,988	0,806	mid
6	1	F18	**pc0657**	strongly similar to ribosomal protein L19	**rplS**	408	pc0657_46-91	CAAATGAAAAAGGATATTACTCCTTTCCGCATTGGCGATACAGTTC	74,2	46	0,979	1	0,995	1	0,996	0,787	random
6	1	J18	**pc0658**	similar to ribonuclease HII	**rnh**	669	pc0658_271-323	GGCATTATTGGTCAAGCGGAGATAGATCGAGTAAATATTTATCAAGCCACTAT	74,2	53	0,978	1	0,998	1	0,994	0,776	random
6	1	N18	**pc0659**	unknown protein	**-**	525	pc0659_24-70	ATTAATTACCATTCTTGCAGTTGTGACAGCCCTACCTTTAGCTGCAC	74,2	47	0,985	1	0,999	1	0,989	0,852	5´preference
6	1	B22	**pc0660**	conserved hypothetical protein	**-**	885	pc0660_443-488	TGAAATCCCATGAAGGGGCTGTTTTACAAGGGGATATTTTAGCTAG	74,3	46	0,978	1	0,995	0,997	0,999	0,774	mid
6	1	F22	**pc0661**	unknown protein	**-**	201	pc0661_7-57	CGCCATGGATTATTTTGCTTCGCAAGTTTAATAATAAAGGCTAATTTAGGG	74,3	51	0,936	1	0,994	0,845	0,905	0,666	mid 2.Wahl
6	1	J22	**pc0662**	similar to guanylate kinase	**gmk**	594	pc0662_92-140	TTCAAGAATTTCCAACAGTGATTGCAAGTATTTCTTACACGACAAGAGC	74,3	49	0,974	1	0,998	0,999	0,955	0,781	5´preference
6	1	N22	**pc0663**	conserved hypothetical protein	**-**	324	pc0663_103-150	AAAAGTGGCCGTGACACAAGAGTCAAATCTGATATACAAAATAGAGCG	74,2	48	0,977	1	0,999	1	0,94	0,832	mid
6	2	B02	**pc0664**	unknown protein	**-**	594	pc0664_250-296	TTTTGTCGAGAAACAGGCCGTATCTTTACAGACTGTGTAACATGGTT	74,2	47	0,976	1	0,997	0,96	0,952	0,873	mid
6	2	F02	**pc0665**	similar to methionine-tRNA ligase	**metG**	2097	pc0665_1094-1142	GCTATGCTATTGCTTCCAACGCTCCTGAAACATCTGATAGTGAATTTAC	74,3	49	0,975	1	0,995	1	0,956	0,806	mid
6	2	J02	**pc0666**	similar to ribosomal protein L28	**rpmB**	276	pc0666_16-68	CAAGTTACAGGTAGAAAACCTACACGTGGCTATAAATATGCCATTCGTGGTAT	74,1	53	0,983	1	0,99	1	0,999	0,846	random
6	2	N02	**pc0667**	unknown protein	**-**	216	pc0667_41-95	CGCTCAATCATAATATCCAAGAGGGTACAGTTCTCATTAATGTGAATATTTGTCC	74,4	55	0,97	1	0,984	1	0,932	0,809	mid
6	2	B06	**pc0668**	unknown protein	**-**	327	pc0668_9-54	TTCCCCTCAATCTATTCAAACAATGATTGCGAGTTTTGAAAAACAG	74,2	46	0,968	1	0,999	1	0,996	0,653	5´preference
6	2	F06	**pc0669**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain B	**gatB**	1485	pc0669_776-821	AAGCGACTTATCGTTGGGATCCTGAAAAACAAGAAACCGTTTTAAT	74,2	46	0,971	1	0,991	0,996	0,968	0,76	mid
6	2	J06	**pc0670**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain A	**gatA**	1470	pc0670_708-761	AACAAGTATTGCCTTAGGACCCGAAGATTACTTGAGTCAGTTTAAAGATTCCAT	74,2	54	0,98	1	0,995	1	0,972	0,838	mid
6	2	N06	**pc0671**	similar to glutamyl-tRNA(Gln) amidotransferase chain C	**gatC**	300	pc0671_25-70	ATCCATACTTTAACACGTCTTTGCAGAATTGATTGCACAGAAGCTG	74,2	46	0,981	1	0,999	1	0,999	0,792	random
6	2	B10	**pc0672**	similar to photolyase	**phrB**	1416	pc0672_652-705	TTAACAGGAGTTATAGATCAATACTTGGACATTCGCGATTTACCAGATCATGAT	74,2	54	0,978	1	0,996	1	0,943	0,852	mid
6	2	F10	**pc0673**	conserved hypothetical protein	**-**	852	pc0673_494-542	AATTGGGTTTAGGTGGAGAGTTGGGATCAGGAAAACAATATATGAGTTG	74,2	49	0,972	1	0,992	0,999	0,933	0,807	mid
6	2	J10	**pc0674**	hypothetical protein	**-**	3465	pc0674_1807-1857	CTTTCACTAGGAAGTTATTCGCTTAGTCAACTGCCAACATTTACAGATCCA	74,3	51	0,976	1	0,998	1	0,927	0,851	mid
6	2	N10	**pc0675**	hypothetical protein	**-**	963	pc0675_430-479	TGGTTTTGGAGAAGTCAATTAGACATCAACTACGATACAACAGGAAGCTC	74,2	50	0,978	1	0,999	1	0,948	0,839	mid
6	2	B14	**pc0676**	conserved hypothetical protein	**-**	1914	pc0676_808-858	AATATAGGAAACAGTTGTTACCTAGATAGCTCTTTGCAGGCCCTGATTGCT	74,3	51	0,965	1	0,996	1	0,85	0,836	mid
6	2	F14	**pc0677**	similar to DNA repair protein RecN	**recN**	1626	pc0677_870-920	ACTTAATCATAATCCAGAACGCCTACAAATTGTCAATGAGCGCTTAAGTCT	74,2	51	0,973	1	0,999	1	0,944	0,783	mid
6	2	J14	**pc0678**	unknown protein	**-**	441	pc0678_195-240	TTTAATTGAGATATTGAACCGTGCAGTTCGGGTTGTTGGAGTTAAG	74,2	46	0,979	1	0,991	0,995	0,973	0,839	mid
6	2	N14	**pc0679**	similar to ribonuclease HII	**rnhB**	906	pc0679_641-	AATTAGATGTGAACCTCACTCAAAGGCATCGAGCAGAAGATGATTT	74,2	46	0,985	1	0,999	1	0,999	0,834	random

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6	2	B18	**pc0680**	conserved hypothetical protein	-	489	pc0680_7-55	AAGTTTATGCTTGAGTTTAGCCCAAATGAGGAGAAAAGAGTGGAACGTA	74,2	49	0,968	1	0,995	1	0,997	0,664	5´preference
6	2	F18	**pc0681**	conserved hypothetical protein	-	1170	pc0681_679-723	TTAATTATCTGTGGAGCGATTGCTGTATGTGCTTTGCTTTTACCG	74,3	45	0,971	1	0,995	1	0,907	0,831	mid
6	2	J18	**pc0682**	similar to tRNA-pseudouridine synthase I	**truA**	789	pc0682_420-464	TCCCTATTCTTGGCATTGCCCTTTCCCTCTTATGTTAGGAAAAAT	74,2	45	0,977	1	0,999	1	0,975	0,785	mid
6	2	N18	**pc0683**	conserved hypothetical protein	-	600	pc0683_63-114	TTCTTATCAAACCATGGTCAAAGAGCTCGATCGTAGACATCAATCTAAAATT	74,2	52	0,963	1	0,999	1	0,969	0,645	5´preference
6	2	B22	**pc0684**	conserved hypothetical protein	-	597	pc0684_332-379	CTCTTTTATCAGGTGCTGGACTCCTTACAATGATCATGCTTTATTCCA	74,3	48	0,971	1	0,994	1	0,968	0,746	mid
6	2	F22	**pc0685**	similar to aspartate transaminase	**aspC**	1263	pc0685_682-729	AGCTTCGTCAGAAGTTCACATATCCCTCGTTCAATCTATGAAATTGAA	74,2	48	0,976	1	0,996	1	0,951	0,818	mid
6	2	J22	**pc0686**	similar to dihydrodipicolinate synthase	**dapA**	869	pc0686_431-475	TTCAAACGCATACGCTTAAACGAATCAGCACTCTTTCTTCGATTA	74,2	45	0,983	1	0,999	1	0,995	0,82	mid
6	2	N22	**pc0687**	similar to dihydrodipicolinate reductase	**dapB**	657	pc0687_450-498	TTTACCCCACTATTCATTGAAATTTAGTAGCATTCGATGCGGACATATG	74,3	49	0,968	1	0,998	1	0,88	0,825	mid
6	3	B02	**pc0688**	conserved hypothetical protein	-	1125	pc0688_585-632	GAGTATGGATGAAGAGGGAAATAGTAAAAAACTCATGCATTGCCAAGC	74,2	48	0,976	1	0,999	1	0,979	0,768	mid
6	3	F02	**pc0689**	similar to exodeoxyribonuclease V	**recD**	2166	pc0689_1154-1198	AAATTACCAAACGAAAAGCCTCTACGATTCACAGCCTTCTGGAAT	74,2	45	0,975	1	0,995	1	0,93	0,837	mid
6	3	J02	**pc0690**	similar to DNA primase	**dnaG**	1779	pc0690_912-956	AGTTTTTTTAGCTCTCGACTCTGACCTTGCTGGACAAGAAGCAAC	74,4	45	0,967	1	0,987	1	0,979	0,702	mid
6	3	N02	**pc0691**	conserved hypothetical protein	-	417	pc0691_130-177	AAGCAGCGCCTTTCTCACTTACCTTTTACCGCTAGAAATATTGACACT	74,3	48	0,972	1	0,997	1	0,92	0,819	mid
6	3	B06	**pc0692**	unknown protein	-	294	pc0692_61-115	TTCATGACTTTGGACTTTAAAGTGCTAATAGGTAAATCCATACAAGTGTATTTCA	71,8	55	0,884	1	0,752	0,89	0,913	0,718	mid 2.Wahl
6	3	F06	**pc0693**	strongly similar to glycyl-tRNA synthetase	**glyS**	3054	pc0693_1514-1559	TTTCGGACAGAATAACTTATGGACACAGACAACTATCTCCCCAAGC	74,2	46	0,984	1	0,996	0,994	0,986	0,864	mid
6	3	J06	**pc0694**	unknown protein	-	228	pc0694_70-114	ACTGAACCAAAAGAGACAACAAATGATGCATTTGCTAATTGCAGA	74,1	45	0,968	1	0,986	0,99	0,972	0,737	random
6	3	N06	**pc0695**	conserved hypothetical protein	-	993	pc0695_481-532	ATCACAGTTTCTACAGTTGGAGTCGTGGAAGGTATCAAACGCTTATCTAAAG	74,2	52	0,982	1	0,998	1	0,983	0,835	mid
6	3	B10	**pc0696**	unknown protein	-	393	pc0696_36-80	TTGGTCAAACGCTCTTCCATCTTATGCACAAGATGAATATCTTCC	74,3	45	0,98	1	0,991	1	0,996	0,806	random
6	3	F10	**pc0697**	similar to Excinuclease ABC subunit C	**uvrC**	1833	pc0697_876-925	TCACGAATTGTTAACTTCTTTTCTTCTACAACATTATGAAGGCGCAACTG	74,2	50	0,969	1	0,999	1	0,959	0,717	mid
6	3	J10	**pc0698**	unknown protein	-	534	pc0698_298-348	TTTTGCTATCTGCAAGATAATATTGGAATGCTTAGAGAAGGTGGATATGGC	74,2	51	0,98	1	0,999	1	0,97	0,829	mid
6	3	N10	**pc0699**	unknown protein	-	1344	pc0699_646-693	TCCATTGTTAGTTTAGGGACTTTGCTTTTTTCTCCTAGTAACGCTGCC	74,3	48	0,973	1	0,991	1	0,973	0,769	mid
6	3	B14	**pc0700**	unknown protein	-	411	pc0700_45-98	CTTCTTCGACACTGATTCTGTAAAAACTCATGCAAATGAAGTTACTGACAAAGT	74,2	54	0,977	1	0,997	1	0,978	0,787	5´preference
6	3	F14	**pc0701**	similar to threonine-tRNA ligase	**thrS**	1662	pc0701_817-861	AAAGAAGGATTATTCAATGCCGTTGGTTGGAGTGGAGATTTTTCT	74,2	45	0,973	1	0,992	1	0,985	0,742	mid
6	3	J14	**pc0702**	strongly similar to translation initiation factor IF-3	**infC**	555	pc0702_295-343	ACAAGACATGCCCGAGACTTTTTAGCAAGTGGTAACAAAGTTAAAGTCA	74,3	49	0,979	1	0,994	1	0,984	0,805	mid
6	3	N14	**pc0703**	strongly similar to 50S ribosomal protein L35	**rpmI**	195	pc0703_5-49	CTAAAATGAAAACCCGCAAAGCCGTTGCTTCTAAGTTTCGCGTGA	78,3	45	0,862	1	0,589	1	0,906	0,795	mid 2.Wahl
6	3	B18	**pc0704**	strongly similar to ribosomal protein L20	**rplT**	357	pc0704_131-179	CATACAATTATGCACATCGTAAACAAAAGAAGCGCGATTTTCGTAGTTT	74,3	49	0,978	1	0,997	1	0,999	0,773	random
6	3	F18	**pc0705**	strongly similar to phenylalanine-tRNA ligase alpha chain	**pheS**	1041	pc0705_515-560	GTACTCATACGTCGAATATTCAAGCGCGAGCAATGGAGCTAAATAG	74,1	46	0,979	1	0,981	0,989	0,993	0,848	mid
6	3	J18	**pc0706**	conserved hypothetical protein	-	897	pc0706_453-499	GAAAGTGTCTAAAAGTTATCGGGCCATTGTTGACGGGATATTAACGT	74,2	47	0,983	1	0,995	1	0,997	0,83	mid
6	3	N18	**pc0707**	similar to heptosyltransferase I	**waaC;rfaC**	1089	pc0707_547-591	TTAAAAAAATCACTCAAGGTCATGGTTTGCCCTGGATCTAATTGG	74,2	45	0,964	1	0,995	0,954	0,999	0,681	mid
6	3	B22	**pc0708**	conserved hypothetical protein	-	477	pc0708_298-342	ATTAAACTTTTGGCAGATCGAGGCAACGCAACTGCTCAGCATAAG	77,1	45	0,899	1	0,715	0,967	0,942	0,835	mid
6	3	F22	**pc0709**	conserved hypothetical protein	-	930	pc0709_12-64	ATACATAGATAGCAATGTTCTCCCCAATAAATATGCTAATTTCTCCCCCTGCT	74,3	53	0,976	1	0,994	0,999	0,968	0,795	random
6	3	J22	**pc0710**	conserved hypothetical protein	-	1140	pc0710_758-802	ATGCAGCTGCTCAGTATTGCTTAGGAGTTTTTTATGCACATGGAC	74,3	45	0,953	1	0,99	1	0,813	0,781	mid
6	3	N22	**pc0711**	conserved hypothetical protein	-	1239	pc0711_1087-1132	GATGCTCAATACTTTGTCGGAATGATGTACCAAAAAGGAAGAGGTG	74,3	46	0,92	1	0,99	1	0,534	0,81	mid
6	4	B02	**pc0712**	unknown protein	-	219	pc0712_28-82	AAGCAAAAAAATATTTACTCGTTCTCTTCCGCATTTTTACCGAAAATAAATAAAA	72,6	55	0,765	0,673	0,833	1	0,917	0,407	mid
6	4	F02	**pc0713**	conserved hypothetical protein	-	1344	pc0713_668-715	AGCTCAAGCTCATTATAGAAAGCCATGATATTGCACAAACGAATCAAG	74,2	48	0,974	1	0,992	0,991	0,995	0,761	mid
6	4	J02	**pc0714**	conserved hypothetical protein	-	1338	pc0714_878-922	AATATAATCTTGGAGTCAGGTATGTGAATGGGCAAGGCGTTATGC	74,3	45	0,63	0,15	0,996	1	0,792	0,885	mid
6	4	N02	**pc0715**	strongly similar to sugE protein	**sugE**	333	pc0715_169-214	ACTATTCCATTAGGAACAGCTTATGCTATTTGGACTGGCATGGGAG	74,3	46	0,964	1	0,994	0,866	0,98	0,844	random
6	4	B06	**pc0716**	conserved hypothetical protein	-	438	pc0716_25-70	CAAAAGTGGCTTCCTCCAGGTGGACATGTAGAAAATAATGAAACAC	74,3	46	0,979	1	0,998	1	0,988	0,787	5´preference
6	4	F06	**pc0717**	conserved hypothetical protein	-	654	pc0717_314-365	ATTCAGTTGCACAAGTGAAGCATCAATGGGAAATAATTAAGAAAAATGAAAA	74,2	52	0,962	1	0,995	1	0,986	0,621	mid
6	4	J06	**pc0718**	hypothetical protein	-	876	pc0718_410-458	TTGGAATACAGGCTTGGCTGATTAGTTATCCTTTTGTGATGGTGTTAAG	74,2	49	0,981	1	0,996	1	0,971	0,84	mid
6	4	N06	**pc0719**	similar to serine protease	-	1233	pc0719_679-732	AGCCAAGTTAGACAAGTAGATATGATGCATACTCTGGGTCAGTATCCAATTTTG	74,3	54	0,974	1	0,998	1	0,938	0,813	mid
6	4	B10	**pc0720**	similar to serine/threonine phosphoprotein phosphatase	-	780	pc0720_357-402	AGGGGTGATTTTTGGACACGTAGGAGATAGTCGAATTTATCGATTG	74,2	46	0,976	1	0,998	1	0,966	0,792	mid
6	4	F10	**pc0721**	similar to cysteine sulfinate desulfinase	**nifS**	1170	pc0721_582-630	TAATATTCCTAAAGGGGTATCAGCCATGTTTTTTAGTGGCCACAAAGTG	74,2	49	0,979	1	0,994	1	0,996	0,794	mid
6	4	J10	**pc0722**	conserved hypothetical protein	-	324	pc0722_209-263	TTAATAGTCAGAGCGACCTAGCTTGGATAGAGCTTACTTTAATGAAGGGGTTAGG	74,2	55	0,98	1	0,998	1	0,954	0,852	mid

6	4	N10	**pc0723**	conserved hypothetical protein	**-**	507	pc0723_169-216	CTGAAGGTCAAAGTCATGAGGCAGGTTGCTGAATATACACCAATTAAT	74,2	48	0,972	1	0,996	1	0,914	0,825	mid
6	4	B14	**pc0724**	unknown protein	**-**	255	pc0724_16-70	TTGAATTTAGGAGATAGGATGCCAGATTTATTTCCATTAGACTCTTACACTCCGT	74,1	55	0,976	1	0,981	1	0,993	0,797	5´preference
6	4	F14	**pc0725**	strongly similar to soluble pyridine nucleotide transhydrogenase	**udhA**	1398	pc0725_643-688	TTAGACGCAGAAATCGGCATTCATTTACAAACAGCTTTGACAGATA	74,2	46	0,972	1	0,994	1	0,943	0,79	mid
6	4	J14	**pc0726**	unknown protein	**-**	495	pc0726_97-148	AGAAAAGGTGGACAAAGTCAAACTCATTATGATTCTGATGGTAATCCTACCA	74,3	52	0,983	1	0,992	1	0,994	0,839	random
6	4	N14	**pc0727**	unknown protein	**-**	1209	pc0727_632-680	AAGATAATTTGGATGAAATTAAGCGCCGTTTAATCGAGGATGATAGTCC	74,2	49	0,973	1	0,996	0,986	0,974	0,772	mid
6	4	B18	**pc0728**	strongly similar to endopeptidase Clp ATP-binding chain	**clpB**	2607	pc0728_1273-1317	GAACAAGAAGCGATGAAACGAGAAAGCACTCCCCTAGCTAAAAAT	74,2	45	0,97	1	0,995	1	0,968	0,734	mid
6	4	F18	**pc0729**	conserved hypothetical protein	**-**	2748	pc0729_1632-1686	AACAATCTCTGCTTGGCATTATGCTTATGATTTACATTATTCCTCAGAAGACTTC	74	55	0,924	1	0,976	0,93	0,743	0,702	mid
6	4	J18	**pc0730**	unknown protein	**-**	192	pc0730_1-54	TTGTCAAACATTAACAAGAGTTATCTAGGGAGACGGAATCTAAAAGTTTTATTT	70,6	54	0,852	1	0,636	0,997	0,904	0,552	mid
6	4	N18	**pc0731**	unknown protein	**-**	243	pc0731_79-133	TTCTTAGGAGTAATAGGAGCGTGTTATATAAAGGCACCTTTTATTAATCAGCACA	72,4	55	0,916	1	0,817	0,901	0,956	0,798	mid
6	4	B22	**pc0732**	unknown protein	**-**	186	pc0732_36-81	TGTTACAATGTCTTCATGCGGTTTGTTCTTATGTGTCCTTCCAATT	74,2	46	0,979	1	0,997	1	0,942	0,855	mid
6	4	F22	**pc0733**	unknown protein	**-**	2826	pc0733_1805-1849	ATAAAAAATTACCAACATCCTTTTCTGAGTTAACATGGGGGCGGG	74,6	45	0,91	1	0,959	1	0,609	0,689	mid
6	4	J22	**pc0734**	hypothetical protein	**-**	2847	pc0734_1432-1478	ATGGCCTACTTTATAACTAGCGGGCGTCATGGTATAACCTTTTTTCG	74,3	47	0,98	1	0,995	0,97	0,993	0,846	mid
6	4	N22	**pc0735**	unknown protein	**-**	3228	pc0735_1604-1648	TACTCAAAGAAGTGCTTCACATTCCTACCCATGTCCCAAGAGATC	74,2	45	0,982	1	0,998	1	0,989	0,827	mid
6	5	B02	**pc0736**	conserved hypothetical protein	**-**	2598	pc0736_1186-1231	GCCTACTTTACAGGTGATAAACACGATGAAGTCTTTTTTCGCACCC	74,6	46	0,959	1	0,964	1	0,886	0,81	mid
6	5	F02	**pc0737**	conserved hypothetical protein	**-**	879	pc0737_404-451	AAAGAGGGAAGAACACTTCAGGATGGTTTTACGGTTTCAAATTACACA	74,3	48	0,593	0,02	0,998	1	0,963	0,78	mid
6	5	J02	**pc0738**	unknown protein	**-**	474	pc0738_252-306	GATTCGTCCCTATCTCAGAGATTACCCTATTTCTAACACTAATGTAGACATGGGC	74,2	55	0,986	1	0,999	1	0,986	0,874	mid
6	5	N02	**pc0739**	similar to rhs core protein with extension	**rhs**	5508	pc0739_2770-2824	CGTATTATTGAAGATAGGCTAGAAGATGCTCAAAATCAGCTCTATCAATGCAATC	74,2	55	0,97	1	0,997	0,961	0,985	0,756	mid
6	5	B06	**pc0740**	strongly similar to gcpE protein	**gcpE**	1965	pc0740_923-970	ATTATCGTCAGATAGAAGCAATCGAACGACGTCAAGTGCACTTATCTT	74,2	48	0,979	1	0,998	0,999	0,94	0,857	mid
6	5	F06	**pc0741**	conserved hypothetical protein	**-**	585	pc0741_290-338	TTCGGTTAGTAGAAAAATGGATCGATCAAATGGAAACTGAACTACCTCC	74,3	49	0,975	1	0,996	1	0,997	0,746	mid
6	5	J06	**pc0742**	conserved hypothetical protein	**-**	1536	pc0742_747-792	ACTTGAAATGGTCACTCCTCCTGGTCATATCTATATTCGTCATCGC	74,3	46	0,983	1	0,996	1	0,978	0,859	mid
6	5	N06	**pc0743**	conserved hypothetical protein	**-**	2298	pc0743_1073-1117	CTTTACAGCATTTAAACTTGAGCCATTGTGGAAAGCTTACGGACG	74,6	45	0,596	0,076	0,964	1	0,923	0,726	mid
6	5	B10	**pc0744**	unknown protein	**-**	216	pc0744_3-47	GTTTCTCCCAATTTCTTTCCAACTAAGTCGGTGTTGCATCGAAGG	76,3	45	0,69	0,433	0,789	1	0,894	0,779	mid
6	5	F10	**pc0745**	similar to 4-alpha-glucanotransferase	**malQ**	1671	pc0745_1126-1178	ATTATGTGTGTTATGCTTAGAGAATGTGAAATGCTTCCTATCGGAGAAGACCT	74,2	53	0,987	1	0,999	1	0,987	0,874	random
6	5	J10	**pc0746**	strongly similar to type III secretion chaperone sycE	**scc1, sycE**	459	pc0746_144-189	GTTATTAATTGGCTGCCGTATAGCCACACTTCCATTAGGGAGATTC	73,7	46	0,971	1	0,948	1	0,998	0,828	random
6	5	N10	**pc0747**	unknown protein	**-**	351	pc0747_1-48	ATGAAAAGAGATTCCTTTCGAGCTCACTTCAACTTTGAATCTATCGGA	74,3	48	0,963	1	0,991	0,904	0,996	0,766	random
6	5	B14	**pc0748**	unknown protein	**-**	1086	pc0748_569-613	AAGATAGCAAACGCTTGACAGAAGTTGCGGCTCATATTAAAGTCG	74,6	45	0,967	1	0,962	0,981	0,975	0,804	mid
6	5	F14	**pc0749**	strongly similar to type III secretion pathway protein SctV	**sctV;lcrD**	2181	pc0749_1110-1157	AGGTCATAAAGTTATCTCTGGGGGTGGAGTTGACAGCTATGCATTAAC	74,2	48	0,985	1	0,999	1	0,981	0,861	mid
6	5	J14	**pc0750**	similar to type III secretion pathway protein sctU	**sctU;yscU**	1074	pc0750_829-878	CACATGGATGCAGCTCCTTATATCTTAGCAATGGGTAAAGATGTTTTAGC	74,2	50	0,981	1	0,999	1	0,999	0,799	random
6	5	N14	**pc0751**	unknown protein	**-**	1815	pc0751_955-1002	AAAAGCATCAAAGATCGAGATATGGTTGGACCTCCTCAAAATTATCAA	74,2	48	0,969	1	0,998	1	0,953	0,733	mid
6	5	B18	**pc0752**	conserved hypothetical protein	**-**	1098	pc0752_508-561	TCCGAACATTTAAATGAGAATAAACCCGTTAGAACTCTTGAATTAACAGACGAG	74,3	54	0,967	1	0,995	1	0,958	0,71	mid
6	5	F18	**pc0753**	conserved hypothetical protein	**-**	1143	pc0753_502-550	GGTTATCGACAAGAAACAGTTGAAGCTCCTCTTCAAGAAACATTAGCTG	74,2	49	0,97	1	0,997	1	0,93	0,781	mid
6	5	J18	**pc0754**	hypothetical protein	**-**	1506	pc0754_834-878	TTTAAGTACAAGCCCTTACTATGGGAAATGTGTGAATGCTTGCCC	74,2	45	0,977	1	0,996	1	0,92	0,874	mid
6	5	N18	**pc0755**	unknown protein	**-**	210	pc0755_2-56	TGGCATTTTTCAAATCGATAATACGTTTCTTTCGTTTTAACGACTTAAAAAAATC	73,7	55	0,737	0,623	0,951	0,663	0,896	0,493	mid
6	5	B22	**pc0756**	unknown protein	**-**	186	pc0756_1-53	GTGCATTTAACGATTTTAGAAAAATTAACGCATTTAAATCTAGACAATTGCAA	72,1	53	0,653	0,435	0,782	0,904	0,907	0,496	mid 2.Wahl
6	5	F22	**pc0757**	unknown protein	**-**	228	pc0757_2-56	TGGTAGTTGATTTTAAAGTTCCTTTGGAAAGCATCTATTGTTTCTTTCAATTAGC	73,1	55	0,62	0,232	0,889	0,96	0,887	0,645	mid
6	5	J22	**pc0758**	similar to riboflavin kinase/FMN adenylyltransferase	**ribF**	942	pc0758_464-518	ATCGCTATGAAGGATTAGCAGTTTCTAGCACCTCTATAAGAAAGCTTGTTCAAGA	74,4	55	0,973	1	0,983	1	0,992	0,766	mid
6	5	N22	**pc0759**	strongly similar to tRNA pseudouridine synthase B	**truB**	789	pc0759_337-387	GGAGTTGTTACAGATTCTTACGATTGTGAAGGCCAGGTATTATCTCAATCA	74,3	51	0,968	1	0,998	0,958	0,941	0,799	mid
6	6	B02	**pc0760**	similar to ribosome binding factor A	**rbfA**	298	pc0760_39-83	AAAAGAAGTTATTTCAGAGGTCATTAGACGTGACGTGCGGAATCC	74,3	45	0,986	1	0,997	1	0,999	0,856	random
6	6	F02	**pc0761**	similar to translation initiation factor IF-2	**-**	2763	pc0761_1367-1413	ATATTGGTGCATTCCGTTGTCATACGACTGTAGGTGATATCGCTATC	74,2	47	0,987	1	0,997	0,985	0,984	0,909	mid
6	6	J02	**pc0762**	similar to transcription termination-antitermination factor nusA	**nusA**	1275	pc0762_667-713	ATTATTGACAAGATTGTTCGTGATGCAGGTTATCGCACGAAACTAAC	74,2	47	0,982	1	0,997	0,985	0,972	0,872	mid
6	6	N02	**pc0763**	unknown protein	**-**	183	pc0763_1-53	TTGATCTGGTTTAGGAACAAATTGTTATTTGATAAGACCTCCCTAAATGGAGG	74,2	53	0,975	1	0,998	0,989	0,985	0,768	random
6	6	B06	**pc0764**	strongly similar to ribosomal protein S1	**rpsA**	1764	pc0764_805-859	ATCTTAAGTGTAGACAAAGACAAAGGTCGTGTTGCTTTAGGTCTCAAACAAAAAG	74,2	55	0,971	1	0,996	0,998	0,922	0,802	mid
6	6	F06	**pc0765**	strongly similar to aspartate kinase II precursor	**lysC**	801	pc0765_415-468	ATTGTTATAGTGGCGGGCTTTCAAGGAGTTAGTCAAGATAAAGAGGTAACAACT	74,2	54	0,981	1	0,994	1	0,987	0,831	mid
6	6	J06	**pc0766**	unknown protein	**-**	1908	pc0766_725-771	CTTTTCTCGTAACGCCGAAAGGTCGTAAAAGGGTGTTAGGATTACTT	74,2	47	0,956	1	0,999	0,984	0,77	0,871	mid
6	6	N06	**pc0767**	similar to branched-chain amino acid transport system II	**braB**	1182	pc0767_596-	TTTTTTGTTCAGTCGTACTAGCTTGCTTGAAAAAAGGGGTTGAACC	74,2	46	0,975	1	0,998	1	0,996	0,733	mid

				carrier protein			641											
6	6	B10	**pc0768**	similar to ribulose-phosphate 3-epimerase	**rpe**	732	pc0768_334-380	TGTAATATACGAGCAGGTTTGGCATTCAATCCAGAAACATCTGTTTC	74,2	47	0,979	1	0,999	1	0,967	0,819	mid
6	6	F10	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
7	1	C02	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
7	1	G02	**pc0769**	similar to elongation factor P	**efp**	555	pc0769_277-323	GTTCCAGCTGAAATCGTGAGTGGCAAAGTTAATTATCTCAAAGAAGG	74,2	47	0,98	1	0,995	1	0,998	0,797	mid
7	1	K02	**pc0770**	unknown protein	**-**	342	pc0770_208-261	AACTATTGCTTACTTTGGTCGTTTTCCTTATCGAAATGCTATTTTAGGTCGAGA	74,3	54	0,976	1	0,996	1	0,964	0,803	mid
7	1	O02	**pc0771**	similar to biotin carboxyl carrier protein of acetyl-CoA carboxylase	**accB, BCCP**	513	pc0771_252-303	TGAAGCTCCCAAAGTCGATACTAATAGCCTTTATGTCACATCTCCTATGGTA	74,2	52	0,984	1	0,996	0,978	0,994	0,871	mid
7	1	C06	**pc0772**	strongly similar to biotin carboxylase	**accC**	1362	pc0772_673-717	GAAAGAGATTGCACTACTCAACGACGCAGACAAAAACTCATTGAA	74,3	45	0,978	1	0,997	0,982	0,991	0,802	mid
7	1	G06	**pc0773**	unknown protein	**-**	711	pc0773_383-434	TTTCTAACTATGCCTATGTCTTACAAAATCGATCGACTCGTGAAATTGTTGA	74,2	52	0,974	1	0,993	1	0,974	0,772	mid
7	1	K06	**pc0774**	unknown protein	**-**	678	pc0774_311-361	ATTGGTGTAGCACTCCATACTATTGGGCAGCCAAAAGAATGTATTTACTTC	74,2	51	0,973	1	0,998	0,962	0,971	0,805	mid
7	1	O06	**pc0775**	conserved hypothetical protein	**-**	693	pc0775_393-437	AGTGATGTTTATTCGCTACGCGCAAGGATATGTCTTTTTACCTGG	74,3	45	0,972	1	0,996	0,959	0,955	0,831	mid
7	1	C10	**pc0776**	conserved hypothetical protein	**-**	957	pc0776_466-514	TTTACTGTTGGTCAAGTCGTTTTAGTTTGCAATATTTTTGTGTTTGGGG	74,3	49	0,974	1	0,995	1	0,986	0,745	mid
7	1	G10	**pc0777**	unknown protein	**-**	411	pc0777_116-165	TTATCCAAGAGTTGCGAGAAATTCGAAATAGAGATCAATTACTTGCTTCG	74,2	50	0,97	1	0,998	0,974	0,943	0,795	5´preference
7	1	K10	**pc0778**	similar to exopolysaccharide synthesis protein	**exoD**	627	pc0778_322-376	AAATTGCGCTATTTTGTTTATCCTAGGCTTCCAAATCTGGTAAAAAATCCTATTC	74,2	55	0,97	1	0,999	1	0,993	0,688	mid
7	1	O10	**pc0779**	hypothetical protein	**-**	1968	pc0779_913-957	CAATCCCATCTAATATCTGTGCAAACTCAATTGGAGCGAACAACT	74,2	45	0,969	1	0,999	1	0,928	0,769	mid
7	1	C14	**pc0780**	strongly similar to methionyl aminopeptidase	**map1**	888	pc0780_490-541	AAACGACTCGTTGTTGACGTCTCTTATAATTGTTTAATGTGTGCGATAGAGA	74,3	52	0,973	1	0,99	1	0,955	0,794	mid
7	1	G14	**pc0781**	similarity to Glucose-6-phosphate isomerase (GPI), (Phosphoglucoseisomerase, PGI), (Phosphohexose isomerase, PHI)	**pgi**	1614	pc0781_795-839	GATAGGAGGACGTTACTCAACAACTTCCATGTGCGGAGCTTTAAT	74,3	45	0,983	1	0,998	1	0,987	0,837	mid
7	1	K14	**pc0782**	unknown protein	**-**	453	pc0782_2-50	TGGAATATTATTCGTTAATTGTTGAAGGGGAAGATCAACAAGTGATTCG	74	49	0,968	1	0,976	0,979	1	0,752	5´preference
7	1	O14	**pc0783**	strongly similar to XerD protein	**XerD**	876	pc0783_466-510	TATGATGTGGACGATACTTTTGTGCGAGTTTTAGGAAAAGGTGGA	74,3	45	0,973	1	0,994	1	0,973	0,763	mid
7	1	C18	**pc0784**	unknown protein	**-**	432	pc0784_173-218	TAATGGGTTTTACTATAGGGGTTGTTCTTGAACGTCATGTACGCGA	74,2	46	0,981	1	0,999	1	0,956	0,855	mid
7	1	G18	**pc0785**	unknown protein	**-**	219	pc0785_55-102	GGAATCTGCATTCCCTACTCTTATCCTTACATTTCCTACCTAACCGCA	74,3	48	0,977	1	0,99	1	0,944	0,855	mid
7	1	K18	**pc0786**	unknown protein	**-**	318	pc0786_58-110	TTAGCGAGACAAGATATCAGTTCAGCTGTTCAAGAAGATGACTCTTTAGAACC	74,2	53	0,969	1	0,995	1	0,898	0,82	mid
7	1	O18	**pc0787**	similar to regulatory protein, involved in type III secretion lcrH, sycD	**lcrH**	501	pc0787_88-132	GAAGGTAAAACTGCTCAACAGATCATGGAACTTCAAGATTCCACG	74,4	45	0,974	1	0,988	1	0,957	0,815	5´preference
7	1	C22	**pc0788**	unknown protein	**-**	267	pc0788_102-146	GCGATTAAATCAGCAAGCTGTTTGTGTTAATAAAGCCATGACTGC	74,2	45	0,965	1	0,998	0,969	0,967	0,715	mid
7	1	G22	**pc0789**	similar to alcohol dehydrogenase class III	**adh3**	1128	pc0789_532-580	GGTGTAGCTCCTTTACTTTGTGCAGGAATTACGACTTACTCACCTTTGA	74,2	49	0,977	1	0,997	0,982	0,967	0,832	mid
7	1	K22	**pc0790**	hypothetical protein	**-**	738	pc0790_385-436	TATACAACGACGACACAAAACCCGACTTACAATTACCCTTATCCTACTTCAA	74,2	52	0,986	1	0,997	1	0,985	0,878	mid
7	1	O22	**pc0791**	hypothetical protein	**-**	1452	pc0791_757-807	AAAAAAGGTGTAGGTAACCATAGTGATTGGGTAGGAAGAAATTTGCTCGAC	74,2	51	0,977	1	0,998	1	0,97	0,799	mid
7	2	C02	**pc0792**	hypothetical protein	**-**	1299	pc0792_731-775	TTGAAGTATTAGATAGTGAGGTGCTTGGGCTTAAGTGGAGAGCGC	74,4	45	0,975	1	0,985	1	0,92	0,887	mid
7	2	G02	**pc0793**	similar to mechanosensitive channel of large conductance	**mscL**	402	pc0793_120-170	CATTATGCCTTTAATTGGTCTTCTATTAGGAGGCGCTGATTTTAGTGCTCT	74,2	51	0,981	1	0,998	1	0,999	0,797	random
7	2	K02	**pc0794**	strongly similar to queuine tRNA-ribosyltransferase (guanine insertion enzyme)	**-**	1164	pc0794_608-653	CTTTAGAGGCTCACTTAAAAAATCCTCAAGAGCAAGCCATGTACGC	74,3	46	0,971	1	0,995	1	0,975	0,731	mid
7	2	O02	**pc0795**	conserved hypothetical protein	**-**	654	pc0795_300-344	CCAAATCCATTTGCTTTATGAACCCAGCTTGAATGATACTTCACA	74,5	45	0,971	1	0,977	1	0,972	0,783	mid
7	2	C06	**pc0796**	similar to tonoplast intrinsic protein (Aquaporin)	**-**	699	pc0796_351-401	TTTAGCAGATGGAGTTTCTATGGGAATAGGTATTATGGCTGAGGCAATTTT	74,3	51	0,977	1	0,996	1	1	0,761	mid
7	2	G06	**pc0797**	hypothetical protein	**-**	630	pc0797_275-326	AAGTCACATGTTGTGAGAAAGATGAATTGGAAGTGGCTAAACTTGAAGTAGA	74,3	52	0,607	0,06	0,99	1	0,959	0,793	mid
7	2	K06	**pc0798**	unknown protein	**-**	222	pc0798_67-113	CTTTCATTTTTAGGAAAAAGAGACCTACAAGCAATTGCCTGCACATG	74,4	47	0,958	1	0,984	0,997	0,955	0,652	mid
7	2	O06	**pc0799**	unknown protein	**-**	243	pc0799_37-89	TCTGATAATATGGAATATAAAGAGGATTTGAAGAAGACTAACTTCAGGCTCCTGA	74,2	53	0,61	0,08	0,999	1	0,914	0,781	mid 2.Wahl
7	2	C10	**pc0800**	hypothetical protein	**-**	942	pc0800_507-555	AACAACTGCCACTATCCGATATTTAACACAAACGAATACTCTTCAAGCG	74,2	49	0,979	1	0,998	1	0,965	0,828	mid
7	2	G10	**pc0801**	strongly similar to triose-phosphate isomerase	**tpiA**	795	pc0801_488-533	AGACCTTAATAATTGCTTACGAACCTGTTTGGGCTATTGGGAATGG	74,2	46	0,981	1	0,999	1	0,998	0,797	random
7	2	K10	**pc0802**	similar to integral membrane component of the sec protein-translocation machinery, secG	**secG**	294	pc0802_40-87	ATTATTTGCGCATTACTTTGTGCAGTTATTTTGATGCAAGAAAGCAAA	74,2	48	0,967	1	0,998	0,953	1	0,709	random
7	2	O10	**pc0803**	similar to polypeptide deformylase	**def**	531	pc0803_281-325	GTCAAGAAGCTTGTCTTTCCATTCCAGGTATGAGGGAAACTGTTT	74	45	0,975	1	0,974	1	0,986	0,822	mid
7	2	C14	**pc0804**	unknown protein	**-**	189	pc0804_14-68	TTTCTCTTGAAGGAATTTGCCGCATATTTAAAGTTAGTATGCTTTGGATTTTAGA	73,9	55	0,948	1	0,968	0,961	0,919	0,696	mid
7	2	G14	**pc0805**	unknown protein	**-**	1857	pc0805_986-1039	GGGGTATTGTTGCCGATGCTTATGAAAAATATGTAGATGATAAGGTTCAGTATC	74,2	54	0,972	1	0,996	1	0,944	0,785	mid
7	2	K14	**pc0806**	unknown protein	**-**	408	pc0806_64-118	GAAATTTTAGATCCAAAAATGAAAGAGCGGCTAGAATTATCAGGTATTACAGTGG	73,7	55	0,955	1	0,944	1	0,997	0,671	random
7	2	O14	**pc0807**	unknown protein	**-**	270	pc0807_53-98	CTATTATGAAACCATTCCTTGGATCCAGCATCAAGCAGTTAGCAAG	74,2	46	0,604	0,06	0,994	1	0,917	0,808	mid
7	2	C18	**pc0808**	hypothetical protein	**-**	366	pc0808_77-121	GTTTAGAGTGTGGCAAACAGTGGAGCGAAAACAATGAAGCTAAAA	74,2	45	0,613	0,07	0,999	1	0,999	0,738	random

7	2	G18	**pc0809**	similar to copper-transporting ATPase	**copB**	2295	pc0809_1136-1180	CGATTGTCAAATGGTTTGTTCCGTTTGTTTTATGTTTAGCGATTG	74,2	45	0,974	1	0,998	1	0,987	0,741	mid
7	2	K18	**pc0810**	strongly similar to threonine 3-dehydrogenase	**tdh**	1029	pc0810_582-631	CACAGATGTAAACGATTATCGTCTAGACCTTGCAAGAACTATGGGTGTCT	74,2	50	0,979	1	0,994	1	0,934	0,881	mid
7	2	O18	**pc0811**	strongly similar to 2-amino-3-ketobutyrate coenzyme A ligase (Glycine acetyltransferase)	-	1191	pc0811_638-682	TTGGCTTCATGGGAGTAAAAGGAAAAGGAACTTCTGAGTTTTGTG	74,2	45	0,971	1	0,997	1	0,959	0,752	mid
7	2	C22	**pc0812**	unknown protein	-	1083	pc0812_465-519	ATCATTTATCATTTTAGGATTTCTCATGGCATTTGTAGGGATCTCAAAAGTTGAT	74,3	55	0,964	1	0,997	0,984	0,922	0,75	mid
7	2	G22	**pc0813**	unknown protein	-	831	pc0813_528-572	CCGCGCATTGATTGAACAAGTTAAAGAATCTTTCGTTACCTCAAT	74,3	45	0,96	1	0,995	1	0,889	0,732	mid
7	2	K22	**pc0814**	unknown protein	-	696	pc0814_367-420	TGTCATTTAGTAACACAAGAAAATGTACAGGATGCTTCCTTTCTTGAGATGTGT	74,3	54	0,978	1	0,995	1	0,982	0,8	mid
7	2	O22	**pc0815**	strongly similar to lipoprotein releasing system ATP-binding protein	**lolD**	687	pc0815_373-417	GAACAACGAGGAATGGAACTTCTTCATCAAGTTGGACTTCAAGAA	74,2	45	0,977	1	0,999	1	0,972	0,788	mid
7	3	C02	**pc0816**	conserved hypothetical protein	-	2133	pc0816_1090-1139	GCCAAAAGATTAGATGATCTTACTTTTGAGATAACCGTGCCTATCCAAGG	74,3	50	0,978	1	0,998	1	0,978	0,794	mid
7	3	G02	**pc0817**	strongly similar to 50S ribosomal protein L33	**rpmG**	159	pc0817_4-58	GCCAGCAAACGTGAAAACATTAAAATGAAAAGTTCAAAAAGTCACTATCATTACT	74	55	0,81	0,624	0,98	0,988	0,923	0,705	mid 2.Wahl
7	3	K02	**pc0818**	strong similarity to O-sialoglycoprotein endopeptidase	-	1032	pc0818_498-545	TTTTGATAAAGTCGCTAAGATGCTTAATCTTCCCTATCCTGGTGGACC	74,4	48	0,977	1	0,986	1	0,981	0,81	mid
7	3	O02	**pc0819**	similar to 6-phosphogluconolactonase (6PGL).	**devB;pgl**	639	pc0819_361-405	GGCTTACACGCAAAAGATCGTCTAGTCATTGCTAATTACGTTCCC	74,2	45	0,978	1	0,994	1	0,959	0,836	mid
7	3	C06	**pc0820**	hypothetical protein	-	1077	pc0820_541-587	GCTCGTATTGGAGGCTGGAGAGAAATTGTAGCACAAACTTTTGATAG	74,2	47	0,976	1	0,998	1	0,999	0,743	mid
7	3	G06	**pc0821**	similarity to glucose-6-phosphate 1-dehydrogenase (G6PD)	**zwf**	1551	pc0821_782-827	GAGATATTGTCCAAAATCATGTGATGCAACTCCTTTCTCTTGTTGC	74,2	46	0,978	1	0,991	1	0,994	0,789	mid
7	3	K06	**pc0822**	similarity to bumetanide-sensitive Na-K-Cl cotransporter	-	2295	pc0822_1169-1215	TACCATGGATTATCTCCTTAACAGGGACCCTACTTTGCGTTATAGCG	74,2	47	0,985	1	0,999	1	0,98	0,867	mid
7	3	O06	**pc0823**	conserved hypothetical protein	-	405	pc0823_20-71	CTCAATCCGACGAAAGAAAGATTATAGCCATGCCTCTTATCACTGTACATAC	74,2	52	0,982	1	0,999	1	0,995	0,817	random
7	3	C10	**pc0824**	strongly similar to CTP synthase	**pyrG**	1635	pc0824_877-925	GGAACTGTAACTGTAGGCATCGTTGGAAAATATGTTCAACATCAAGATG	74,3	49	0,974	1	0,997	1	0,942	0,806	mid
7	3	G10	**pc0825**	strongly similar to 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)	**kdsB**	780	pc0825_352-397	ATCAATTTAGCTGTTCAGGCACTTGTTAATGACCCTCAAGGACAAG	74,2	46	0,978	1	0,996	1	0,961	0,82	mid
7	3	K10	**pc0826**	conserved hypothetical protein	-	951	pc0826_478-525	GAAATGGATTGGTGGGATGAAGTTTCTCTCTATTCGTCTAATCAGCTC	74,3	48	0,979	1	0,995	1	0,999	0,789	mid
7	3	O10	**pc0827**	similarity to 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO transferase)	**gseA;kdtA**	1254	pc0827_569-617	AATTAGATGATGAGTATCCACAACTGACAAAAGAAGGGGTGTATGCATG	74,1	49	0,972	1	0,99	1	0,941	0,81	mid
7	3	C14	**pc0828**	unknown protein	-	189	pc0828_1-45	TTGGTAGAGCAACGGAATCATAATCCGTGTGTCGTCGGTTCAAGT	78,1	45	0,874	1	0,614	0,885	0,987	0,903	random
7	3	G14	**pc0829**	unknown protein	-	1311	pc0829_619-664	AAGGAATACACAGTAGGAGCAAGAGGATATGGCGGAGAATGGATTA	74,2	46	0,979	1	0,997	1	0,962	0,837	mid
7	3	K14	**pc0830**	unknown protein	-	696	pc0830_353-400	CACTAGTCCTGAGTGTTTTTAGGTGGCACTTATGCGGTGAATGTCTAT	74,4	48	0,979	1	0,985	1	0,996	0,814	mid
7	3	O14	**pc0831**	unknown protein	-	201	pc0831_10-54	TTATTTGATGGCAGGAACGTCTTGTTTCTTAGCAAAAAAAGCCCT	74,4	45	0,815	0,644	0,979	0,991	0,908	0,695	mid 2.Wahl
7	3	C18	**pc0832**	unknown protein	-	186	pc0832_36-88	TTTCCCATTATTAGTTTTCACATTTGAGTTCTCTGTCCAAAAGCCTTTCCTAT	74,2	53	0,976	1	0,996	1	0,962	0,8	random
7	3	G18	**pc0833**	unknown protein	-	366	pc0833_22-76	AAATTTGTCACTGCTTGCAATAAGTCAGCTATAGACTTACATTACGATGCTCATT	73,8	55	0,973	1	0,957	0,997	0,997	0,836	random
7	3	K18	**pc0834**	unknown protein	-	252	pc0834_73-125	TTCTTACGTTGTGGGGATTTACATCAAAATAATCTATTTGTCTCATGGAAAGC	74,3	53	0,975	1	0,996	1	0,987	0,755	random
7	3	O18	**pc0835**	hypothetical protein	-	1149	pc0835_545-590	AACACAAAGAAATTTCGACATATGAAGAGGGGACAACTGACTGTCA	74,2	46	0,976	1	0,999	1	0,97	0,78	mid
7	3	C22	**pc0836**	unknown protein	-	267	pc0836_3-52	GCAAAGAAAGTACCAGAGGTCAAATGCCTTAAATGAATTGAGAGAGTTTG	74,2	50	0,979	1	0,996	1	0,998	0,778	random
7	3	G22	**pc0837**	unknown protein	-	423	pc0837_4-51	GATTCTTCGTTACTTACATTATTTCGGGGACCAGCAAGAAAGGTTTGT	74,2	48	0,982	1	0,998	1	0,993	0,823	random
7	3	K22	**pc0838**	unknown protein	-	1239	pc0838_598-642	CTCAAACAACGTATGGATGAGGTTCAAGATTCTTCCGCTTATGAA	74,2	45	0,972	1	0,998	1	0,977	0,73	mid
7	3	O22	**pc0839**	unknown protein	-	1020	pc0839_618-663	TAAGCAAGAATTATCTCGAGAAGGAAGTTGGCTACAAAGCGAGGAA	74,3	46	0,966	1	0,989	1	0,893	0,809	mid
7	4	C02	**pc0840**	unknown protein	-	759	pc0840_428-474	GTTTCTGGGTTTTGCGCTGTCTTTACCAGCCCTATATCGTTAATAAA	74,1	47	0,971	1	0,982	1	0,953	0,805	mid
7	4	G02	**pc0841**	unknown protein	-	279	pc0841_63-116	GCCAGAAAATGAACAAATTGAAAAAACTAAGAAGAATCAACTCGAAAAACCTTT	74,2	54	0,812	0,63	0,991	1	0,997	0,552	random
7	4	K02	**pc0842**	unknown protein	-	444	pc0842_93-138	AACCCAAACTGTCTCGCGTGTAGTCATTGAAGTGCTAAAGACTGTA	74,3	46	0,987	1	0,997	1	0,996	0,867	random
7	4	O02	**pc0843**	hypothetical protein	-	1164	pc0843_607-656	AAAGAAGACTTGAAAGAGCGTGCTAAAATAATCAATGAATTTTCTCCCGA	74,3	50	0,966	1	0,991	1	0,976	0,685	mid
7	4	C06	**pc0844**	unknown protein	-	291	pc0844_39-84	AAGGCTAGGGGTACCTTTTTCTTGTGATTGGATCGTTGATTTCTCT	74,2	46	0,976	1	0,993	1	0,999	0,752	random
7	4	G06	**pc0845**	conserved hypothetical protein	-	366	pc0845_77-131	AGAACTTTGTTAGCCAGTCTGCGATTAGCCAAGCAATTCATAAATTAGAGATTAC	74,2	55	0,979	1	0,999	1	0,999	0,772	random
7	4	K06	**pc0846**	hypothetical protein	-	618	pc0846_318-362	TCGAACTCGACATAGCCACCGCTCTCCTGAATTTATTGAATTATT	74,2	45	0,979	1	0,999	1	0,992	0,78	mid
7	4	O06	**pc0847**	unknown protein	-	219	pc0847_66-110	TTATATTGAAAGACTTAATTGCACCCTCGGATACCGATGCTCACG	74,8	45	0,955	1	0,947	0,909	0,955	0,846	mid
7	4	C10	**pc0848**	hypothetical protein	-	492	pc0848_155-203	TATTAGAGTGCATTGCTCTTGAAGGAGTATGTTGGGTATTTGACGTCAG	74,2	49	0,987	1	0,998	1	0,997	0,867	random
7	4	G10	**pc0849**	unknown protein	-	288	pc0849_87-131	CGACCTAATACTTTCTCAACATCTCTCACAAGCTCTTCAGCCTGC	74,2	45	0,983	1	0,998	1	0,995	0,828	random
7	4	K10	**pc0850**	hypothetical protein	-	747	pc0850_407-454	AACAGTTCAACTTGGCAAATGAGGGCAACTGGGTTATCTCTATAAAGA	74,4	48	0,976	1	0,987	1	0,967	0,815	mid
7	4	O10	**pc0851**	conserved hypothetical protein	-	1371	pc0851_679-725	GAAGTGCAAGTGGCTAAAGGTTTGTTTTCTGAGGATGAAGAAGTGTT	74,2	47	0,978	1	0,998	1	0,993	0,775	mid
7	4	C14	**pc0852**	conserved hypothetical protein	-	684	pc0852_333-382	CATTAGGGATCGGCATATGTTTGAAACCTTAGAAACTCTGATGAGTCTTC	74,2	50	0,982	1	0,996	1	0,99	0,83	mid
7	4	G14	**pc0853**	conserved hypothetical protein	-	192	pc0853_1-45	ATGATTCGTCTCCTGCATCGCGCCATTGGTGTTATTTACCAACCT	79,1	45	0,849	1	0,518	1	0,904	0,858	mid 2.Wahl
7	4	K14	**pc0854**	unknown protein	-	255	pc0854_22-73	GCTCAGTCCATTCTCAATAATATACTAAGTGAATGGGATCATTTCTCAACGC	74,3	52	0,967	1	0,997	0,981	0,893	0,827	mid
7	4	O14	**pc0855**	conserved hypothetical protein	-	432	pc0855_209-253	ATTATGAAGGCTGGGTCCCAGCACATACTCCTATCAAAGTTCATC	74,3	45	0,983	1	0,997	0,97	0,992	0,878	mid

7	4	C18	**pc0856**	strongly similar to L-isoaspartyl protein carboxyl methyltransferase	**pcm**	633	pc0856_320-368	AAAAACGGCTGCAAGAGTTTGGCTATAATAATGTGACAGTATCAGTTGG	74,2	49	0,985	1	0,998	1	0,997	0,84	mid
7	4	G18	**pc0857**	conserved hypothetical protein	**-**	246	pc0857_26-72	ACCTATGCATAAAACAACTCGACATGGCTTTTCCCTCATTTACAGAG	74,2	47	0,979	1	0,999	1	0,996	0,777	random
7	4	K18	**pc0858**	unknown protein	**-**	411	pc0858_25-72	ATTGATCACAAGTTCTATGTTAGCTCCATTGGTGTCCATAAAAGACGC	74,2	48	0,986	1	0,999	1	0,995	0,859	random
7	4	O18	**pc0859**	conserved hypothetical protein	**-**	333	pc0859_104-156	AAGTCACTTCATTAGGAAAACGTAAATTTACTGCTAAAATTCTCAGCAGCGGT	74,2	53	0,979	1	0,999	1	0,999	0,77	random
7	4	C22	**pc0860**	conserved hypothetical protein	**-**	741	pc0860_491-535	AAATTCACATGCAAGAATATGGTGTGACAATTATTCGACCGTTGA	74,2	45	0,967	1	0,999	1	0,88	0,807	mid
7	4	G22	**pc0861**	hypothetical protein	**-**	855	pc0861_342-386	GGCTCTTGTAACAGCCATGATTCGAGGAGGTGTCTGTATTCTAGA	74,3	45	0,987	1	0,993	1	0,988	0,896	random
7	4	K22	**pc0862**	unknown protein	**-**	1827	pc0862_823-867	ATGAAGTTTGTGCGTAACTATGCATTAGTCGGAGGGCAGTTAATG	73,9	45	0,97	1	0,97	1	0,908	0,885	mid
7	4	O22	**pc0863**	hypothetical protein	**-**	1014	pc0863_571-617	GCAATTGAAGAACCTCTTAAGCATCTCGTTGAACTGAAAACACATGT	74,2	47	0,971	1	0,999	1	0,937	0,779	mid
7	5	C02	**pc0864**	similar to acid phosphatase	**surE**	786	pc0864_330-377	TTATAGTGGGACTGTTGCAGCTATTATGGAAGGAGTTATGCAGGGAAT	74,2	48	0,979	1	0,993	1	0,936	0,875	mid
7	5	G02	**pc0865**	strongly similar to aconitate hydratase	**acnB**	2847	pc0865_1454-1506	CTATTACAAGTTGTACCAATACGAGTAATCCAAATGTGATGTTAGCAGCAGGG	74,2	53	0,982	1	0,998	1	0,971	0,85	mid
7	5	K02	**pc0866**	unknown protein	**-**	186	pc0866_37-91	TTTTTTATCAGTTTTTTAGTTTATTTCATTATTTCCTATCAGCAAGCTGCTGAAA	71,5	55	0,761	0,691	0,725	1	0,943	0,56	mid 2.Wahl
7	5	O02	**pc0867**	conserved hypothetical protein	**-**	699	pc0867_412-457	AAAAAATTCACAGGTTCTCGTTTTCTTTGGCTACGCAGTAATGGAG	74,3	46	0,969	1	0,998	1	0,939	0,749	mid
7	5	C06	**pc0868**	conserved hypothetical protein	**-**	390	pc0868_95-140	TCCATCTCGTGATTAATCATCATGCAGAAATTGTCGCATTTAAGTT	74,2	46	0,61	0,06	0,994	1	0,999	0,758	random
7	5	G06	**pc0869**	unknown protein	**-**	960	pc0869_464-509	AAATGTATGAGGCAGACCTCTGCGTACCAGCTGTAGCTAGTAATCG	74,3	46	0,987	1	0,993	1	0,983	0,905	mid
7	5	K06	**pc0870**	unknown protein	**-**	891	pc0870_310-355	CAACAACATGCTCGTTTCGAATCTAGCAAACTCAAAGGAATGACTA	74,3	46	0,967	1	0,998	1	0,864	0,832	mid
7	5	O06	**pc0871**	strongly similar to spermidin/putrescin transport ATP-binding protein, component of ATP-transporter system	**potA**	1122	pc0871_601-650	GTTAGTGATCGCATTGCTGTTTTACATAAAGGGAGTTTAGAGCAAATTGG	74,2	50	0,973	1	0,993	1	0,961	0,775	mid
7	5	C10	**pc0872**	strongly similar to spermidine/putrescine transport system permease, component of ATP-transporter system	**potB**	915	pc0872_510-564	AGTTATGGTTTACACTTATTTACCTTTTGCCGTTTTTCCTATTTATGCAGCAGCT	74,2	55	0,971	1	0,997	1	0,949	0,766	mid
7	5	G10	**pc0873**	strongly similar to spermidine/putrescine transport system permease, component of ATP-transporter system	**potC**	768	pc0873_386-433	TTACGGTCTTTATTGCACACACCACATTTTGCATGAGTTATGTTACAA	74,1	48	0,981	1	0,989	1	0,999	0,824	mid
7	5	K10	**pc0874**	similar to spermidine/putrescine-binding protein precursor, component of ABC transporter system	**potD**	1038	pc0874_531-578	TTTAGGCTATAGTGCCAATACAACTCAATTGCAACAAATCGATCAAGC	74,3	48	0,98	1	0,991	1	0,989	0,824	mid
7	5	O10	**pc0875**	unknown protein	**-**	186	pc0875_23-70	GCTCTAGCCAGCTAGTGACAATAACTCAATTGAGCAGACATTGCTTTT	74,2	48	0,968	1	0,993	1	0,929	0,766	mid
7	5	C14	**pc0876**	unknown protein	**-**	201	pc0876_56-109	ATTCATGTGACTATCAACGTCTATACACATTAAGCAGAGTCGTGGAAGAAGAAG	74,2	54	0,98	1	0,999	1	0,954	0,846	mid
7	5	G14	**pc0877**	similar to Mg2+ transporter	**mgtE**	1365	pc0877_653-701	ATGATCGCTCAGCTTTACCTGTCATTGACAATGAAGGAGTCTTATTAGG	74,3	49	0,977	1	0,991	1	0,969	0,815	mid
7	5	K14	**pc0878**	strongly similar to L-serine ammonia-lyase	**sdaB**	1392	pc0878_780-824	AGAAAAGCGAGATCGTGCTGAAGTTATAGATTGGGTCAGTCTGTG	74,3	45	0,977	1	0,994	1	0,917	0,888	mid
7	5	O14	**pc0879**	conserved hypothetical protein	**-**	792	pc0879_314-360	AAATTGATCTTAACCGTATAGGAATACTTGGGCGCTCTTTAGGTGGG	74,1	47	0,97	1	0,982	1	0,917	0,841	mid
7	5	C18	**pc0880**	similar to 6-phosphofructokinase 1	**pfkA**	1662	pc0880_779-823	CTCATCTTGCTCTCGAGTGCGCTTTATTGACACACCCTAATTTAG	74,2	45	0,969	1	0,995	1	0,947	0,751	mid
7	5	G18	**pc0881**	hypothetical protein	**-**	603	pc0881_285-334	TTTCATGATCAGTGTCATCACTTATCCCCAAGACTTCAATACAACCAATA	74,3	50	0,974	1	0,998	0,99	0,982	0,764	mid
7	5	K18	**pc0882**	similar to 3-phosphoshikimate 1-carboxyvinyltransferase(5-enolpyruvylshikimate-3-phosphate synthase, EPSP synthase)	**aroA**	2820	pc0882_1322-1366	CTGACTGGATTCCCCAACAAATTACTGCTTTAGACGTGATTTCAC	74	45	0,968	1	0,979	1	0,911	0,831	mid
7	5	O18	**pc0883**	similar to shikimate kinase precursor	**aroL**	612	pc0883_391-443	AACTGGAAAGAGCGTATTTTCAGTCAAACTGAGTTACCAGCCTATATTTCTCA	74,2	53	0,978	1	0,996	0,98	0,998	0,806	random
7	5	C22	**pc0884**	strongly similar to chorismate synthase	**aroC**	1104	pc0884_498-547	TGAATTATCAGACCATGTAAATAACGTGCCTTTATTGCAACAAACCATTC	74,2	50	0,974	1	0,994	1	0,945	0,812	mid
7	5	G22	**pc0885**	unknown protein	**-**	738	pc0885_408-460	TTTAGTTTTAGGGGATTGTTGCAACAATTACATTGAAAAAGGCTTTTTAGGTG	74,2	53	0,967	1	0,998	1	0,962	0,697	mid
7	5	K22	**pc0886**	unknown protein	**-**	702	pc0886_250-294	GAGGGTGGAGATCATCTTCTGAATGTGTCTAGCAATATCGGTGTT	74,3	45	0,973	1	0,998	1	0,898	0,849	mid
7	5	O22	**pc0887**	unknown protein	**-**	387	pc0887_138-182	AATTAGTGCACTAACCACTCCCTTATTTCGCAAAATGTTTGCTGC	74,3	45	0,975	1	0,997	1	0,943	0,819	mid
7	6	C02	**pc0888**	conserved hypothetical protein	**-**	1962	pc0888_752-800	AAGTACTCCATTTAGAGAAATGTCAGGTTATTACGGACGATGGTTTGGC	74,2	49	0,611	0,122	0,998	1	0,77	0,819	mid
7	6	G02	**pc0889**	strongly similar to riboflavin synthase beta chain	**ribH;ribE**	519	pc0889_262-306	CATTTTGACTATGTTGCTAGCCAATCTGCTGCAGGAATTCTGAAT	74,3	45	0,98	1	0,988	1	0,999	0,815	mid
7	6	K02	**pc0890**	strongly similar to 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	**ribA;ribB**	1239	pc0890_558-607	TCAAATTCCCATTATTACGATTGCAGAGCTTATTCGTTTTAGAAGAAGGC	74,2	50	0,966	1	0,998	1	0,937	0,726	mid
7	6	O02	**pc0891**	strongly similar top riboflavin synthase alpha chain	**ribC**	606	pc0891_261-305	TAAATATAGCGACCGCTTAGGAGGCCATCTTGTACAAGGCCATAT	74,2	45	0,982	1	0,999	0,989	0,957	0,887	mid
7	6	C06	**pc0892**	similar to formamidopyrimidine-DNA glycosidase	**mutM, fpg**	831	pc0892_345-399	TGGTCGTTGGTATTTAGTTTCTGATGTAGAGGAAATTATAGGACACTTAGGTCCC	74,2	55	0,976	1	0,997	1	0,929	0,847	mid
7	6	G06	**pc0893**	strongly similar to nucleic acid-binding protein	**rbp**	339	pc0893_68-112	AAGCTTTCGGTAAAGTTGTTAGCGCCAAGATCGTTACTGATCAAA	74,2	45	0,983	1	0,995	1	0,999	0,833	random
7	6	K06	**pc0894**	unknown protein	**-**	4047	pc0894_2070-2123	TGCAGAACCAACTCAAGTCAATCTTGAATCAAAGAATCTAAGTAGCCTATTGTT	74,2	54	0,975	1	0,998	1	0,955	0,795	mid
7	6	O06	**pc0895**	similar to outer membrane protein	**-**	1614	pc0895_697-746	ACAGCTGATATTGCTTCAAACTACTTCCAATTGCGTGATTTAGATTCTCA	74,2	50	0,964	1	0,999	1	0,889	0,765	mid
7	6	C10	**pc0896**	hypothetical protein	**-**	1422	pc0896_740-791	TTGTTATCTCTTTACTGACCTGCATTCCTTCACTTATCGTTGTTGTTTACCA	74,3	52	0,98	1	0,996	1	0,972	0,83	mid
7	6	G10	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
8	1	D02	**Cont**	Cont				GGAAGGAAGGAAGGAAG									

8	1	H02	**pc0897**	unknown protein	**-**	183	pc0897_1-53	TTGCTAAGCCGCTATTTAAATGTGTTTTTATTTAGAATCTTTCAAAAAAAATT	70,5	53	0,704	0,717	0,625	0,851	0,908	0,376	mid
8	1	L02	**pc0898**	similar to RNase BN, tRNA processing enzyme	**rbn**	1170	pc0898_597-642	TAAATTCCAAATTGGGGTTGCTAGCTATGGAGCTATCTACGGAAGC	74,4	46	0,977	1	0,982	1	0,989	0,815	mid
8	1	P02	**pc0899**	unknown protein	**-**	2406	pc0899_1218-1266	TTTTTGGGATTCAAATTTACCTTCCGCTAGTACTGCTACCAAGACACTC	74,3	49	0,98	1	0,997	1	0,986	0,81	mid
8	1	D06	**pc0900**	conserved hypothetical protein	**-**	606	pc0900_196-240	AAAAACACATTAGAAGCTGTAATTAGTGCGCGCAATCAAGCTCAA	74,2	45	0,97	1	0,999	1	0,892	0,824	mid
8	1	H06	**pc0901**	hypothetical protein	**-**	981	pc0901_490-536	GAATTCGGGCATATATATAATCGAGATATGCTGATTGGAATGCGTGT	74,2	47	0,984	1	0,992	0,987	0,998	0,868	mid
8	1	L06	**pc0902**	conserved hypothetical protein	**-**	371	pc0902_22-68	ATCAGGGTCATTATTACAGAAGGCACAACAGCAGATTGTACTCAAGC	74,2	47	0,983	1	0,999	1	0,99	0,833	5´preference
8	1	P06	**pc0903**	conserved hypothetical protein	**-**	516	pc0903_29-74	GGTAATCAGAGCATGAGTCGTACAAAAGGGGGCTCAATACAAAATT	74,5	46	0,606	0,04	0,974	1	0,99	0,873	random
8	1	D10	**pc0904**	strongly similar to rhamnosyltransferase	**rgpB**	939	pc0904_484-536	CAAAATAACGTGACAGGATGCACTTCAATGATAAATCGATCTTTAGTTGAACT	74,3	53	0,98	1	0,998	1	0,987	0,805	mid
8	1	H10	**pc0905**	unknown protein	**-**	1650	pc0905_789-843	CATTAATAAACGTTCTCCTAAGCAAACTCCACCTGTTCAAATTTCACTCATAGAA	74,3	55	0,974	1	0,997	1	0,963	0,77	mid
8	1	L10	**pc0906**	conserved hypothetical protein	**-**	1317	pc0906_676-723	CTTAGCATGACAAGATCGGATATCAAGCTTGTTTTCCTGGGAATTAAG	74,2	48	0,977	1	0,998	0,981	0,984	0,806	mid
8	1	P10	**pc0907**	hypothetical protein	**-**	1815	pc0907_999-1043	ATTAATTTCCCAAACCTACCGAGCTATTCCAGCTTTAACCGCTGT	74,2	45	0,967	1	0,996	1	0,91	0,778	mid
8	1	D14	**pc0908**	hypothetical protein	**-**	468	pc0908_66-115	GATTCTAATGCTTTGTCGGCTATATTGGGGAACGTTATTTTTGTTAGCAG	74,2	50	0,978	1	0,998	1	0,994	0,772	random
8	1	H14	**pc0909**	conserved hypothetical protein	**-**	729	pc0909_84-128	AGGATATCGACTCATCATGAATACACCACACTATGCGCCTGAGTA	74,3	45	0,986	1	0,989	1	0,982	0,899	random
8	1	L14	**pc0910**	unknown protein	**-**	192	pc0910_10-54	AGTTTAACCATCCGTCGATTTGGCTACATCGCCTCCCTCTTAATT	75,9	45	0,914	1	0,835	0,941	0,985	0,634	random
8	1	P14	**pc0911**	unknown protein	**-**	2232	pc0911_1179-1233	AATTTTGGTAGATGGATCTTTAGCATACTATCGTATTATTGCACGGAAAAATGGA	74,2	55	0,974	1	0,999	1	0,938	0,803	mid
8	1	D18	**pc0912**	conserved hypothetical protein	**-**	558	pc0912_283-330	GTGTGGATTTTCTTACTTTGGGCTCTGGTAGCTGTTAACCTTCCTCTT	74,3	48	0,971	1	0,996	1	0,997	0,701	mid
8	1	H18	**pc0913**	hypothetical protein	**-**	594	pc0913_316-365	CAGGCATTAGTCACTCGTTGGCAAAACCTCAATGATAGTTTAAGAAGTTT	74,2	50	0,981	1	0,999	1	0,982	0,823	mid
8	1	L18	**pc0914**	similar to cation efflux system protein	**czcD**	942	pc0914_353-398	TCAATGGATTTATTCAGGAAGCTCCTCAACCTTTTTTACATCCCTG	74,3	46	0,959	1	0,995	0,992	0,881	0,741	mid
8	1	P18	**pc0915**	similar to glutathione-regulated potassium-efflux system protein	**kefC**	2016	pc0915_967-1016	TTACCCATGCGAACAGCTATTTTAACAGGTTTAATGCTAAGTCAAGTTGG	74,2	50	0,969	1	0,998	0,987	0,958	0,747	mid
8	1	D22	**pc0916**	similar to CPAF (chlamydia protease-like activity factor)	**-**	1713	pc0916_779-823	GTAAAATGATGTCTGAAACAAAGCGGGATGGAACATTATGTGCTC	74,4	45	0,97	1	0,988	1	0,921	0,815	mid
8	1	H22	**pc0917**	unknown protein	**-**	192	pc0917_8-56	AAGTAATTCCTACACAAACAACCAACAGGTTATCGGGCTTTACAAATGG	74,3	49	0,977	1	0,993	1	0,986	0,784	random
8	1	L22	**pc0918**	hypothetical protein	**-**	954	pc0918_483-528	CATCCATCCTTTTAGTGATGGAAATGGAAGAACTGCTCGATTACTC	73,9	46	0,973	1	0,969	1	0,995	0,794	mid
8	1	P22	**pc0919**	conserved hypothetical protein	**-**	825	pc0919_393-437	GCCTTATCTTAACTATGCCGATTCTTTTCAATGCCAAAAACAGGG	74,2	45	0,976	1	0,998	1	0,98	0,766	mid
8	2	D02	**pc0920**	conserved hypothetical protein	**-**	312	pc0920_61-105	GGCGAATGGATCCCTGAGCCAATGCCAGCCATTAAATCTAAACAT	79	45	0,829	1	0,527	0,869	0,904	0,791	mid 2.Wahl
8	2	H02	**pc0921**	hypothetical protein	**-**	441	pc0921_57-109	TGAAATTGAAACAATTCGTTCATTAGCTATTGTAGAGACTTTTGAACACCCTG	74,2	53	0,977	1	0,998	1	0,995	0,755	random
8	2	L02	**pc0922**	unknown protein	**-**	1509	pc0922_774-820	ATTTATGCTTGAATCACTCATGCTAAAAAGTTATCGCGCTTCTCTCG	74,2	47	0,976	1	0,998	1	0,982	0,764	mid
8	2	P02	**pc0923**	hypothetical protein	**-**	858	pc0923_490-535	TGGCAAGATCAACAAACTCAACAGGAACAGACAGACTATTTTTCGT	74,3	46	0,972	1	0,995	1	0,94	0,79	mid
8	2	D06	**pc0924**	unknown protein	**-**	471	pc0924_14-60	TTGATTATGCAGTGATCAAGAACGGTATTCTTTCTGGTGTCGCTTAT	74,1	47	0,983	1	0,99	1	0,994	0,849	5´preference
8	2	H06	**pc0925**	unknown protein	**-**	435	pc0925_107-161	TAAGCCAAACTTCAAAATATACGCGAAATAATTACTTGCCTATTTTAGCGACCAT	74,3	55	0,967	1	0,994	1	0,947	0,732	5´preference
8	2	L06	**pc0926**	unknown protein	**-**	675	pc0926_341-385	GCTCAGCAAAACTTCATAATCCTCATTATGCCTGTCCTGTAGTCG	74,2	45	0,982	1	0,994	0,994	0,998	0,831	mid
8	2	P06	**pc0927**	similar to cationic amino acid transport protein	**-**	1308	pc0927_652-696	CGTAACTTACCAATAGCGGTGATGGCTGTTATTAGCTTTTGCTCG	74,4	45	0,976	1	0,984	0,982	0,997	0,816	mid
8	2	D10	**pc0928**	similar to anthranilate synthase component II	**trpD**	804	pc0928_478-531	TCTTTACACTCAAACCAAGTTTATCAACACATTCAACAAGCTCAGGTACATGTA	74,2	54	0,973	1	0,994	1	0,925	0,826	mid
8	2	H10	**pc0929**	conserved hypothetical protein	**-**	459	pc0929_4-56	AAGCACTCCTCCTCATTACCTTGGTATAAAAAAGGACTTCACTTTAGTTGCAC	74,3	53	0,971	1	0,996	0,93	0,999	0,792	5´preference
8	2	L10	**pc0930**	similar to carbonic anhydrase	**cynT**	651	pc0930_85-132	GGTCAAACACCTGATGTTCTCTTTATTGCTTGTTCGGATAGTAGGGTT	74,2	48	0,982	1	0,995	1	0,986	0,838	random
8	2	P10	**pc0931**	hypothetical protein	**-**	1014	pc0931_649-693	CAATCGCGTAATGGATGGTTGATTAATCGTTTAATGCATATCCCT	74,3	45	0,982	1	0,997	1	0,996	0,818	random
8	2	D14	**pc0932**	unknown protein	**-**	207	pc0932_59-103	TGTTAAAGAAAATGAGTTTGATGCGCTCGTTATTCCTGGTCAATC	74	45	0,964	1	0,98	0,998	0,96	0,724	random
8	2	H14	**pc0933**	strongly similar to fructose-bisphosphate aldolase class I	**dhnA;fbaB**	1056	pc0933_801-849	AAACCATCCGATTGATCTAACAAGGTATCAAGTTGCCAACTGCTATATG	74,2	49	0,987	1	0,998	1	0,999	0,865	
8	2	L14	**pc0934**	conserved hypothetical protein	**-**	630	pc0934_332-377	TACAAATTGTTGTCGTAAGTAATGAAGGCCGTGAATTGATGCAAAA	74,3	46	0,977	1	0,996	1	0,984	0,779	mid
8	2	P14	**pc0935**	similar to glucokinase	**glk**	984	pc0935_403-447	ATTTGTTTATTCGTAGGAACAGGAATTGGCAGTGGTATCGTTTGC	74,2	45	0,97	1	0,995	1	0,91	0,816	mid
8	2	D18	**pc0936**	unknown protein	**-**	291	pc0936_29-76	TTTTGCCAAGAAATTTATCTTTCTATGTTGGATTAGGGCCGAGTTTTG	74,3	48	0,954	1	0,991	1	0,882	0,684	mid
8	2	H18	**pc0937**	unknown protein	**-**	372	pc0937_135-188	AAATTTAACTAATGTAGCAGCAAGCTTAGAAATCAAAGCAGAGGCAAAAAGTCA	74,1	54	0,968	1	0,989	1	0,999	0,686	random
8	2	L18	**pc0938**	hypothetical protein	**-**	9546	pc0938_8992-9045	TATAAACAACCTGTGACATTTACATCTACTGTTACCTCTGGCTCAGAAACTCCA	74,3	54	0,985	1	0,998	1	0,986	0,861	random
8	2	P18	**pc0939**	hypothetical protein	**-**	546	pc0939_314-361	GTGTTGCCAAAATCATCATGGGATTTCAACTGAAATCTACTAACAGCT	74,2	48	0,98	1	0,999	1	0,999	0,785	random
8	2	D22	**pc0940**	unknown protein	**-**	183	pc0940_14-68	TGAAAACTTTTCAGACTGTCCCTCTAAACACTCTACGCATTAAAGAAAAAGGATT	74,2	55	0,962	1	0,997	0,95	0,978	0,697	random
8	2	H22	**pc0941**	unknown protein	**-**	219	pc0941_6-55	TCAACATGAGGAAAAGGAAAGGGTAAATCCGTTAAATTGTTACAAACATG	74,1	50	0,977	1	0,989	1	0,994	0,786	random
8	2	L22	**pc0942**	conserved hypothetical protein	**-**	1407	pc0942_663-713	TGAAGAAACAGAATGGATTAAAAGTATTAGTCAGGATTTGCCTGCAATTCC	74,3	51	0,968	1	0,989	1	0,958	0,743	mid
8	2	P22	**pc0943**	similar to outer membrane lipoprotein	**blc**	579	pc0943_135-	AATTGCCCGTTTAGATGAGCCATGGGATAGAGGATGTTATCATAAC	74,1	46	0,981	1	0,982	1	0,992	0,849	random

							180										
8	3	D02	**pc0944**	hypothetical protein	-	723	pc0944_353-402	CTTACGAATCATTGCTTAGTTTAGCCAGTTTACGCTCAGACTTGCAAGAT	74,4	50	0,982	1	0,986	0,993	0,99	0,864	mid
8	3	H02	**pc0945**	unknown protein	-	786	pc0945_314-358	GAATTGGTTATACCTTAGCGTCAAATTGTGGGTGGAAGCCTTCTT	74,2	45	0,971	1	0,999	1	0,92	0,795	mid
8	3	L02	**pc0946**	unknown protein	-	534	pc0946_289-336	CGTATGGTTCCCCAGTACTATGAAAAAACATGCTGCAGATATATTCCA	74,2	48	0,977	1	0,994	1	0,979	0,796	mid
8	3	P02	**pc0947**	similar to thioredoxin	**trxA**	435	pc0947_161-205	AACCTGTTATTTTGATGATTTATGCAGAATGGTGTGGGTGTTGCT	74,2	45	0,97	1	0,998	1	0,942	0,755	mid
8	3	D06	**pc0948**	conserved hypothetical protein	-	648	pc0948_328-378	GGTAATCATGACAAAAACCTTGTTAAACATTTGCCTAAAACATGGTCGTTT	74,3	51	0,976	1	0,99	1	0,997	0,77	mid
8	3	H06	**pc0949**	conserved hypothetical protein	-	2415	pc0949_1045-1090	CCTCTTACGCCTTGTTACATTGAAGTTGTTCCTACACATGCCCTAG	74,2	46	0,963	1	0,998	1	0,836	0,835	mid
8	3	L06	**pc0950**	similar to DNA ligase	**lig**	1593	pc0950_805-850	CTTCCAGACGGGACGGTATTAGATGGAGAATTGATTGCTTATCAAT	74,3	46	0,979	1	0,993	1	0,993	0,801	mid
8	3	P06	**pc0951**	conserved hypothetical protein	-	1005	pc0951_503-549	CTATTTTATTTTGTTATTCACTTGGCAAAGCACAACGGGTTTTGTCG	74,3	47	0,971	1	0,998	1	0,999	0,692	mid
8	3	D10	**pc0952**	strongly similar to putative oxidoreductases	-	867	pc0952_389-439	CTGAACAGCACCCGCAAGTTTCTATTGAAGATATTACTGAAGAGCAGTTAG	74,2	51	0,975	1	0,997	0,997	0,954	0,802	mid
8	3	H10	**pc0953**	strongly similar to yciF protein	**yciF**	525	pc0953_150-202	GAAAGAAACAAAAACTCAAGTAGCTCGTCTGGAACAAATCTTTGAGATAATGG	74,2	53	0,964	1	0,998	0,99	0,926	0,734	5´preference
8	3	L10	**pc0954**	unknown protein	-	357	pc0954_59-105	ATTACAGAAAAAATGCCCAAACTCGTTATGAGGAAAAAGGTCTGCAT	74,2	47	0,972	1	0,992	1	0,999	0,72	random
8	3	P10	**pc0955**	strongly similar to ferritin	**ftn**	489	pc0955_29-83	ATGAGCAAATCAAGCACGAGTTTTATTCCTCTTACCTTTATCTTTCTATTGCATC	74,2	55	0,975	1	0,999	0,99	0,991	0,752	random
8	3	D14	**pc0956**	conserved hypothetical protein	-	618	pc0956_272-316	TTGGATTAACCCAAAAACATCTCGATAAAGCACATCAATGGTTTG	74,1	45	0,972	1	0,991	1	0,962	0,771	mid
8	3	H14	**pc0957**	conserved hypothetical protein	-	1002	pc0957_517-562	CTTTTTGCTTATACCTGTTCTTTTAGCGTTCATGCAGCTGCTTCAG	74,2	46	0,976	1	0,998	1	0,985	0,768	mid
8	3	L14	**pc0958**	strongly similar to dctp deaminase	**dcd**	567	pc0958_237-283	TGATGTGTGCGTTATTCCTCCTAATAGCTTTGCGCTAGCAATAACTT	74,3	47	0,976	1	0,997	1	0,953	0,815	mid
8	3	P14	**pc0959**	conserved hypothetical protein	-	276	pc0959_6-53	AATGACTGCTAACAACTGGGAAGTTTATATTATCCAAACGCGTTCTGG	74,2	48	0,983	1	0,997	1	0,999	0,818	random
8	3	D18	**pc0960**	unknown protein	-	1005	pc0960_479-523	ATTTAGCTTGGGACCGTGTATGTATCAATCTCGCTGTGATCTTTG	74,2	45	0,983	1	0,998	1	0,975	0,858	mid
8	3	H18	**pc0961**	unknown protein	-	195	pc0961_1-45	ATGATGAAGCTCCTTGGATGCAACAACGACTTAGTTGGAAAGGAA	76,2	45	0,657	0,335	0,805	0,963	0,902	0,831	mid
8	3	L18	**pc0962**	unknown protein	-	201	pc0962_18-69	AATAGTCGATCGTCTTGTGCGTTTATTCCTTGCCTTCACTTTTTTATTTCTA	74,2	52	0,971	1	0,999	1	0,986	0,705	random
8	3	P18	**pc0963**	conserved hypothetical protein	-	288	pc0963_89-136	GACGTTATCACGACCATCACGATGATCATCACTATCACCACTATTATG	74,2	48	0,986	1	0,999	0,983	0,995	0,876	random
8	3	D22	**pc0964**	strongly similar to protein-methionine-s-oxide reductase	**msrA**	855	pc0964_431-484	AAAAGCTTACAGGAGTTATTAAGACGAAAGTAGGATATAGCGGGGGAGTAACCA	74,2	54	0,987	1	0,999	1	0,998	0,861	mid
8	3	H22	**pc0965**	unknown protein	-	291	pc0965_106-151	GCTTTTTACAATTACTTGGGGATTTTCGTTAGATGCTTTCACCCGT	74,3	46	0,974	1	0,997	1	0,959	0,779	mid
8	3	L22	**pc0966**	unknown protein	-	255	pc0966_75-127	TCCAATAGCCTTTGTTTTACTATTTACAAGCAGCACTTTCGAACTTGATCATT	74,2	53	0,976	1	0,998	1	0,987	0,758	random
8	3	P22	**pc0967**	unknown protein	-	366	pc0967_187-234	TTTCAGGTGCTTGAATGCGTTGGCCGTTATAGCTATTCATTAGTAAAT	74,2	48	0,985	1	0,997	1	0,997	0,845	mid
8	4	D02	**pc0968**	unknown protein	-	771	pc0968_336-380	AATTGATGTAGGCGTAACACGAGAAATGGCCAAAGTTTTACCAAA	74,3	45	0,97	1	0,994	1	0,949	0,76	mid
8	4	H02	**pc0969**	conserved hypothetical protein	-	198	pc0969_1-47	GTGAAAGGAAAAGCATTCGCAGATAAAGGGGATATGTCAGAAAAACT	74,1	47	0,625	0,104	0,988	1	0,99	0,761	random
8	4	L02	**pc0970**	conserved hypothetical protein	-	4818	pc0970_1788-1839	ACTAAAACACTGTCTCTCCAATCCAGAATGCTATGAATTGAAAATTTGCATT	74,2	52	0,771	0,692	0,995	1	0,378	0,704	mid
8	4	P02	**pc0971**	conserved hypothetical protein	-	210	pc0971_29-77	TCGCAGATAGAGGGTCTATTTCAGAAAAACTGGCTCATACTTTAATGCA	74,3	49	0,616	0,08	0,996	1	0,985	0,757	random
8	4	D06	**pc0972**	unknown protein	-	222	pc0972_13-63	TTAAATGCTTGCAATATTCACTTGAACAGATCGTTAAATGGAAATACTCGC	74,1	51	0,977	1	0,988	0,996	0,994	0,796	random
8	4	H06	**pc0973**	conserved hypothetical protein	-	597	pc0973_293-337	ATTGGACCACGCGTCAGGCTACACCTGAAGAAGTCTATTTAAGTT	74,1	45	0,973	1	0,985	0,969	0,993	0,801	mid
8	4	L06	**pc0974**	conserved hypothetical protein	-	2265	pc0974_1106-1152	CTTTTATTCAGTTCTACAAACCTTATGCGGTTGCGATTGGTAATGGA	74,2	47	0,981	1	0,997	1	0,972	0,841	mid
8	4	P06	**pc0975**	similar to SOS mutagenesis and repair protein UmuC	**umuC**	1182	pc0975_560-604	AACGACTGGGTGTGATTGGAGAGCGAATACTATGGGAATTAAGAG	74,2	45	0,983	1	0,999	1	0,968	0,858	mid
8	4	D10	**pc0976**	strongly similar to SOS mutagenesis and repair protein UmuD	**umuD**	432	pc0976_166-211	TTTTTCCTTAAGGTGTCTGGTTCTTCGATGATTAATGCAGGGATTC	74,3	46	0,973	1	0,992	1	0,949	0,803	mid
8	4	H10	**pc0977**	unknown protein	-	552	pc0977_223-268	GCTCAAGTCGCTAAAGATTATGTCGAGACTCTGGATAAAGGGCAAT	74,2	46	0,977	1	0,995	1	0,946	0,841	mid
8	4	L10	**pc0978**	unknown protein	-	444	pc0978_3-51	GTCTTGTCAAGATCAATCTTGTGGAACTCATCATCATCATTATCATTCC	73,9	49	0,97	1	0,965	0,974	0,999	0,81	5´preference
8	4	P10	**pc0979**	conserved hypothetical protein	-	441	pc0979_133-177	AAATCTTCTATTCGCCACCTTTTTCCTGCAGATATGAAAGCTGCT	74,3	45	0,962	1	0,989	1	0,934	0,707	5´preference
8	4	D14	**pc0980**	conserved hypothetical protein	-	339	pc0980_17-65	AAGTTATCTGGATTTACGCCATTATTGTATTGATTGGAGGAATTGTCGG	74,2	49	0,983	1	0,999	1	0,992	0,825	5´preference
8	4	H14	**pc0981**	hypothetical protein	-	1404	pc0981_712-759	AAAGGGACTAACAAATGGCGAATTAATAAACGTCTTTTTCGGAAAAGC	74,1	48	0,973	1	0,989	1	0,991	0,751	mid
8	4	L14	**pc0982**	unknown protein	-	282	pc0982_3-55	GTGTCTACATACCGAGCCTCAATATCTTGCTTTATTAAAACAAAGGTTGATGG	74,2	53	0,596	0,036	0,991	1	0,999	0,711	random
8	4	P14	**pc0983**	unknown protein	-	243	pc0983_10-54	AAATGCAGGCGAGGCTTTCTCATGGTTAGTAAAAATAGGGCTTTT	74,3	45	0,601	0,04	0,995	1	0,996	0,743	5´preference
8	4	D18	**pc0984**	unknown protein	-	378	pc0984_9-60	GCATAAAGTAGAGAGGCAGGAGTATAAAGTAGAGAGGCAAGAGCATAAGGCA	74,3	52	0,963	1	0,995	1	0,819	0,866	mid
8	4	H18	**pc0985**	unknown protein	-	264	pc0985_116-163	CTAAGGCATTCCTCTACTACATCTTCTTCAACGGAAGGTGTGTGACAT	74,2	48	0,982	1	0,994	0,999	0,983	0,846	mid
8	4	L18	**pc0986**	conserved hypothetical protein	-	262	pc0986_149-199	CCGAAGCTCAACGATTAAGGAGCCTTGAATCTGAAATTACTAAGCTTAAAA	74,2	51	0,85	0,71	0,999	0,897	0,983	0,769	mid
8	4	P18	**pc0987**	conserved hypothetical protein	-	336	pc0987_8-61	AAAGGGGCTTTAAGATTAACCATGAGAAGCTTTTTAGACTTTATCAGGAAATGG	74	54	0,719	0,407	0,975	1	0,839	0,75	mid 2.Wahl
8	4	D22	**pc0988**	unknown protein	-	276	pc0988_2-55	TGAATTCATTTGGTTTTATGATAGGAGAAACAGCAGTAATGATGAAGGAAATTG	74,3	54	0,971	1	0,994	1	1	0,701	5´preference
8	4	H22	**pc0989**	unknown protein	-	249	pc0989_64-109	ATGGCTTGCGTTAAGAAAGGAGTCTCTGTGAAAGACTTTGTCACTC	74,3	46	0,975	1	0,993	1	0,938	0,837	mid
8	4	L22	**pc0990**	conserved hypothetical protein	-	258	pc0990_29-83	GGGTTGAAAAAGCGCTATCTAAAATTGATAAGCATATGGCTTTAAAAATAAGAAA	72,9	55	0,897	1	0,868	0,913	0,899	0,514	mid
8	4	P22	**pc0991**	unknown protein	-	186	pc0991_92-138	GAGAAATTTTTCCATCACCTGTCTGTAGCCTTACCATCAATCCAAAA	74,2	47	0,938	1	0,999	1	0,786	0,624	random

8	5	D02	**pc0992**	conserved hypothetical protein	-	1752	pc0992_839-885	ATCTAGATTTAAGCGATTGTGAGAATCTCACCGATGTTGGATTAGCG	74,4	47	0,595	0,058	0,985	0,987	0,962	0,701	mid
8	5	H02	**pc0993**	conserved hypothetical protein	-	1437	pc0993_756-800	AAAAATACTTACTTTCGAGACATGCCAAGCTCTCACTGACGATGG	74	45	0,653	0,17	0,977	1	0,964	0,855	mid
8	5	L02	**pc0994**	conserved hypothetical protein	-	306	pc0994_2-53	TGCAGAGCCTTAGAAACTATCTCGAAAATAGAACGGGTCAAATTTTTATCAC	74,2	52	0,971	1	0,993	1	1	0,698	5´preference
8	5	P02	**pc0995**	conserved hypothetical protein	-	303	pc0995_2-56	TGGCAAGTAATAAGAAGTATCAAGATTTTCTCTTAGAACAGCTAAAGGATCATGA	72,2	55	0,925	1	0,795	0,999	0,998	0,766	random
8	5	D06	**pc0996**	conserved hypothetical protein	-	342	pc0996_5-53	AAGAGATCGATATTGAAATCTACGAAACCGCTAATGGTAAACGACCCTT	74,2	49	0,985	1	0,999	1	0,997	0,842	random
8	5	H06	**pc0997**	unknown protein	-	198	pc0997_83-129	TTTGGAAAGACTTAAACCAAAACAACCTCAATGGCCCATTAGCTAAG	74,2	47	0,967	1	0,998	1	0,889	0,798	random
8	5	L06	**pc0998**	unknown protein	-	219	pc0998_1-52	ATGGAAAAAGCAAAAGTAATGAGCTTCGTAGAATTCCGTCAAAACTTATCAG	74,1	52	0,614	0,078	0,99	1	0,995	0,737	random
8	5	P06	**pc0999**	conserved hypothetical protein	-	270	pc0999_9-59	TCTAAATCTATTTGGCTGTAATAATCTCACCGATGATGGATTAGCGCATTT	74,3	51	0,598	0,05	0,993	1	0,996	0,673	5´preference
8	5	D10	**pc1000**	conserved hypothetical protein	-	813	pc1000_384-436	GGATACGTGTGACAGAAAAGTCATGCGTTATATTGCCTCTACAATAGGTATTG	74,3	53	0,981	1	0,992	1	0,976	0,849	mid
8	5	H10	**pc1001**	conserved hypothetical protein	-	378	pc1001_84-138	ATATCAAGAAGGTCAATCTGTCTCCCAAATAGCAAGGAGATATGATATAACACCA	74,2	55	0,601	0,04	0,997	0,966	0,959	0,842	5´preference
8	5	L10	**pc1002**	unknown protein	-	717	pc1002_273-322	TGATAGTAAAATTACAAGTTTTTACGCGGATCAAAGCAAAATGGAACAGG	74	50	0,951	1	0,978	0,985	0,914	0,667	mid
8	5	P10	**pc1003**	hypothetical protein	-	366	pc1003_177-222	GATTTAATTGTACTCGCAGACAAAGATGTGCAAGACTTGTAAGGAAAACACTTT	74,3	46	0,611	0,05	0,998	0,985	0,993	0,827	mid 2.Wahl
8	5	D14	**pc1004**	conserved hypothetical protein	-	264	pc1004_46-98	GAAGTAGAAGCAGGCTCAGCAGTAGCTGAAGTTTGTCGTAAATATAGCATAGC	74,4	53	0,983	1	0,985	1	0,997	0,857	random
8	5	H14	**pc1005**	conserved hypothetical protein	-	846	pc1005_428-481	ATTTTACTAGGAAAAGTCTTAAGATGGTGGTAGATACCTCGATCAGCGGAGTTC	74,2	54	0,987	1	0,991	1	0,996	0,885	mid
8	5	L14	**pc1006**	unknown protein	-	2874	pc1006_1487-1531	ATCAAGCAGATGAAAGCCTTGCACGCTTAGTTGAGCCTTATAAAA	74,3	45	0,962	1	0,992	0,913	0,951	0,796	mid
8	5	P14	**pc1007**	unknown protein	-	264	pc1007_162-209	GATGAGATCACTAAATGGTTCAATTTTCAAAATACTTGGGGGAACCAA	74,2	48	0,687	0,301	0,996	0,918	0,971	0,724	mid 2.Wahl
8	5	D18	**pc1008**	unknown protein	-	186	pc1008_1-55	TTGAATTTTAGATGTAACCAACCTAATAGGTGTAGCAAGTTATACTTGAGAAGCA	71,4	55	0,884	1	0,717	1	0,907	0,661	mid
8	5	H18	**pc1009**	unknown protein	-	2811	pc1009_1362-1411	TTTACTCGCATTACTTCCCGATTCTAATAATACAATGACCGTTCAACAGG	74,2	50	0,979	1	0,998	1	0,955	0,839	mid
8	5	L18	**pc1010**	conserved hypothetical protein	-	1251	pc1010_849-894	AATGAAACGAAGCAACCCTGCTAAGTTAGTAATGTCGGAATCCTTG	74,3	46	0,987	1	0,998	1	0,994	0,87	random
8	5	P18	**pc1011**	conserved hypothetical protein	-	1941	pc1011_1019-1066	AGAATGTTTCATTTGAAATAGAACGAGGAGATCGTTTGGCGATTATTG	74,3	48	0,97	1	0,99	1	0,952	0,767	mid
8	5	D22	**pc1012**	unknown protein	-	228	pc1012_42-93	GTCCTGTACAGAGGGTTTGATAATGAAATTAATAAAATCTAGCAGCCATGGC	74,2	52	0,711	0,364	0,999	0,983	0,927	0,683	mid
8	5	H22	**pc1013**	unknown protein	-	276	pc1013_103-157	CGAATACAAAGATTTTTCAACTGGCTAACTTCTTTGAATGATTATCAAGAGGTCA	74,3	55	0,954	1	0,99	0,9	0,985	0,691	random
8	5	L22	**pc1014**	hypothetical protein	-	339	pc1014_29-76	TTAGCATTCCTCTAGCTTGGATTTCCTTAGGAAGAGCAGGTAATTCCA	74,3	48	0,977	1	0,99	0,989	0,998	0,798	random
8	5	P22	**pc1015**	hypothetical protein	-	366	pc1015_104-149	AAGAAAAAGCATATTCAGGACAAGCTTTGAGGGAACAAGAAAATGTTTATTGT	74,2	46	0,593	0,04	0,998	1	0,92	0,761	mid
8	6	D02	**pc1016**	unknown protein	-	216	pc1016_12-59	ATTGTCCTGTACACAGTTCATTGGCACAGAAAGACGATTAAGTCTTTG	74,1	48	0,777	0,516	0,986	0,952	0,903	0,871	mid
8	6	H02	**pc1017**	conserved hypothetical protein	-	210	pc1017_45-93	AAAAAGAGGGGGCTTTAGGGTTGGCTATTTAGATATTCCAGAAAAGAGC	74,2	49	0,6	0,05	0,999	1	0,939	0,76	mid
8	6	L02	**pc1018**	conserved hypothetical protein	-	357	pc1018_87-133	AAAAGTTAGGATCGATACTGGAGAAATTCCACAGCAGCCAAAAGAGT	74,2	47	0,981	1	0,998	1	0,999	0,803	random
8	6	P02	**pc1019**	unknown protein	-	270	pc1019_75-122	AGAAATTAGAGAGTATCAAAAAGGGCTGCCTTATGGAGCCAATGACAT	74,3	48	0,608	0,052	0,995	0,993	0,993	0,787	random
8	6	D06	**pc1020**	unknown protein	-	282	pc1020_45-98	TTTTTCGGTAGGTGCGTTTTGGATTTCATATTTATCCTCTATATTTTCCTTTCA	74,2	54	0,729	0,363	0,999	1	0,999	0,757	random
8	6	H06	**pc1021**	similar to death on curing protein	**doc**	378	pc1021_42-89	TCATCTCGTTTCTGCATACGGAGGTCTACATGGTATTAGAGATATGGG	74,2	48	0,99	1	0,998	1	0,997	0,895	random
8	6	L06	**pc1022**	conserved hypothetical protein	-	231	pc1022_121-174	ACAGGTGTTACTATTCAATCGGTAAAACCAGTAAACAGCAAATTTGAAGAAGCT	74,1	54	0,956	1	0,988	1	0,872	0,736	random
8	6	P06	**pc1023**	unknown protein	-	186	pc1023_99-146	TGTTTACGCCAAGTCTTATGCCTTAAGATTTAAAAGCGGAGATCTTCG	74,6	48	0,922	1	0,961	0,938	0,735	0,726	random
8	6	D10	**pc1024**	unknown protein	-	186	pc1024_92-138	GAGAAATTTTTCCATCACCTGTCTGTAGCCTTACCATCAATCCAAAA	74,2	47	0,938	1	0,999	1	0,786	0,624	random
8	6	H10	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
9	1	A03	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
9	1	E03	**pc1025**	conserved hypothetical protein	-	2088	pc1025_1073-1117	GCTACTGTGAGAAACTCACTGACGATGGTTTGGTGCATTTAAGAC	74	45	0,614	0,071	0,979	1	0,972	0,836	mid
9	1	I03	**pc1026**	conserved hypothetical protein	-	249	pc1026_1-46	ATGGATAAAGCCCTAACTTCCAAATCCGTCGCATTGATTATTAAGC	74,2	46	0,617	0,071	0,991	1	0,997	0,8	random
9	1	M03	**pc1027**	unknown protein	-	204	pc1027_1-48	ATGATTCTCTCCTTCTATTCTTGGTCGGTTTTCGATTTCCTAAGCGTA	74,3	48	0,622	0,08	0,994	1	0,992	0,809	random
9	1	A07	**pc1028**	conserved hypothetical protein	-	378	pc1028_166-210	ATGGAACAAGGAGCACTACAAGGAATTAGCAGCCGAGAAGAACTA	74,2	45	0,984	1	0,998	1	0,997	0,833	random
9	1	E07	**pc1029**	conserved hypothetical protein	-	813	pc1029_378-424	CTCGTTGGATACATGTGACAGAGAAGTCATGCGTTATATTGCCTCTA	74,2	47	0,984	1	0,997	1	0,97	0,871	mid
9	1	I07	**pc1030**	unknown protein	-	210	pc1030_48-101	TACAGGGACAAAAGCACCTACAGTTTTTCCATTACGAGTAATCAAAAATCTTTC	74,2	54	0,6	0,05	0,999	0,99	0,974	0,722	random
9	1	M07	**pc1031**	conserved hypothetical protein	-	1662	pc1031_802-849	TTAACAGCTTTGCAACACCTAGATCTGAGCTATTGTGAGAATCTCACG	74,3	48	0,63	0,11	0,992	1	0,97	0,805	mid
9	1	A11	**pc1032**	conserved hypothetical protein	-	2205	pc1032_1050-1095	TTTGCAACATCTAAATCTAAATAGGTGCAAGGATCTCACCGATGCT	74,2	46	0,612	0,097	0,997	0,982	0,946	0,711	mid
9	1	E11	**pc1033**	hypothetical protein	-	1989	pc1033_983-1027	ATCTAGGTTTAAGCGGTTGTCAGAATCTCACGGATGCAGGATTAG	74,3	45	0,618	0,086	0,992	1	0,987	0,757	mid
9	1	I11	**pc1034**	unknown protein	-	432	pc1034_155-202	AATCAGTAATAGGACAAAAGCCCAAATGGCAAAGCTTGGATAAGGTAA	74,2	48	0,974	1	0,995	1	0,938	0,818	mid
9	1	M11	**pc1035**	similar to sporulation initiation inhibitor protein	**soj, parA**	597	pc1035_242-294	TTGCAAGTAACTATTATTTAGTGCCAGTGAGTGCAGAGTACCTTCCACTTGTT	74,3	53	0,977	1	0,994	0,992	0,942	0,857	mid
9	1	A15	**pc1036**	unknown protein	-	201	pc1036_35-80	ATAATAAGGCTGATCGCAAGCTAGCTCACCTTTTAAACTTGCATGG	74,2	46	0,976	1	0,993	1	0,977	0,784	random
9	1	E15	**pc1037**	unknown protein	-	285	pc1037_54-108	TTCTGCTGAACTAAATTTCAAAGGAAAAGGAATATTGCAAAGTGATGAATTACAA	74,2	55	0,968	1	0,999	1	0,999	0,65	random
9	1	I15	**pc1038**	unknown protein	-	2598	pc1038_1384-1428	GAAATAGTGCTTGATTGCCCTTATGGTGAAACGGCTAATTCTGAC	74,2	45	0,97	1	0,995	0,961	0,916	0,86	mid
9	1	M15	**pc1039**	unknown protein	-	2607	pc1039_1318-1363	AAAATCGGAAGAGCTTCTGAGCTAGAAATGAGGCCTTCTAATCCTG	74,3	46	0,979	1	0,994	1	0,987	0,805	mid
9	1	A19	**pc1040**	unknown protein	-	231	pc1040_106-160	TCCCACAATAGCGAAAATTCAACTTTAAGAGCTGTAACTAAATTTCCAATTTTGT	74	55	0,955	1	0,976	1	0,92	0,687	random

9	1	E19	**pc1041**	strongly similar to adenylate kinase (EC 2.7.4.3)	**adk**	696	pc1041_375-420	ATATTTAGAAGTTCCCGATGCAGTGATTGTTAAGCGAGCAGAAGGT	74,2	46	0,98	1	0,999	1	0,974	0,824	mid
9	1	I19	**pc1042**	strongly similar to diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	**ribD, ribG**	1107	pc1042_602-648	CGACTATTGACTCGCCTCAACTTACAGTTCGACATCCAACTATTCAT	74,2	47	0,98	1	0,997	1	0,953	0,853	mid
9	1	M19	**pc1043**	conserved hypothetical protein	**-**	1173	pc1043_676-721	TCTTACACTGGTGGTTTTAGCGTATATGCTATGGCTGGAGGAGCTA	74,2	46	0,976	1	0,993	1	0,912	0,878	mid
9	1	A23	**pc1044**	conserved hypothetical protein	**-**	441	pc1044_130-174	GCTTTCGGCTCACACCTACTCAAGTCAAGGTTGACATCTGAATAT	74,2	45	0,985	1	0,999	1	0,998	0,839	random
9	1	E23	**pc1045**	unknown protein	**-**	441	pc1045_158-212	ATACATTGATCGAAGGAACCTTAGAGAATAGAAAATTAGTTTTGGCAAATGGACA	74,2	55	0,961	1	0,999	1	0,936	0,66	mid
9	1	I23	**pc1046**	conserved hypothetical protein	**-**	771	pc1046_494-545	ACAAAATTCAATACCGAAGAATGGACCGTTATATGAGTGAAATGAAAATTCC	74,3	52	0,961	1	0,998	1	0,893	0,733	mid
9	1	M23	**pc1047**	strongly similar to leucyl-tRNA synthetase	**leuS**	2538	pc1047_1162-1207	AATAGTGCTTGTGGCGATCTCTCCCTCAATGGTTTAAATCTAGACC	74,1	46	0,965	1	0,984	1	0,892	0,811	mid
9	2	A03	**pc1048**	similar to ribonuclease R	**vacB, rnr**	2328	pc1048_1171-1224	GTGATTAAAAGCGCGAAACGCTTTACCTATAAAGAAGCCAAAAAAGTCTTAGAT	74,3	54	0,974	1	0,996	1	0,994	0,733	mid
9	2	E03	**pc1049**	conserved hypothetical protein	**-**	708	pc1049_367-412	AAGGCTAATTCCTTTAAACAAGTCGTGCTTGTCCGCTTTCCTAATC	74,1	46	0,974	1	0,99	1	0,988	0,765	mid
9	2	I03	**pc1050**	conserved hypothetical protein	**-**	657	pc1050_361-413	TCCTCCCACTCTAAATCCTTTGCTTATGTAGTACTAGCTCCATATCCCTCTGT	74,2	53	0,981	1	0,999	1	0,969	0,835	mid
9	2	M03	**pc1051**	unknown protein	**-**	453	pc1051_115-160	TTTGAGCAAGAGAAACGACTACAAATCCTCGTCCCAACAATAGAAG	74,3	46	0,984	1	0,997	1	0,997	0,838	random
9	2	A07	**pc1052**	unknown protein	**-**	1506	pc1052_746-790	AAGCTTTTGCATGGAAGGAAAAATGGCACAGTAAATATGAGTTGG	74,2	45	0,974	1	0,998	1	0,992	0,728	mid
9	2	E07	**pc1053**	conserved hypothetical protein	**-**	160	pc1053_4-48	TCTAGACACCCAAGTTTTGGTAAGGCAGGAAAAACTGCCACAAAG	75,6	45	0,928	1	0,86	0,877	0,967	0,827	random
9	2	I07	**pc1054**	conserved hypothetical protein	**-**	453	pc1054_285-331	TCTTTCCCATGAACTAGACCCGTACGAAGAAACAACGCTATATCTTG	74,2	47	0,978	1	0,999	0,997	0,943	0,845	mid
9	2	M07	**pc1055**	conserved hypothetical protein	**-**	1374	pc1055_710-757	TAGCCCACGACACAACAATAGAACAGGCCGCAGTTCTAATATATAATG	74,2	48	0,984	1	0,997	1	0,978	0,865	mid
9	2	A11	**pc1056**	conserved hypothetical protein	**-**	1560	pc1056_720-764	CGTTAACTTTATTATCGACGATACGCCAGGTGCAGTTGTCTTGTC	74,3	45	0,976	1	0,993	1	0,939	0,841	mid
9	2	E11	**pc1057**	conserved hypothetical protein	**-**	1998	pc1057_976-1020	GATGAAGACGAACGGTTTTCCACACTATTAGGCTTTCAATGGAGT	74,2	45	0,982	1	0,998	0,991	0,976	0,856	mid
9	2	I11	**pc1058**	similar to carbonate dehydratase, cynT	**cynT**	786	pc1058_398-449	ATGTTAAGCATATCATTATTTGTGGTCATTCGCATTGTGGAGCTATTAAAGG	74,3	52	0,977	1	0,995	1	0,996	0,772	mid
9	2	M11	**pc1059**	unknown protein	**-**	270	pc1059_48-92	TATCGCAATTGCTTGTTTAGCTATTGGTTGGTTGATTACAGGCAA	74,4	45	0,975	1	0,986	1	0,997	0,766	random
9	2	A15	**pc1060**	similar to ubiquinone/menaquinone biosynthesis methyltransferase, ubiE	**ubiE**	729	pc1060_362-406	AAACAATGGATTGTGCGACGATGGCTTATGGAATTCGTAATATTC	74,5	45	0,978	1	0,971	1	0,996	0,845	mid
9	2	E15	**pc1061**	conserved hypothetical protein	**-**	414	pc1061_72-122	TTTTGGACATACCTTTACTTTAGCTCATCAAGTTTTTGAAAGCTTCGTCGT	74,2	51	0,973	1	0,995	1	0,997	0,721	random
9	2	I15	**pc1062**	similar to o-succinylbenzoate-CoA ligase, menE	**menE**	1134	pc1062_518-562	AATTAGGGTGGCCTTTAATGCCAAGTTATGGTTTGACAGAATGCT	74,4	45	0,976	1	0,988	1	0,95	0,843	mid
9	2	M15	**pc1063**	similar to 1,4-dihydroxy-2-naphthoate octaprenyltransferase, menA	**menA**	903	pc1063_555-606	TTTAGCCATGATTCCTAATGCCGTGAATAACTTAAGAGATAGACAAAGCGAT	74,3	52	0,97	1	0,992	1	0,897	0,835	mid
9	2	A19	**pc1064**	strongly similar to naphthoate synthase, menB	**menB**	828	pc1064_451-496	TCATTTGACGGTGGATTGGGAAGCAGTTATTTAGCTCGTATTGTAG	74,2	46	0,979	1	0,998	1	0,964	0,829	mid
9	2	E19	**pc1065**	conserved hypothetical protein	**-**	4518	pc1065_3966-4019	TATGAATAATTCGAACCTCACCATACTTAACTTTTTTGACAAAAGAATAAGCGA	72,5	54	0,916	1	0,829	0,915	0,986	0,704	random
9	2	I19	**pc1066**	conserved hypothetical protein	**-**	306	pc1066_1-52	GTGGTCGAAACCTTATCGAAAGGAATTTTTAGGAAGCTATTTGATGATAAGG	74,1	52	0,643	0,191	0,982	0,927	0,998	0,698	random
9	2	M19	**pc1067**	conserved hypothetical protein	**-**	711	pc1067_419-464	TTTATCGTTCCCATAATGATTATCAGCGGTCGAATCTAGCTATGCA	74,3	46	0,979	1	0,996	1	0,938	0,868	mid
9	2	A23	**pc1068**	similar to menaquinone biosynthesis protein, menD	**menD, menCF**	1563	pc1068_804-851	AACAGCGAGATTATGGAGAGATTTGGAAGAGACAAATAACGTGAAGGT	74,2	48	0,98	1	0,995	1	0,979	0,823	mid
9	2	E23	**pc1069**	similar to menaquinone-specific isochorismate synthase, menF	**menF**	1056	pc1069_746-791	CTTTTGAAGTTCTAGTTAGAGCTTTGCATCCAACACCTGCTCTTGG	74,2	46	0,98	1	0,992	1	0,998	0,802	random
9	2	I23	**pc1070**	hypothetical protein	**-**	1095	pc1070_411-455	AGGGGGGGACATAAGTAATGATAATACAGCGGTTGCAAACTCTTC	74,2	45	0,965	1	0,999	1	0,862	0,814	mid
9	2	M23	**pc1071**	hypothetical protein	**-**	1428	pc1071_680-724	AATCAGATTTAGATGTTGGAGAAATCGTTAATGTTGCCCGAGCAT	74,2	45	0,977	1	0,995	1	0,965	0,807	mid
9	3	A03	**pc1072**	similar to DNA polymerase III, delta' subunit, holB	**holB**	1110	pc1072_527-579	TCGAACGAATGTATTTAGAAACTGAATTTGCTCAAAACATAGCAAGCTTATCA	74,3	53	0,972	1	0,997	0,995	0,971	0,754	mid
9	3	E03	**pc1073**	similar to thymidylate kinase, tmk	**tmk**	678	pc1073_399-451	ACTTCCTAATTGGACATTATTTCTAGATGTGTCTCCAGAGATTGGCTTAGCAC	74,1	53	0,976	1	0,988	1	0,941	0,85	mid
9	3	I03	**pc1074**	strongly similar to DNA gyrase subunit A	**gyrA**	2571	pc1074_1174-1219	TTAGATGAAGTTGTTCGTCTGATTCGTGCAAGTAGTAATCGGGATG	74,2	46	0,973	1	0,997	1	0,887	0,874	mid
9	3	M03	**pc1075**	strongly similar to DNA gyrase subunit B	**gyrB**	2508	pc1075_1237-1281	GAATTAACTTTACGTAAATCGGCTTTGGATAGTGCGCGACTTCCT	74,1	45	0,978	1	0,988	0,985	0,982	0,836	mid
9	3	A07	**pc1076**	conserved hypothetical protein	**-**	339	pc1076_3-48	GAGCAAGCCCTATTCTCGCACATCTAGAAGTTATGATGGAACAGAG	74,3	46	0,987	1	0,996	1	0,997	0,876	random
9	3	E07	**pc1077**	unknown protein	**-**	1038	pc1077_505-552	CGTCATTTAAGATTTGCAACTAGCCCTATAGGTGAAAGCAGCAGTAGC	74,3	48	0,983	1	0,996	1	0,985	0,843	mid
9	3	I07	**pc1078**	strongly similar to protein involved in isoprenoid biosynthesis and penicillin tolerance	**lytB, ispH**	942	pc1078_476-530	TTTATATTACACAAACAACTTTGAGTTTGGATGATGTGAAAGAGATTACGCAAGC	74,2	55	0,979	1	0,999	0,982	0,996	0,803	mid
9	3	M07	**pc1079**	similar to low molecular weight protein-tyrosine-phosphatase	**wzb**	483	pc1079_166-210	ATGCAAGAAGCTGCGAAATCAAGAGGAATCATTTTGACTAGTCAA	74,3	45	0,967	1	0,996	1	0,923	0,756	mid
9	3	A11	**pc1080**	conserved hypothetical protein	**-**	1968	pc1080_1015-1068	GAGGGAAAATGCAATGTTCAAAAAGGTGTTAGCGAGTCTCTAGTTACATTAAAA	74,3	54	0,966	1	0,993	1	0,97	0,69	mid
9	3	E11	**pc1081**	similar to 60 kDa inner-membrane protein	**yidC**	2601	pc1081_1299-1343	TTTTGGTGATTCCTTACAAGAAGGGCCTTATTGCCTTAATCTTGC	74,1	45	0,98	1	0,986	1	0,997	0,827	mid

9	3	I11	**pc1082**	similar to chromosomal replication initiator protein, dnaA	**dnaA**	1356	pc1082_659-708	CTAGAAAAGGCGCCACGCAAGAAGAATTTTTCCATACTTTTAATACATTG	74,2	50	0,965	1	0,999	1	0,98	0,647	mid
9	3	M11	**pc1083**	similar to prolipoprotein diacylglycerol transferase	**lgt**	1125	pc1083_592-637	CATGGTGGAGCCTTGGGAGTGATGTTAGCCCTCTTTTTTTATACTA	74,2	46	0,971	1	0,999	1	0,972	0,725	mid
9	3	A15	**pc1084**	similar to ferredoxin [2Fe-2S] 4	**fdlV**	267	pc1084_131-184	TAGAAGTTAAAGAGGGAAAAGAAAATCTTTCTCCTCCCACCAAAGAAGAAGAAG	74,2	54	0,946	1	0,998	0,879	0,997	0,589	mid
9	3	E15	**pc1085**	conserved hypothetical protein	**-**	705	pc1085_342-391	ACGCTTAAATGCTTTATTACAAGAACCTGTCGATCAATCCTCTATTTGCA	74,2	50	0,977	1	0,999	1	0,989	0,761	mid
9	3	I15	**pc1086**	hypothetical protein	**-**	1098	pc1086_599-648	TTAATCGTGACAATTGGCAACTTCGAGAGTCAAAAAATGAGCTAGAACTA	74,2	50	0,971	1	0,997	1	0,951	0,758	mid
9	3	M15	**pc1087**	hypothetical protein	**-**	1146	pc1087_487-540	AAAAGAATGCATCAGCAATGTGATGACTTACAGTTATCTCATAAGCAGGATATG	74,3	54	0,97	1	0,991	0,994	0,913	0,834	mid
9	3	A19	**pc1088**	strongly similar to dihydrolipoamide dehydrogenase precursor (E3 component of pyruvate dehydrogenase multi-enzyme complex)	**dld1, pdhD, aceD, citL**	1398	pc1088_777-821	AAATATTAGCGGGGAAGTGGTATTAGTTGCTGTTGGTCGAAGACC	74,2	45	0,979	1	0,999	1	0,923	0,884	mid
9	3	E19	**pc1089**	strongly similar to dihydrolipoamide S-succinyltransferase, (2-oxogluturate dehydrogenase complex E2 component), sucB	**sucB, odo2, E2o**	1215	pc1089_564-609	AAATCGTTTAATAGAAGCTCAGCAAACTATGGCGATGTTGACAACG	74,3	46	0,974	1	0,995	1	0,955	0,792	mid
9	3	I19	**pc1090**	strongly similar to 2-oxoglutarate dehydrogenase E1 component, sucA	**sucA, odo1, E1o**	2673	pc1090_1266-1314	AGGAGATGAACCTGCTTATACCCAGCCTCTAGAATGTCGTTTAATCAAA	74,2	49	0,975	1	0,998	1	0,928	0,833	mid
9	3	M19	**pc1091**	unknown protein	**-**	663	pc1091_359-404	AAGATTTAGACCTTTTGTCTGTCAATGTGACAACCCAATCACATGG	74,3	46	0,975	1	0,994	0,966	0,974	0,824	mid
9	3	A23	**pc1092**	unknown protein	**-**	2376	pc1092_1375-1419	AATGACAGCCACACCCCTCTTTTTTCCTCTTTATCTCTAGCGTCT	74,2	45	0,953	1	0,997	1	0,814	0,757	mid
9	3	E23	**pc1093**	similar to carboxymethylenebutenolidase	**ysgA**	732	pc1093_359-403	TTGGAGGGTTGACAGTGATAGAACTATTACGTAGTGGGGCTGATG	74,4	45	0,988	1	0,988	1	0,992	0,91	mid
9	3	I23	**pc1094**	hypothetical protein	**-**	1905	pc1094_959-1007	AACTTTATGCTGAATATGCGTATTATCAATTCCCCTGGATCAAACTGCT	74,2	49	0,98	1	0,998	1	0,995	0,789	mid
9	3	M23	**pc1095**	conserved hypothetical protein	**-**	468	pc1095_172-216	AAAGAAAGTGGAGAAGCGGAAGAATATATCACTCCCAAGCGAATC	74,2	45	0,977	1	0,995	1	0,937	0,85	mid
9	4	A03	**pc1096**	similar to oxygen-independent coproporphyrinogen III oxidase, hemN	**hemN**	1158	pc1096_645-691	TGTACGTCCCCTATTACCCGATGAAGAGACCAGTTTAGCCATGTATA	74,3	47	0,98	1	0,996	1	0,935	0,888	mid
9	4	E03	**pc1097**	unknown protein	**-**	2091	pc1097_1024-1068	TTCAAAGATATTGGAGTGATTCGCGTTGCTGCAGATAATGAATTT	74,2	45	0,977	1	0,999	1	0,977	0,78	mid
9	4	I03	**pc1098**	unknown protein	**-**	387	pc1098_30-75	TGTAGAGTCTTCCGATCTTGGAAAAGCCTATAATCCTGTTGCCATT	74,2	46	0,983	1	0,998	1	0,996	0,824	random
9	4	M03	**pc1099**	conserved hypothetical protein	**-**	726	pc1099_391-438	TTAATGGCGCTTATGCTATCTGGGTTACCAGGTCAAAAGTTTTTCTTT	74,2	48	0,971	1	0,995	1	0,973	0,739	mid
9	4	A07	**pc1100**	hypothetical protein	**-**	1032	pc1100_632-682	AAATTTGCAATTATCAACCTTCCGATACTATTTGGCAGTTAGGAGAAGCTC	74,2	51	0,958	1	0,995	1	0,885	0,718	mid
9	4	E07	**pc1101**	unknown protein	**-**	255	pc1101_46-99	CAGGCATCGACAGAAAATAAACAGATCACAAAACTTACTTCCAAAAATGAAATA	74,3	54	0,97	1	0,998	1	0,995	0,679	random
9	4	I07	**pc1102**	similar to aspartate-semialdehyde dehydrogenase	**asd**	1068	pc1102_548-596	GGGCTGGATATCCTGGTGTGGCAAGTTTGGATATCAATGATAATATTAT	74,3	49	0,971	1	0,996	0,958	0,987	0,77	mid
9	4	M07	**pc1103**	similar to aminopeptidase A, pepA	**pepA, xerB, carP**	1500	pc1103_814-860	AATATTAAGCCAACGGGAGGAATAGAAACCATGAAATGCGATATGTC	74,1	47	0,974	1	0,985	1	0,937	0,85	mid
9	4	A11	**pc1104**	similar to Single-strand binding protein	**ssb, lexC, exrB**	477	pc1104_106-150	AAGGGAAAAGAGGACATTACTATCTGGGTGCGTGTTACTGTTTGG	74,1	45	0,984	1	0,987	1	0,995	0,87	random
9	4	E11	**pc1105**	conserved hypothetical protein	**-**	504	pc1105_255-299	GGCTGGTGGTGGAGTTGGAGTAGCAGTAAAAGAAGAACTCATTCT	74,2	45	0,98	1	0,999	1	0,998	0,785	mid
9	4	I11	**pc1106**	strongly similar to isoamylase	**-**	2013	pc1106_910-955	AAAGAATTTATTATCCAATCGCTTCGCTACTGGGTGACAGAAATGC	74,1	46	0,962	1	0,99	1	0,902	0,754	mid
9	4	M11	**pc1107**	hypothetical protein	**-**	864	pc1107_482-526	AAGCCTTATCTGCACTGGCGATTATAGCTCGGACTAATGCCTACT	74,3	45	0,981	1	0,991	1	0,951	0,883	mid
9	4	A15	**pc1108**	strongly similar to holliday junction DNA helicase, ruvB	**ruvB**	999	pc1108_500-547	AACCTCTTCGTTCCCGATTTGCTTTTACATGTCGTCTTGAATATTATG	74,3	48	0,98	1	0,998	1	0,999	0,786	mid
9	4	E15	**pc1109**	unknown protein	**-**	540	pc1109_272-317	AATTAAACACTGCAAAAGGAATGGGCATCAATATACCGATGGATTC	74,3	46	0,978	1	0,996	1	0,999	0,771	mid
9	4	I15	**pc1110**	similar to low calcium response protein lcrH	**lcrH, ycD**	387	pc1110_64-108	GAAGCCTCACTCTTCTTTCGTTTGCTGACGGTGGTAAATCATAAT	74,3	45	0,981	1	0,993	1	0,998	0,813	random
9	4	M15	**pc1111**	unknown protein	**-**	963	pc1111_485-531	ACTCCTTTGATCAATTACAAAACCTACGCAAGATTCAAGAACGAACG	74,2	47	0,979	1	0,999	1	0,998	0,772	mid
9	4	A19	**pc1112**	unknown protein	**-**	579	pc1112_335-383	CAGGAGCTCAAATTGGACAAGGAATCAGTCAGACTATTAGTACAACACG	74,3	49	0,981	1	0,994	1	0,955	0,867	mid
9	4	E19	**pc1113**	conserved hypothetical protein	**-**	633	pc1113_213-259	ATTATCTGTAAGAGACACTGTGTTTGAGCTGGGATGTGGAAGAGGAC	74,2	47	0,975	1	0,995	1	0,895	0,892	mid
9	4	I19	**pc1114**	unknown protein	**-**	963	pc1114_516-568	ACAATTACGGGAAATAATGGATTGTTTTCGAGAAGCAACCTTATCTCCTTATT	74,2	53	0,969	1	0,999	0,965	0,967	0,757	mid
9	4	M19	**pc1115**	similar to Mg2+ transporter	**mgtE**	1473	pc1115_735-780	TGAAGCCGTTGATATTGTGGAGCGCTATAAAATTTCTGCTTTACCT	74,3	46	0,973	1	0,997	1	0,997	0,716	mid
9	4	A23	**pc1116**	similar to Elongation factor G (EF-G), fusA	**fusA**	1821	pc1116_917-967	AACCTACAGTTTCCGTCGATATGACAGTTAATAATAGCCCATTTGTTGGTC	74,2	51	0,983	1	0,994	1	0,994	0,836	mid
9	4	E23	**pc1117**	hypothetical protein	**-**	2049	pc1117_1052-1097	CTGAGTCTCCAGATGGGTGGTATCTTTACGGCTCTTGTTTAAATGA	74,2	46	0,978	1	0,997	1	0,974	0,807	mid
9	4	I23	**pc1118**	conserved hypothetical protein	**-**	2157	pc1118_1121-1172	AAATTCTAGGGGATCATAGCCAATTATTTTGCGAATATTATGATATCACCGC	74,2	52	0,976	1	0,998	1	0,959	0,799	mid
9	4	M23	**pc1119**	conserved hypothetical protein	**-**	966	pc1119_503-551	CTCATTATATAAATTATGCAGGAGTCGCTTTAAATTGGCGCTGTTTTGG	74,3	49	0,972	1	0,998	0,998	0,981	0,729	mid
9	5	A03	**pc1120**	conserved hypothetical protein	**-**	1260	pc1120_631-685	ATGGATATCGAATGGTTAGACTTAAATCATCATACAGAAGAGCTTCTCCAACAAA	74,2	55	0,979	1	0,998	1	1	0,771	mid
9	5	E03	**pc1121**	similar to 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase)	**yedO**	1008	pc1121_504-556	AACGCTTCCTTTAGATATCATTCAAAACGAAACAGATACGCAACTAGAATTCA	74,3	53	0,978	1	0,998	1	0,999	0,77	mid

9	5	I03	**pc1122**	unknown protein	-	216	pc1122_1-54	TTGGGATTTAAACAAGACAATATACACATACTTTCTATCCCTCAATGCTTAGGA	72,7	54	0,909	1	0,841	0,924	0,892	0,712	mid 2.Wahl
9	5	M03	**pc1123**	unknown protein	-	909	pc1123_480-525	ATATGCTCCTGGTGTAGTGGTTAATTGGGTTATGTACGGAACCTCC	74,1	46	0,985	1	0,985	1	0,976	0,911	mid
9	5	A07	**pc1124**	similar to calcium-dependent protein kinase 9	-	1395	pc1124_718-772	CCACAAGTCGTTAAAACGTATTCCATTCATTACTATCCAGCAAATCTATCTTTTG	74,1	55	0,973	1	0,989	1	0,981	0,763	mid
9	5	E07	**pc1125**	strongly similar to hemolysin III	**hlyE;hly3**	585	pc1125_226-273	GGATCTTATACGCCTTTTACACTAATAGCCTTACAGGGGTTTTGGGGA	74,3	48	0,978	1	0,997	1	0,932	0,867	mid
9	5	I07	**pc1126**	unknown protein	-	291	pc1126_87-131	AATAGGGCAGGATAAAGCGGGCAAGAAGGAATCCAGTTTAGTTAA	74,3	45	0,981	1	0,998	1	0,996	0,805	random
9	5	M07	**pc1127**	unknown protein	-	207	pc1127_43-93	TTTTATCTCATCTATTTATTTTTCCCCGAAGCCTTTGATATGCTTGTGTCA	74,3	51	0,97	1	0,998	1	0,976	0,705	random
9	5	A11	**pc1128**	unknown protein	-	2325	pc1128_1115-1161	AATATCCCCTCAACCAACCCCCTTCTTTATTTCTCATGATTTACGAC	74,2	47	0,969	1	0,998	1	0,951	0,738	mid
9	5	E11	**pc1129**	unknown protein	-	3321	pc1129_1455-1499	TTTGACACGTATCGATACAGGTAACCAACAAGAGCCTAGCGAAAG	74,2	45	0,96	1	0,995	1	0,793	0,868	mid
9	5	I11	**pc1130**	unknown protein	-	183	pc1130_26-70	TTGCGATTTCACTTTCGACAGAGAGTGCAAACTTAGATCAAGAGA	74,2	45	0,968	1	0,998	0,991	0,933	0,765	mid
9	5	M11	**pc1131**	hypothetical protein	-	969	pc1131_558-602	CTTATGGTTTTCCTTTGTTTCTCCGCCAGTCATAAGGATTGGATT	74,3	45	0,969	1	0,998	1	0,928	0,768	mid
9	5	A15	**pc1132**	similar to pyrroline-5-carboxylate reductase, proC	**proC,**	795	pc1132_472-516	GATGCATTAACGGCTCTAACTGGATCTGGGCCAGCTTTTATATTT	74,2	45	0,97	1	0,992	1	0,927	0,793	mid
9	5	E15	**pc1133**	strongly similar to peptidylprolyl isomerase II (cyclophilin A)	**ppiB**	480	pc1133_318-368	TATTACCACAGCTGCTACACCTTGGTTGAATAAAAAACATACGATCTTTGG	74,2	51	0,964	1	0,992	0,996	0,923	0,741	mid
9	5	I15	**pc1134**	unknown protein	-	675	pc1134_318-369	TGAAAAGAAAAACTATCTCAAAGCTCGCCAAGCCTTAATCTGTTTAACAAAA	74,3	52	0,96	1	0,994	1	0,979	0,609	mid
9	5	M15	**pc1135**	unknown protein	-	2256	pc1135_1022-1067	TAGGAGAAAGAGTATTGATTTGTGATCCTTGCGGTGCTACAGCTCT	74,2	46	0,969	1	0,999	1	0,893	0,815	mid
9	5	A19	**pc1136**	unknown protein	-	1242	pc1136_614-666	GAGCTTCGTTTAAAGTTCTACTAGGTATTTTGCCTTCCACAGTTGGAACACTT	74,3	53	0,982	1	0,996	1	0,992	0,828	mid
9	5	E19	**pc1137**	unknown protein	-	1233	pc1137_644-692	CAATTGGTGCACTCCCAACTTCACCAGGCACTATTACCTTAGACTATAC	74,2	49	0,987	1	0,998	1	0,974	0,905	mid
9	5	I19	**pc1138**	unknown protein	-	1119	pc1138_449-495	TTTTAGATACTTGCATTGGATTGGGGGTAGCGGTCTTTATTGCTAAA	74,2	47	0,964	1	0,995	1	0,888	0,777	mid
9	5	M19	**pc1139**	unknown protein	-	186	pc1139_55-109	AAAATTCCTGTAGTAAAACAATCTAGCCAGGCAGAGTTGACAATAGAAGAAATGG	74,3	55	0,852	0,709	0,992	0,991	0,932	0,755	random
9	5	A23	**pc1140**	conserved hypothetical protein	-	186	pc1140_1-52	GTGCTAACTATTTTGCTTCTCTTTCATCGTTCCAATGACAGAACATTTAAGC	74,3	52	0,604	0,075	0,997	0,919	0,986	0,753	random
9	5	E23	**pc1141**	conserved hypothetical protein	-	585	pc1141_10-54	CCAAGAACACCAAAGGTAATTGACAGAAGTGGCGAAGAATTTAGG	74,3	45	0,774	0,485	0,994	0,99	0,985	0,777	random
9	5	I23	**pc1142**	conserved hypothetical protein	-	1773	pc1142_1574-1618	CGGCTTTGCAATCTCTAGATCTAATTGGCTGTAATAACCTCACCG	74,2	45	0,638	0,127	0,996	1	0,996	0,773	random
9	5	M23	**pc1143**	conserved hypothetical protein	-	1011	pc1143_544-592	GTGTTAGCAAAATTTAGGTCGGTAGATATGGTCAATATGGAAAATCAGTTAGCAA	74,3	49	0,613	0,07	0,996	1	0,963	0,789	mid
9	6	A03	**pc1144**	unknown protein	-	219	pc1144_89-134	TTTTGATTACTCGTAATGGAAAAACCGTAGGTGCTTTTGTCCCTGT	74,3	46	0,609	0,06	0,997	0,988	0,978	0,785	mid
9	6	E03	**pc1145**	conserved hypothetical protein	-	264	pc1145_46-99	GAAGCAATTGCTTATTACCTTATTTCCAATGCGACTATTGAGTCACTCTACCTT	74	54	0,756	0,494	0,971	0,928	0,913	0,791	mid 2.Wahl
9	6	I03	**pc1146**	conserved hypothetical protein	-	273	pc1146_121-166	TTAAAAAGTAGCTGTCAGATAGAACATCATCGGCACCGAAATCGAT	74,2	46	0,619	0,07	0,997	1	0,983	0,832	mid
9	6	M03	**pc1147**	conserved hypothetical protein	-	543	pc1147_243-293	TGAGGTCGAAGAAATTATCACTCGTTTTCCTACTCCCTCTTCATTAAAAGA	74	51	0,952	1	0,978	0,93	0,97	0,681	mid 2.Wahl
9	6	A07	**pc1148**	conserved hypothetical protein	-	540	pc1148_158-210	CAGCATCTCAGACAAGCTTAAGTCCTAAACTACGAGAACAACTTGCTTTAGTG	74,2	53	0,983	1	0,995	0,994	0,995	0,845	random
9	6	E07	**pc1149**	conserved hypothetical protein	-	465	pc1149_252-305	TTTAGAAATGACCTCATTAAAAGAATCTGATGGAGATTTGGGTGGAGATGATAT	74,3	54	0,975	1	0,998	1	0,997	0,74	random
9	6	I07	**pc1150**	unknown protein	-	240	pc1150_5-59	TGAAAGCAATCGCTCTAGAAAAGTATAGAGAATCAAACGAATTAGCAATTAAGGG	74,1	55	0,974	1	0,983	1	0,997	0,767	random
9	6	M07	**pc1151**	unknown protein	-	936	pc1151_520-567	ATAGATCTTGATCAAATGGAATTTTGCGTACAGCGTCGAGCTACTATG	74,1	48	0,971	1	0,988	1	0,949	0,791	mid
9	6	A11	**pc1152**	strongly similar to NADH-dependent enoyl-ACP reductase	**fabI**	912	pc1152_481-527	CATCTTGGACCTTATCTCAATTCTCAAGGGTCAGCCTTAACTCTGAC	74,2	47	0,983	1	0,994	1	0,976	0,865	mid
9	6	E11	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
10	1	B03	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
10	1	F03	**pc1153**	unknown protein	-	873	pc1153_471-518	AACTTTAAACGATGGTTATTTTCAACAAGGAACAGGAGGGCATAGACC	74,2	48	0,974	1	0,997	1	0,967	0,774	mid
10	1	J03	**pc1154**	unknown protein	-	1110	pc1154_571-617	GAACACACTTGGGTAGCTCTCGAAAAGAAAGTATCTGCTGGTTTGAT	74,3	47	0,981	1	0,995	1	0,985	0,829	mid
10	1	N03	**pc1155**	unknown protein	-	276	pc1155_74-120	TCTATCAAAGTTCGCAAACGGGCTATCTTCATTATTATCATGGGATG	74,3	47	0,971	1	0,99	1	0,935	0,807	mid
10	1	B07	**pc1156**	similar to 3-ketoacyl-acyl carrier protein reductase, fabG	**fabG**	708	pc1156_384-434	TAAAGGTCAAATTATTAATTTAGGGGTAAGCGGTTTGTACGAAAACCCTGC	74,3	51	0,974	1	0,998	1	0,971	0,766	mid
10	1	F07	**pc1157**	similar to dGTP pyrophosphohydrolase/dihydroneopterin aldolase (mutT/folB, fusion protein)	**folB, mutT**	789	pc1157_372-419	TCACAAAGCATGTCGACTTCTCATTGAAAGATATTTGACACAACAAAA	74,3	48	0,975	1	0,994	1	0,977	0,773	mid
10	1	J07	**pc1158**	hypothetical protein	-	879	pc1158_546-599	ATTAGGTTTACATGCCCCTACTATTCGCGATCCTTTTAACGAAGAATATTTTGT	74,2	54	0,966	1	0,999	1	0,895	0,776	mid
10	1	N07	**pc1159**	conserved hypothetical protein	-	573	pc1159_341-386	AAGTCACTCAAATGAACCAAGCCAGCTCCATTAAGGTCCTAGAAAC	74,3	46	0,98	1	0,996	1	0,946	0,864	mid
10	1	B11	**pc1160**	conserved hypothetical protein	-	480	pc1160_10-57	CCCATTGAAATGAGCCTAAAGGCTTTATTAACTTCGATGCAGAGAAAT	74,2	48	0,975	1	0,995	1	0,996	0,742	5´preference
10	1	F11	**pc1161**	similar to DNA polymerase III, epsilon chain, mutD	**dnaQ, mutD**	651	pc1161_350-395	AAATTTATGGAATAACTGCTAACAATGCGCACAGGGCATTAGATGA	74,2	46	0,98	1	0,994	0,995	0,977	0,832	mid
10	1	J11	**pc1162**	conserved hypothetical protein	-	810	pc1162_489-535	GATTACTGATCGCGTTATTAGAATGCACCAATATTCATTTCCAGGGA	74,3	47	0,972	1	0,991	1	0,917	0,835	mid
10	1	N11	**pc1163**	similar to transport ATP binding protein	**msbA**	1941	pc1163_1114-1162	GCAGAAAGAATGCAAGAGGTTTTACATGTACAACCGCAGATTAAGAATC	74,2	49	0,965	1	0,997	1	0,858	0,827	mid
10	1	B15	**pc1164**	strongly similar to acetyl-CoA carboxylase	**accA**	951	pc1164_537-589	TCGTGAAATGATGCGTATTAATACTCCAATCATTATTACAATTATCGGGGAAG	74,3	53	0,974	1	0,995	1	0,94	0,811	mid
10	1	F15	**pc1165**	hypothetical protein	-	978	pc1165_565-	GTGGGATTAGGAAGATTGGATTCTTCTAGTAGTTCGGGCTTATTAACACCTCT	74,1	53	0,972	1	0,99	1	0,925	0,833	mid

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10	1	J15	**pc1166**	unknown protein	-	297	pc1166_48-100	TGAGTTTTCTCGAGGTAAGCTATCTTTTAGAGAAACATGCGATAAGTGTGGTT	74,2	53	0,984	1	0,999	1	0,999	0,823	random
10	1	N15	**pc1167**	hypothetical protein	-	1497	pc1167_799-847	CTTCCAGAACATATCTATGATCCTTCGACATCTCTTGTTGGGTATCGTT	74,3	49	0,981	1	0,997	1	0,951	0,867	mid
10	1	B19	**pc1168**	similar to integration host factor	**himD; ihfB**	363	pc1168_6-50	AAAAATGAAGGAGTGTGGCCTTATGGCAACCAGTACAAAGAAGAG	74,2	45	0,982	1	0,995	1	0,996	0,818	random
10	1	F19	**pc1169**	strongly similar to tyrosine-tRNA ligase	**tyrS**	1278	pc1169_623-667	GTAAAGTGCATGCCAAGCCAGCTTATGGAATTACATTTCCTCTTC	74,2	45	0,979	1	0,999	0,976	0,983	0,825	mid
10	1	J19	**pc1170**	unknown protein	-	243	pc1170_15-69	TTTTTCCATGTCTATGACTAAGTTTTGTATCCCTCAGTTTATTATCTCAATGCGC	74,1	55	0,964	1	0,988	1	0,892	0,792	mid
10	1	N19	**pc1171**	similar to hyperosmotically inducible periplasmic protein	**osmY**	393	pc1171_70-115	ACTAATGCTGACAATACTGCTCGTAATGCTCGTGATCGTAATGGTC	74,3	46	0,989	1	0,997	1	0,998	0,89	random
10	1	B23	**pc1172**	hypothetical protein	-	627	pc1172_237-282	TAACCTAGGTCACGAAAAAAACACTAAAGCACCTGAAGGAGCAACA	74,3	46	0,97	1	0,994	1	0,922	0,796	mid
10	1	F23	**pc1173**	conserved hypothetical protein	-	759	pc1173_357-401	ATGGGAAAAGTTAGAACCCTTCGCCTTTATGAATGGAATTCCAAT	74,2	45	0,976	1	0,994	1	0,976	0,782	mid
10	1	J23	**pc1174**	unknown protein	-	855	pc1174_427-473	ACTGGATCGCAAACGATTGAGGCTAGTATCAAAGCATTTAATTTTGA	74,2	47	0,972	1	0,999	1	0,999	0,697	mid
10	1	N23	**pc1175**	similar to ribose 5-phosphate isomerase A	**rpiA**	699	pc1175_365-419	TCGTTGTTATCGATGAGACTAAACTTGTGAATAAATTAGGAAAATTTCCCGTAGC	74,3	55	0,974	1	0,991	1	0,986	0,76	mid
10	2	B03	**pc1176**	conserved hypothetical protein	-	414	pc1176_120-169	TAAAACCCTACAAATGTTTTTGACTGAAGCGGAAAGACTAAGGCCTCTAA	74,2	50	0,971	1	0,995	1	0,912	0,822	mid
10	2	F03	**pc1177**	strongly similar to PTS phosphocarrier protein HPr	**ptsH**	294	pc1177_66-119	TCATACAAGACCTTCAACAGAACTTGTAAAGTGCGCAAATAGTTTTAGATCTCA	74,2	54	0,977	1	0,991	0,994	0,999	0,78	random
10	2	J03	**pc1178**	similar to oligoendopeptidase F	**pepF**	1845	pc1178_918-969	ATTAGACCAACTCCATCTTTACGATATTTACGTCCCTCTAACTAGTGCCGTG	74,2	52	0,988	1	0,999	1	0,994	0,88	mid
10	2	N03	**pc1179**	strongly similar to chlamydial heat shock protein groES	**groES**	321	pc1179_1-55	ATGACACAAACTCAAACAGTCTCTCAAATCACGAAACTAAAACCTTTAGGAAATC	74,2	55	0,981	1	0,999	1	0,998	0,801	random
10	2	B07	**pc1180**	strongly similar to chlamydial hypB stress response protein	**groEL**	1623	pc1180_1435-1487	TATAACGCATTAACAGGCGAATATGTAGACATGATCACAGCCGGTATCTTAGA	75.5	53	0,988	1	0,997	1	0,993	0,887	testchip
10	2	F07	**pc1181**	hypothetical protein	-	963	pc1181_459-504	AGAATTATTAGGAGCAGATGTAATCAACATTCATGCGGGAGGAACA	74,2	46	0,98	1	0,994	1	0,976	0,835	mid
10	2	J07	**pc1182**	similar to DNA topoisomerase I	**topI**	1077	pc1182_578-624	TTGGTAAAAGCGGAAAGCAGCATACCATCACTCTATACGATAAACGT	74,2	47	0,98	1	0,991	1	0,962	0,858	mid
10	2	N07	**pc1183**	similar to mannosyltransferase	**wbdA**	1086	pc1183_542-587	ACTTCGATGATGTCTGTTTGGTTGTCAAAGATGTGGGAGTTAAAGA	74,2	46	0,984	1	0,999	1	0,998	0,829	mid
10	2	B11	**pc1184**	hypothetical protein		1644	pc1184_642-686	CCCTTGTGTGCATGGTGTTTATTTGATTCAAGCTCCATTCTTAAG	74,3	45	0,955	1	0,994	1	0,819	0,778	mid
10	2	F11	**pc1185**	unknown protein	-	216	pc1185_111-165	AGTTAATCAAACAATTATCGTACTCCCCCTAACACCATACTTTAAAACGAGGGAG	74,2	55	0,979	1	0,995	1	0,998	0,784	mid
10	2	J11	**pc1186**	unknown protein	-	423	pc1186_147-195	GGCAGTTGTTGCAGGAGCTTTCAGTTATGCTGTTAGTTTCTTAATCC	74,4	49	0,624	0,1	0,983	1	0,935	0,862	mid 2.Wahl
10	2	N11	**pc1187**	unknown protein	-	420	pc1187_226-277	AATAATCGGCAGGAGCTAAGTTTTGTAGGAGAAGCTTTGAGAACTAGCATTT	74,2	52	0,626	0,1	0,991	0,991	0,985	0,807	mid 2.Wahl
10	2	B15	**pc1188**	similar to outer membrane protein tspO	**tspO**	465	pc1188_76-130	TCCTCTAGTGTTCATCAGTGGTATCCAACGCTTATAAAATCATCTCTTACTCCTC	74,3	55	0,98	1	0,99	1	0,994	0,815	random
10	2	F15	**pc1189**	strongly similar to cytochrome o ubiquinol oxidase chain II cyoA	**cyoA**	888	pc1189_407-456	AAATCACTATTCAAGTCATCGCTTTGCAATGGAAATGGCTGTTTATCTAT	74,2	50	0,973	1	0,999	1	0,962	0,764	mid
10	2	J15	**pc1190**	strongly similar to cytochrome o ubiquinol oxidase chain I cyoB	**cyoB**	1962	pc1190_920-968	AAAGGTTATTTGGGTATGTCTCTATGGTTTGGGCTCTCGTTTTAATTGC	74,3	49	0,964	1	0,996	1	0,938	0,702	mid
10	2	N15	**pc1191**	strongly similar to cytochrome o ubiquinol oxidase chain III cyoC	**cyoC**	636	pc1191_244-298	ATCTTACTATTAAGTAGTATGACATGTGGATTAAGCATGCTCGCTGCCGTTAAAA	74,2	55	0,975	1	0,999	1	0,925	0,837	mid
10	2	B19	**pc1192**	similar to cytochrome O ubiquinol oxidase chain IV cyoD	**cyoD**	363	pc1192_144-198	TTTAGTCTATACCTTGATAGGTTTCGCCCTAACACAGACATTTGTTCAGCTAGTC	74,1	55	0,979	1	0,982	1	0,998	0,823	random
10	2	F19	**pc1193**	strongly similar to heme O synthase (=protoheme IX farnesyltransferase) cyoE	**cyoE**	852	pc1193_367-413	TATAGTATTTGGAAAAGTCGGACAGTTTACGGAACGGCGATAGGAAG	74,2	47	0,979	1	0,998	1	0,94	0,86	mid
10	2	J19	**pc1194**	unknown protein	-	5046	pc1194_2502-2552	TCTGGATATCACGCTTAATCACTTGTCTGATCCTATACTTCAAAGAACGCT	74,2	51	0,98	1	0,999	1	0,978	0,816	mid
10	2	N19	**pc1195**	conserved hypothetical protein	-	231	pc1195_29-74	GCTTAAATGTGCTACTTTTCTACGCTCATCAATGGAGCATCTTATGGA	74,5	46	0,603	0,03	0,974	1	0,993	0,873	random
10	2	B23	**pc1196**	conserved hypothetical protein	-	309	pc1196_22-66	GCTGGTCTTACAGCTGAGTGGTTACTGGCAGACAAAGGATATGAT	74,2	45	0,983	1	0,999	0,963	0,99	0,882	5´preference
10	2	F23	**pc1197**	hypothetical protein	-	2001	pc1197_928-974	GGTTTGCAGCATCTTGATTTAAGCAATTGTAAGAATCTTACCGATGC	74,3	47	0,609	0,093	0,997	1	0,926	0,698	mid
10	2	J23	**pc1198**	conserved hypothetical protein	-	360	pc1198_92-137	TTAATCGGCATGGTCAAATCATGGATAAAGCCTTAACTTCCAAATC	74,3	46	0,615	0,06	0,991	1	0,999	0,826	random
10	2	N23	**pc1199**	conserved hypothetical protein	-	333	pc1199_57-101	AATCCTTGAATCTATCCGAAAGAAAACACGTCCCCGAAAGATAGA	74,2	45	0,977	1	0,997	1	0,972	0,794	5´preference
10	3	B03	**pc1200**	conserved hypothetical protein	-	357	pc1200_125-172	CTGGAGAACCATTTTCAAATGGTATTCATGAGATATGGGGATGTACAG	74,3	48	0,959	1	0,997	0,898	0,945	0,786	mid 2.Wahl
10	3	F03	**pc1201**	conserved hypothetical protein	-	711	pc1201_378-425	AAACAAGGTCTTTAAAGGTTTAGCAAAGAGGGGGAAAACAACTTCAGG	74,2	48	0,595	0,027	0,998	1	0,979	0,755	mid
10	3	J03	**pc1202**	conserved hypothetical protein (chlamydia plasmid)	-	417	pc1202_3-47	GTCTCTACAAATTCACCAGATTGATTGGGAGCGCTGTGAAATCAC	76	45	0,713	0,489	0,826	1	0,793	0,822	mid
10	3	N03	**pc1203**	conserved hypothetical protein (chlamydia plasmid)	-	483	pc1203_12-59	GCCAACAGTGATTGAACCCTCTATTGGATTTAGCTTAGAGACCTACGA	74,3	48	0,954	1	0,992	1	0,77	0,845	mid
10	3	B07	**pc1204**	unknown protein	-	783	pc1204_404-457	CTTTAAGTTTACAGATGACCAGTGAATTCAAGACGTACTCAGGAGAATCTGGAT	74,2	54	0,985	1	0,998	1	0,989	0,857	mid
10	3	F07	**pc1205**	unknown protein	-	726	pc1205_365-415	AGGTGCTTAAGAAGTCGAATCTACAATCCAAAACCGTTTTAGCTCTTCATT	74,2	51	0,983	1	0,998	1	0,999	0,816	mid
10	3	J07	**pc1206**	unknown protein	-	234	pc1206_54-105	TGACGCTTACTTTGTGGCAAAAGAATTAGTTTATCTACAAGATTATTGGCGA	74,2	52	0,608	0,06	0,997	1	0,986	0,748	random
10	3	N07	**pc1207**	unknown protein	-	1404	pc1207_1098-1146	GATTACAATGCACCCTTTTGGTACTTCTCCTGTCCAGTTCCTTAACTTC	74,3	49	0,62	0,06	0,991	1	0,998	0,873	random
10	3	B11	**pc1208**	unknown protein	-	2523	pc1208_1232-1282	GCAAACTCTCTGTTTATATTAAGTCATTATCCTGTGTCTAGCGCCACGC	74	51	0,618	0,09	0,978	1	0,969	0,804	mid
10	3	F11	**pc1209**	conserved hypothetical protein	-	183	pc1209_6-56	CAATATGTGCCCCCAGAGTCCTTCATTCTATAGAGGTTATTGGTCTAAATG	74,1	51	0,73	0,393	0,989	0,938	0,913	0,877	mid
10	3	J11	**pc1210**	unknown protein	-	183	pc1210_6-58	TTTTTCGATGCTTGTCATCCCAAAATTACCAACTTTTTTAGATTGTCAATTTA	74,2	53	0,593	0,07	0,991	1	0,982	0,556	random
10	3	N11	**pc1211**	similar to metalloprotease	**cnp; nprC**	831	pc1211_67-113	GGTTCCTTTACCAGTGGAGGACTTAAACAGCTAGGTTACCTACCGCT	74,2	47	0,941	1	0,997	1	0,65	0,863	mid
10	3	B15	**pc1212**	unknown protein	-	1110	pc1212_574-	ATTCAAGCGGAAATAGAGCATCTTAAAAGCAAGCTAGAGAAATTGGAGG	74,3	49	0,598	0,04	0,993	1	0,982	0,738	mid

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10	3	F15	**pc1213**	conserved hypothetical protein	-	267	pc1213_2-51	TGTTAACGGTTTTGCTTCTCTTTCATCATTCCAATGACAGAACATTTAAA	74,3	50	0,623	0,128	0,989	0,923	0,998	0,73	random
10	3	J15	**pc1214**	conserved hypothetical protein	-	336	pc1214_146-199	AAAAGAGGACTATGATTGAAAGTGTGAATCATCTGTTGAAAAGTAGCTGTCAGA	74,2	54	0,615	0,07	0,993	1	0,977	0,805	mid
10	3	N15	**pc1215**	conserved hypothetical protein	-	381	pc1215_34-80	ATCAGGGTCATTATTACAGAAGGCACAACAGCAGATTGTACTCAAGC	74,2	47	0,982	1	0,999	1	0,984	0,833	5´preference
10	3	B19	**pc1216**	hypothetical protein		1152	pc1216_401-446	TAAGACGAGAAGGAGCAGTGATTGTAGACGTATATGCGGCACATAG	74,3	46	0,967	1	0,996	1	0,824	0,899	mid
10	3	F19	**pc1217**	similar to ABC transporter, ATP-binding protein	**glnQ**	690	pc1217_279-329	TCAATCCTTACTTTTGATTCCCACTTTGACCGTTTTAGAGAATGTCTCTCT	74,2	51	0,97	1	0,994	1	0,933	0,781	mid
10	3	J19	**pc1218**	hypothetical protein	-	1065	pc1218_622-666	CAAACGAAAGCTCGCATGAATGCTGCCAAAATAGATATAGAGAGA	74,2	45	0,972	1	0,996	1	0,912	0,828	mid
10	3	N19	**pc1219**	similar to outer membrane protein of AcrAB(MexAB)-OprM multidrug efflux pump	**oprM**	1461	pc1219_759-803	AATCTATCATTTATCGATTCTGCTCGGACAATTTCCAGGGGAAGT	74,2	45	0,979	1	0,999	1	0,973	0,814	mid
10	3	B23	**pc1220**	similar to 7-dehydrocholesterol reductase	**DHCR7**	1308	pc1220_760-806	TCGTTAGATATCATGCACGACAGAGCTGGTTACTATATTTGTTGGGG	74,2	47	0,973	1	0,995	1	0,895	0,867	mid
10	3	F23	**pc1221**	similar to DNA mismatch repair protein mutS	**mutS**	2577	pc1221_1273-1318	AATGCATTAATATCCAATGCAATCGTAGAAGAGCCGCCTCTAAGAC	74,2	46	0,983	1	0,997	1	0,983	0,846	mid
10	3	J23	**pc1222**	unknown protein	-	201	pc1222_2-56	TGGTATACAGTAGACAAGTATGGCTACTAGCCACGACAATTAAAAAGCAGTCAAA	74,1	55	0,825	0,709	0,986	0,903	0,9	0,639	mid 2.Wahl
10	3	N23	**pc1223**	unknown protein	-	723	pc1223_337-381	GATTCTGTTTACCAAACGTGGCATCTCGCTAATCATCAAATGAAC	74,4	45	0,974	1	0,984	1	0,974	0,792	mid
10	4	B03	**pc1224**	unknown protein	-	945	pc1224_386-430	TTCCTCCTCTTCTTACTTTAGAACCCATGGTTGCCGTTTCTCCTA	74,4	45	0,966	1	0,982	1	0,912	0,807	mid
10	4	F03	**pc1225**	similar to primosomal protein N'	**priA**	2238	pc1225_1148-1192	CCTTGAGTGTTTTACACAAACGAGCAGATGTAGCTACCCTTCCAG	74,3	45	0,985	1	0,997	1	0,972	0,883	mid
10	4	J03	**pc1226**	conserved hypothetical protein	-	1428	pc1226_779-823	TTTGGCTTCGCCTCCTTTATTTGTACCCTGATGAAATTACTGATG	74,3	45	0,968	1	0,997	1	0,936	0,753	mid
10	4	N03	**pc1227**	unknown protein	-	243	pc1227_93-142	TATTTTCATGTTTGTTCTTTATACGCTGGCATTAATTTGGACAACAGTGC	74,2	50	0,97	1	0,997	0,984	0,965	0,756	random
10	4	B07	**pc1228**	strongly similar to lysyl-tRNA synthetase	**lysS**	1590	pc1228_804-848	AGTTTATGAAATGGCACGTGTATTTCGTAATGAAGGCATTGATCG	74,2	45	0,982	1	0,996	0,999	0,992	0,822	mid
10	4	F07	**pc1229**	unknown protein	-	276	pc1229_32-82	TTTTACTCTTTATCACGCTATTTCCTAGGTTGACAATGCTTTTTGCGGTTA	74,2	51	0,981	1	0,996	1	0,999	0,806	random
10	4	J07	**pc1230**	unknown protein	-	1266	pc1230_538-584	ACTCTTCGAGTTGCCAGACTGGTAGCAAAGCTAGAAAAACATTATGC	74,1	47	0,968	1	0,988	1	0,904	0,814	mid
10	4	N07	**pc1231**	unknown protein	-	1065	pc1231_786-836	TGGTAAAGAGGTAACAGAAGAGCAGATTGAGCAAGCCCTTATTAACGAATA	74,3	51	0,95	1	0,997	1	0,748	0,818	mid
10	4	B11	**pc1232**	unknown protein	-	357	pc1232_66-118	GCTCCAAAAATATAATGCCGTCTTATTCGCATATTTAAAAGCGAAAATTTGTT	74,2	53	0,914	1	0,999	0,805	0,886	0,498	mid 2.Wahl
10	4	F11	**pc1233**	unknown protein	-	1308	pc1233_690-742	TGTTGAACCTATAGAAGGCAAGGTTAATATTGCTATTCAAGTAAGAGACGGGG	74,3	53	0,977	1	0,993	1	0,965	0,812	mid
10	4	J11	**pc1234**	unknown protein	-	252	pc1234_88-137	ATAGATCGTTATCAGATTGGAAAATTAGCGGGACTTCAAAAAACTGCTGT	74,2	50	0,973	1	0,999	1	0,978	0,739	random
10	4	N11	**pc1235**	similar cysteinyl tRNA synthetase	**cysS**	1437	pc1235_684-731	CATGCACCTACTTGGAGAAACGATAGATATTCATGTGGGAGGAATAGA	74,3	48	0,981	1	0,998	1	0,964	0,845	mid
10	4	B15	**pc1236**	similar to bifunctional AAS protein	**aas**	2718	pc1236_1332-1382	CTCAAGTGTTGTGACTTATTTTACGATCTTAGCTTGCCAGTTAGCTGGAAA	74,3	51	0,98	1	0,995	1	0,972	0,831	mid
10	4	F15	**pc1237**	similar to dGTP pyrophosphohydrolase, mutT	**mutT**	354	pc1237_209-259	CTTTAGTAGAGGGAGAAGTTGTTATTCAATGGTCAGAAATTCGGTCGAGTC	74,2	51	0,979	1	0,994	1	0,969	0,831	mid
10	4	J15	**pc1238**	strongly similar to beta-ketoacyl-ACP synthetase	**fabF**	1257	pc1238_634-678	TGTAAAGCCCTTTCTCAACGAAACGAAAATCCAGCTAAAGCTTCT	74,3	45	0,978	1	0,995	1	0,996	0,782	mid
10	4	N15	**pc1239**	conserved hypothetical protein	-	381	pc1239_91-138	GGCATCTGTACTATGACCGATTATTTCATCATTGCTGAAGGAACTGTT	74,3	48	0,981	1	0,996	1	0,999	0,807	random
10	4	B19	**pc1240**	similar to glutamate-ammonia ligase (=glutamine synthetase) type III	**glnA**	2178	pc1240_1113-1165	AATGACAGCCATTCTGTATGGTGTTTATCAACATTCGACTTTATTAAGAGCTG	74,2	53	0,979	1	0,999	1	0,977	0,804	mid
10	4	F19	**pc1241**	hypothetical protein	-	642	pc1241_282-326	GCAAAGACTGCAAGAAGCCAAACAAAGAGGGGATTACACACTTAT	74,3	45	0,978	1	0,997	1	0,96	0,821	mid
10	4	J19	**pc1242**	hypothetical protein	-	1722	pc1242_878-923	AATTAACCTTGAACACAAATTCCTTCACGCAAACACGTACTCGATT	74	46	0,977	1	0,977	1	0,984	0,839	mid
10	4	N19	**pc1243**	similar to tRNA delta-2-isopentenylpyrophosphate transferase	**MiaA**	1035	pc1243_475-526	TTTGAAGATGAAATTGAACGATTGGGATCAGAAATACTTTATGAAAGGCTTT	74,3	52	0,966	1	0,997	1	0,956	0,699	mid
10	4	B23	**pc1244**	similar to sigma regulatory factor	**spoIIAA**	354	pc1244_41-85	TAAAAGGTGATGTGCTTGTCTTAAGAATGCAAGGTCGGTTAGACG	74,2	45	0,986	1	0,995	1	0,998	0,867	random
10	4	F23	**pc1245**	similar to excinuclease ABC chain A	**uvrA**	2814	pc1245_1420-1470	CTCGACCAAGTAGGATTGGGATACTTGACATTAACTAGAGAAGGGAAAACA	74,2	51	0,986	1	0,999	1	0,988	0,866	mid
10	4	J23	**pc1246**	hypothetical protein	-	771	pc1246_500-544	CAGTCAAACAAATAGACGTGGCTGAGGCTTATGCTGACAGTTATG	74,3	45	0,97	1	0,993	1	0,887	0,856	mid
10	4	N23	**pc1247**	similar to UDP-N-acetylmuramate-alanine ligase murC	**murC**	1365	pc1247_682-730	AGTTATGGCTTTGGAGAGCATTGCAATTGGAGAATTTCTAATGTTTTTC	74,2	49	0,962	1	0,992	1	0,999	0,604	mid
10	5	B03	**pc1248**	similar to UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase MurG	**murG**	1131	pc1248_557-609	AAAATAACTCTACACTTTTAGTTTTCGGTGGATCTCAGGGAGCTTTAGCCATT	74,2	53	0,981	1	0,999	1	0,99	0,809	mid
10	5	F03	**pc1249**	similar to cell division protein ftsW	**ftsW**	1110	pc1249_558-603	TCTTCCACTGATGTGTTTTATGGTGATTGGTGCAATTTCTGCTTAT	74,3	46	0,979	1	0,994	1	0,998	0,791	mid
10	5	J03	**pc1250**	similar to muropeptidase (autolysin)	**lytF**	735	pc1250_388-438	GTATTAGAAAAGATTGCTCGTGCTAATGGGACAACGATTAATGCGATTAAG	74,3	51	0,975	1	0,997	1	0,98	0,763	mid
10	5	N03	**pc1251**	similar to UDP-N-acetylmuramoylalanine-D-glutamate ligase murD	**murD**	1335	pc1251_733-785	TCTTGTCATACTTATACAGATTTATGCTCGGTCTTCTTAGAAGGAATGCAGCA	74,3	53	0,975	1	0,995	1	0,936	0,832	mid
10	5	B07	**pc1252**	similar to phospho-N-acetylmuramoyl-pentapeptide-transferase mraY	**mraY**	1233	pc1252_628-680	TTTAAAGAGCCTGTTGTTACGTTTGGAGGTATTTCTCTTATTCTCATGGCTTT	74,2	53	0,972	1	0,998	1	0,99	0,714	mid
10	5	F07	**pc1253**	similar to UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate -D-alanyl-D-alanine-ligase murF	**murF**	1338	pc1253_638-690	ATACTCGATTAGGTGTGGTTGATCGAGAGATAGAAGCTTATGAAACAATTGCT	74,3	53	0,975	1	0,997	1	0,968	0,782	mid
10	5	J07	**pc1254**	unknown protein	-	237	pc1254_92-144	AAATGACGACTCCAATATTTCATTCCATTTACATTGTTTTGCCTCATTATGTT	74,3	53	0,971	1	0,99	1	0,958	0,77	random
10	5	N07	**pc1255**	similar to eucaryotic stearoyl-CoA 9-desaturase	-	1146	pc1255_627-	AGAGCAATCAGCGGTCAACAATTATATTTTGGCCCTATTAACTTTTGG	74,3	48	0,97	1	0,993	1	0,947	0,765	mid

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10	5	B11	**pc1256**	similar to virulence protein ipgD (Shigella flexneri plasmid pINV)	**ipgD**	1818	pc1256_953-999	CTGGCGAACTCTTAAAAGCCGCTGTGTTACAACATTTATCAGATGTA	74,2	47	0,976	1	0,999	1	0,957	0,805	mid
10	5	F11	**pc1257**	conserved hypothetical protein	**-**	816	pc1257_440-494	TTTTTACCTATACAGGGACAACTATCTGCTATGAATCTCCTCATCGTTTAATCGA	74	55	0,975	1	0,978	1	0,969	0,831	mid
10	5	J11	**pc1258**	unknown protein	**-**	198	pc1258_1-54	ATGAAAGAATCGCAATCTAAATCTTATGACCAATTCCTTCATCCTTACGTTTTT	74,3	54	0,758	0,519	0,995	0,898	0,901	0,699	mid 2.Wahl
10	5	N11	**pc1259**	strongly similar to heat shock protein GroEL	**groEL**	1605	pc1259_791-839	TCGTCAATAAACTTCGTGGTACTCTAAAAGTAGCTGCTGTTAAAGCCCC	74,3	49	0,979	1	0,994	1	0,987	0,805	mid
10	5	B15	**pc1260**	conserved hypothetical protein	**-**	1401	pc1260_687-734	TTTAGGTCAAGGGATCATGTTGACTTACGGGAGCTATATGAGAAGAGG	74,3	48	0,987	1	0,994	1	0,985	0,893	mid
10	5	F15	**pc1261**	conserved hypothetical protein	**-**	447	pc1261_183-228	CTCTATTAATGGGCGTTTTTCACTGCTTGAGAGGCCACAAACTTAT	74,3	46	0,977	1	0,994	1	0,959	0,825	mid
10	5	J15	**pc1262**	similar to phosphoglucomutase/phosphomannomutase	**pgm**	1779	pc1262_904-951	CTACAATCAAAATGTGATCTTTTAATCGCTAATGATCCAGATGCCGAC	74,2	48	0,975	1	0,997	1	0,987	0,747	mid
10	5	N15	**pc1263**	hypothetical protein	**-**	828	pc1263_427-479	TTGAAAGTAACAGTCTTAGCTTCTCAAGATGGGTGCCCTTTTAGAGTTATCCT	74,2	53	0,982	1	0,999	1	0,988	0,822	mid
10	5	B19	**pc1264**	similar to sialic acid synthase	**neuB**	1056	pc1264_542-589	TTTTACTCAAATGTACAGCTGCCTATCCTGCGAAATCGATAGATATGC	73,9	48	0,977	1	0,97	1	0,987	0,856	mid
10	5	F19	**pc1265**	similar to ATP-dependent RNA helicase	**deaD**	1224	pc1265_601-645	GCGATTCAACGTTTAGCTAAGCATCACATGAAAGATCCTCAAGAG	74,3	45	0,98	1	0,997	0,993	0,988	0,816	mid
10	5	J19	**pc1266**	conserved hypothetical protein	**-**	834	pc1266_422-467	ATGTATCCTCGGCTATTTCTTTTCAGGTAGCGCCTAATATGGCTGT	74,3	46	0,979	1	0,995	1	0,996	0,793	mid
10	5	N19	**pc1267**	conserved hypothetical protein	**-**	2076	pc1267_1002-1047	GGTTGCTACATTTTCAGCAGGATTTCTTTCTGTGGTGTCTTCAATT	74,2	46	0,97	1	0,999	1	0,963	0,728	mid
10	5	B23	**pc1268**	hypothetical protein	**-**	678	pc1268_343-388	AAACAAATCATTGAATTCGGGGGTGCTCAACCATTTTTACCTTATT	74,3	46	0,97	1	0,992	0,969	0,997	0,738	mid
10	5	F23	**pc1269**	similar to SOS response regulator lexA	**lexA;dinR**	612	pc1269_339-390	TACTTATATCTTACGCGTTCAGGGTAATAGCCTGTCAGAAGAGCTCATTCAA	74,3	52	0,983	1	0,996	1	0,968	0,873	mid
10	5	J23	**pc1270**	similar to CDPdiacylglycerol-serine O-phosphatidyltransferase	**pssA**	864	pc1270_343-396	GCAATTGTCTTTTCACTTTGTGGAGTTCTTCGTCTAGTTAGGTTTAATGTAGCA	74,3	54	0,973	1	0,998	1	0,91	0,832	mid
10	5	N23	**pc1271**	conserved hypothetical protein	**-**	2976	pc1271_1386-1430	AATTGATAATCCCCATTTCGTTCAGATTGTTATGACACCTGACCA	74,3	45	0,969	1	0,998	1	0,897	0,817	mid
10	6	B03	**pc1272**	conserved hypothetical protein	**-**	1857	pc1272_169-213	CAAATTTCATGCTTTGCCTCACCTCCCCCTATATTGAGCTTCCAG	77,1	45	0,809	1	0,709	1	0,239	0,823	mid
10	6	F03	**pc1273**	hypothetical protein	**-**	1245	pc1273_710-756	AACATACGCAAATAGGGCAGAACTTGCTTAAAGAACGAGCAGGATAT	74,3	47	0,973	1	0,998	0,999	0,914	0,837	mid
10	6	J03	**pc1274**	conserved hypothetical protein	**-**	417	pc1274_13-63	GGAGCGAAAACAAGAAAGCTAAAATCATTAACGAACAAGCATAAGGAACTT	74,2	51	0,61	0,07	0,995	1	0,994	0,714	5´preference
10	6	N03	**pc1275**	unknown protein	**-**	222	pc1275_31-75	TGGTCAGACAAGCTACATTGAAAGATTTAATTGTACTCTTAAGACAAAGATGTGC	74,2	45	0,6	0,05	0,992	0,999	0,919	0,814	mid
10	6	B07	**pc1276**	conserved hypothetical protein	**-**	2004	pc1276_1065-1118	ATCTTTGGTGGCTTTACAGCATTTAGATCTGAGCTGTTGTAGAAATCTTACTGA	74,3	54	0,597	0,045	0,998	1	0,938	0,757	mid
10	6	F07	**pc1277**	conserved hypothetical protein	**-**	426	pc1277_143-191	AAAGCCTTCTAGAACAGGGCTTAGAATTGTTTACGAGTGTACGAGCAAA	74,2	49	0,974	1	0,997	0,989	0,929	0,839	mid
10	6	J07	**pc1278**	conserved hypothetical protein	**-**	2196	pc1278_1073-1125	ACAAACTCACTGACACTGGTTTAGTATATTTGGCGCCTTTAGTGTCTTTACAA	74	53	0,631	0,142	0,978	0,932	0,974	0,82	mid
10	6	N07	**pc1279**	conserved hypothetical protein	**-**	276	pc1279_32-86	TTCCAGAGCTTAAAACTGGACAAGTGATTATTATGGATAATGCTACTTTTCACAA	73,6	55	0,567	0,05	0,931	0,801	0,999	0,796	random
10	6	B11	**pc1280**	conserved hypothetical protein	**-**	303	pc1280_49-93	ACTGGACATTCTGCAGAAGAAGTCAGACAAGTTTTCGGTATAGCG	74,3	45	0,612	0,05	0,998	1	0,976	0,838	5´preference
10	6	F11	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
11	1	C03	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
11	1	G03	**pc1281**	conserved hypothetical protein	**-**	222	pc1281_2-56	TGGCAAATGATCTAGACAACAGTGCTGACGATAACTATAAAGTCTACAAAAAAAG	73,2	55	0,948	1	0,894	1	0,995	0,743	random
11	1	K03	**pc1282**	conserved hypothetical protein	**-**	3249	pc1282_1612-1656	ATTGAGTCCTCCACACAACCTTTAGGCTTTTTCTCTTCACCTCAG	74,2	45	0,98	1	0,998	1	0,986	0,809	mid
11	1	O03	**pc1283**	unknown protein	**-**	282	pc1283_87-139	TCAAAAAGAAATGACTTTGTTGCACAATAGCTTTTACAGGAACTTATATTGTT	71,5	53	0,901	1	0,73	1	0,994	0,69	random
11	1	C07	**pc1284**	unknown protein	**-**	255	pc1284_45-92	AATCGCATCATCTGAGTATGTTTGTGGTCTACCTACCAAACCACTACA	74,2	48	0,977	1	0,994	1	0,917	0,888	mid
11	1	G07	**pc1285**	conserved hypothetical protein	**-**	678	pc1285_304-352	CTCTTAACAATTTGTGGAGAAGGGTTTCATGTTACCCGAGATTTTTTTG	74,3	49	0,963	1	0,994	1	0,964	0,666	mid
11	1	K07	**pc1286**	unknown protein	**-**	1059	pc1286_484-535	TCAATGGAATACATCTCACTTCTTATTTCTCGTTTACCTGACACTTTACCCG	74,4	52	0,973	1	0,981	1	0,954	0,823	mid
11	1	O07	**pc1287**	unknown protein	**-**	198	pc1287_50-98	GTTTTTCCATCTATCAATGTAAGTGTGGGCATAGGCAAGAAAAGTTCCT	74,3	49	0,974	1	0,997	1	0,96	0,781	random
11	1	C11	**pc1288**	conserved hypothetical protein	**-**	990	pc1288_560-606	TCGATCAACAGTCGTTAACCCTTCCTTTAATCGCTAGCCATTCTAAT	74,2	47	0,976	1	0,999	1	0,936	0,827	mid
11	1	G11	**pc1289**	conserved hypothetical protein	**-**	1443	pc1289_627-675	CACAATGGATGTCGAAGTACAAGGTTCAGATAATGATTTACATTCTGGC	74,3	49	0,971	1	0,993	1	0,904	0,838	mid
11	1	K11	**pc1290**	unknown protein	**-**	864	pc1290_368-418	ATAACAAACAGGTATTGGCCGTTGTTTTGGGTCTAGTTGTAGGAGGTATTT	74,2	51	0,977	1	0,998	1	0,935	0,842	mid
11	1	O11	**pc1291**	similar to serine proteinase	**htrA, degP**	1455	pc1291_708-753	AGGCGGTCCTTTGCTCACATTAAATGGAGAAATTGTAGGGATTAAT	74,2	46	0,976	1	0,994	1	0,979	0,784	mid
11	1	C15	**pc1292**	unknown protein	**-**	1635	pc1292_731-776	CTAACAGTCCATGGAGATGGGGTAGACAAATATTCACGAAAAGTGG	74,2	46	0,975	1	0,998	1	0,912	0,859	mid
11	1	G15	**pc1293**	unknown protein	**-**	228	pc1293_119-173	CACTTAAAAAGTTACTTTTGTGTATCTTTCGTCATTTAACATATGCAAGCCTTTT	71,8	55	0,886	1	0,753	0,954	0,867	0,71	random
11	1	K15	**pc1294**	conserved hypothetical protein	**-**	990	pc1294_512-558	TTCATGCATCTGCTGCTGTTCCCTTTGTATTTTCTCCTGTTTATCTA	74,2	47	0,978	1	0,996	1	0,984	0,797	mid
11	1	O15	**pc1295**	unknown protein	**-**	600	pc1295_190-240	AATACCCCATCTAAAGGACATTTGCATATTTTTACAAGTGCAACACAAACA	74,2	51	0,962	1	0,999	1	0,889	0,747	mid
11	1	C19	**pc1296**	hypothetical protein	**-**	1146	pc1296_579-628	CTTAATGATGGGTTTTGAAAGTTATCGTTCTTGGATCGATGTACGAAAAA	74,2	50	0,976	1	0,999	1	0,995	0,746	mid
11	1	G19	**pc1297**	strongly similar to succinate-CoA ligase (ADP-forming) alpha	**sucD**	906	pc1297_502-	CAATTAGGTTTGGGACAATCAACCTGTGTAGGAATAGGAGGGGAT	74,4	45	0,977	1	0,986	1	0,952	0,861	mid

				chain			546										
11	1	K19	**pc1298**	strongly similar to succinate-CoA ligase (ADP-forming) beta chain	**sucC**	1170	pc1298_591-635	AATTAACCCTCTTGTGGAAACAAAGGAAGGCCATTTATTAGCGCT	74,2	45	0,981	1	0,997	1	0,995	0,808	mid
11	1	O19	**pc1299**	strongly similar to signal recognition particle	**ftsY**	930	pc1299_466-519	GAGTTATGGGCTCATAAATTACACATAGAAATTGTCAAGGGTCATCCAAAAAGT	74,2	54	0,98	1	0,999	1	1	0,782	mid
11	1	C23	**pc1300**	unknown protein	**-**	516	pc1300_247-301	ACGCTCTACTTTGCTAATAATGCTAAAATTGCCGAGTTAATAGAAAGATGGATCA	74,2	55	0,974	1	0,991	1	0,988	0,752	mid
11	1	G23	**pc1301**	unknown protein	**-**	552	pc1301_269-313	ATCAAGACATGAAATGGACGCAGGAAACGTTTCGTATTATCTTCA	74,4	45	0,981	1	0,987	1	0,992	0,845	mid
11	1	K23	**pc1302**	similar to UDP-glucose 4-epimerase	**galE**	969	pc1302_478-531	GCTTATGGTCTTAAATATTCTTGTCTTCGCTATTTTAATGCAGCTGGAGGAGAT	74,3	54	0,974	1	0,994	1	0,992	0,748	mid
11	1	O23	**pc1303**	unknown protein	**-**	192	pc1303_2-56	TGGTCATTTTTTGGGAGGCAAAGAAAAGTAGATCTAGTTATTTTTGTAGTTTAGG	72,7	55	0,928	1	0,842	1	0,988	0,672	random
11	2	C03	**pc1304**	unknown protein	**-**	405	pc1304_174-218	CTACAGAAATGGGAGTCAAGAATGCCACTGCAGCTATGAGTGTAG	74,1	45	0,982	1	0,984	0,988	0,999	0,861	random
11	2	G03	**pc1305**	similar to tyrosine-specific transport protein	**tyrP**	1215	pc1305_583-627	TTTGCTTATCAAGGAATTATTCCAACGCTTGCGAGTTATTTGCAT	74,3	45	0,974	1	0,998	0,985	0,974	0,773	mid
11	2	K03	**pc1306**	strongly similar to glutamine-fructose-6-phosphate transaminase (isomerizing)	**glmS**	1824	pc1306_931-982	GCTTACCTAATTGAAGATAAGGCGCGGATTCCTGTACAAGTAGAGATTTCTT	74,2	52	0,978	1	0,999	1	0,982	0,792	mid
11	2	O03	**pc1307**	strongly similar to phosphoglucomutase	**pgm**	1464	pc1307_1020-1064	ATCTCAGGTGGGAGATCGCTACGTCATTCAAGATATGCTCAAATA	74,2	45	0,986	1	0,998	1	0,992	0,864	random
11	2	C07	**pc1308**	similar to Poly(A) polymerase	**pcnB**	1275	pc1308_636-687	AATTCTTCGTATGCTAGAATCAGGAGCTTCGGCTCCTTTTATTAAACTTTTG	74	52	0,969	1	0,98	0,993	0,998	0,726	mid
11	2	G07	**pc1309**	unknown protein	**-**	771	pc1309_360-406	TATTGCTGTTGCTGGGTTATCAAGAGGAGGATTTATCGCTACTCACT	74,2	47	0,98	1	0,998	1	0,973	0,828	mid
11	2	K07	**pc1310**	similar to dolichol-phosphate mannosyltransferase	**dpm1**	642	pc1310_241-285	AAAGAAATTAACACTTGTGACCTCGTCTGCGGGATTCGTCTTAAC	74,2	45	0,974	1	0,998	1	0,919	0,839	mid
11	2	O07	**pc1311**	conserved hypothetical protein	**-**	684	pc1311_410-457	TGGAGTATTCGTTGTGGTGGCATGGTTTGGGAACTATTTCTTATTTAT	74,3	48	0,967	1	0,997	1	0,933	0,743	mid
11	2	C11	**pc1312**	similar to lipid A-disaccharide synthase	**lpxB**	1128	pc1312_610-654	AAAAATCATCCTTCAATTCATTTCGCTATTTCCTGCTCAGACGAC	74,2	45	0,972	1	0,992	1	0,955	0,782	mid
11	2	G11	**pc1313**	conserved hypothetical protein	**-**	654	pc1313_286-330	ATTGTTCGCTCCTATAAAACAGGCAGAGTCATTCGAGTTCCTCAT	74,2	45	0,98	1	0,997	1	0,958	0,85	mid
11	2	K11	**pc1314**	similar to fatty acid/phospholipid synthesis protein PlsX	**plsX**	1020	pc1314_673-717	GGTGTTTTTGAGGGTTGTGTCGATGTACTTGTTACAGACGGATTT	74,3	45	0,965	1	0,998	1	0,838	0,85	mid
11	2	O11	**pc1315**	similar to 50S ribosomal protein L32	**rpmF**	222	pc1315_8-56	GAATAAGTTTAATTGATCAGGAGACTTTAACCATGGCAGTGCCACGTAA	74,2	49	0,981	1	0,999	1	0,994	0,804	random
11	2	C15	**pc1316**	hypothetical protein	**-**	477	pc1316_131-185	TAGATGGTGTTGCTTATAAGGCAGATGATGAACTGATATTAAATTGGAAAATTCG	74,3	55	0,975	1	0,99	1	0,996	0,764	random
11	2	G15	**pc1317**	similar to ribonuclease G (axial filament protein)	**cafA;rng**	1539	pc1317_752-796	CCACCTATCAAACTTGTAAACGGCTTTATAGTCGTTATGCCAGCG	74,3	45	0,981	1	0,991	0,993	0,981	0,849	mid
11	2	K15	**pc1318**	similar to glycerol-3-phosphate acyltransferase	**ats1**	999	pc1318_428-474	AAAAGTTAGCAACAGAGATGATCTTTATTGCGGGTCATCGCGTTATA	74,2	47	0,969	1	0,999	0,948	0,927	0,836	mid
11	2	O15	**pc1319**	conserved hypothetical protein	**-**	342	pc1319_60-109	AGAGTTTTCTAATCTCAATTTATGCTTGCCCGATCCCAACCTTTTTATTC	74,2	50	0,971	1	0,995	1	0,999	0,696	random
11	2	C19	**pc1320**	hypothetical protein	**-**	750	pc1320_325-370	CTTTTTGTTGTGCAATCCAATATGCATGATCCACAAGATTTGCTAT	74,2	46	0,969	1	0,998	0,984	0,949	0,764	mid
11	2	G19	**pc1321**	conserved hypothetical protein	**-**	819	pc1321_489-539	TTTAGTATTTGCCATCGATTCTATTCCTGCCATTCTAGGTATTACAACGGA	74,2	51	0,975	1	0,997	0,994	0,922	0,85	mid
11	2	K19	**pc1322**	unknown protein	**-**	333	pc1322_157-201	TTTGCTTCTAATGCATCCAATTATTCCGCTCCTATATGGGAACAA	74,2	45	0,98	1	0,999	1	0,99	0,799	mid
11	2	O19	**pc1323**	conserved hypothetical protein	**-**	879	pc1323_464-508	AGAAAGGAGAAATTTTGGCTTTTCAGCTAACTCCTGGAAATGTCG	74,1	45	0,594	0,04	0,989	1	0,977	0,715	mid
11	2	C23	**pc1324**	similar to prolyl-tRNA synthetase	**proS**	1524	pc1324_772-826	TTTAGTAATATGGAAGGGCAATTAGAATATGCTTATACGACATCTTGGGGAATGA	74,2	55	0,984	1	0,999	1	0,991	0,837	mid
11	2	G23	**pc1325**	similar to 4-amino-4-deoxychorismate lyase	**pabC**	843	pc1325_378-428	ATTTACTCCTTGTCGACTAACTTTATATCCCAGTCCCATCGTTAAACCGAC	74,2	51	0,982	1	0,998	1	0,955	0,875	mid
11	2	K23	**pc1326**	unknown protein	**-**	492	pc1326_89-135	AAAGGCACTATTGGGAAACGATAGAAATCATTGCTAGAGGAGCCATA	74,3	47	0,983	1	0,996	1	0,994	0,83	random
11	2	O23	**pc1327**	similar to para-aminobenzoate synthase component I	**pabB**	1305	pc1327_648-695	AATCAATCCCGCTCCCTTTTCCGCTTATTTGAAAGCAGATTATTATAC	74,2	48	0,976	1	0,999	1	0,994	0,752	mid
11	3	C03	**pc1328**	conserved hypothetical protein	**-**	738	pc1328_313-358	AAAAATCGAATTTCTTCTGACATGCGTATAGCGACAAATAAGCGTG	74,1	46	0,97	1	0,986	1	0,943	0,791	mid
11	3	G03	**pc1329**	conserved hypothetical protein	**-**	708	pc1329_415-465	AAACATCGACCTAATCGCATTACTTTTGGGTTATTTCACGATCCTTTAAAG	74,3	51	0,972	1	0,996	1	0,94	0,784	mid
11	3	K03	**pc1330**	conserved hypothetical protein	**-**	513	pc1330_23-69	CTACTGGGATTGAAGTGCGCTATACGGAATCTGGAGATGCTAAGTAC	74,2	47	0,988	1	0,997	1	0,989	0,893	random
11	3	O03	**pc1331**	strongly similar to peptide chain release factor RF-2	**prfB**	981	pc1331_507-551	TAATGCTAAGAGGCATACCAGTTTTGCATCAGTGGATGTTTCTCC	74,3	45	0,98	1	0,996	0,994	0,985	0,824	mid
11	3	C07	**pc1332**	conserved hypothetical protein	**-**	846	pc1332_381-425	TTCGCTATTTTCCTGGAATTGGTACGTTTTATCCAACGCAAAATT	74,4	45	0,968	1	0,985	1	0,957	0,756	mid
11	3	G07	**pc1333**	similar to ABC transporter ATP-binding protein	**-**	1824	pc1333_885-930	ATGGAACATTACTATCATGGCTTGGTTAGCTGGTTTAGAACTCCCG	74,2	46	0,981	1	0,997	0,992	0,972	0,848	mid
11	3	K07	**pc1334**	similar to thioredoxin peroxidase	**tpx**	288	pc1334_7-51	TTTATCCCCCTAATTGAAGTCCTGCTCTGCAACAATCAATTAACG	74,3	45	0,952	1	0,997	0,917	0,862	0,791	mid
11	3	O07	**pc1335**	hypothetical protein	**-**	528	pc1335_262-313	CAAATGCATGAATGTCTTTATCATCATCACCATGCTCTAAGTTTAGAAGCTT	74,1	52	0,972	1	0,988	1	0,997	0,731	mid
11	3	C11	**pc1336**	similar to aminoglycoside N6'-acetyltransferase	**aac**	501	pc1336_149-203	AACAAATTCCAATAGGTTATATCCAAAAGTATTCTGTTAGCGATTATCCCTGGGA	74,2	55	0,971	1	0,996	1	0,926	0,794	5´preference
11	3	G11	**pc1337**	conserved hypothetical protein	**-**	606	pc1337_129-173	TAAAATAGCCGAAGAAATGGGAGCGAAGGTTCAAATCATTGATCT	74,5	45	0,969	1	0,97	1	0,99	0,76	random
11	3	K11	**pc1338**	strongly similar to 3-methyladenine-DNA glycosylase I	**tag**	567	pc1338_338-386	GCTTTAATACCTATATTTGGCAATTTGTAAACGGGAAACCCATCCAGAA	74,3	49	0,973	1	0,997	1	0,947	0,786	mid
11	3	O11	**pc1339**	unknown protein	**-**	192	pc1339_67-120	GAGGAAACGATAACTACAAACGATATGAATGCTACATTTATCAGGTCTTGCATC	74,2	54	0,973	1	0,998	0,996	0,918	0,837	random

11	3	C15	**pc1340**	conserved hypothetical protein	**-**	222	pc1340_805-849	AAAGTTAACCAAAGATATGGGTATCCAAAAAGCGGTATGACAAATTTTTTTATGG	74,1	45	0,732	1	0,985	1	-0,844	0,734	mid
11	3	G15	**pc1341**	unknown protein	**-**	5295	pc1341_100-154	GATTCTGGGACCATCGCGCTTGGCTTTTCTCGCGTTGGAATAAAC	74	55	0,957	1	0,979	1	0,988	0,609	mid
11	3	K15	**pc1342**	unknown protein	**-**	204	pc1342_71-122	TAGAATCCGTTGTATCCACTACTGTTTCGGACATAAAGTGCATTTTTTTCTTC	74,2	52	0,967	1	0,999	0,955	0,968	0,748	mid
11	3	O15	**pc1343**	similar to ADP/ATP translocase	**ntt_5**	1470	pc1343_774-828	TATGGATGTTTTAAGAACAGGTCCCTTACTTTGTATAGCTGTATTGGTAGTGGGG	74,4	55	0,977	1	0,988	1	0,962	0,839	mid
11	3	C19	**pc1344**	similar to arsenate reductase	**arsC;arsG**	348	pc1344_10-57	TATGTTTATTCTAAATGTTCGACTTGTCAACAAGCCATCCGCTTTTTG	74,2	48	0,97	1	0,999	1	0,996	0,682	5´preference
11	3	G19	**pc1345**	unknown protein	**-**	672	pc1345_334-388	ATTTTTACTGTATTAGCTATGCTAAAACCCTTGATTCCGTCGTATTGGTTTTGCT	74,2	55	0,979	1	0,997	0,985	0,997	0,807	mid
11	3	K19	**pc1346**	unknown protein	**-**	2448	pc1346_1249-1293	TTAAGTGGATGGGTTGAAAGACAAGGTCCTGAAGAGTGTAAAGCA	74,3	45	0,982	1	0,995	1	0,976	0,851	mid
11	3	O19	**pc1347**	conserved hypothetical protein	**-**	1368	pc1347_737-781	TAGGCAAGTTCTGGGATTCCCTCGATTCTATACAAACTGATGGAC	74,3	45	0,98	1	0,995	1	0,948	0,865	mid
11	3	C23	**pc1348**	strongly similar to ribonucleoside-diphosphate reductase large chain	**nrdA**	2322	pc1348_1280-1328	ATTTGTGTACAGAAATTATAGAGTACACTTCACCCCATGAAGCGGCTGT	74,3	49	0,97	1	0,996	1	0,882	0,847	mid
11	3	G23	**pc1349**	strongly similar to ribonucleoside-diphosphate reductase small chain	**nrdB**	972	pc1349_532-580	TTTTGGCTTAAAAAACGAGGGTTAATGCCTGGATTAAGTTTTGCTAATG	74,3	49	0,964	1	0,993	0,992	0,955	0,696	mid
11	3	K23	**pc1350**	unknown protein	**-**	186	pc1350_30-74	AAAAAGCACGCAGCGCATTTTAGGTTTTTTCAACCTTTTTCATTT	74,9	45	0,936	1	0,932	0,975	0,936	0,614	mid
11	3	O23	**pc1351**	unknown protein	**-**	249	pc1351_1-45	GTGTTGGCTAGGCAATTAGATCCTCGAGACAAAAAAACCGCTGAG	76,4	45	0,619	0,232	0,78	1	0,997	0,734	random
11	4	C03	**pc1352**	unknown protein	**-**	228	pc1352_74-119	TAAATGTACACGTCACTTGTCATGAGAACGATGAGCTAGAAGTGGC	74,2	46	0,644	0,14	0,994	0,976	0,968	0,87	random
11	4	G03	**pc1353**	conserved hypothetical protein (possible outer surface protein wsp)	**-**	438	pc1353_4-48	GAGTACTATGTTGGGGCAGCAATTGGCTATAAACTGTCCGATTTC	74,1	45	0,984	1	0,991	1	0,992	0,861	random
11	4	K03	**pc1354**	unknown protein	**-**	1410	pc1354_1233-1287	GGGAGCTTTTTGCTCTATTAAACAAAAAAAGAAATTGGAAGATAGAGAAGCAGAA	74,1	55	0,718	0,636	0,986	0,807	0,473	0,528	mid
11	4	O03	**pc1355**	unknown protein	**-**	2604	pc1355_1266-1310	TTTATTCCAATATATAGAGGAGCGACAAAGGCAGCCGCAAGAAAT	74,3	45	0,624	0,1	0,991	1	0,963	0,795	mid
11	4	C07	**pc1356**	unknown protein	**-**	186	pc1356_10-62	TTTGCAAATTTAAGCAGGTCAAAAAAAACGGCTATTTATTTCTTTTACCTAGA	72,7	53	0,608	0,256	0,841	0,954	0,916	0,517	mid
11	4	G07	**pc1357**	unknown protein	**-**	195	pc1357_96-142	TTGTCTGACCAGATTACTTGCTAACTGGTTGATGTTGACTCCAAAGA	74,3	47	0,615	0,05	0,997	1	0,997	0,844	mid
11	4	K07	**pc1358**	unknown protein	**-**	435	pc1358_12-56	AAATCCAATAGAACCCTTGCTTTCGCAAATTACAGAGATTCTGCA	74,2	45	0,977	1	0,999	1	0,993	0,759	random
11	4	O07	**pc1359**	hypothetical protein	**-**	2166	pc1359_1080-1125	TGTTGGATTGGATCTTTCCTATCAAGAAGGAGAGCATTATGCATCT	74	46	0,972	1	0,977	0,966	0,996	0,817	mid
11	4	C11	**pc1360**	hypothetical protein	**-**	2832	pc1360_1328-1374	ACTCTGATATACAAATGATTAACGCGACTGAAGGCGGCTTAGGTTTT	74,2	47	0,968	1	0,998	0,972	0,911	0,822	mid
11	4	G11	**pc1361**	hypothetical protein	**-**	1896	pc1361_932-978	AAGCTCTTGAGGTAATTTCTGGCCCTAAACTTTATCTGTCTGGGACA	74,2	47	0,978	1	0,995	1	0,983	0,801	mid
11	4	K11	**pc1362**	strongly similar to acetate kinase	**ackA**	1188	pc1362_623-667	ATTGTCATTTAGGAAATGGAGCATCTCTTTGTGCGATACGAGATG	74,3	45	0,978	1	0,992	1	0,972	0,825	mid
11	4	O11	**pc1363**	hypothetical protein	**-**	3366	pc1363_1622-1672	TAGCTCTTAATTCTGTTCTGACAACTCCAAGTAATTCCCCAATTGATGTTG	74,2	51	0,975	1	0,999	1	0,938	0,812	mid
11	4	C15	**pc1364**	strongly similar to two-component response regulator	**-**	1326	pc1364_657-701	TTTTACAGGAGCAGCTAATAAAAGGCTGGGTCGCTTTGAGTTAGC	74,4	45	0,974	1	0,981	1	0,993	0,778	mid
11	4	G15	**pc1365**	similar to two-component sensor histidine kinase	**-**	1233	pc1365_675-719	TCGACCCGAACTTCAACAAATGGCTTATCATATTATCGAAGGAAC	74,3	45	0,974	1	0,994	1	0,943	0,814	mid
11	4	K15	**pc1366**	unknown protein	**-**	219	pc1366_78-130	ATTGCCTGCAAAGGTCAGTTCTATCCGATTATTTTTTTACGAACACTTTTTTAA	74,2	53	0,962	1	0,996	1	0,967	0,636	mid
11	4	O15	**pc1367**	strongly similar to 30S ribosomal protein S4	**rpsD**	621	pc1367_232-279	CGCTTAGAAGGTAATACAGCTAGTCATTTTGCCGAAATGCTAGAATGC	74,1	48	0,972	1	0,985	1	0,92	0,849	mid
11	4	C19	**pc1368**	conserved hypothetical protein	**-**	249	pc1368_40-88	CAATATACCTTAAGTCCCTTACTCGGACTAACTTGCCGCTTTTATCCCA	74,3	49	0,987	1	0,995	1	0,995	0,882	random
11	4	G19	**pc1369**	similar to glycosyltransferase	**-**	1131	pc1369_530-574	AACATTTTGTTCATGCGGAAGATTATGAGCTCATGATTCGGTTAG	74	45	0,971	1	0,98	1	0,963	0,793	mid
11	4	K19	**pc1370**	hypothetical protein	**-**	1449	pc1370_765-812	TATCCAATTAGGATCTTCTTCAGCTGCCTCATTTCTTGTCAAAACAGA	74,3	48	0,972	1	0,998	1	0,96	0,755	mid
11	4	O19	**pc1371**	strongly similar to Phosphoenolpyruvate carboxykinase [GTP]	**pckG**	1776	pc1371_868-912	GAAGATGGGCAGTTATACGCGATTAATCCAGAAGCTGGTTTTTTT	74,1	45	0,972	1	0,988	1	0,979	0,761	mid
11	4	C23	**pc1372**	strongly similar to rod shape-determining protein mreB	**mreB;envB**	1092	pc1372_774-823	TCAAGTTGCAGGACTACCTGTTACTAAACGCATTAACTCTGTTGAGATCC	74,2	50	0,959	1	0,998	1	0,773	0,879	mid
11	4	G23	**pc1373**	unknown protein	**-**	186	pc1373_78-132	AAAAATACTACAAATTAGAGGCATAAGGGGGAACATCATGGATAAACAAATGCTT	74,2	55	0,976	1	0,995	1	0,984	0,778	mid
11	4	K23	**pc1374**	conserved hypothetical protein	**-**	3486	pc1374_1673-1717	AATCGAATCGAATTGACATGTATGAAGTCGAGGTCAAAGTTGATG	73,9	45	0,968	1	0,97	0,999	0,929	0,832	mid
11	4	O23	**pc1375**	similar to trigger factor	**tig**	1308	pc1375_604-651	GACAATCAACGCACTCAAGTTAATCAATCTGGCTTACCTTCTTGGATA	74,3	48	0,975	1	0,995	1	0,949	0,812	mid
11	5	C03	**pc1376**	strongly similar to ATP-dependent Clp protease proteolytic subunit P	**clpP;lopP**	624	pc1376_224-275	ACTCTTTAGGTGGATATATCACTTCAGGCCTTGCGATCTATGATACTATGCA	74,3	52	0,976	1	0,997	1	0,911	0,877	mid
11	5	G03	**pc1377**	strongly similar to ATP-dependent Clp protease ATP-binding subunit X	**clpX**	1242	pc1377_649-699	GTCCCTCCTAAAGGAGGTCGTAAGCACCCAAATCAAGAGTATATTAAAGTG	74,2	51	0,978	1	0,991	1	0,973	0,826	mid
11	5	K03	**pc1378**	hypothetical protein	**-**	750	pc1378_428-474	AGGAGCACGTTCATTTAGGAACTAGTGTAGGCCTACGCTATTTGGAC	74,3	47	0,98	1	0,995	1	0,948	0,873	mid
11	5	O03	**pc1379**	hypothetical protein	**-**	924	pc1379_415-461	AGTTATCAATTTGATCCTTCCTGGCTTTATTTACCCTTTCGCCCTTT	74,3	47	0,97	1	0,998	1	0,952	0,739	mid
11	5	C07	**pc1380**	unknown protein	**-**	2610	pc1380_2021-2069	AAGCTGATGCAATTGCAAATGAAGTTGTTTCAAGGACACTAAGTGATAG	74,3	49	0,978	1	0,998	1	0,984	0,786	random
11	5	G07	**pc1381**	unknown protein	**-**	1245	pc1381_503-555	TATTAGCCTCGCCAGGACGTTCTCTGCAAAGTATGCTTGAATTAGAGTATATA	74,3	53	0,971	1	0,991	1	0,879	0,882	mid
11	5	K07	**pc1382**	unknown protein	**-**	1449	pc1382_749-795	AAACCACTTATAATAATGACGTAGCCACTGCCAAACAAAATGCTGCT	74,1	47	0,975	1	0,986	1	0,977	0,796	mid
11	5	O07	**pc1383**	unknown protein	**-**	1308	pc1383_631-676	TCAAATATTAGTTTACTCAATACTCCCGATTCGAGCACTCCTGCCA	74,2	46	0,981	1	0,994	1	0,976	0,839	mid

11	5	C11	**pc1384**	similar to low calcium response protein H	**lcrH;sycD**	573	pc1384_320-373	ATGCCATACAAACTTATACAATGTGTAGTGCGATCGATCCTAATACACCTATCC	74,2	54	0,984	1	0,997	0,996	0,968	0,884	mid
11	5	G11	**pc1385**	unknown protein	**-**	2250	pc1385_1170-1223	TATTGGGCCTATTATTGCTGCTTTATCAACGATTATAGGAACTCTTATTGCCAT	74,3	54	0,972	1	0,992	1	0,956	0,78	mid
11	5	K11	**pc1386**	similar to low calcium response protein H	**lcrH;sycD**	594	pc1386_285-329	CCACCAATTTAAACAAGAATACTCGGAAGCAGCAGCCAATTACAT	74,2	45	0,973	1	0,999	1	0,987	0,725	mid
11	5	O11	**pc1387**	unknown protein	**-**	675	pc1387_288-332	CTATTACCAAAGTCGATTCGAAGGCTTACCCTTTGAGCTACAGGC	74,2	45	0,983	1	0,999	1	0,949	0,888	mid
11	5	C15	**pc1388**	unknown protein	**-**	951	pc1388_431-475	CTAAGGAGGGGGGCGAACTTTTAAGGGAACTGGGAATTACTTTTA	74,3	45	0,973	1	0,996	1	0,954	0,784	mid
11	5	G15	**pc1389**	unknown protein	**-**	1083	pc1389_525-575	AACAGTCGATAACAATATTAGTCATGAACGAAGCTTAATGAAATCCGCAGA	74,2	51	0,981	1	0,998	0,996	0,982	0,826	mid
11	5	K15	**pc1390**	hypothetical protein	**-**	387	pc1390_80-129	TTACTATCCCTTTTGCAGATGATATTCAGGTTGATATGACGCAGTTTCAC	74,3	50	0,983	1	0,995	1	0,998	0,828	random
11	5	O15	**pc1391**	conserved hypothetical protein	**-**	1830	pc1391_936-987	TGGGCCTTATGTTTTGCTAGCTATTATATCAGGTCTCTTCTTATTGACAGGG	74,1	52	0,979	1	0,99	1	0,98	0,826	mid
11	5	C19	**pc1392**	conserved hypothetical protein	**-**	243	pc1392_1-55	ATGTTTGGTTTAGAAGATCAAAAAAAGAAAAAAACTTCAGAAGAATTTGTTTTTG	71,8	55	0,633	0,426	0,761	0,825	0,997	0,362	mid
11	5	G19	**pc1393**	conserved hypothetical protein	**-**	465	pc1393_200-249	CAACGCGTATCTTTGAAGGCATTATAGCTGCAGAACCTGATAATTATCTC	74,3	50	0,978	1	0,992	1	0,966	0,833	mid
11	5	K19	**pc1394**	similar to UDPgalactose-glucose galactosyltransferase	**-**	684	pc1394_262-309	TCAGACTATTCTTATCCAATTGTTCCTACTCATCTTGCAGCTGACGTG	74,3	48	0,973	1	0,996	0,99	0,919	0,845	mid
11	5	O19	**pc1395**	unknown protein	**-**	279	pc1395_1-45	ATGGCGACTGGTGGAGGAAGTAGTGGTGATTTTCAAGGTAACTAC	74,4	45	0,983	1	0,986	1	0,999	0,857	random
11	5	C23	**pc1396**	unknown protein	**-**	852	pc1396_423-476	AAATCAGGCTCAATCTGTTATTGCTCAAATAGACCAAGTCAAAACACAACTTAG	74,3	54	0,982	1	0,997	1	0,996	0,812	mid
11	5	G23	**pc1397**	strongly similar to type III secretion pathway protein sctN	**sctN;yscN**	1365	pc1397_672-716	GGATTTAGGTCCCGAAGGACTAAAAAGATCTGTCCTTGTGGTCTC	74,2	45	0,975	1	0,991	0,944	0,988	0,85	mid
11	5	K23	**pc1398**	conserved hypothetical protein	**-**	498	pc1398_182-235	TAAGAGAGCAATTAGATCAAGGAACGACTAGCCCAAAAGTTATTCAAATGAAAG	74	54	0,961	1	0,974	0,997	0,932	0,745	mid
11	5	O23	**pc1399**	unknown protein	**-**	993	pc1399_498-546	ATTCGAAGCACGAGAAGAACAGGTAGATTTATCAGCCATTAATTCACAA	74,2	49	0,981	1	0,998	1	1	0,802	mid
11	6	C03	**pc1400**	similar to flagellar motor switch protein (= type III secretion translocase SctQ)	**sctQ**	1338	pc1400_700-744	ATTGTTTTGGATAGCTGCTCATTAGACCCTCAAGAATTGACAGGC	74,3	45	0,976	1	0,989	1	0,97	0,808	mid
11	6	G03	**pc1401**	similar to serine/threonine protein kinase	**pkn**	1590	pc1401_779-833	ATCAAGATATCGTTGATTTTATGACAGATGTCTCTGCTTACCTTTATTCTCCAGC	74,2	55	0,978	1	0,996	1	0,983	0,797	mid
11	6	K03	**pc1402**	conserved hypothetical protein	**-**	477	pc1402_169-214	GTATTTTGGATATTAAGAACGAAAGCTCCATGGAGGGATTTGCCTC	74,3	46	0,6	0,04	0,997	1	0,929	0,82	mid
11	6	O03	**pc1403**	unknown protein	**-**	402	pc1403_213-264	AAATTATCTTCTCCATCTTAAGCCTGTTCAAGGAGATTGCATTGAAGAAAAG	74	52	0,961	1	0,976	0,932	0,989	0,749	mid
11	6	C07	**pc1404**	unknown protein	**-**	873	pc1404_441-491	AACTTCAATTCCAGAGATGCAAATTAATCCATCAACTCTACAAACTCCCTC	74,3	51	0,602	0,04	0,991	1	0,997	0,771	mid
11	6	G07	**pc1405**	conserved hypothetical protein	**-**	321	pc1405_16-70	ATCGTTGACACTGTACGTTTTCATGCTATTAAGTTAGGCTTAATAATCGAAAGGC	74,3	55	0,963	1	0,99	1	0,854	0,835	mid
11	6	K07	**pc1406**	unknown protein	**-**	297	pc1406_92-141	TTGAGCGTTTTGGTATCGATCTTACAGATAGCCAAGCTAGAATTATGGAA	74,3	50	0,981	1	0,994	0,994	0,996	0,822	random
11	6	O07	**pc1407**	unknown protein	**-**	348	pc1407_43-89	TATTATGACAGATTGGTGTTAGATGCTAATGGCAACCCTGAAAAGGG	74,4	47	0,965	1	0,979	1	0,868	0,859	mid
11	6	C11	**pc1408**	unknown protein	**-**	552	pc1408_43-87	ATCAATTGCAATTGGGAAGATATTGCCATCGCGATAAAAATGCCT	76,9	45	0,872	1	0,732	0,966	0,766	0,738	mid
11	6	G11	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
12	1	D03	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
12	1	H03	**pc1409**	unknown protein	**-**	261	pc1409_151-195	TCGAATACTGAGCAGGCCTTTGGTATTCAAAATTTTGACCAGAAC	74,5	45	0,792	0,58	0,971	0,933	0,981	0,72	mid
12	1	L03	**pc1410**	conserved hypothetical protein	**-**	1119	pc1410_547-591	AACTTCAAAACTACCTTACCAGCTCCGCAATCAGATTTAGCCCAG	74,5	45	0,975	1	0,969	1	0,986	0,83	mid
12	1	P03	**pc1411**	unknown protein	**-**	201	pc1411_31-76	TTCGATGTTCCAGCTTTGGCAACAGCATTAGGTATTAAAGAGAAGA	74,2	46	0,979	1	0,998	0,999	0,979	0,808	random
12	1	D07	**pc1412**	unknown protein	**-**	204	pc1412_5-50	GCACAGAAAGGCAATTGAGTCTTTGGGATGTAGGTACTCCTGTAGA	74,5	46	0,61	0,07	0,975	1	0,991	0,778	random
12	1	H07	**pc1413**	unknown protein	**-**	300	pc1413_123-170	TAATTTGCGTCACCCTTCGTTAAATACTCACAAATTTGGGGCTATTTT	74,3	48	0,607	0,05	0,989	1	0,988	0,793	random
12	1	L07	**pc1414**	unknown protein	**-**	315	pc1414_176-229	ACCCAATTTTTACCCAAAGGTCTTGAAATTAGTTCATTTCGAGCTTATCAAG	74,2	54	0,603	0,04	0,999	1	0,952	0,82	random
12	1	P07	**pc1415**	unknown protein	**-**	1497	pc1415_738-782	TAAAGATTGGATCGGAAAATCGAATAAGGGTGAAGAATGGCTAGC	74,2	45	0,979	1	0,994	1	0,988	0,803	mid
12	1	D11	**pc1416**	unknown protein	**-**	186	pc1416_68-112	TAAAAGTTCGCGCTCAGACATACAGCATTAAAAAATGCAACAAGC	74,4	45	0,953	1	0,988	1	0,898	0,666	random
12	1	H11	**pc1417**	unknown protein	**-**	1473	pc1417_789-836	CTTCTTTGAAATCTTAAATGAACAGGATGATATTCAGCCTTTGGACGG	74,2	48	0,971	1	0,995	1	0,949	0,771	mid
12	1	L11	**pc1418**	unknown protein	**-**	1104	pc1418_486-530	ATCCTTTGCTACGCGAGCAGATATCTCTTCTTCTGAAACAAGTCC	74,2	45	0,973	1	0,997	1	0,933	0,808	mid
12	1	P11	**pc1419**	hypothetical protein	**-**	828	pc1419_427-479	TTGAAAGTAACAGTCTTAGCTTCTCAAGATGGGTGCCCTTTTAGAGTTATCCT	74,2	53	0,982	1	0,999	1	0,988	0,822	mid
12	1	D15	**pc1420**	unknown protein	**-**	405	pc1420_255-303	CACTCGCTACCTTCATCTTCAACTTGAAACAGACCTTTTTGAAGAAATC	74,2	49	0,963	1	0,994	1	0,949	0,678	mid
12	1	H15	**pc1421**	unknown protein	**-**	318	pc1421_15-63	ATTATTGACCTATGCCTGTTTAGGAATTGCCTTAGGAATGATCATCCCT	74,2	49	0,983	1	0,999	0,999	0,998	0,825	random
12	1	L15	**pc1422**	unknown protein	**-**	306	pc1422_103-147	TTTGTTGGCATTTTCCTTCGAAGCTTAGTGTTATTAGGATTGGCA	74,4	45	0,972	1	0,982	0,98	0,996	0,779	random
12	1	P15	**pc1423**	similar to F pilus assembly protein traE	**traE**	570	pc1423_57-105	TTTAGTGGGATTGTCGTTAACCTTACTGATGGGAGTGATCTTAGCTGTC	74,2	49	0,987	1	0,997	1	0,988	0,888	random
12	1	D19	**pc1424**	unknown protein	**-**	693	pc1424_298-343	ATTTGTTTTATAGAGCGTCAGCCTGAAGTTGTTGTCTTGCAGGAAC	74,3	46	0,98	1	0,996	1	0,994	0,803	random
12	1	H19	**pc1425**	similar to F pilus assembly protein traB	**traB**	1227	pc1425_611-657	CTAGTGTGGATGCTGTTTGTAGACTAGACGCTCAAAGCGATCCTATC	74,2	47	0,987	1	0,995	1	0,996	0,882	mid
12	1	L19	**pc1426**	conserved hypothetical protein	**-**	495	pc1426_54-99	TAAAGGCCACCATACATTATTGGGAGTAAGCGTTCAAATAGCTGCT	74,2	46	0,608	0,04	0,994	1	0,992	0,833	random
12	1	P19	**pc1427**	conserved hypothetical protein	**-**	441	pc1427_27-80	CATCGTGAAGACAGTGAATCTGTCAGAGCTAGCAACAGTTTTATATAGTAAGGC	74	54	0,974	1	0,975	1	0,987	0,805	5´preference
12	1	D23	**pc1428**	unknown protein	**-**	474	pc1428_181-	AGGACATTGCTAGAAGCATTATTTGACTCTCTTCAGGTTCAAGATGGTC	74,1	49	0,968	1	0,988	1	0,91	0,807	5´preference

						229											
12	1	H23	**pc1429**	unknown protein	**-**	375	pc1429_119-166	GAATTCCTTGTACATCTGTGACAGCTATCGAAAGCCTAATCGTTGAAA	74,3	48	0,614	0,05	0,991	1	0,999	0,855	random
12	1	L23	**pc1430**	similar to inner-membrane protein traC	**traC**	2487	pc1430_1244-1288	GAACCACTCTCAATCGAGAGTGTGGTAACTACGTTCCTTTGCAAG	74,5	45	0,98	1	0,969	1	1	0,864	mid
12	1	P23	**pc1431**	similar to F pilus assembly protein traF	**traF**	483	pc1431_26-70	AAACTTTATGCATTTCTTTGCTCATAGGGATCAACGCGTATGGTC	74,3	45	0,98	1	0,992	1	0,988	0,817	5´preference
12	2	D03	**pc1432**	similar to F pilus assembly protein traW	**traW**	633	pc1432_322-366	AAAAAAGGAACGCGGATCAATCCTCTGTCTTTAGTAATGCTGGAT	74,2	45	0,98	1	0,999	1	0,996	0,789	mid
12	2	H03	**pc1433**	similar to F pilus assembly protein trbC	**trbC**	597	pc1433_288-336	CCAAGAGTTAGAGAAACTAGGAGGAATTTTTGTGTTAAGAGGGCTTCCG	74,2	49	0,976	1	0,996	1	0,989	0,762	mid
12	2	L03	**pc1434**	similar to F pilus assembly protein traU	**traU**	936	pc1434_446-490	ATCCAGAGGCGGCCCTATTTAACTCTCCTTTAGCACAAGTTTCTT	74,3	45	0,979	1	0,997	1	0,977	0,811	mid
12	2	P03	**pc1435**	unknown protein	**-**	768	pc1435_386-430	CTAATCAAACACCCGAACTTCCAGCTGAAAAGGACAAAGAAGAAG	74,1	45	0,971	1	0,988	1	0,999	0,714	mid
12	2	D07	**pc1436**	unknown protein	**-**	186	pc1436_22-67	TTGATGGACAGTCTGTTAATCGTCCCTGTTGGAAAGAGAAAATTTC	74,2	46	0,965	1	0,998	1	0,975	0,657	random
12	2	H07	**pc1437**	similar to conjugative transfer protein traN precursor	**traN**	555	pc1437_280-327	GATGAGCATGTCTTTTGCTGTTTTCCCTCTAAATTATCTCGTCTTGTG	74,2	48	0,978	1	0,996	1	0,998	0,767	mid
12	2	L07	**pc1438**	similar to F pilus assembly protein traF	**traF**	792	pc1438_346-390	AATTTATTGACGTACCCTCAATTGGATTCTCGTTTAACGGCAGGA	74,8	45	0,962	1	0,94	1	0,949	0,825	mid
12	2	P07	**pc1439**	similar to F pilus assembly protein traH	**traH**	1359	pc1439_715-762	ATCATGAGTTTGACAGGAACCTTGATCATTCGAAGAGATAAATCCCTT	74,2	48	0,978	1	0,996	1	0,966	0,816	mid
12	2	D11	**pc1440**	similar to conjugative transfer protein traG	**traG**	2784	pc1440_1382-1427	ACTCTTATGACAATATCAGCATGGGCCAAACCTCCTATGGGAATAC	74,2	46	0,986	1	0,998	1	0,989	0,866	mid
12	2	H11	**pc1441**	similar to conjugative transfer protein traD	**traD**	1671	pc1441_796-840	CCTCAAAGTCTTTCCGATAGTGATAATTATTGGCGAACTTCAGCG	74,2	45	0,98	1	0,997	1	0,959	0,844	mid
12	2	L11	**pc1442**	conserved hypothetical protein	**-**	354	pc1442_2-55	TGGAACGAACAATTATTCAGTTATCGCCTTTTTCTCGCTATTTAGATGAATTAA	74,1	54	0,945	1	0,986	1	0,824	0,691	mid
12	2	P11	**pc1443**	conserved hypothetical protein	**-**	357	pc1443_85-138	AAAAAAGTTAGAATTGATACTGGAGAAATTCCACAGCAGCCAAAAGAGTATCAA	74,2	54	0,97	1	0,999	1	0,958	0,729	5´preference
12	2	D15	**pc1444**	unknown protein	**-**	264	pc1444_53-99	AGATAACCTATCGTGAATTTGCTGATAAGCTTGGCATTCATTTGCAT	74,3	47	0,975	1	0,997	1	0,974	0,774	5´preference
12	2	H15	**pc1445**	unknown protein	**-**	282	pc1445_20-64	AGGAAAAGAAAGCCAAAAATCAGCCAACAAATACGGAAGAAAGTG	74,3	45	0,955	1	0,994	1	0,878	0,701	mid
12	2	L15	**pc1446**	conserved hypothetical protein	**-**	681	pc1446_274-328	TCATTTATGGGTAGGCAGTACCCCATTGTAGTAGAAGGAGATACTTCATACATTG	74,2	55	0,978	1	0,994	1	0,932	0,871	mid
12	2	P15	**pc1447**	unknown protein	**-**	333	pc1447_93-142	AATTTCTGTGGTTGATGGACATAAAGTGTATTTAAAGCCAGGCTCTGTTC	74,2	50	0,982	1	0,999	1	0,999	0,809	random
12	2	D19	**pc1448**	unknown protein	**-**	774	pc1448_465-518	TAAAGACAGAGACTACATGATTCGTTATAACATAACTTTGCTGGGCATTTTGCT	74,2	54	0,974	1	0,995	1	0,923	0,841	mid
12	2	H19	**pc1449**	hypothetical protein	**-**	2094	pc1449_1039-1087	CTTGAAACAGAGAAAAACCTTGTTAATCACCCAAATCTAAGACGTGGTG	74,2	49	0,98	1	0,999	1	0,991	0,799	mid
12	2	L19	**pc1450**	unknown protein	**-**	195	pc1450_77-130	TATTGATCAGATATCTCCATACTAAACCTGCCCCTTTTCAAAGTCTTCAAACAT	74,2	54	0,974	1	0,996	1	0,978	0,762	mid
12	2	P19	**pc1451**	hypothetical protein	**-**	336	pc1451_2-52	TGTCTACGTTTGAAGTTATTTCCGTTCTGCTATCCTCTGGTGTTTTCATAG	74,2	51	0,985	1	0,998	1	0,997	0,85	random
12	2	D23	**pc1452**	unknown protein	**-**	1035	pc1452_420-467	TTTTTGGGAAAAATGGAAGGTATGGAAAAAATACGAACATCTGTTTCC	74,2	48	0,955	1	0,997	1	0,901	0,655	mid
12	2	H23	**pc1453**	conserved hypothetical protein	**-**	324	pc1453_139-188	ATTTCTATTGATGGATACTTGGATTGGTGTAAAGAGCTAGGCCAAGAACC	74,1	50	0,976	1	0,985	1	0,976	0,808	mid
12	2	L23	**pc1454**	unknown protein	**-**	192	pc1454_1-47	ATGAAAACCCAAGTCAACGCTATAGCCAATCGCTCTAGAGTTTTTCT	74	47	0,616	0,119	0,979	0,955	0,904	0,808	mid
12	2	P23	**pc1455**	conserved hypothetical protein	**-**	5601	pc1455_4875-4921	GTCACTCTACCTTGATGATAGCCAAATCAGTGATAAGGGAGCACAAG	74,1	47	0,655	0,171	0,989	0,969	0,977	0,869	random
12	3	D03	**pc1456**	strongly similar to doc (death on cure) protein of bacteriophage P1	**doc**	378	pc1456_40-93	GATCATCTCGTTTCTGAATACGGAGGTCTACATGGTATTAGAGATATGGGACTT	74,3	54	0,986	1	0,991	0,998	0,997	0,882	random
12	3	H03	**pc1457**	conserved hypothetical protein	**-**	231	pc1457_121-174	ACAGGTGTTACTATTCAATCGGTAAAACCAGTAAACAGCAAATTTGAAGAAGCT	74,1	54	0,972	1	0,988	1	0,996	0,736	mid
12	3	L03	**pc1458**	unknown protein	**-**	186	pc1458_96-142	TGGTGTTTACGCCAAGTCTTATGCCTTAAGATTTAAAAGCGGAGATC	74,4	47	0,851	0,689	0,988	0,969	0,998	0,77	mid
12	3	P03	**pc1459**	unknown protein	**-**	726	pc1459_58-102	GGGGCTATTCTGGGTTCTACGTTAGCAATGCCTTGTTATGCTTAT	74,1	45	0,981	1	0,984	1	0,981	0,861	random
12	3	D07	**pc1460**	unknown protein	**-**	201	pc1460_34-82	TATCATGAGTTAGGCCATGCTCTCACAAATATATTAATTGATAGCGCCG	74,4	49	0,976	1	0,985	1	0,978	0,815	random
12	3	H07	**pc1461**	conserved hypothetical protein	**-**	321	pc1461_84-128	ATCAGAAATAATTGAAATACCCGATGCTCCAGCCGATTACAAAGC	74,6	45	0,611	0,08	0,96	1	0,999	0,775	mid
12	3	L07	**pc1462**	conserved hypothetical protein	**-**	2613	pc1462_2336-2382	CGGATAAGGGGTTGGCATATTTAACCTCCTTCGCAGGTTTAAAGTAT	74,7	47	0,638	0,53	0,951	0,95	-0,028	0,714	mid
12	3	P07	**pc1463**	unknown protein	**-**	189	pc1463_91-145	GTGTTGAGCTATAATGTCGAAGTGTTTAAACATCCACATAATATTCTCATACGCA	73,8	55	0,572	0,04	0,955	0,79	0,995	0,844	mid
12	3	D11	**pc1464**	unknown protein	**-**	222	pc1464_27-71	ATGCTTCTCCAAGGGGGAAATCCTAGGTCATCTGTCCAGTAATTA	74,4	45	0,633	0,1	0,983	1	0,991	0,882	random
12	3	H11	**pc1465**	hypothetical protein	**-**	828	pc1465_427-479	TTGAAAGTAACAGTCTTAGCTTCTCAAGATGGGTGCCCTTTTAGAGTTATCCT	74,2	53	0,982	1	0,999	1	0,988	0,822	mid
12	3	L11	**pc1466**	unknown protein	**-**	795	pc1466_442-495	TCAGATGGCAGTAGAGGATATAAAGTCTTATTGGGAGAAGCTTTCATTGATCTT	74,1	54	0,599	0,04	0,989	1	0,957	0,8	mid
12	3	P11	**pc1467**	unknown protein	**-**	2103	pc1467_1080-1130	TGATCCTGTCGCTTATAAAGACGCTTTGGAAACACTAGCAGATAAGGTTAT	74,3	51	0,623	0,08	0,998	1	0,972	0,845	mid
12	3	D15	**pc1468**	unknown protein	**-**	390	pc1468_133-184	TATCAATATCAATTTTCTTGCCAGTGTACTGTTCTACCCCATGCTTTAGGTC	74,2	52	0,98	1	0,999	1	0,999	0,779	random
12	3	H15	**pc1469**	strongly similar to resolvase	**tnpR**	558	pc1469_285-329	ATTTTCAGGTGAAGATTCTCCTATGGCCATCCTTATGCTGTCAGT	74,2	45	0,978	1	0,994	0,948	0,995	0,861	mid
12	3	L15	**pc1470**	strongly similar to transposase, partial length	**tnpA**	531	pc1470_216-266	TGCAACCTATGTACTTGGCGGTCTGCTATATCACGAATCTGATATAAGAAT	74,2	51	0,988	1	0,997	1	0,998	0,879	random
12	3	P15	**pc1471**	strongly similar to transposase, partial length	**tnpA**	321	pc1471_174-227	CTATCGTGACTCTGGTCTTAATTTTGTGATAGCTGCAATCGTTTTATGGAATAC	74,2	54	0,98	1	0,995	1	0,987	0,809	mid
12	3	D19	**pc1472**	unknown protein	**-**	246	pc1472_40-86	TTTGATTGCCCTATAGATTTGCATGCTATTGCAAAAATGAAAGCTTC	74,2	47	0,96	1	0,997	1	0,916	0,692	mid
12	3	H19	**pc1473**	strongly similar to doc (death on cure) protein of bacteriophage P1	**doc**	378	pc1473_31-75	GAACTACATGATGCTCTTATTGACAAATTTGGTGGGCTTCTTGGA	74,2	45	0,981	1	0,999	1	0,996	0,802	random
12	3	L19	**pc1474**	unknown protein	**-**	192	pc1474_60-108	TAAAGGATTTAGAAATGCAGCCTTTTTAGAGATTGTCGAGAGTGATGCA	74,3	49	0,83	0,653	0,992	1	0,934	0,733	random
12	3	P19	**pc1475**	similar to component D of type II secretion pathway	**gspD;sctC;pulD**	2862	pc1475_1479-1524	GAAGGGGACTCCTTTACGAGCAGGTGACACTACTGGAACATTAAAT	74,2	46	0,977	1	0,995	1	0,953	0,823	mid

12	3	D23	**pc1476**	unknown protein	**-**	969	pc1476_615-666	ACAATCTAGTTTAAATACGTATTCTACATACGCCAAATCACCCAAACGAGCC	74,2	52	0,966	1	0,999	0,983	0,871	0,841	mid
12	3	H23	**pc1477**	conserved hypothetical protein, partial length	**-**	381	pc1477_24-72	TTTTATGTATAGTTTCATTTTTATTGCCCCTTTGTTGAGCGATCCTTGG	74,1	49	0,969	1	0,981	1	0,989	0,729	5´preference
12	3	L23	**pc1478**	similar to sulfate transport protein	**HVST1**	1923	pc1478_995-1039	TAGGAAACTTTTTTGGTGCTTTTATTGGAGCGATGCCTGTATCAG	74,3	45	0,97	1	0,994	1	0,968	0,73	mid
12	3	P23	**pc1479**	unknown protein	**-**	198	pc1479_53-99	CTTTCTGTAGTAATGCTTTTTCGAAGCCCAAAATTCAAGTCAGACCA	74,3	47	0,969	1	0,995	0,978	0,956	0,767	random
12	4	D03	**pc1480**	conserved hypothetical protein	**-**	1464	pc1480_773-817	AAAGGGCTGATTTATGCGTTTTGATGCTAGATGTTCAAGAAGGAA	74,2	45	0,973	1	0,999	1	0,96	0,759	mid
12	4	H03	**pc1481**	hypothetical protein	**-**	915	pc1481_440-485	TAGCGACGATGTCTCACCATCGAGAACTTCAAAATCTTTTATCTGA	74,2	46	0,974	1	0,997	1	0,981	0,75	mid
12	4	L03	**pc1482**	unknown protein	**-**	201	pc1482_1-55	TTGAAATTTAATAGAAAAGCCACTAGGAATAAAAAACCCGTTTGTTTTACAAAGA	72,4	55	0,892	1	0,816	1	0,899	0,487	mid
12	4	P03	**pc1483**	conserved hypothetical protein	**-**	1029	pc1483_484-530	GTTTTAGCCTCTTTTCCAAAACACCACATTGTGAGTGAAGAAAGTCA	74,1	47	0,972	1	0,99	1	0,968	0,767	mid
12	4	D07	**pc1484**	conserved hypothetical protein	**-**	3771	pc1484_2270-2324	AACTTCAAACCCCAGATGTGCCTAATATTACAGGTCTTAACAGTCATTTAAGACC	74,2	55	0,979	1	0,996	1	0,94	0,867	random
12	4	H07	**pc1485**	similar to heat shock protein 70, dnaK	**dnaK, grpF, groP, seg**	2838	pc1485_1403-1450	GTCAAGGGGTTTCTATCAGAGGAGGATTGCCAAGAACTTATTATTTGG	74,2	48	0,975	1	0,994	1	0,983	0,762	mid
12	4	L07	**pc1486**	strongly similar to alanine dehydrogenase	**ald**	1113	pc1486_602-648	ACCGTTTACGGTTTTTGGATGCACTATATGGACCTACTTTGAAGACA	74,2	47	0,98	1	0,999	1	0,956	0,849	mid
12	4	P07	**pc1487**	similar to chromosome segregation SMC protein	**smc**	3540	pc1487_1873-1917	GAAGGTAGCAAAAATTTAAATGAACCAGGCCTAGAGGGGTGGACT	74,3	45	0,954	1	0,995	1	0,898	0,655	mid
12	4	D11	**pc1488**	strongly similar to seryl-tRNA synthetase	**serS**	1362	pc1488_1023-1072	ACTCCATTATCGTAATGCTTTACTAGTAACTGGGGACATGTCTTTCGCTG	74,2	50	0,988	1	0,999	1	0,997	0,876	random
12	4	H11	**pc1489**	unknown protein	**-**	954	pc1489_530-575	ATCCTAACAGCTACGGAAGCTACACACACAAATTTAACAGCCGTTG	74,4	46	0,973	1	0,984	1	0,948	0,827	mid
12	4	L11	**pc1490**	similarity to aspartyl aminopeptidase (metalloprotease)	**-**	1305	pc1490_637-687	CTTGATAAAGCTCGATTTGTTGGCTTCGAAAATCAGTTCATCTCTTCTTAT	74,2	51	0,975	1	0,998	1	0,983	0,759	mid
12	4	P11	**pc1491**	unknown protein	**-**	1221	pc1491_629-675	TGATTAACTTGATGGTTGCATCTACTTTTTATGCGACTGCTTTGGAC	74,3	47	0,98	1	0,997	1	0,983	0,813	mid
12	4	D15	**pc1492**	conserved hypothetical protein	**-**	879	pc1492_464-508	AGAAAGGAGAAATTTTGGCTTTTCAGCTAACTCCTGGAAATGTCG	74,1	45	0,594	0,04	0,989	1	0,977	0,715	mid
12	4	H15	**pc1493**	unknown protein	**-**	210	pc1493_8-53	CCCCAAAACGAAAATTCAGCAGAATTGTGATAGGGCTTAACAAATA	74,2	46	0,974	1	0,998	0,96	0,992	0,787	random
12	4	L15	**pc1494**	unknown protein	**-**	186	pc1494_52-104	ACAGGTAAAATTGGCCATGTTCTGTATACTCAGATAGTTGAGGTCCTTGTTTT	74,1	53	0,862	0,725	0,982	1	0,958	0,77	mid
12	4	P15	**pc1495**	hypothetical protein	**-**	1680	pc1495_840-890	AAATCTAAGTAAGTGCAGGAAACTCACCGATACAGGCTTGGTTCATTTAAC	74	51	0,634	0,12	0,979	0,998	0,999	0,808	mid
12	4	D19	**pc1496**	similar to eucaryotic NAD-specific glutamate dehydrogenase	**gdhB**	3075	pc1496_2314-2359	GTGAATAACGAAGTGATTGAAGACTGGTTATCTGGCAGCGATACAA	74,2	46	0,984	1	0,999	1	0,976	0,859	random
12	4	H19	**pc1497**	similar to Heat-inducible transcription repressor hrcA	**hrcA**	1158	pc1497_511-559	ACTGAAGTCATGCATTTGCCAGTTAAACTCTCTTCTTTTGGAATCAAAC	74,3	49	0,967	1	0,995	1	0,931	0,749	mid
12	4	L19	**pc1498**	strongly similar to heat shock protein GrpE	**grpE**	636	pc1498_226-270	TTACAAAAAGAGCGGCAGGAAATTAGTCGTTATGCCTTGGAAAAT	74,2	45	0,965	1	0,998	1	0,907	0,75	mid
12	4	P19	**pc1499**	strongly similar to chaperone protein dnaK (heat shock protein 70)	**dnaK**	1965	pc1499_998-1044	AAGATGATATCAGTGAAGTGATTCTAGTCGGTGGAATGAGCCGTATG	74,3	47	0,987	1	0,998	1	0,986	0,884	mid
12	4	D23	**pc1500**	unknown protein	**-**	702	pc1500_313-367	ACCTTCACCCCCTACCTATTGTATGATTCGATAAAAGAGATGCTAGAGCTTAAGT	74,1	55	0,976	1	0,983	1	0,961	0,835	mid
12	4	H23	**pc1501**	hypothetical protein	**-**	804	pc1501_427-475	GAAAAAGTGGTAGATGGTAGCCAGCAGTTTTTAAACTTGCCTTACACGT	74,2	49	0,976	1	0,997	0,995	0,976	0,79	mid
12	4	L23	**pc1502**	strongly similar to oligo/dipeptide-binding protein oppA	**oppA, dppA, spo0KA**	1584	pc1502_823-876	AACTTTCACGTTACTCCAGCAGCAGGAATACATCTCTTTCGAGTTAATACTTCT	74,2	54	0,978	1	0,999	1	0,97	0,799	mid
12	4	P23	**pc1503**	strongly similar to oligo/dipeptide ABC transporter (permease) oppB	**oppB, dppB, spo0KB**	936	pc1503_519-565	TATTCTCCCTTCATTATCTTTAGCTCTTCTCCCTATGGCGTTCATCG	74,2	47	0,977	1	0,997	1	0,95	0,825	mid
12	5	D03	**pc1504**	strongly similar to oligo/dipeptide ABC transporter (permease) oppC	**oppC, dppC, spo0KC**	903	pc1504_453-506	CGTTATTTTGTTCACAGTAGTTTTAGGATCTGGCTTTTTCTCTATTGTCCTTGC	74,2	54	0,976	1	0,996	1	1	0,751	mid
12	5	H03	**pc1505**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppD	**oppD, dppD, spo0KD**	987	pc1505_461-506	ATGAGATTAGTGGCGGAATGAAACAACGTGTCATCATAGCTATGAC	74,2	46	0,982	1	0,999	1	0,967	0,847	mid
12	5	L03	**pc1506**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppF	**dppF, oppF, spoOKF**	945	pc1506_435-488	TCCTCAAGAGTTAAGTGGAGGACAAAAACAAAGAGTTTCTTTAGCTAGAGCCTT	74,3	54	0,964	1	0,994	0,96	0,961	0,738	mid
12	5	P03	**pc1507**	hypothetical protein	**-**	1872	pc1507_1009-1062	ACATCCTTAGTGGCTTTACAGTATTTGAATCTGAGTGAGTGCTCTAATTTCACC	74,1	54	0,601	0,062	0,982	1	0,928	0,79	mid
12	5	D07	**pc1508**	hypothetical protein	**-**	1974	pc1508_433-479	TTTCCTTCAGGATTTAAATTGAACTTTCAAGATGGCAATTTTCTGCA	74,2	47	0,893	1	0,999	1	0,445	0,622	mid
12	5	H07	**pc1509**	hypothetical protein	**-**	297	pc1509_1-55	TTGACACCCTTATTGGCTTTACAGTACTTAAATTTGAATTGGTGCTCTAATCTCA	74,4	55	0,621	0,1	0,987	1	0,999	0,725	random
12	5	L07	**pc1510**	hypothetical protein	**-**	2013	pc1510_998-1051	GATTGACGCACTTAACATTCTTAGACGCTCTAAATTATTTAGGTCTGGGTGAGT	74,1	54	0,623	0,092	0,987	0,988	0,991	0,81	mid
12	5	P07	**pc1511**	strongly similar to endopeptidase ATP-binding chain clpC	**clpC**	2544	pc1511_1294-1346	ATGAATCAGCCACAAGACATTAGTAAGTATGAGTCAGAAATAGAGGCCACAAG	74,3	53	0,985	1	0,997	1	0,979	0,872	mid
12	5	D11	**pc1512**	similar to protoporphyrinogen oxidase	**hemG**	1374	pc1512_858-905	GTTTAGTGAAACGGCTTCACTGCTACAGTCTATGGAATCAACCTCTGT	74,2	48	0,967	1	0,997	1	0,83	0,893	mid
12	5	H11	**pc1513**	strongly similar to uroporphyrinogen decarboxylase	**hemE**	1095	pc1513_560-605	AACATTGGATGTATCATGAGCCGCAAGGATTTCATACTTTACTTCG	74,3	46	0,984	1	0,998	1	0,988	0,845	mid
12	5	L11	**pc1514**	strongly similar to transketolase	**tkt**	2034	pc1514_1022-1071	CTAAATTCCAAGAATTAGAAGTCATGCTACATCACAAACTTCCCGACGAT	74,3	50	0,981	1	0,995	1	0,996	0,812	mid
12	5	P11	**pc1515**	hypothetical protein	**-**	312	pc1515_67-112	AAACACCTTATAAAATTTGGAAAGTGCAAAAAGGGCCCAGAATCTG	74,2	46	0,605	0,07	0,999	1	0,967	0,693	5´preference
12	5	D15	**pc1516**	unknown protein	**-**	2385	pc1516_1181-1226	ATAATGCAGGATTAGGTCAAAGAGTGTTTATCTGCGATCCATGTGG	74,5	46	0,977	1	0,974	1	0,988	0,838	mid
12	5	H15	**pc1517**	unknown protein	**-**	1215	pc1517_595-640	TCTAAATCCACTGCAATCTACAAAGTGACCCTTGGTGCTTTTCCTA	74,3	46	0,981	1	0,989	0,986	0,986	0,859	mid
12	5	L15	**pc1518**	unknown protein	**-**	1233	pc1518_538-	CAACTACAAAATGCTAAGGGAGTGGTTTACAGCGAGGGAACTTTAGAAA	74,2	49	0,98	1	0,999	1	0,979	0,818	random

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12	5	P15	**pc1519**	strongly similar to alanyl-tRNA synthetase	**alaS**	2637	pc1519_1275-1320	AAAGCAAAGATCTCGTCATGTTCATAAGACTGTTCATCAAATTGCG	74,3	46	0,973	1	0,995	0,992	0,955	0,788	mid
12	5	D19	**pc1520**	similar to periplasmic immunogenic protein	**-**	732	pc1520_463-507	AATAATCCTCAAGCTTATCGTCAGGAAGTCATTCAACTGGCAACC	74,3	45	0,967	1	0,993	0,974	0,904	0,831	mid
12	5	H19	**pc1521**	strongly similar to transcription-repair coupling factor mfd	**mfd, tcrF**	3306	pc1521_2276-2327	ATACCCCTCCTCAGGATCGACTACCAACAAAGACTATTATCACAGAACCTAG	74,2	52	0,984	1	0,998	1	0,963	0,883	random
12	5	L19	**pc1522**	unknown protein	**-**	198	pc1522_54-98	CGTGCTTCATTTTGAACCTAAAAAGCTGAGTTTTCTCGCATCTTT	74,1	45	0,959	1	0,988	1	0,955	0,643	random
12	5	P19	**pc1523**	unknown protein	**-**	252	pc1523_3-55	GGTGCCATATTATATTTTGGTCTACGAATGTATCAACGAATTTGAGAAGAGGA	74,3	53	0,979	1	0,993	1	0,999	0,787	5´preference
12	5	D23	**pc1524**	hypothetical protein	**-**	1146	pc1524_516-570	AGATATTGTAGGATATCTTACACGTTTAGCCACAATTTTAGCAGTCATCCCCTTC	74,1	55	0,972	1	0,986	1	0,942	0,82	mid
12	5	H23	**pc1525**	similar to regulatory protein lcrH and chaperone sycD	**lcrH, sycD**	540	pc1525_293-338	AAGCAGCTGAAGGTTACATTCGATGTGGAATGCTTGATCTTAAAAA	74,2	46	0,977	1	0,997	0,991	0,978	0,805	mid
12	5	L23	**pc1526**	unknown protein	**-**	1494	pc1526_1011-1057	GGTTATTCATCAATGGTTGAAGGAACGGATAGCCGAACTACTGACTA	74,2	47	0,952	1	0,999	1	0,737	0,85	mid
12	5	P23	**pc1527**	similar to AMP nucleosidase	**amn**	846	pc1527_449-495	AAATTGTGACAAATGTCCTAGATGAAACACAGACGGCTTATCATGTG	74,1	47	0,979	1	0,985	1	0,975	0,852	mid
12	6	D03	**pc1528**	unknown protein	**-**	243	pc1528_64-113	CGGGATCTCGTTCTCCGTTATTATCTTTGTCCAAAATGGGGTTATATTAT	74,3	50	0,979	1	0,996	1	0,986	0,796	random
12	6	H03	**pc1529**	strongly similar to translation elongation factor EF-P	**efp**	573	pc1529_359-412	GAAATGCCGTTAACGTTGAACCTCCTACATTTATGGAAATGGTTATTACAGATA	74,2	54	0,975	1	0,997	1	0,929	0,834	mid
12	6	L03	**pc1530**	similar to lysyl-tRNA synthetase	**lysS**	903	pc1530_460-506	TTTTATACTTCCATTCTTGAAGAAGGACGGGATGCCCTCCTTAATCT	74,3	47	0,976	1	0,998	1	0,992	0,754	mid
12	6	P03	**pc1531**	unknown protein	**-**	462	pc1531_226-271	GCGCTGTCATTAGGCCAATTTTACCCCGATACACTAAATGATGTAT	74,3	46	0,98	1	0,998	1	0,994	0,79	mid
12	6	D07	**pc1532**	unknown protein	**-**	231	pc1532_12-64	AATAGACCAATTAAAATCCATCGATTCTTCATTATTACTCCGCTTCCGTACAA	74,2	53	0,975	1	0,999	1	0,995	0,73	random
12	6	H07	**pc1533**	strongly similar to Na(+)-translocating NADH-quinone reductase, chain F	**nqrF**	1398	pc1533_749-793	AACCCAATGAAGTCATAAGAGCTTACTCGATGGCGTCTTATCCTG	74,3	45	0,981	1	0,992	0,999	0,951	0,889	mid
12	6	L07	**pc1534**	strongly similar to yabJ	**yabJ, yjgF**	390	pc1534_40-94	AAAGCTATTGGTCCTTATTCCCAAGCTGTGTTAGCAGATAAACATTTGTATGTTT	74,2	55	0,979	1	0,993	1	0,981	0,818	5´preference
12	6	P07	**pc1535**	similar to heat shock protein HtpG	**htpG**	1848	pc1535_930-974	ATTGAATGTCTCCAGAAGCTATTTACAAATGGATCGCACTGTTCG	74,3	45	0,981	1	0,996	1	0,995	0,805	mid
12	6	D11	**pc1536**	hypothetical protein	**-**	1365	pc1536_688-736	CCTGAAGGAAGATTAATTCCCATTATTGCAGCAATAGGTAATCATGACC	74,2	49	0,979	1	0,997	1	0,996	0,78	mid
12	6	H11	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
13	1	A04	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
13	1	E04	**pc1537**	unknown protein	**-**	810	pc1537_347-393	CAAGTGAAGCTGTTCTCAAGGTGGATCAAGAAATTCATATTCGTCAT	74,3	47	0,968	1	0,997	1	0,941	0,74	mid
13	1	I04	**pc1538**	unknown protein	**-**	258	pc1538_74-122	CTTTCTCAAGCTCTCTTCATTCCTTATCGCGAGAATGGTTAGGAGTTAA	74,2	49	0,982	1	0,999	1	0,989	0,822	random
13	1	M04	**pc1539**	unknown protein	**-**	225	pc1539_7-61	AGAAAATGTTATGATAATTTAGCACAAGGAGTCAGAATTTCCGAAAAACTCCCTT	74,3	55	0,837	0,658	0,998	0,951	0,995	0,754	random
13	1	A08	**pc1540**	unknown protein	**-**	2571	pc1540_2161-2210	GAAGAAGCTAAGACGCAATATGCACTGAGTCAATCTAAAGTCCAAGAGTG	74,3	50	0,985	1	0,998	1	0,993	0,851	random
13	1	E08	**pc1541**	hypothetical protein	**-**	531	pc1541_43-92	TTTGATTGTTCCTATGTTGCAGCCTCTGAAATAGAGCCATTTGATTATTT	74,3	50	0,972	1	0,998	1	0,979	0,725	5´preference
13	1	I08	**pc1542**	unknown protein	**-**	2214	pc1542_1162-1213	ATTGCTAGCATTAATTTACAGCCTTTATTCGACGACCTTACAGCATTGTCTT	74,3	52	0,974	1	0,997	1	0,946	0,797	mid
13	1	M08	**pc1543**	similar to preprotein translocase YajC subunit	**yajC**	399	pc1543_24-77	TTTAACAACATTGCTATTCCTGTCAAATGGTTATCTATTTGGTGAAGGAGAAGA	74,1	54	0,976	1	0,99	1	0,989	0,779	5´preference
13	1	A12	**pc1544**	similar to rRNA methyltransferse	**ygcA, rumA**	1329	pc1544_684-730	AAAGGGAAGACCTACCAACTTTTATGAAATGCTCCTGTATGGTCCAG	74,2	47	0,979	1	0,995	0,994	0,982	0,817	mid
13	1	E12	**pc1545**	similar to histone H1-like protein	**hctA**	396	pc1545_79-126	GGTAATAAGGCAGCTTCTCAACGCGTTCGCACAGGTACAGTTAAATTA	75.7	48	0,971	1	0,981	1	0,998	0,737	testchip
13	1	I12	**pc1546**	unknown protein	**-**	2691	pc1546_1339-1393	AATGGTTCTGATTCAGGTCAGTTATTAATCTTAGCAGGTTTAATTGTCACTTCCA	74,1	55	0,971	1	0,99	1	0,992	0,724	mid
13	1	M12	**pc1547**	similar to biopolymer transport protein exbB	**exbB, tolQ**	726	pc1547_444-488	TGCTTACATTGCACCTTTAATTGGCCTGCTAGGAACTGTTTTAGG	74,2	45	0,968	1	0,998	1	0,92	0,77	mid
13	1	A16	**pc1548**	similar to biopolymer transport protein exbD	**exbD, tolR**	441	pc1548_154-199	GACTCTACTCCCCTAACAACTCAGCTTCTTTTAGTGATGGATGCCC	74,2	46	0,972	1	0,995	1	0,932	0,8	mid
13	1	E16	**pc1549**	unknown protein	**-**	705	pc1549_260-304	ATCTAACCCCTCCAACACCGATCGACAATCTCTCCTATTTCTTTC	74,3	45	0,971	1	0,992	1	0,906	0,84	mid
13	1	I16	**pc1550**	unknown protein	**-**	249	pc1550_2-55	TGATTGAGCTTAACTTTACAACAGCGTTTATGCTTTACTTGGGTGTTACCATAG	74,2	54	0,983	1	0,996	1	0,997	0,834	random
13	1	M16	**pc1551**	unknown protein	**-**	288	pc1551_128-182	TAAGAAATATTGAAAACAATACTAACAATGTCTTGTCTTGTTATTTGTTTTATCG	68,7	55	0,81	1	0,447	0,894	0,977	0,672	random
13	1	A20	**pc1552**	unknown protein	**-**	294	pc1552_132-186	ACAAAAATATGGAAAAAACCATAATGGCTTTGACGAGTATTTATCCAATACAGAA	73,3	55	0,931	1	0,909	0,903	0,984	0,661	mid
13	1	E20	**pc1553**	unknown protein	**-**	201	pc1553_75-129	TGAGTACAAGTGCTCATCGGCACTCGTTATTCTTACTACTTACATTTTTGTACGT	74,3	55	0,981	1	0,994	1	0,963	0,857	5´preference
13	1	I20	**pc1554**	conserved hypothetical protein	**-**	837	pc1554_396-448	AGATCAGCTCTCAGTTAATTCACCTTCTCAATTCACTACACAAACTGCAAATT	74,2	53	0,979	1	0,994	1	0,976	0,818	mid
13	1	M20	**pc1555**	unknown protein	**-**	561	pc1555_227-279	AGGGTCCCTACAATGCTCCAAATGATCAAGGCGACTACTATCAATACTATAAT	74,2	53	0,978	1	0,997	1	0,945	0,843	mid
13	1	A24	**pc1556**	conserved hypothetical protein	**-**	2871	pc1556_1440-1488	GCTAATTGATATTGTCGCGTGTTTTCCCGTTTATCGTAGTTATATTCGC	74,2	49	0,983	1	0,999	1	0,996	0,817	mid
13	1	E24	**pc1557**	similar to ferrochelatase (heme synthetase), hemH	**hemH**	1044	pc1557_474-525	TATCAATAGTTACCCAGACCATCCTGGTTTAGTAGGAGCTTTCTGTGAAAGG	74,5	52	0,976	1	0,978	1	0,951	0,871	mid
13	1	I24	**pc1558**	similar to heat shock protein ClpB	**clpB**	1944	pc1558_959-1013	CGAACTATGAAGTTGATTGCGGGTTATTAATTTCGAATTATAGTTTTGGACATTC	74,2	55	0,977	1	0,996	1	0,986	0,777	mid
13	1	M24	**pc1559**	similar to ATP-dependent RNA helicase	**deaD**	1548	pc1559_800-845	CGTTAGTGGCTAATGGCTATCATGCTCGAGGTTTACATGGTGATAT	74,2	46	0,984	1	0,999	0,997	0,975	0,87	mid
13	2	A04	**pc1560**	unknown protein	**-**	276	pc1560_23-77	TGAAACTACTTACCGTACTTAGTTCGTTTACATTAGTCACAACAGCTGAAGCAGC	74,2	55	0,988	1	0,997	1	0,999	0,873	random
13	2	E04	**pc1561**	conserved hypothetical protein	**-**	336	pc1561_50-104	TTGGACATTCTGCAGAAGAAGTAAGACTAGTTTTCGGTATAGCGTTAAGAACAGT	74	55	0,614	0,06	0,975	1	0,999	0,854	random
13	2	I04	**pc1562**	conserved hypothetical protein	**-**	333	pc1562_25-69	CATTTAGAGCTAAGTGAATGCCCTAATCTCATGGACGCTGGGTTA	74,6	45	0,619	0,084	0,967	1	0,998	0,836	random
13	2	M04	**pc1563**	hypothetical protein	**-**	1143	pc1563_690-	GACGCCCTTAGTGGTTCTACAGTATTTAAGTCTAGCTGGGTGCGA	74,3	45	0,642	0,118	0,998	1	0,991	0,862	random

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13	2	A08	**pc1564**	unknown protein	-	186	pc1564_25-72	CATCAGCCCACTCCCATTGTTAATTCAGATACTCAATTTTACTCTCCA	74,2	48	0,64	0,14	0,998	1	0,972	0,776	random
13	2	E08	**pc1565**	hypothetical protein	-	3432	pc1565_1609-1656	GCCTTAGCAACTTCGCTTACTCATTTTTACTGCTGGTCTCAAGTAGGT	73,9	48	0,961	1	0,964	1	0,892	0,831	mid
13	2	I08	**pc1566**	conserved hypothetical protein	-	735	pc1566_393-437	AAGAACTTTTCCAAGAGGGCTTGACGTAGAAGTTTTCACGTTTGA	74,1	45	0,974	1	0,987	0,996	0,976	0,792	mid
13	2	M08	**pc1567**	hypothetical protein	-	678	pc1567_271-318	GCCTTGGATTGTCTTCAACGTTTAAGCTCTTATCCGATTTATGTTGTC	74,2	48	0,974	1	0,996	1	0,931	0,829	mid
13	2	A12	**pc1568**	hypothetical protein	-	1794	pc1568_915-966	CAAATCTATTCACGGTTGTGATGCAGATGTTAACTGTATTGGAAAATATGGT	74,1	52	0,978	1	0,989	0,998	0,983	0,817	mid
13	2	E12	**pc1569**	similar to ribosomal-protein-serine acetyltransferase	**rimL**	573	pc1569_230-275	ATCAAGGTCAATGTATTGGATATGGAGGGCTTGTTAATGTGGATTG	74,1	46	0,975	1	0,99	1	0,942	0,838	mid
13	2	I12	**pc1570**	conserved hypothetical protein	-	2763	pc1570_1289-1335	GGATGGGGGGAGATTCTGTTATAGAAGGAGCAAATATTTTATCGCAT	74,2	47	0,961	1	0,993	1	0,907	0,721	mid
13	2	M12	**pc1571**	similar to ribonuclease R	**rnr, vacB**	1569	pc1571_905-953	CTAAACAACTCCCTTCATTTCGCAAAATAGTCAGGGTACCAAAAAAGTG	74,3	49	0,963	1	0,995	1	0,881	0,778	mid
13	2	A16	**pc1572**	similar to tylosin resistance protein	-	1866	pc1572_1173-1224	AGATGTACCTTTAAGAAGAGCACTTGCCCCCGAGGGAGATACTGTATACTAT	74,2	52	0,987	1	0,997	1	0,979	0,895	random
13	2	E16	**pc1573**	strongly similar to peptide chain release factor 3	**rf-3, prfC**	1602	pc1573_797-842	TTGGAATAGAACCTTTTTTTGATGCCTTTGTGAATTTAGCTCCAGC	74,1	46	0,968	1	0,988	1	0,995	0,688	mid
13	2	I16	**pc1574**	hypothetical protein	-	549	pc1574_122-167	CTTTACTGCCTAAACAATTGAATGGAAAGGTGGTTGAATTGGGATC	74,3	46	0,971	1	0,992	1	0,94	0,79	5´preference
13	2	M16	**pc1575**	unknown protein	-	390	pc1575_1-50	ATGGCTAAATGTCGTCAAGCTTCTATGCCATACCCTAAATTCTCCTTCTA	74,3	50	0,978	1	0,995	0,973	1	0,812	5´preference
13	2	A20	**pc1576**	similar to inositol-1(or 4)-monophosphatase	**suhB**	798	pc1576_235-281	CAGATTGAACCAGAAGAAGTGCTTTGGATTATCGATCCTTTAGATGG	74,2	47	0,957	1	0,996	1	0,835	0,77	mid
13	2	E20	**pc1577**	unknown protein	-	1206	pc1577_647-694	CTCTAAGAAAAGGTCCTCGTTCTTACGTTTATGTCGCAAGACACCCTA	74,2	48	0,982	1	0,999	1	0,957	0,869	mid
13	2	I20	**pc1578**	similar to blue fluorescent protein	-	792	pc1578_379-426	GTTCTTAATGCAACAAGACTCATTGTCCCATCCATGTTAAAAGCTGAT	74,2	48	0,978	1	0,999	1	0,982	0,788	mid
13	2	M20	**pc1579**	similar to protein involved in tRNA-dihydrouridine synthesis	**yohI, dusC**	981	pc1579_496-545	AAATATTTGACACTGCATCCTAGAACAAAAGTTGATGGATATGGACCTCC	74,2	50	0,98	1	0,999	1	0,995	0,79	mid
13	2	A24	**pc1580**	hypothetical protein	-	1236	pc1580_606-651	CTTAGCCTTTAACTGGAATACATTTTTCGGGCGCACAATGTTACAT	74,2	46	0,981	1	0,998	1	0,987	0,817	mid
13	2	E24	**pc1581**	unknown protein	-	906	pc1581_414-458	TTCTAATGTGTTAGTCATCGATGCCGACACCCTCTTTATGAATCC	74,2	45	0,981	1	0,999	1	0,96	0,849	mid
13	2	I24	**pc1582**	unknown protein	-	828	pc1582_525-572	CAAAAATCCGAATGGAATGTGCATGCAAATGTACTATCATATGAACAT	74,2	48	0,971	1	0,994	1	0,89	0,853	mid
13	2	M24	**pc1583**	unknown protein	-	777	pc1583_471-515	AGAAATGGATATTTGTGAAGGTGGGGTAGATCCAATGGGAGAAGT	74,3	45	0,973	1	0,991	1	0,919	0,844	mid
13	3	A04	**pc1584**	conserved hypthetical protein	-	186	pc1584_5-50	GAGGGTTGCTTAAAGATTGGTGTTCATTAGGAGGTGGGGTAGAATT	74,2	46	0,97	1	0,997	1	0,911	0,803	mid
13	3	E04	**pc1585**	conserved hypothetical protein	-	258	pc1585_57-106	GGTTTTAGATAAAAATCCATCTTGTTATGTGCTCATTACCTGCGGAGAGC	74,7	50	0,966	1	0,953	1	0,994	0,768	random
13	3	I04	**pc1586**	unknown protein	-	258	pc1586_156-200	GTTTTTATCACTGAAAAGTCTGCTCATGCAGGACCGAGACTTCTC	74,2	45	0,98	1	0,996	1	0,974	0,827	mid
13	3	M04	**pc1587**	similar to bifunctional protein involved in LPS core biosynthesis, hdlE	**hldE,rfaE**	1362	pc1587_686-731	TCACTCAAGCACGCTTGTTAATGATTACTCGTTCAGAAGCTGGTAT	74,1	46	0,981	1	0,991	1	0,996	0,821	mid
13	3	A08	**pc1588**	similar to ADP-D-D-heptose epimerase, hldD	**hldD, waaD, rfaD**	987	pc1588_521-566	TTAATGTATTTGGTCCTAATGAATATCACAAAGGGCGAATGGCCTC	74,3	46	0,982	1	0,996	1	0,974	0,853	mid
13	3	E08	**pc1589**	strongly similar to isopentenyl monophosphate kinase (IPK)	-	867	pc1589_454-498	TCCAAAGGAACTGCTCATTGTACTGGCAGAGGAGAATGTGTAAAT	74,3	45	0,975	1	0,989	1	0,98	0,788	mid
13	3	I08	**pc1590**	similar to ribosomal protein L9	-	486	pc1590_247-295	AAAGTAGACCAAGAAGGACATATGTATGGTTCTGTAACAGTGGCGGAAA	74,3	49	0,99	1	0,998	1	0,997	0,897	mid
13	3	M08	**pc1591**	strongly similar to ribosomal protein S18	**rpsR**	261	pc1591_9-59	AAGAAAACCAAAATATAATTCTGACTACTCTGATGCCCGCTCTAAAAAGCG	74,2	51	0,979	1	0,995	1	0,998	0,784	random
13	3	A12	**pc1592**	similar to ribosomal protein S6 (BS9)	**rpsF**	345	pc1592_10-57	AAAGTACAAAACCTTTACGAAGGAATGTATGTCATTAGCGCAACGCTC	74,3	48	0,981	1	0,996	0,966	0,997	0,852	random
13	3	E12	**pc1593**	similar to peptidyl-tRNA hydrolase	**spoVC**	597	pc1593_268-321	GGTGGGCATAACGGTTTAAAAAGTGTAGAAACTCATTTAGGAACCTCTCACTAT	74,2	54	0,975	1	0,998	1	0,968	0,78	mid
13	3	I12	**pc1594**	similar to general stress protein ctc	**ctc**	555	pc1594_337-385	GTAGATTGTGTGGGGGTTAAATTAGGTGGTGTACTTCGTCAAGTCATTC	74,2	49	0,979	1	0,993	1	0,942	0,872	mid
13	3	M12	**pc1595**	strongly similar to phosphoribosyl pyrophosphate synthetase (PRPP)	**prsA, prs**	942	pc1595_596-650	GTGCTATAGAAGTTGTAGACTATCACCTAATCGGGGATGTTAACGGAAAAGATGT	74,3	55	0,971	1	0,997	1	0,876	0,867	mid
13	3	A16	**pc1596**	similar to starch synthase, precursor, glgA	**glgA**	1503	pc1596_689-734	CACCGAAGGAAGGAAGAGGACTTGAAGCCACCTTAGTAGAATATCA	74,3	46	0,976	1	0,994	1	0,936	0,847	mid
13	3	E16	**pc1597**	similar to phosphatidylglycerophosphate synthase (PGP synthase)	**pgsA**	618	pc1597_332-378	TAAGAACTATTTGTGCTTTGAAAGGATTCGCACTTGCTGCTAGACCT	74,3	47	0,981	1	0,998	1	0,978	0,83	mid
13	3	I16	**pc1598**	similar to D-alanine/glycine transport protein, sodium-dependent	**dagA, cycA**	1362	pc1598_673-726	ATGTGGGTATTGGTCAATAACCTTTCCGCTTTACCTACAGTAATTCAACAAGTA	74,2	54	0,984	1	0,999	1	0,991	0,836	mid
13	3	M16	**pc1599**	unknown protein	-	537	pc1599_250-294	GAAGATTGTAACAGAGGATTACTTGTTTTAGACGCGACCTGGCGT	74,3	45	0,982	1	0,998	1	0,98	0,835	mid
13	3	A20	**pc1600**	hypothetical protein	-	624	pc1600_383-431	AAGCCGAATTTCCAGACTATGGTGAAGATGCTATTATGTCATCTCCATA	74,2	49	0,978	1	0,998	1	0,93	0,86	mid
13	3	E20	**pc1601**	strongly similar to ATP-dependent DNA helicase, mutU	**pcrA, mutU, recL**	2007	pc1601_1050-1097	TTTATATCGATCTAATGCTCTATCTCGCCAATTTGAAACGGCTCTCAT	74,1	48	0,975	1	0,99	1	0,955	0,82	mid
13	3	I20	**pc1602**	unknown protein	-	1875	pc1602_949-1000	CATTTTGGGATTGCTTACCACGCAGAAACAGTGTTTAAATTACTAGAACAAC	74,3	52	0,98	1	0,996	1	0,99	0,805	mid
13	3	M20	**pc1603**	hypothetical protein	-	330	pc1603_28-77	ATGGCTAATGGATCTTCTCGGTACATTGGACGATGGATTATTTTAGATCT	74,2	50	0,976	1	0,999	0,994	0,998	0,75	random
13	3	A24	**pc1604**	strongly similar to 50S ribosomal protein L34	**rpmH**	140	pc1604_57-102	GAAAAGAATGGGCACAGCCAACGGACGTAAAATTATTAGTAGACGT	74	46	0,935	1	0,974	1	0,697	0,788	random
13	3	E24	**pc1605**	strongly similar to 50S ribosomal protein L36	**rpmJ**	141	pc1605_33-77	TTCTAAAGGCGATATACTTGTTCGTCGCAGTGGTCGTTTGTATGT	74,3	45	0,968	1	0,993	1	0,859	0,869	random
13	3	I24	**pc1606**	strongly similar to ribosomal protein S14	-	306	pc1606_90-138	AAGTTACAACATAAACCTTAGCGAAGAAGAAAGAGAGCAAGCTCGCATC	74,2	49	0,981	1	0,999	1	0,998	0,799	random

13	3	M24	**pc1607**	hypothetical protein	-	477	pc1607_228-272	TATTTCTATTTCACAGCCACAACAACCCATTTCCCCCTCTAGTTG	74,4	45	0,978	1	0,986	1	0,988	0,82	mid
13	4	A04	**pc1608**	conserved hypothetical protein	-	480	pc1608_159-203	TATCGATCATCTTCTAGGCCGTATTGCTGAAGGTGTAAAAGGCAT	74,2	45	0,974	1	0,999	1	0,918	0,832	mid
13	4	E04	**pc1609**	unknown protein	-	528	pc1609_281-333	TAATCGAACAATACTTGAAGAGTTATTGGAAAGAGCAATTTTCTCAAAGCGAG	74,2	53	0,973	1	0,996	1	0,984	0,737	mid
13	4	I04	**pc1610**	unknown protein	-	207	pc1610_39-91	AGCAGTGCATTGGCAATTTAATCAGTATTATGTGGTTAGGATGGAAAAGTTAG	74,3	53	0,978	1	0,998	1	0,979	0,799	random
13	4	M04	**pc1611**	conserved hypothetical protein	-	4785	pc1611_1840-1893	AATTTTTGCATTTCCAGCCTAAACTCTCATCAATTAAAGCTTTGCATTTTTAAG	74,2	54	0,834	0,704	0,998	1	0,875	0,623	random
13	4	A08	**pc1612**	unknown protein	-	207	pc1612_49-101	GTTGCTAGAGTTTGGTTCAAGTATTGCAGCTTTAAATTTAGCTCACTAAGGGG	74,2	53	0,618	0,092	0,999	1	0,971	0,733	random
13	4	E08	**pc1613**	unknown protein	-	213	pc1613_89-133	TTAAAAAAACCATAACAGCCAAGCATTGCCAATTCAACGTATCTG	74	45	0,625	0,15	0,971	1	0,916	0,725	random
13	4	I08	**pc1614**	conserved hypothetical protein	-	1512	pc1614_810-855	AAACCTTGCCAAACTAGGAACTTGGAATCTATTCACACGTCCTTGT	74,3	46	0,979	1	0,995	1	0,947	0,857	mid
13	4	M08	**pc1615**	unknown protein	-	213	pc1615_64-118	AGTTCAAAACTTGGAGATTTTGTAGGAAATAAGAAAAATGATCATTGGTTATGGC	73,9	55	0,686	0,306	0,966	0,996	0,956	0,685	mid
13	4	A12	**pc1616**	conserved hypothetical protein	-	2442	pc1616_2149-2195	ATAAATCTGACGGACCAGGGACTGGCATATTTGACCTCTTTAGTAGG	74,2	47	0,621	0,06	0,999	1	0,999	0,862	mid
13	4	E12	**pc1617**	unknown protein	-	216	pc1617_34-84	TCCAGGAGGAAAATCCTAGGAAATATGCCCAGTAATTACTGCATTCAATAT	74,2	51	0,626	0,1	0,999	1	0,986	0,77	random
13	4	I12	**pc1618**	unknown protein	-	2781	pc1618_1340-1389	ATCTGCTTCCTAATTCTGGTAAAGAGATGACTGCCCAAGAAATTGTATCA	74,2	50	0,608	0,07	0,999	1	0,948	0,75	mid
13	4	M12	**pc1619**	unknown protein	-	252	pc1619_77-128	ATGATTTACCTGAGGATTTAAATGCACAAGTCACTTGTCATGAGAAAAATGA	74,3	52	0,614	0,09	0,988	1	0,985	0,705	random
13	4	A16	**pc1620**	conserved hypothetical protein	-	549	pc1620_241-287	AATTTAGGGTATTTACCAGGCGGAGACAAGAAAAAGACGACACTCAC	74,2	47	0,981	1	0,998	1	0,998	0,805	random
13	4	E16	**pc1621**	unknown protein	-	582	pc1621_329-380	CACAAATTGTTGATGTTTATACACAGGAAAAATATCACTGGCCCTATCATTG	74,2	52	0,971	1	0,998	1	0,963	0,741	mid
13	4	I16	**pc1622**	unknown protein	-	309	pc1622_53-98	GTTATCCCACGTCTTTACCCGCAGTAGTTGCAACTGATTTAGGAAT	74,2	46	0,983	1	0,996	1	0,999	0,826	random
13	4	M16	**pc1623**	similar to transcription termination factor, nusB	**nusB, groNB**	465	pc1623_325-373	GAAGAAGTCAATTCAAATCTGCTTGTCGAAAGTTCTCAAATCCTTGAAC	74,3	49	0,965	1	0,998	1	0,909	0,749	mid
13	4	A20	**pc1624**	similar to UDP-N-acetylmuramate dehydrogenase	**murB**	900	pc1624_406-456	GCGAATGGTCGAGAAACTGCAGACAATTTGATTAGTGTAGATTTTGTAGAT	74,3	51	0,973	1	0,992	1	0,955	0,788	mid
13	4	E20	**pc1625**	conserved hypothetical protein	-	843	pc1625_434-487	TAAAAAAGGGTTATGTACCCACTATTCAGAAGGCATTTCAAGAGTATATTGGGG	74,2	54	0,98	1	0,999	1	0,989	0,799	mid
13	4	I20	**pc1626**	similar to folylpolyglutamate synthase	**folC**	1233	pc1626_539-583	AAAAAGCTGGTATCATTAAATCGCACACTCCTGTCATTATTGGCC	74,3	45	0,971	1	0,996	1	0,921	0,806	mid
13	4	M20	**pc1627**	unknown protein	-	462	pc1627_292-336	AGAGAAAATTGTCATCAAGTCATGAATCAAGTCCAGGCCATCTTC	74,3	45	0,971	1	0,993	1	0,94	0,784	mid
13	4	A24	**pc1628**	unknown protein	-	597	pc1628_171-218	TGGAAAAATGTTTGAAGTAAGTCGTCACCAGACAGCTAAAGTTTTTGC	74,2	48	0,965	1	0,996	0,968	0,993	0,682	random
13	4	E24	**pc1629**	similar to cytochrome bd-I oxidase subunit II	**cydB, cyd-2**	933	pc1629_439-485	TCAATTTACATTTTGATGAAAACAGAAGGGGAATTTCATGATCGGAT	74,1	47	0,967	1	0,991	1	0,971	0,7	mid
13	4	I24	**pc1630**	similar to cytochrome bd-I oxidase subunit I	**cydA, cyd-1**	1398	pc1630_686-736	TCATCACATCTATTCTGCAAGCTTATTCAGGGGATAGTAGTGGTAAAGTCG	74,3	51	0,983	1	0,994	1	0,986	0,855	mid
13	4	M24	**pc1631**	unknown protein	-	189	pc1631_67-121	GGCATCTTACAAGGATCGGTTTTTGGAAATAGTAATTTTTATTTCCCTAAATTTC	73,1	55	0,82	0,709	0,886	1	0,971	0,634	mid
13	5	A04	**pc1632**	similar to dihydropteroate synthase	**folP, dhpS**	780	pc1632_279-324	GGCAAGCTTAATCAATGATGTATCTGGTTTTCGAGACCCCTTTATG	74,4	46	0,963	1	0,981	1	0,888	0,805	mid
13	5	E04	**pc1633**	conserved hypothetical protein	-	1338	pc1633_682-728	TCGACAAGTCCATACGACGATGAAATTAACTTTTACATTCCAGATGC	74,2	47	0,977	1	0,999	1	0,988	0,768	mid
13	5	I04	**pc1634**	hypothetical protein	-	706	pc1634_384-430	ATCTCTAATCATCGCCGCTATGAAACAATGTGGTCGTTTAACTCTTC	74,3	47	0,975	1	0,99	1	0,97	0,801	mid
13	5	M04	**pc1635**	unknown protein	-	2793	pc1635_1464-1513	AAATCCGAGCTTAAGTAAGAGCGATCAGGTTTTTCTGATTTGTGCCTATA	74,3	50	0,973	1	0,992	1	0,934	0,815	mid
13	5	A08	**pc1636**	strongly similar to pyruvate kinase	**pyk**	1797	pc1636_953-998	GTCGTTATCCTGTTGAGACGGTTAATGTGATGCGAAGTATCGTAGA	74,2	46	0,982	1	0,995	1	0,946	0,889	mid
13	5	E08	**pc1637**	conserved hypothetical protein	-	453	pc1637_29-78	CGTTTAATAGACCTTTGGCTAGCTCCCTTTCAGGGAAACCTATACTCAGT	74,1	50	0,958	1	0,986	1	0,801	0,866	mid
13	5	I08	**pc1638**	unknown protein	-	279	pc1638_90-137	AATGATTGGTCCTAATAGCGATCAGATTATCTGTGGAGTTATGGGGAA	74,2	48	0,974	1	0,994	0,968	0,949	0,85	mid
13	5	M08	**pc1639**	conserved hypothetical protein	-	4602	pc1639_2261-2305	ATCACTGGCTAAATCCGTTTACATGGGGATTAAACCTCTACTCGC	74,3	45	0,978	1	0,996	0,978	0,959	0,856	mid
13	5	A12	**pc1640**	conserved hypothetical protein	-	291	pc1640_146-190	GATTGACACCCCTAAGATCGAATAGGAAGCAGAAGCTGATGAATC	74,3	45	0,643	0,13	0,993	1	0,999	0,822	mid
13	5	E12	**pc1641**	strongly similar to excinuclease ABC subunit A, uvrA	**uvrA**	5703	pc1641_2879-2932	CCAAAAAGCAAAGAGAGGCTCTCTTAATTAAAGACATCAATGTAATAGGTGCTG	74,3	54	0,973	1	0,996	1	0,974	0,749	mid
13	5	I12	**pc1642**	unknown protein	-	1176	pc1642_565-609	AATAGCTGGCAATTAATGAAGCAACGACCTGATTTTCGCAACTAC	74,3	45	0,977	1	0,989	1	0,976	0,809	mid
13	5	M12	**pc1643**	unknown protein	-	702	pc1643_287-332	ATTGTGTGCTATCTGATGATGATTCTGAAAGAATGTCCGCTATTGC	74,4	46	0,974	1	0,988	1	0,935	0,84	mid
13	5	A16	**pc1644**	unknown protein	-	342	pc1644_114-161	TGTTTTGGGTATTACATTTGGTTTAAGGCAATACTTAATGGGCAGACG	74,1	48	0,974	1	0,989	1	0,942	0,823	mid
13	5	E16	**pc1645**	conserved hypothetical protein	-	2949	pc1645_1518-1566	GCGAGATGCTGATTTTGAAATCAGTCCTCTTGAAATTTATGTTGGTAAC	74,2	49	0,964	1	0,998	1	0,958	0,673	mid
13	5	I16	**pc1646**	similar to mutT protein	**mutT**	564	pc1646_328-372	TTTCACCTCTTAGGAAGTGCTTACCCTTATCCAGGAATTAGCGGA	74,2	45	0,978	1	0,997	1	0,955	0,829	mid
13	5	M16	**pc1647**	unknown protein	-	243	pc1647_55-109	CAACTTCATCAGCTATGCATCATATTCGACTTTAGGGGAGTAAATAGTTCAAGAC	74,2	55	0,63	0,11	0,999	1	0,932	0,839	mid
13	5	A20	**pc1648**	unknown protein	-	189	pc1648_61-107	TGGGCAAACACTTGCTGCACTATTGGGACTAATTACTTAAACAACAA	74,2	47	0,976	1	0,999	1	0,965	0,792	mid
13	5	E20	**pc1649**	conserved hypothetical protein	-	1566	pc1649_247-295	TTTATGGAACATCGCCTATCATCCGATCCAACTTCACTAAGTAAGATTG	74,3	49	0,911	1	0,995	1	0,463	0,798	mid
13	5	I20	**pc1650**	conserved hypothetical protein	-	273	pc1650_71-116	AGATAAGCGAAAGAAGAGGCTGTGAACTCATCAAAGTAGTGCGATC	74,2	46	0,974	1	0,994	1	0,933	0,83	mid
13	5	M20	**pc1651**	conserved hypothetical protein	-	339	pc1651_41-91	TGCCAGAAAGCATAAGAGTAGACAATGACCCTGAGTATACTTCAAAAATGG	74,3	51	0,981	1	0,997	1	0,999	0,802	random
13	5	A24	**pc1652**	unknown protein	-	960	pc1652_210-	TACTCCTGAGAATAAGCCTTGTGTTATAGGCGAGAATAAACTTCCTGTTGAAGAT	74,3	55	0,98	1	0,996	1	0,977	0,827	random

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13	5	E24	**pc1653**	conserved hypothetical protein	**-**	213	pc1653_107-155	TTCCATCGATAGATGTTTGCCACAATAAACGCATAAAAAGAAACAAGAT	74,2	49	0,602	0,06	0,993	1	1	0,675	mid
13	5	I24	**pc1654**	strongly similar to valyl-tRNA synthetase	**valS**	2850	pc1654_1354-1398	TTAGATACCTGGTTTTCTTCAGCTTTATGGCCTTTCTCGACGCTT	74,3	45	0,973	1	0,996	1	0,928	0,815	mid
13	5	M24	**pc1655**	unknown protein	**-**	3312	pc1655_1733-1781	CTCAAATACGTGTGAGTCTAGCTCTTGTGCATGAATTTCTTAGCGATTC	74,2	49	0,974	1	0,999	1	0,924	0,821	mid
13	6	A04	**pc1656**	similar to D-alanine/glycine transport protein, sodium-dependent	**dagA, cycA**	1398	pc1656_712-761	TATCACTACGATCGTATCTTTGATGTCATTGTTGCTATCATTACCCATGC	74,2	50	0,985	1	0,999	1	0,988	0,851	mid
13	6	E04	**pc1657**	similar to D-alanine/glycine transport protein, sodium-dependent	**dagA, cycA**	1386	pc1657_777-826	GGCTTTACAGATGGGTGTAGCAAGAAGTGTATTTTCTAATGAAGCAGGAC	74,2	50	0,968	1	0,994	1	0,917	0,781	mid
13	6	I04	**pc1658**	strongly similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (tyrosine-sensitive), aroF	**aroF**	1092	pc1658_521-567	AAAATGGAATTGCTGGTAATATTTCAGCTGCTGTTCAAGGAGCCTAT	74,3	47	0,977	1	0,997	1	0,974	0,795	mid
13	6	M04	**pc1659**	hypothetical protein	**-**	534	pc1659_58-104	ATAGCTATCATCTGCTTTCTTTGTCCGACTAGCTGTAGCCTTCAACG	74,2	47	0,979	1	0,993	1	0,972	0,832	5´preference
13	6	A08	**pc1660**	stongly similar to fumarate hydratase class II, fumC	**fumC**	1392	pc1660_784-831	AATAAATTTGAGTCGCTCGCGACTAATGACGCTCTTGTAGAAGTTAGC	74,2	48	0,971	1	0,998	1	0,913	0,809	mid
13	6	E08	**pc1661**	conserved hypothetical protein	**-**	972	pc1661_551-602	ATAATGGTTCTTTAGAGGCGAGATATCGACTTTCGTTGCTATATTTAAGCGG	74,2	52	0,977	1	0,999	1	0,936	0,841	mid
13	6	I08	**pc1662**	unknown protein	**-**	183	pc1662_78-128	TTTGCTTAACCATACTGCAACAAAACACAAATACCTAACCATAAACAACTT	72	51	0,921	1	0,772	1	0,985	0,801	mid
13	6	M08	**pc1663**	similar to o-succinylbenzoate synthase II, menC	**menC**	939	pc1663_487-539	ATAGATGTTAATCGAGCCTGGAAAACGGAAGATTCTTTACAATTCTTTTCAGA	74,3	53	0,973	1	0,993	1	0,984	0,742	mid
13	6	A12	**pc1664**	conserved hypothetical protein	**-**	333	pc1664_45-93	AATCGATGATCGGGCATTTAAGCAACTTTATGGGTATGTTACCAACTAC	74,2	49	0,619	0,06	0,999	1	0,999	0,838	random
13	6	E12	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
14	1	B04	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
14	1	F04	**pc1665**	unknown protein	**-**	237	pc1665_142-195	AACGACAAAAAAAGACGCCATTTTATTAAGAATAGGAAGGAAGACAAAAGAACA	74,2	54	0,656	0,213	0,998	1	0,978	0,625	mid
14	1	J04	**pc1666**	hypothetical protein	**-**	1557	pc1666_823-867	GCTGGGTTAACACATTTGACTCCTTTAGCGGCTTTACAGCATTTA	74,3	45	0,614	0,09	0,996	1	0,957	0,722	mid
14	1	N04	**pc1667**	similar to H+-transporting two-sector ATPase (epsilon chain, atpC)	**atpC**	444	pc1667_206-252	AGGTTTCTCATAACAGTGCAACAATTATTGCTGATGCAATTGAATCC	74,3	47	0,977	1	0,997	1	0,983	0,78	mid
14	1	B08	**pc1668**	strongly similar to H+-transporting two-sector ATPase (beta chain, atpD)	**atpD**	1461	pc1668_723-770	AATGCGAGTAGGTTTAACAGGATTAACGATGGCAGAGCATTTTAGAGA	74,2	48	0,982	1	0,999	1	0,991	0,82	mid
14	1	F08	**pc1669**	similar to H+-transporting two-sector ATPase (gamma chain, atpG)	**atpG**	858	pc1669_496-543	ATTTGGCTTGTTTATACGCATTATGTGACAATGATGACCCGTAAAGTC	74,2	48	0,975	1	0,992	1	0,934	0,843	mid
14	1	J08	**pc1670**	strongly similar to H+-transporting ATP synthase (alpha chain, atpA)	**atpA**	1527	pc1670_775-827	ATCTGCTTTTATGATGACCTTTCTAAACATGCACAAGCTTATCGAGAAATAGC	74,2	53	0,974	1	0,999	1	0,99	0,732	mid
14	1	N08	**pc1671**	similar to H+-transporting two-sector ATPase (delta chain, atpH)	**atpH**	546	pc1671_79-124	CATTTGTTGGCTTTAGAAGAGTTTGTGGGGATATTGGAAACCATTC	74,3	46	0,971	1	0,992	1	0,961	0,759	5´preference
14	1	B12	**pc1672**	similar to H+-transporting two-sector ATPase (chain b, atpF)	**atpF; uncF**	483	pc1672_195-239	GTTACATGATATTGATGCTGAAGCTCGTCGGAGAATTCAAGAAGC	74,3	45	0,973	1	0,993	1	0,952	0,797	mid
14	1	F12	**pc1673**	strongly similar to H+-transporting two-sector ATPase lipid-binding protein (chainC, atpE)	**atpE**	297	pc1673_60-104	AACAATGAGTATTGGAACAGCATTAGCTCTCTCTGCTCCATTTGC	74,1	45	0,965	1	0,988	0,961	0,91	0,837	mid
14	1	J12	**pc1674**	similar to H+-transporting two-sector ATPase (chain a, atpB)	**atpB**	816	pc1674_389-435	CTTCGTCTAGTTTGAATATTACCGCAGCTTTGGCGATTTGTGTATTC	74,2	47	0,98	1	0,995	1	0,98	0,827	mid
14	1	N12	**pc1675**	unknown protein	**-**	396	pc1675_102-146	TAGTCTCGGTATTTTAAGCGGAGCATGTTGGGCTTGTCTGAATAT	74,2	45	0,971	1	0,995	1	0,903	0,832	mid
14	1	B16	**pc1676**	similar to V-type sodium ATP synthase subunit K (ntpK)	**ntpK**	423	pc1676_6-52	TATTAATATGGTTGGCCCTGCAATGGCACTAGGATTGAGTAGTATGG	74,2	47	0,988	1	0,997	0,999	0,993	0,885	random
14	1	F16	**pc1677**	similar to V-type sodium ATP synthase subunit I (ntpI)	**ntpI**	1917	pc1677_886-931	TATGATACACCGTCATCTTCAGATCATGATCCTTCAAATTGGGTTC	74,2	46	0,973	1	0,998	1	0,926	0,819	mid
14	1	J16	**pc1678**	similar to V-type sodium ATP synthase (subunit D, ntpD)	**ntpD**	648	pc1678_326-370	ATAGCTTATTTGAAACATCTCCGTGGATTGATGCAGCCGTTTTAG	74,3	45	0,978	1	0,991	1	0,999	0,788	mid
14	1	N16	**pc1679**	similar to H+-transporting two-sector ATPase (chain B, atpB)	**atpB**	1317	pc1679_615-660	AACTGACCCAGCTGTTGAATGCTTACTTGTACCAGATATGGCTCTT	74,1	46	0,978	1	0,986	1	0,955	0,862	mid
14	1	B20	**pc1680**	strongly similar to V-type sodium ATP synthase (subunit A, ntpA)	**ntpA**	1782	pc1680_933-981	TATGCCTGTTGCCGCTCGAGAGTCATCTATTTATATGGGTATTACCATA	74,2	49	0,981	1	0,996	1	0,959	0,866	mid
14	1	F20	**pc1681**	hypothetical protein	**-**	792	pc1681_419-471	GATTGGTGTGGACAGGATATCGTGCTAAAAAGTTAGGAAGAGATTTGAGTATC	74,2	53	0,979	1	0,996	1	0,978	0,814	mid
14	1	J20	**pc1682**	similar to V-type sodium ATP synthase (subunit E, ntpE)	**ntpE**	513	pc1682_247-295	AAAGCCATCGATAGAGACGGATTAAACACAGACTTAACCGCTGTTATTC	74,3	49	0,985	1	0,991	1	0,989	0,875	mid
14	1	N20	**pc1683**	hypothetical protein	**-**	816	pc1683_345-398	AGGTAATGCCAGCTTATCTCAGGTTGATACTAAATCTGAATGGGGTAGTGTAAG	74,1	54	0,975	1	0,981	1	0,936	0,869	mid
14	1	B24	**pc1684**	unknown protein	**-**	297	pc1684_21-75	GAATTTTTTAAATAAGTGGATCGTAATCGTTACAGCCATTGTCATGACAGGTTTA	74,2	55	0,965	1	0,999	1	0,999	0,622	random
14	1	F24	**pc1685**	unknown protein	**-**	477	pc1685_203-247	AGGCTCCACCTTGTAAAGAAGATTCCACCCTTACAAAAGTTGACC	74,2	45	0,969	1	0,995	1	0,963	0,722	mid
14	1	J24	**pc1686**	unknown protein	**-**	366	pc1686_173-217	GTACGGCTCATTGGTCTGCTTATGTACCCATCGTAGCACTTATTG	74,3	45	0,988	1	0,993	1	0,989	0,905	mid
14	1	N24	**pc1687**	unknown protein	**-**	297	pc1687_75-119	TCACACGCTCACGCTCATTTTAGCTCATCGTCTCTATAATGCTAA	74,3	45	0,968	1	0,997	1	0,925	0,768	mid
14	2	B04	**pc1688**	hypothetical protein	**-**	828	pc1688_427-479	TTGAAAGTAACAGTCTTAGCTTCTCAAGATGGGTGCCCTTTTAGAGTTATCCT	74,2	53	0,982	1	0,999	1	0,988	0,822	mid
14	2	F04	**pc1689**	unknown protein	**-**	1776	pc1689_1010-1057	CAATAGGACATTACCGAACTTTCCTTCTTAAAACGGATCCTGATCCAT	74,3	48	0,969	1	0,997	1	0,879	0,838	mid
14	2	J04	**pc1690**	hypothetical protein	**-**	393	pc1690_12-57	ACATCTTCTTCAATTTTGTTGCCAGACATGTCAACATCTCATTCAA	74,3	46	0,967	1	0,994	1	0,995	0,659	5´preference
14	2	N04	**pc1691**	strongly similar to transaldolase B	**talB**	969	pc1691_444-489	AATGGGTATCCACTGCAACATGACACTTCTTTTTAGTATGCCACAA	74,2	46	0,975	1	0,996	1	0,958	0,797	mid
14	2	B08	**pc1692**	hypothetical protein	**-**	1296	pc1692_564-609	GGTTAAAGAGACAAGGTTAATTCGCCTAGGACAACCGATTTGTCAA	74,2	46	0,975	1	0,998	1	0,915	0,853	mid
14	2	F08	**pc1693**	unknown protein	**-**	942	pc1693_444-	CATTCAACTTAACCCCTCAAACCTCTCTAAATGGATTACCTTAGTCGATAAAGGT	74,1	55	0,974	1	0,982	1	0,972	0,803	mid

							498										
14	2	J08	**pc1694**	unknown protein	**-**	1857	pc1694_938-982	TAGAACGTGTCATGGCTGGTGAAGTTGATGTAACTCAATCTCTCA	74,3	45	0,976	1	0,997	0,99	0,991	0,769	mid
14	2	N08	**pc1695**	strongly similar to UDPglucose 6-dehydrogenase	**rkpK**	1410	pc1695_809-857	GTTATGGTGGATCATGCCTGCCAAAAGATGTAAAAGCTCTAATTACTCA	74,3	49	0,967	1	0,993	1	0,897	0,803	mid
14	2	B12	**pc1696**	strongly similar to farnesyltranstransferase	**crtE**	885	pc1696_421-466	ATTACTATTTTATCCAGACAAAGCGGATACGATGGAATGATTGGCG	74,3	46	0,977	1	0,992	0,999	0,977	0,804	mid
14	2	F12	**pc1697**	strongly similar to exopolysaccharide production protein	**exoY**	654	pc1697_374-418	AATTTTGGAATGTCCTAAAAGGAGATTTGAGCGTCGTAGGTCCTC	74,1	45	0,973	1	0,984	1	0,954	0,811	mid
14	2	J12	**pc1698**	conserved hypothetical protein	**-**	519	pc1698_63-111	ATTACCGCACCTTCCCCTCTTATATTTCGCTCCATTTCTAGTTATAGCC	74,2	49	0,96	1	0,996	1	0,802	0,85	mid
14	2	N12	**pc1699**	conserved hypothetical protein	**-**	1269	pc1699_697-746	GATCAACATTATAATCTCATTTCAGCATTGCATAAGTCTGTGAGGGGATC	74,2	50	0,976	1	0,999	1	0,939	0,83	mid
14	2	B16	**pc1700**	unknown protein	**-**	504	pc1700_251-304	AAGCTTCTAAACTAGATCCGAATCCTTTTAAAGATCTTAGTCAACGGGATGTTG	74	54	0,969	1	0,973	1	0,998	0,74	mid
14	2	F16	**pc1701**	strongly similar to bifunctional protein folD	**folD**	879	pc1701_452-497	AAGTTTGTGGGAAACATGCTCTGATTATTGGACGAAGCAATATTGT	74,1	46	0,979	1	0,985	1	0,989	0,832	mid
14	2	J16	**pc1702**	similar to Thiamine biosynthesis lipoprotein apbE precursor	**apbE**	1074	pc1702_463-509	CTTCCCTCTCCAGATGAAATAGCTCTCATTAAACCCTCTATTGGGTG	74,2	47	0,973	1	0,996	1	0,925	0,817	mid
14	2	N16	**pc1703**	unknown protein	**-**	261	pc1703_16-64	AATCCTCCAAATTACGATAATCAAAAACCTGTTTCTTCCAAGAGGCAAT	74,2	49	0,976	1	0,996	1	0,998	0,747	random
14	2	B20	**pc1704**	unknown protein	**-**	1359	pc1704_672-726	TGTTACTCCTTTTCATGAATACCATGAATACCTTCTCGTTAAAGCTCAGAATACG	74,3	55	0,98	1	0,994	1	0,991	0,809	mid
14	2	F20	**pc1705**	similar to DNA polymerase III, beta chain	**dnaN**	1212	pc1705_607-653	AAGCGATTAGCTCGAGCAAAAGGCGTAATAGATAATGATCCCTCTTT	74,2	47	0,983	1	0,995	1	1	0,823	mid
14	2	J20	**pc1706**	similar to DNA replication and repair protein recF	**recF, uvrF**	1080	pc1706_431-475	CTCTTTATGTTCACCATTTAAATCGTTATGGGCGAGCTCTCAAGC	74,2	45	0,966	1	0,999	1	0,89	0,787	mid
14	2	N20	**pc1707**	conserved hypothetical protein	**-**	462	pc1707_164-210	ATGAACTTTGGCTTATTGGATGTAACATTGCTCATTATCGTTTTGGC	74,3	47	0,98	1	0,996	1	0,999	0,795	random
14	2	B24	**pc1708**	conserved hypothetical protein	**-**	423	pc1708_97-141	CAAATCGAATGTCTGTGGGCTAAAGATTCTTACCAACTGCTTGAA	74,2	45	0,983	1	0,999	1	0,997	0,825	random
14	2	F24	**pc1709**	unknown protein	**-**	399	pc1709_63-108	GATGAAATGGGTAGGAGGGGCTGATCAAGCAGTCTTATTTTTGATA	74,3	46	0,967	1	0,989	1	0,969	0,716	5´preference
14	2	J24	**pc1710**	conserved hypothetical protein	**-**	1095	pc1710_534-582	GGATTTATATACTCAAGCTGAGAGCACGGAAGAAAATGTCAAAGCAAGA	74,2	49	0,976	1	0,994	1	0,985	0,78	mid
14	2	N24	**pc1711**	strongly similar to holo-(acyl carrier protein) synthase	**acpS**	369	pc1711_2-50	TGACTTTAGGAATTGGCAACGATATTATTGAGATTGAGCGAATACAAGC	74,2	49	0,976	1	0,992	1	0,995	0,764	random
14	3	B04	**pc1712**	unknown protein	**-**	822	pc1712_348-392	ATTAACCTTAGGAATCAACCTTGTTCATGCGTTTCCCTGGAGTCT	74,3	45	0,977	1	0,988	1	0,936	0,873	mid
14	3	F04	**pc1713**	strongly similar to thioredoxin-disulfide reductase 2	**trxB**	951	pc1713_437-481	CTATTTTTCGCAATCGCCCTTTATTTGTCATAGGTGGAGGAGATT	74,1	45	0,971	1	0,986	1	0,961	0,776	mid
14	3	J04	**pc1714**	unknown protein	**-**	498	pc1714_290-334	AACATAACCCCTACTTAGATGGCACAAAATTCGGCCCAAATTATG	74,2	45	0,979	1	0,994	1	0,96	0,842	mid
14	3	N04	**pc1715**	strongly similar to sodium/proline symporter	**putP**	1431	pc1715_727-777	GGATGGGGACTTGGTTATTTTGGGATGCCTCATATTATCACTAAATTTATG	74,4	51	0,974	1	0,988	1	0,99	0,765	mid
14	3	B08	**pc1716**	unknown protein	**-**	1794	pc1716_915-959	CGTCGATCAGTTACCTCACGGAAAAGGAATTTACAAACAAGAAGG	74,3	45	0,975	1	0,994	1	0,983	0,768	mid
14	3	F08	**pc1717**	strongly similar to acyl carrier protein	**acpP**	234	pc1717_99-149	TGCAGATTCTCTAGATCTAACAGAACTCATCATGACATTTGAAGAGCGTTT	74,3	51	0,972	1	0,996	1	0,942	0,788	random
14	3	J08	**pc1718**	strongly similar to 3-oxoacyl-[acyl-carrier protein] reductase, fabG	**fabG**	756	pc1718_363-409	TTTTAACACTTGTAAATCTGTCGTTCGTGGAATGATGAAAGCCAAAA	74,3	47	0,97	1	0,994	1	0,984	0,709	mid
14	3	N08	**pc1719**	similar to malonyl CoA-acyl carrier protein transacylase, fabD	**fabD**	990	pc1719_777-823	ACTTGTCCGAACTCATTTAAGCAAACAAATCACACATTCTGTTCGAT	74,3	47	0,981	1	0,994	1	0,998	0,809	random
14	3	B12	**pc1720**	strongly similar to 3-oxoacyl-[acyl-carrier-protein] synthase III, fabH	**fabH**	999	pc1720_437-483	TGTCTGCCTTTATTGATTATAAGGATCGGACGACATGTGTTTTGTTC	74,2	47	0,973	1	0,995	0,991	0,936	0,818	mid
14	3	F12	**pc1721**	unknown protein	**-**	228	pc1721_114-166	AAACTGTTTTATATGTAAATTTGAATCCAAACCCCGATTAATTCGACATCGAC	74,2	53	0,975	1	0,999	1	0,999	0,728	mid
14	3	J12	**pc1722**	unknown protein	**-**	237	pc1722_67-113	AGCCTCGTACTGCTTCCGCTTATTTGGACAACTTTTATTTCCTATGA	74,2	47	0,973	1	0,999	1	0,981	0,732	random
14	3	N12	**pc1723**	unknown protein	**-**	189	pc1723_99-146	TGATCATATTTTAGACGACCTTTATCAATTTACTTCTGGCGCTGCTCA	74,3	48	0,975	1	0,997	0,997	0,997	0,742	mid
14	3	B16	**pc1724**	strongly similar to recombination protein RecR	**recR**	597	pc1724_283-329	GAAGAAACTCACGAATATCGGGGTTTATATCACGTTTTAGGAGGGGT	74,2	47	0,984	1	0,999	1	0,984	0,85	mid
14	3	F16	**pc1725**	unknown protein	**-**	231	pc1725_65-109	AAGTAGCTAAGCAAATTGACGGATCTAGCTGCCGAACAAATCTTG	74,1	45	0,975	1	0,991	1	0,948	0,828	mid
14	3	J16	**pc1726**	similar to outer membrane protein Omp85	**-**	2448	pc1726_1374-1427	AGATGTTTATATCGAAGTCGAGGAAACGAATACAGGACAATTTAGTGCTTTTGT	74,2	54	0,962	1	0,995	1	0,851	0,814	mid
14	3	N16	**pc1727**	conserved hypothetical protein	**-**	573	pc1727_242-286	ATGAAGATTACATGGATAGCATTTCGGAAGAAGCTGCTAGCGAAC	74,2	45	0,977	1	0,998	1	0,954	0,82	mid
14	3	B20	**pc1728**	similar to UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	**lpxD;firA**	1050	pc1728_576-620	AACTAACCAACAAGGACAACACATCAAACTGAATCAAGTTGGCAA	74,1	45	0,977	1	0,99	1	0,95	0,846	mid
14	3	F20	**pc1729**	similar to phosphoprotein phosphatase	**ptc1**	1461	pc1729_600-646	TTTACGAACGATAGCAGAAAATGTGAAGTTTAGCGTTACCAGTGCAG	74,2	47	0,969	1	0,998	1	0,868	0,851	mid
14	3	J20	**pc1730**	unknown protein	**-**	774	pc1730_15-61	TAATCCTCCAACTAACTCTCAAGGTATCTTCCCAGGAAGCCCTTCTT	74,2	47	0,985	1	0,999	1	0,993	0,847	5´preference
14	3	N20	**pc1731**	strongly similar to pyruvate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	**pdhC;aceF**	1302	pc1731_707-753	ATGTCACTTTAACAATCGATGCTAGTCCATTGACCCAAATCAGAGAG	74,2	47	0,978	1	0,998	1	0,945	0,837	mid
14	3	B24	**pc1732**	strongly similar to pyruvate dehydrogenase (lipoamide), E1 component, beta chain	**pdhB**	993	pc1732_690-734	GGGAATTTGTGCTGAACTTATTGATCTTCGGACAGTCAAACCTTT	74,2	45	0,98	1	0,999	1	0,998	0,782	random
14	3	F24	**pc1733**	similar to pyruvate dehydrogenase (lipoamide), E1 component, alpha chain	**pdhA**	1029	pc1733_534-586	ATTATGGAACTTACCTTGCATCTACGTTATTGAAAATAATCAATGGGGAATGG	74,2	53	0,976	1	0,999	1	0,981	0,762	mid
14	3	J24	**pc1734**	similar to neutral amino acid (glutamate) transporter	**aaaT**	1260	pc1734_623-672	TAAAACAAGGATTAGACGTCAAAAGCCTTGCACTTTATTTAACCGTTGTG	74,2	50	0,975	1	0,994	1	0,992	0,753	mid
14	3	N24	**pc1735**	conserved hypothetical protein	**-**	633	pc1735_154-199	CCTAGGGACATACAGTGGCATTTAATCGGAACGTTGCAGAGTAATA	74,2	46	0,972	1	0,994	0,964	0,924	0,868	5´preference
14	4	B04	**pc1736**	unknown protein	**-**	474	pc1736_111-160	ACAACAATGGGGGAATGAGCCTCTACAAGTTTTTCTTACAAAAAGAGAAG	74,2	50	0,953	1	0,999	1	0,873	0,662	mid

14	4	F04	**pc1737**	conserved hypothetical protein	**-**	1029	pc1737_481-526	ATTCAATTAAATTGCCGTGCCAGAGTAACAGTGAGGACAAATATCG	74,2	46	0,975	1	0,997	1	0,965	0,781	mid
14	4	J04	**pc1738**	hypothetical protein	**-**	480	pc1738_283-328	TACGATCGAAATGCGATTGGAAAATTAGGAATGGTACTTACCGATC	74,3	46	0,979	1	0,992	1	0,995	0,8	random
14	4	N04	**pc1739**	hypothetical protein	**-**	2232	pc1739_1060-1104	GCTGCTGAACCTGTTTATACGAATGAGAATGGAAAAATGGAGTCA	74,3	45	0,97	1	0,995	1	0,943	0,765	mid
14	4	B08	**pc1740**	unknown protein	**-**	423	pc1740_194-239	ATGAATATGCTCGTGAAGTTATGAAAGCCCTCGCTCAAATACCTCT	74,3	46	0,983	1	0,996	1	0,981	0,849	mid
14	4	F08	**pc1741**	unknown protein	**-**	603	pc1741_147-191	AATTCGCTGTTACATGAATTACCTTTCTCAGACCCTTTCCTCACG	74,2	45	0,967	1	0,999	1	0,844	0,864	mid
14	4	J08	**pc1742**	unknown protein	**-**	846	pc1742_494-540	TCGACATCCTCATTCCCAAAGCTCTAGAGAATAAGGGAACACATTTA	74,2	47	0,972	1	0,996	0,974	0,93	0,836	mid
14	4	N08	**pc1743**	unknown protein	**-**	330	pc1743_2-52	TGCAAACAAAGGAGATGTTTATGATAAGTGGATTAAATGGATTTGGACATC	74,2	51	0,974	1	0,999	1	0,997	0,725	random
14	4	B12	**pc1744**	unknown protein	**-**	276	pc1744_53-107	AAAGCAGTTTTTCTACAGAAAAAACTTCTGCTCAATTACAACTAATTTCTGAGCA	73	55	0,789	0,675	0,877	0,853	0,998	0,634	random
14	4	F12	**pc1745**	unknown protein	**-**	834	pc1745_247-299	AAAGCACAGGAAAGTGAAACAATTTCTGTAAATCCAAATGCACTTAGACTAGC	74,3	53	0,975	1	0,993	0,989	0,985	0,783	random
14	4	J12	**pc1746**	unknown protein	**-**	222	pc1746_62-112	AAGCTCCTAGAGGAAGGGTGTCTCTTCATGGAATTTTTGATATAAGAATGC	74,2	51	0,633	0,134	0,998	0,999	0,95	0,748	mid
14	4	N12	**pc1747**	unknown protein	**-**	183	pc1747_55-109	TTTAGAAATTTAGAACTTTGTTCTAACGTTGCTTGCGTTCAATTAAATAGAAGGC	73	55	0,931	1	0,875	1	0,962	0,651	mid
14	4	B16	**pc1748**	strongly similar to glutamate-1-semialdehyde 2,1-aminomutase	**hemL**	1299	pc1748_706-751	ATGGGAGCGTTACTGATTTTTGATGAGGTCATGACTGGATTTAGAG	74,2	46	0,973	1	0,998	1	0,945	0,785	mid
14	4	F16	**pc1749**	hypothetical protein	**-**	1953	pc1749_989-1042	CAAAACAAAGAAGTATGGGTTTTGGAGTAAATTATACCACTCAATTTGGACCTG	74,2	54	0,973	1	0,998	0,964	0,989	0,776	mid
14	4	J16	**pc1750**	hypothetical protein	**-**	3867	pc1750_1773-1821	TCAAATACATTTAGATAAAATCTCATCTGTGAGGGGCGAAGCACAATCT	74,2	49	0,958	1	0,999	1	0,838	0,772	mid
14	4	N16	**pc1751**	unknown protein	**-**	363	pc1751_32-85	ATATCAACCTATTACGACCAATTTTACAAACCTCAGCAGTGACTGCAATAAATG	74,2	54	0,976	1	0,995	1	0,985	0,774	5´preference
14	4	B20	**pc1752**	conserved hypothetical protein	**-**	723	pc1752_252-297	TATGTGTGCAGAATTAGGAACCATGAGGGTCACAGAGCAGATAGAT	74,4	46	0,972	1	0,988	1	0,889	0,887	mid
14	4	F20	**pc1753**	conserved hypothetical protein	**-**	714	pc1753_414-459	AATTATCTTATATGATGAGCCTACAACAGGCCTGGATCCCATCACC	74,3	46	0,98	1	0,994	1	0,944	0,877	mid
14	4	J20	**pc1754**	hypothetical protein	**-**	1230	pc1754_627-676	TACTAACTTTGTTAATTTATCTGAACGAACCCACCAATCGTGGAAGACGT	74,2	50	0,981	1	0,999	1	0,989	0,808	mid
14	4	N20	**pc1755**	conserved hypothetical protein	**-**	570	pc1755_355-400	AATGGACCTCATATTCACTTATGTTTTGGTTATTCAGGCTGGGGAG	74,2	46	0,985	1	0,994	1	0,998	0,851	random
14	4	B24	**pc1756**	strong similarity to small subunit ribosomal protein S9	**rpsI, rs9**	390	pc1756_3-47	GTTAGAAGAAACAGTAGCAACTGGACGACGAAAAACAGCTGTTGC	74,4	45	0,978	1	0,987	1	0,999	0,794	5´preference
14	4	F24	**pc1757**	strongly similar to large subunit ribosomal protein L13	**rl13, rplM**	432	pc1757_149-196	ATTGTGGAGATGGTGTTATTGTGGTCAACGCTGATAAAGTAGAAGTCA	74,2	48	0,988	1	0,999	1	0,999	0,871	random
14	4	J24	**pc1758**	strongly similar to 2-methylthioadenine synthetase	**miaB**	1353	pc1758_726-773	AAGAGTCAGATTTATGACAAGCCACCCTGTTGATATTTCGAAAGAGCT	74,2	48	0,977	1	0,999	1	0,952	0,815	mid
14	4	N24	**pc1759**	similar to Superoxide dismutase (Cu-Zn)	**sodC**	618	pc1759_264-308	TATTGCAGATGTAATGGGATTAACGCCAGGTAAACATGGTTTTCA	74,3	45	0,98	1	0,997	1	0,954	0,849	mid
14	5	B04	**pc1760**	strongly similar to DNA ligase	**dnlJ, ligA**	1998	pc1760_1001-1049	TGACTCCAGTTGCAGAATTAGAGCCTATCTTTTTGTCAGGAAGTACGAT	74,2	49	0,983	1	0,997	0,999	0,999	0,823	mid
14	5	F04	**pc1761**	strongly similar to 1,4-alpha-glucan branching enzyme (= Glycogen branching enzyme)	**glgB**	2184	pc1761_1082-1126	CTCTTTATGAACATGCAGATCCTCGTCAAGGCTATCATCCTCATT	74,1	45	0,974	1	0,986	0,941	0,989	0,853	mid
14	5	J04	**pc1762**	hypothetical protein	**-**	1059	pc1762_488-539	TAGGACAATGGATCCCCAGTAGTTTAGGAATCAATAACGCTTTAGAGGAAAT	74,2	52	0,977	1	0,997	0,999	0,957	0,817	mid
14	5	N04	**pc1763**	similar to 2-methylthioadenine synthetase	**yqeV, miaB, yleA**	1305	pc1763_665-710	CTTCAATAGACCCTGACGAGGTAGATGATGAATTAAGTGACGCCAT	74,2	46	0,981	1	0,999	1	0,989	0,815	mid
14	5	B08	**pc1764**	unknown protein	**-**	7209	pc1764_3565-3609	GCTATGGAACAAGCCTTAACTGATGAAATGCAAAAGCAAGGGTTA	74,3	45	0,971	1	0,991	0,998	0,959	0,773	mid
14	5	F08	**pc1765**	similar to DNA repair protein radC	**radC**	696	pc1765_308-353	AATCTCGCTATTTAATCGAACATTCCTCTCATGCCTACCAGTTGGT	74,2	46	0,979	1	0,996	1	0,959	0,834	mid
14	5	J08	**pc1766**	conserved hypothetical protein	**-**	1335	pc1766_692-736	CAGGAAAGTCTACTCTTCTCAATGCTTTGACTGATGCAGGCGTAT	74,3	45	0,979	1	0,99	1	0,977	0,825	mid
14	5	N08	**pc1767**	similar to phnP protein	**phnP**	717	pc1767_381-429	TTATATGACCTATGAACAGGGAGGAATGGCTGTTAATGGATTTCGTTTT	74,1	49	0,977	1	0,989	0,98	0,979	0,836	mid
14	5	B12	**pc1768**	unknown protein	**-**	555	pc1768_277-321	GAGTTTTATCGATTCATTGCTTCCGAAAACATTTTGCAGTCAGTG	74,4	45	0,974	1	0,983	1	0,998	0,768	mid
14	5	F12	**pc1769**	hypothetical protein	**-**	1005	pc1769_484-532	AGAGGGGCTCAATTCCAAAAACAACATATACACTCCTTACAAGAAATCG	74,2	49	0,973	1	0,999	1	0,981	0,728	mid
14	5	J12	**pc1770**	unknown protein	**-**	750	pc1770_226-274	ATGATAGGCGCATCGTATTTTGCTATTCCGATTATTCTGAGTTATTTGC	74,2	49	0,96	1	0,999	1	0,85	0,774	mid
14	5	N12	**pc1771**	similar to citrate (si)-synthase	**gltA**	1161	pc1771_620-665	ATTTATATGGATCTATGTCAGCAGCTATGTGTGCATTAGCAGGGCC	74,4	46	0,982	1	0,988	1	0,962	0,892	mid
14	5	B16	**pc1772**	strongly similar to NADP-dependent malate dehydrogenase	**mdh**	993	pc1772_501-547	TTCCCAAAAAAGTCAAGTTTCAACAAAGGATGTCTCTTGTGTAACGA	74,2	47	0,977	1	0,999	1	0,997	0,752	mid
14	5	F16	**pc1773**	unknown protein	**-**	894	pc1773_428-472	ACATACCAAACTACGTCATTGTCGATGATGGATCTTACTCTGGCA	74,3	45	0,982	1	0,997	1	0,98	0,84	mid
14	5	J16	**pc1774**	unknown protein	**-**	822	pc1774_432-483	TAAAAGCCCAGAAGAAGTCAGAGAATTTGCAATAACAATAGACCCCAAATTA	74,2	52	0,978	1	0,999	1	0,98	0,785	mid
14	5	N16	**pc1775**	unknown protein	**-**	324	pc1775_108-161	CGCGTTTTGTTTTTCAACGTTTATTGCGGAAGAGACTACTAACATACAAAATAT	74,2	54	0,965	1	0,999	1	0,945	0,698	mid
14	5	B20	**pc1776**	unknown protein	**-**	210	pc1776_106-151	AAGATCGAGATCTCTCATCTACAAACATGCCATGGGAATTTCAGAT	74,2	46	0,982	1	0,999	1	1	0,809	mid
14	5	F20	**pc1777**	unknown protein	**-**	246	pc1777_55-105	TATGCCTCGAAATCAGTAGGGATAGTAAAGCTCCAAAGCGAAATAAAAGTC	74,2	51	0,971	1	0,999	1	0,931	0,782	mid
14	5	J20	**pc1778**	hypothetical protein	**-**	993	pc1778_548-599	AAGTACAAGATCCAGATGACAGAGTACATATTACTTTAGCACAGCCCCCAAG	74,2	52	0,981	1	0,997	1	0,95	0,868	mid
14	5	N20	**pc1779**	unknown protein	**-**	357	pc1779_20-72	CAGTTAGTTTTTTAGGAGGTTTATTAGGAGGATACTGCGGAGTTAATCCCCCT	74,1	53	0,977	1	0,986	1	0,997	0,794	random

14	5	B24	**pc1780**	unknown protein	**-**	249	pc1780_133-180	TTTGAAAGTATTTATGCCACTGGTCAATTGATTGACATCCAAACTCAC	74,1	48	0,964	1	0,989	1	0,895	0,783	random
14	5	F24	**pc1781**	unknown protein	**-**	453	pc1781_3-50	GCTTGGACTTATTCCAATGATTTATGTAGGAGGATTTGCCGAATTACC	74,2	48	0,978	1	0,998	1	0,999	0,769	5´preference
14	5	J24	**pc1782**	similar to Gut Q protein	**gutQ**	960	pc1782_454-498	ATTTTCCAAGGGCTTTTTGGAGACTTAGTGACTGCTGCACTAATG	74,3	45	0,98	1	0,996	1	0,973	0,833	mid
14	5	N24	**pc1783**	strongly similar to isocitrate dehydrogenase (NADP)	**icd**	1452	pc1783_753-798	ATCTGCAAATATTGGTAATTCGGGAGCCATGTTTGAAGCTATTCAT	74,2	46	0,969	1	0,998	0,933	0,974	0,796	mid
14	6	B04	**pc1784**	unknown protein	**-**	804	pc1784_409-453	CTTGATGCTCTATTTGAAACATGTCAAAATGGGTCTGGATTTGCT	74,2	45	0,977	1	0,999	0,994	0,994	0,766	mid
14	6	F04	**pc1785**	similar to proton/sodium-glutamate symporter	**gltT**	1230	pc1785_497-546	TAGCTGATGTCATGTACCGTTTAACTTCATTAGTGATGGAATTTTCTCCG	74,2	50	0,966	1	0,997	1	0,881	0,802	mid
14	6	J04	**pc1786**	similar to tetraacyldisaccharide (lipid A) 4'-kinase	**lpxK**	1107	pc1786_530-574	ATTATGATGTTGTCGTGATAGATGTTTCAGATCCTTTTGGCCGAG	74,2	45	0,981	1	0,999	1	0,975	0,835	mid
14	6	N04	**pc1787**	strongly similar to phosphoheptose isomerase	**gmhA, lpcA**	645	pc1787_352-396	GAATGGATCTTTTCAAGAGGCGTAGAGGCTTATGGTAAAACTGGC	74,3	45	0,979	1	0,996	1	0,972	0,819	mid
14	6	B08	**pc1788**	hypothetical protein	**-**	594	pc1788_303-352	TTGGACTTATTTACATGATAGCTCTCAAGGCATCGCTTTAGCTTATGGAG	74,2	50	0,981	1	0,997	1	0,995	0,811	mid
14	6	F08	**pc1789**	unknown protein	**-**	270	pc1789_92-143	CCCCTCTATATTTGTCCATCTCTATTAATTGTTACAGCCCTTTTCTTGCTGA	74,1	52	0,97	1	0,987	1	0,956	0,767	mid
14	6	J08	**pc1790**	unknown protein	**-**	1233	pc1790_521-565	GCAAAATTGCCCTTAGTACTCAAACACTCAAGTCTTTTCCTCCCA	74,2	45	0,97	1	0,999	1	0,903	0,814	mid
14	6	N08	**pc1791**	similar to 23S rRNA pseudouridine synthase	**rlu**	660	pc1791_398-442	CAAAACTGACTTATCGTGTCATAGAACGAAAGAGCGTAGGGGCTT	74,3	45	0,976	1	0,997	0,933	0,999	0,843	random
14	6	B12	**pc1792**	similar to rRNA methylase	**rlmB, yjfH**	798	pc1792_419-468	GGATTGATGGGTTGATTGTTTGCGATCGATGTACAGATATTTATAATCCT	74,3	50	0,977	1	0,995	1	0,981	0,787	mid
14	6	F12	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
15	1	C04	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
15	1	G04	**pc1793**	hypothetical protein	**-**	864	pc1793_407-451	GAGCTGCGGTATGTCATTTAGATGCTTCTAAAGGAATGGTGACCT	74,3	45	0,975	1	0,99	1	0,974	0,787	mid
15	1	K04	**pc1794**	similar to exopolyphosphatase	**ppx**	1029	pc1794_758-810	AAATGATTGCTGTCGGAAGTCTATTTAACTATGGAATTAGACCAGTGGTTGAC	74,2	53	0,98	1	0,999	0,972	0,999	0,824	random
15	1	O04	**pc1795**	unknown protein	**-**	291	pc1795_43-97	GCTTTTCAACTAGTTTTAATCGATAAATTGCTAATACTTCAGAGGCCAATTCTTT	72,2	55	0,917	1	0,801	0,988	0,999	0,67	random
15	1	C08	**pc1796**	unknown protein	**-**	702	pc1796_381-425	CTTTGATTACTCTTTGGCTGATGGGAAGTTTCGTTCGATGATTCT	74,3	45	0,98	1	0,991	1	0,971	0,845	mid
15	1	G08	**pc1797**	similar to signal peptidase II (prolipoprotein signal peptidase)	**lspA**	528	pc1797_264-311	TCTGATGCTCTTTCGTATAGGATTGATTGTTGGGTTGTGTGTGTACTT	74,2	48	0,985	1	0,999	1	0,999	0,842	mid
15	1	K08	**pc1798**	similar to dnaK suppressor	**dksA**	366	pc1798_118-162	ACTGGTTACTCTCAACACCAAGCAGATCAAGGGACAGATGACTTT	74,3	45	0,987	1	0,995	1	0,999	0,868	random
15	1	O08	**pc1799**	conserved hypothetical protein	**-**	489	pc1799_86-140	GAGAGTGCTTGAATTGTCTTAAGCGTTTTACTACTTTTGAAACAATCGAATTGAC	74,2	55	0,969	1	0,999	0,957	0,958	0,778	5´preference
15	1	C12	**pc1800**	strongly similar to tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase/ Antisuppressor	**ycfB, trmU, mnmA, asuE**	1131	pc1800_575-620	AGGACAGCACTGGAATATGCTTTATTGGAGAAAGAGATTTTCGCTC	74,2	46	0,977	1	0,996	1	0,991	0,768	mid
15	1	G12	**pc1801**	similar to ferric uptake regulator protein	**fur**	393	pc1801_2-53	TGTGTTTACTAACTTTACTTAAATATCGGTTGGCAATGAAAAGAATGACGCG	74,2	52	0,979	1	0,998	1	0,994	0,786	random
15	1	K12	**pc1802**	unknown protein	**-**	819	pc1802_409-460	CGGGTTTCTCATTTTATCGCTCATGGATTATTTACAACATCATTACTTGGTA	74,2	52	0,977	1	0,999	1	0,998	0,754	mid
15	1	O12	**pc1803**	conserved hypothetical protein	**-**	1071	pc1803_540-584	GAAATTAATGTTTTTGAGTCATTCGGACGCTATAGCCGCTTTTCC	74,3	45	0,977	1	0,995	1	0,997	0,768	mid
15	1	C16	**pc1804**	similar to small heat shock protein	**sHsp**	447	pc1804_299-348	ATCAAATAGATATTCCTACTCAAGTCGAAGAAAGCACAGAACAAGCCTGC	74,2	50	0,977	1	0,994	1	0,965	0,81	random
15	1	G16	**pc1805**	similar to zinc ABC transporter membrane protein	**znuA, ycdH**	858	pc1805_351-396	AGATACTCAATGTCATTGCTGTTCGGGATCTGAAGATCTCCATTTT	74,2	46	0,97	1	0,996	1	0,921	0,794	mid
15	1	K16	**pc1806**	strongly similar to zinc ABC transporter ATP-binding protein	**znuC**	738	pc1806_280-325	TTTGAAGTCGTTTTATCTGGGCTTCTATCCCAACTTCCTTGGTATG	74,2	46	0,974	1	0,999	1	0,91	0,849	mid
15	1	O16	**pc1807**	similar to zinc ABC transporter membrane protein	**znuB**	1056	pc1807_557-609	ACATTTTATGGGTTTCCCAGACAGATCTTTATATTCTTTGGGGATTGGATATT	74,2	53	0,974	1	0,993	1	0,972	0,779	mid
15	1	C20	**pc1808**	unknown protein	**-**	354	pc1808_198-242	TGGCTATTATGGATATGGTTTAGGAGGTTTTGGCTTGGGATATGG	74,2	45	0,983	1	0,999	1	0,98	0,844	mid
15	1	G20	**pc1809**	similar to NADH2 dehydrogenase	**ndh**	1245	pc1809_862-907	GGATTTACAAATGTATTTGTCATCGGAGATGCTGCTGCTGTAGTGT	74,2	46	0,95	1	0,998	1	0,762	0,8	mid
15	1	K20	**pc1810**	similar to replicative DNA helicase	**dnaB**	1446	pc1810_796-840	CGCATTGTTTGTTCACAAGCAGAAGTCCAATCCGATAAAATTAAA	74,2	45	0,958	1	0,998	1	0,928	0,649	mid
15	1	O20	**pc1811**	unknown protein	**-**	462	pc1811_2-46	TGACAGTAACAATAACTGCACAACCTATAGAACGAGTGCGGCAAG	74,4	45	0,983	1	0,985	1	0,991	0,866	random
15	1	C24	**pc1812**	hypothetical protein	**-**	1092	pc1812_513-557	TACTGACTTGCCTTGTCCTATTATTGCAGGAATTGCCCACTATCA	74,4	45	0,978	1	0,987	1	0,966	0,841	mid
15	1	G24	**pc1813**	unknown protein	**-**	792	pc1813_364-418	TTTAATGATCCTTATGCTGAGCAAAGATTATTAAACGAGTTACCAGCTTTACGCT	74,1	55	0,965	1	0,988	1	0,967	0,692	mid
15	1	K24	**pc1814**	unknown protein	**-**	654	pc1814_440-489	TCAAAAACACAAGAGAGGATATCTTAACACAATGCGCAAGCTCATTAGTT	74,2	50	0,968	1	0,995	1	0,888	0,826	mid
15	1	O24	**pc1815**	similar to fibronectin/fibrinogen binding protein	**fbp**	1416	pc1815_619-663	TTAAAAGCAGAAAGAGAGTGCCTTGATTGGGAAACCATTCAACAT	74,4	45	0,964	1	0,983	1	0,91	0,784	mid
15	2	C04	**pc1816**	hypothetical protein	**-**	2199	pc1816_1077-1125	TAATTGCGGTGCTGTTAATCATCGGTTATTAGATACTATTGCAAGTCGC	74,3	49	0,981	1	0,99	1	0,976	0,854	mid
15	2	G04	**pc1817**	unknown protein	**-**	261	pc1817_112-158	GTAGATACTTTTGGTACGGGAACTGTCAGTGAAGCAGAGTTGAGTCG	74,3	47	0,985	1	0,996	1	0,981	0,879	mid
15	2	K04	**pc1818**	unknown protein	**-**	183	pc1818_25-77	CGATTCGAATTCATATCATTGTTATTTCAACTCGACATTCTGAGGAAGTTAGA	74,3	53	0,971	1	0,99	0,998	0,932	0,815	mid
15	2	O04	**pc1819**	unknown protein	**-**	279	pc1819_21-72	AACCCGTAGGCAAAGGTTTAGTCATACCTCACTTTCTTTTACTTCTGAATCC	74,3	52	0,981	1	0,997	1	0,999	0,806	random
15	2	C08	**pc1820**	strongly similar to DNA polymerase IV	**dinP;dinB**	1053	pc1820_577-628	AAATTACACAGTTTAGGATTAATGAATTGCGGGGATTTACAGACACTTGACA	74,3	52	0,976	1	0,995	1	0,951	0,824	mid
15	2	G08	**pc1821**	unknown protein	**-**	438	pc1821_53-97	TTCTCTTCTCTTTATCTGCAGAAACGCAATCGCAAAAAATTGATG	74,2	45	0,957	1	0,993	1	0,974	0,587	5´preference

15	2	K08	**pc1822**	similar to sodium/pantothenate symporter (pantothenate permease)	**panF**	1368	pc1822_672-725	CAGTGGATGGCTATTAATGCCTCTACTTTTTATGGTCATAGAACAAGATATGGC	74,4	54	0,976	1	0,98	1	0,987	0,811	mid
15	2	O08	**pc1823**	conserved hypothetical protein	**-**	570	pc1823_241-285	ATAGCGGTTGGCATGCCAGTTTTATCTAATTTCGAAATGAATCCT	74,2	45	0,974	1	0,999	1	0,955	0,778	mid
15	2	C12	**pc1824**	unknown protein	**-**	819	pc1824_277-327	ATTTACTTACAAAAGCACGGAATCCTTTTACCCGAATGGTTAAAGATAGCG	74,5	51	0,957	1	0,972	1	0,866	0,803	mid
15	2	G12	**pc1825**	similar to beta-N-acetylglucosaminidase	**nagA**	1653	pc1825_807-853	TTTGAATTGCGTAACATTTTCGAAATCTGCGATTGATGTTCTAAGAA	74,2	47	0,974	1	0,998	1	0,979	0,752	mid
15	2	K12	**pc1826**	unknown protein	**-**	681	pc1826_359-413	AACAAGCAAATTGGAGCCATTACAAAGAAGTAGATTGGTCTAACCCTTTAAGTTT	74,2	55	0,974	1	0,994	1	0,982	0,755	mid
15	2	O12	**pc1827**	unknown protein	**-**	1209	pc1827_610-664	AATTCTCCTGCACTCAATGACAAATACAATCAATTTGAACAATTGATTATGAAGT	74,1	55	0,97	1	0,99	1	0,996	0,703	mid
15	2	C16	**pc1828**	conserved hypothetical protein	**-**	936	pc1828_507-560	AGAATTAGTAGAATCTTTTGGCTATACATATATTCGTTTGCCAATCACGGACCA	74,2	54	0,973	1	0,997	0,963	0,962	0,82	mid
15	2	G16	**pc1829**	conserved hypothetical protein	**-**	471	pc1829_210-254	ATCAGGATATACATTATTTACGACCGCAGAACCATGTCCCATGTG	74,4	45	0,981	1	0,987	1	0,973	0,872	mid
15	2	K16	**pc1830**	conserved hypothetical protein	**-**	855	pc1830_632-685	CAAATGTCTGGAATACAGATTATATCATCCGATTAGATAAAGAGACAGGCATCG	74,2	54	0,984	1	0,999	0,992	0,999	0,835	random
15	2	O16	**pc1831**	conserved hypothetical protein	**-**	678	pc1831_311-357	TCCATAAAGCTGAGTTAAGTCACCTCGTTAAAATTCGGCAAGGCTAT	74,2	47	0,98	1	0,999	1	0,971	0,824	mid
15	2	C20	**pc1832**	hypothetical protein	**-**	1371	pc1832_589-634	GAATTGAACGTTGTGAGCGCATTATTGAACCAGAGTTCTCAGTTAA	74,2	46	0,634	0,13	0,999	1	0,902	0,85	mid
15	2	G20	**pc1833**	conserved hypothetical protein	**-**	2487	pc1833_1244-1298	CCAGAGAGCATTTCGGATCTCTACTTTTAGGAGTCTACAAAGATAATGAATTGCT	74,2	55	0,978	1	0,999	0,988	0,999	0,779	mid
15	2	K20	**pc1834**	similar to DNA-3-methyladenine glycosidase II	**alkA**	1431	pc1834_697-751	ATTAGAGAGTATAAAGGCTGGATTCACGTTTCTCATGTAGAGGATAAACATTGCC	74,4	55	0,98	1	0,986	1	0,981	0,852	mid
15	2	O20	**pc1835**	similar to methylated-DNA-[protein]-cysteine S-methyltransferase	**ada**	522	pc1835_111-155	AAATCCTGCAGAACTTCAATTACTCCTTCAAGCTCGTTTTCCTCA	74,2	45	0,978	1	0,999	1	0,993	0,775	random
15	2	C24	**pc1836**	similar to H1-like protein	**hctB**	636	pc1836_421-468	TCGACAACAACTTCTCCTCGTACTAATACAATCAAGAAAACGACAGCA	74,3	48	0,978	1	0,992	1	0,998	0,788	random
15	2	G24	**pc1837**	hypothetical protein	**-**	417	pc1837_95-139	TGTTTGGGCAACGTTCTAAACGGTACGAAGGAGTTATTAATCCAC	74,1	45	0,967	1	0,988	1	0,885	0,84	mid
15	2	K24	**pc1838**	similar to lipoate-protein ligase	**lplA**	702	pc1838_353-399	AAGAAAACGATTATGTTATGGGCCTAAGGAAATTTGGAGGTAATGCG	74,3	47	0,981	1	0,994	1	0,999	0,811	mid
15	2	O24	**pc1839**	similar to glucose-inhibited division protein	**gidA**	1878	pc1839_974-1018	CATTTATCAAAAGTATCCCTGCACTTCGTCATGCTGAAATCATGA	74,2	45	0,977	1	0,998	1	0,966	0,8	mid
15	3	C04	**pc1840**	hypothetical protein	**-**	1554	pc1840_848-896	TATTTTGTGGAGGACTTTCATTAATATGCTTAGCGTGTGCTTTAGGCCT	74,2	49	0,976	1	0,999	1	0,93	0,838	mid
15	3	G04	**pc1841**	strongly similar to succinate dehydrogenase iron-sulfur protein	**sdhB**	774	pc1841_423-472	AAATATTGGTCCAGAAAAGCAAAAAGTGATGTATTCTTTAGCAACCTGCA	74,2	50	0,97	1	0,994	1	0,965	0,736	mid
15	3	K04	**pc1842**	strongly similar to succinate dehydrogenase flavoprotein	**sdhA**	1884	pc1842_930-974	AGTTTTACGTATTTGCGAAATGGGATTAGGGATCAATGGGGAAAT	74,4	45	0,98	1	0,986	1	0,987	0,838	mid
15	3	O04	**pc1843**	similar to succinate dehydrogenase cytochrome b558	**sdhC**	963	pc1843_420-465	TCCAGTAACTGCTCAATTGGACACTCAACATTATTATCTCGTTCGC	74,2	46	0,976	1	0,999	1	0,938	0,83	mid
15	3	C08	**pc1844**	similar to deoxyribonuclease TatD	**tatD;mttC**	798	pc1844_369-417	GCATTTAGCTCTTGAATGTCGATTACCTGTAGTCATTCATTGTCGAGAG	74,2	49	0,979	1	0,997	1	0,969	0,825	mid
15	3	G08	**pc1845**	unknown protein	**-**	198	pc1845_3-49	GTTCATTCAAACATCTCCTGGCTTTATACGGCTTATTGAAGCCTTTC	74,3	47	0,972	1	0,996	0,975	0,99	0,752	random
15	3	K08	**pc1846**	similar to thiol-disulfide interchange protein	**dsbD**	2244	pc1846_1140-1189	ATTTTGGCTATTAGCTTCTGCAATGCTAACTCTACGTGCTTATGGTCAAG	74,2	50	0,98	1	0,991	0,993	0,983	0,843	mid
15	3	O08	**pc1847**	similar to TolQ protein	**tolQ**	753	pc1847_367-420	TCGTTAAGTGATATAGACTACGTTGCCTCTCATTTATCCACTCAAGTTGCTTCT	74,2	54	0,981	1	0,997	1	0,989	0,817	mid
15	3	C12	**pc1848**	similar to TolR protein	**tolR**	429	pc1848_104-154	TTATTGTAATTGCCCCCTTATTAGAACAAGATCATGTTGAACTTGCTGATG	74,2	51	0,968	1	0,999	1	0,888	0,816	mid
15	3	G12	**pc1849**	similar to tolA protein of Tol-Pal system	**tolA**	1068	pc1849_543-588	AAATATTGCTAAGGAAACTCTTGCCAAAGATGCTGACAAGCGACTT	74,3	46	0,98	1	0,996	1	0,992	0,799	mid
15	3	K12	**pc1850**	similar to TolB protein	**tolB**	1410	pc1850_763-812	AAAGATGGCAAAGGACAGCGTTTATTGAAGCTTAAAGGTAATCAACTGAT	74,2	50	0,973	1	0,999	1	0,943	0,792	mid
15	3	O12	**pc1851**	strongly similar to peptidoglycan-associated lipoprotein precursor (pal)	**pal;excC**	741	pc1851_342-390	AGGTAGTTCCATTCCGAGTATTGAATCTTTTCAAGATCCTTGCATGATT	74,2	49	0,976	1	0,998	1	0,97	0,789	mid
15	3	C16	**pc1852**	hypothetical protein	**-**	720	pc1852_324-373	AGAAGGGAAAATTGATACTCTTGATAAAGCTGTCAACGGTTTGATGAATG	74,3	50	0,968	1	0,995	1	0,963	0,718	mid
15	3	G16	**pc1853**	strongly similar to glutamate racemase	**murI**	750	pc1853_370-420	ATTGCATGTCCTCTATTGGTTTCTCTCGTTGAAGAAGGTTTTCTCTATCAT	74,2	51	0,981	1	0,999	1	0,994	0,802	mid
15	3	K16	**pc1854**	unknown protein	**-**	351	pc1854_153-207	TTCTACTAATCAAATGGTGACAGTTCAAGGGATATTAAAGTTACAAGCGCAAGAG	74,3	55	0,978	1	0,995	1	0,976	0,812	mid
15	3	O16	**pc1855**	similar to two-component response regulator phoP	**phoB**	690	pc1855_263-311	AAGAGCTCGATGTTGTTTTAGGACTTGAGCTAGGTGCAGATGATTATGT	74,2	49	0,973	1	0,999	0,998	0,917	0,829	mid
15	3	C20	**pc1856**	conserved hypothetical protein	**-**	933	pc1856_457-501	GAATTATCTGTCATGATGGCTGCTATCTGCAGTGTTTATGGATGG	74,1	45	0,975	1	0,99	0,947	0,99	0,842	mid
15	3	G20	**pc1857**	conserved hypothetical protein	**-**	1032	pc1857_552-603	GCACATCAAGTTAGTTAGACTTGAACCAACTGACCTAGAAGCTCATACAGGA	74,2	52	0,982	1	0,999	0,985	0,965	0,881	mid
15	3	K20	**pc1858**	unknown protein	**-**	1272	pc1858_727-776	ACAGCCTCATATCATAAACGGAAAGTAAGTGATGGAATAGGAACACTTGC	74,3	50	0,972	1	0,997	0,998	0,91	0,835	mid
15	3	O20	**pc1859**	conserved hypothetical protein	**-**	597	pc1859_42-89	TCGCCATAAACGCTTAGTAACTCCTAAAGACGATTTAACACGTCCAAC	74,2	48	0,982	1	0,999	0,991	0,98	0,85	5´preference
15	3	C24	**pc1860**	unknown protein	**-**	978	pc1860_530-584	CTTCCTCTAACCCACTCTATGGTAATGACTCTAATCCTTTTGTAAAACCATCCAG	74,1	55	0,975	1	0,988	1	0,96	0,818	mid
15	3	G24	**pc1861**	hypothetical protein	**-**	1203	pc1861_709-753	ACCCTAGGTTTAGCCGAATGGATTTATTATGGAGGAGGGCATCTA	74,2	45	0,967	1	0,998	0,989	0,894	0,813	mid
15	3	K24	**pc1862**	unknown protein	**-**	495	pc1862_158-	CCCATTCTACTCGGAGTGATTTAGCTGATAATTATTCGTATGGATGTGACAATA	74,3	54	0,982	1	0,995	1	0,997	0,82	random

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15	3	O24	**pc1863**	unknown protein	-	441	pc1863_46-95	TTAGTATTAGCATCTAGCCCTGTTACTGCTCAGACAACAGATGGAACAGC	74,3	50	0,963	1	0,991	0,99	0,824	0,882	mid
15	4	C04	**pc1864**	unknown protein	-	633	pc1864_310-355	GACTGGAATGCAGCGCATATCTCTAATCATTCTTATTCTCAAACGG	74,3	46	0,983	1	0,994	1	0,993	0,841	mid
15	4	G04	**pc1865**	conserved hypothetical protein	-	861	pc1865_348-392	TTATACACGAGAAGTCGTTGATTATGTGGCAGAAAGAGCTCGGAT	74,2	45	0,973	1	0,994	1	0,916	0,841	mid
15	4	K04	**pc1866**	unknown protein	-	897	pc1866_324-368	TTTATCGGAATGTCCTCCCAATCACTGGGCATTATCATTAGTAGG	74,2	45	0,984	1	0,998	0,985	0,985	0,869	random
15	4	O04	**pc1867**	unknown protein	-	648	pc1867_366-410	TTTGCATATAAAGCATCGCTGGGAAGATTTTAGTCGGGACAGTAG	74,3	45	0,974	1	0,99	1	0,959	0,806	mid
15	4	C08	**pc1868**	conserved hypothetical protein	-	771	pc1868_373-417	TTATTTTATGATCCTCAACATCACGTGATTGCGAATGTTCATGCT	74,4	45	0,976	1	0,987	1	0,986	0,797	mid
15	4	G08	**pc1869**	similar to phosphoglycerate mutase	-	648	pc1869_437-481	TCTCTCCATTGTACTTAGGCTCTACAATTTTGCTGTCTTCCCACG	74	45	0,964	1	0,974	1	0,888	0,84	mid
15	4	K08	**pc1870**	unknown protein	-	1551	pc1870_842-895	TTATTAACACTTCCGATAAATGGATATTTAATGGTCCCAGTTGCGTGTTTAGTC	74,2	54	0,975	1	0,997	1	0,935	0,831	mid
15	4	O08	**pc1871**	unknown protein	-	492	pc1871_151-205	CTCATGGAGTTAGTTAGAGTGGATTTTGATTTTAGTGAGGACGAACGATTAATTG	74,2	55	0,963	1	0,991	1	0,904	0,757	mid
15	4	C12	**pc1872**	unknown protein	-	240	pc1872_27-74	AAGTTCGGAGTGCTTATCCTTAAAGGAGTTGAAATGTGGAGTTTTGTG	74,2	48	0,971	1	0,996	1	0,906	0,825	mid
15	4	G12	**pc1873**	hypothetical protein	-	1095	pc1873_550-594	TTGTATGCTCCAACTTGTCATGACCAAGATCATACGACATCCTTT	74,3	45	0,986	1	0,997	1	0,999	0,859	mid
15	4	K12	**pc1874**	similar to arginine kinase	-	990	pc1874_517-561	GGAATTGAGCAAACAGGTTTACAAGGAAATCCCCATGAAATCATA	74,2	45	0,978	1	0,998	1	0,979	0,798	mid
15	4	O12	**pc1875**	conserved hypothetical protein	-	579	pc1875_75-127	TGTTCGCTACACAGAAATTGTGGGTGAGAATATGACTCATACTAGTATGTGTG	74,3	53	0,985	1	0,993	1	0,989	0,875	random
15	4	C16	**pc1876**	similar to ribosome recycling factor (ribosome releasing factor)	**rrf**	552	pc1876_261-306	AATGCCTATTGTTGATGCGCATTCTGTTCGTATAAAAATTCCTCCT	74,2	46	0,973	1	0,997	1	0,984	0,738	mid
15	4	G16	**pc1877**	strongly similar to uridylate kinase	**pyrH;smbA**	756	pc1877_284-328	AAGTCAAAACGTGCGTGATGAGTGCCTTAGACTGTCCAAAAGTAG	74,7	45	0,965	1	0,957	1	0,905	0,877	mid
15	4	K16	**pc1878**	similar to procollagen-lysine 5-dioxygenase	-	888	pc1878_465-517	AAAAGACCTTATCAAACAAGATAAGCCTATTATTGCGCCCTTGTTACGATCTT	74,3	53	0,974	1	0,995	0,995	0,98	0,769	mid
15	4	O16	**pc1879**	hypothetical protein	-	1086	pc1879_499-553	GGATTAGGAGTGGAACTTTTAGGAGATTGTGTTGAATTTAGAGTCAATGGCTATC	74,2	55	0,975	1	0,999	1	0,955	0,794	mid
15	4	C20	**pc1880**	similar to X-Pro dipeptidase	-	999	pc1880_558-605	TTTACAGGCTAACATGCCTGTGTTAATTGATATTGGAGTTGTCGTTCA	74,3	48	0,975	1	0,998	1	0,943	0,81	mid
15	4	G20	**pc1881**	similar to two-component sensor histidine kinase phoR	**phoR**	1770	pc1881_764-809	TCTTAGAATCACTTGTGGAAGGAGTAATTGCCGTTGACCGTACAAT	74,3	46	0,971	1	0,995	1	0,878	0,872	mid
15	4	K20	**pc1882**	conserved hypothetical protein	-	996	pc1882_476-521	AAAATCCGATTGAGCAAGAAGGAACCTATCCTTTATCTGAAGCACA	74,3	46	0,977	1	0,997	1	0,977	0,79	mid
15	4	O20	**pc1883**	conserved hypothetical protein	-	879	pc1883_430-478	GTTTTGAGAGTTATTCGTGAGCTTCTATTTTTTCAGCCTCAGTATCGGG	74,3	49	0,974	1	0,997	1	0,989	0,734	mid
15	4	C24	**pc1884**	unknown protein	-	1095	pc1884_589-633	ACGGTTCCTTGGCTAACAATCCTGCTGTTATTGTGTTTACTGCTT	74,3	45	0,981	1	0,994	1	0,96	0,866	mid
15	4	G24	**pc1885**	hypothetical protein	-	654	pc1885_365-410	ATCCGTATGCAAGTTTATATGTCGGAGCAGGTGCTTCTTACAATTG	74,2	46	0,982	1	0,999	1	0,963	0,856	mid
15	4	K24	**pc1886**	conserved hypothetical protein	-	1110	pc1886_550-594	TTAACAATGTTGGTGGGGTTAATTGTGACAGCTTTATCTGTCGCT	74,2	45	0,983	1	0,999	1	0,994	0,821	mid
15	4	O24	**pc1887**	conserved hypothetical protein	-	1128	pc1887_549-597	AGGATCCTTAGCGATTATTATGACCTTAATTGGAACACTTTTGACCGCT	74,2	49	0,982	1	0,999	1	0,984	0,826	mid
15	5	C04	**pc1888**	conserved hypothetical protein	-	1731	pc1888_851-895	GATTATCTGCAACTGTCATCCCAATCCTACCTCGTTTTGAAGATG	74,1	45	0,979	1	0,987	1	0,984	0,824	mid
15	5	G04	**pc1889**	conserved hypothetical protein	-	849	pc1889_492-539	TTTAACACGTATCAGAGAGCCAGGTTCTATTGTAAGGGAAGCAGATCC	74,3	48	0,979	1	0,992	1	0,934	0,886	mid
15	5	K04	**pc1890**	conserved hypothetical protein	-	972	pc1890_585-629	GATTCGACTTATTCGCCAAACATTAATCGATATGGGAGGACACAT	74,3	45	0,985	1	0,995	1	0,994	0,861	random
15	5	O04	**pc1891**	unknown protein	-	885	pc1891_461-515	TTAGGCAAATCGAAGATATTCAACGTATTCGCTTAGAAGATCCTGTATTACAACA	74,3	55	0,977	1	0,997	1	0,983	0,775	mid
15	5	C08	**pc1892**	unknown protein	-	798	pc1892_383-433	TTTCTACCGACATATTAGCTAGGCTGTATGTTGATCAACAACATCGTCTTG	74,2	51	0,983	1	0,997	1	0,983	0,844	mid
15	5	G08	**pc1893**	unknown protein	-	567	pc1893_6-57	GAGATATATCCTGATACCAACTCAGATCTGCAATAATCAAATGCTTCAACCC	74,3	52	0,976	1	0,997	1	0,986	0,769	random
15	5	K08	**pc1894**	unknown protein	-	588	pc1894_303-349	GATTGAGCGCCCATTAATGTTATCTGCTATCGAAACTTATCAACTGG	74,2	47	0,985	1	0,999	1	0,992	0,846	mid
15	5	O08	**pc1895**	conserved hypothetical protein	-	405	pc1895_49-98	ATGATCGTCATGTTCTTAATCGCAATGATTACAGGCGTGATAGCTTATAA	74,2	50	0,983	1	0,999	0,974	0,996	0,855	random
15	5	C12	**pc1896**	similar to protein of the general secretion pathway	**gspF;xcpS**	1188	pc1896_515-562	CGTTGTTGATTATCACCCTCTTACTTGGATTTGTCGTTCCCTCTTTAG	74,3	48	0,966	1	0,994	1	0,92	0,759	mid
15	5	G12	**pc1897**	strongly similar to protein of the general secretion pathway	**gspE;xcpR**	1632	pc1897_848-892	AAAAGCTCGTTTCATTACCAGAAGGTATTGTTTTAGTGACGGGGC	74,2	45	0,975	1	0,999	0,968	0,969	0,821	mid
15	5	K12	**pc1898**	similar to protein of the general secretion pathway	**gspD;xcpQ**	2490	pc1898_1248-1294	TCCTATTCTTAACCCACAAAAAGAGCCTCCCCAAACCTTATATGGAC	74,3	47	0,982	1	0,998	1	0,998	0,811	mid
15	5	O12	**pc1899**	conserved hypothetical protein	-	1419	pc1899_856-901	GAGCGATTATTGACTTTGGAATTGTGGGATGTAGAAGGGAAAGGTA	74,3	46	0,963	1	0,997	1	0,855	0,805	mid
15	5	C16	**pc1900**	unknown protein	-	525	pc1900_258-312	GATTGTTCTCATGATGTTTATGTACGGTAGCCTATTAGGAGAGCTAATCATTGGA	74,3	55	0,981	1	0,989	0,993	0,995	0,841	mid
15	5	G16	**pc1901**	similar to RNA polymerase sigma-54 factor (sigma-N)	**rpoN**	1479	pc1901_826-873	TTCTCTGCTCAAACATCTCAAGTACTTATTCCCGATGTTACTTTGCGT	74,2	48	0,973	1	0,991	1	0,915	0,852	mid
15	5	K16	**pc1902**	unknown protein	-	240	pc1902_39-87	ATCTGAAAAGTATGAAACGCAAGATTCCAAAAACATTACTCCCTCAACC	74,3	49	0,98	1	0,997	1	0,993	0,797	random
15	5	O16	**pc1903**	unknown protein	-	429	pc1903_13-60	TTAAGCCCAGATAATGAATTTGGTGTAGCGATCAAAGAAAGTGGAGAT	74,2	48	0,98	1	0,998	1	0,993	0,796	random
15	5	C20	**pc1904**	unknown protein	-	207	pc1904_46-94	TTTTTTCTACTATATGTTTTTTGGGGATTTTCCGTGTCTTGGGTTGGTT	74,3	49	0,973	1	0,997	1	0,973	0,753	random

15	5	G20	**pc1905**	unknown protein	-	261	pc1905_112-161	GAAACAGACGCGGCTACTTTTTACAAATCAATAGTTGATGCTAAAAATGC	74	50	0,966	1	0,979	1	0,964	0,732	random
15	5	K20	**pc1906**	conserved hypothetical protein	-	486	pc1906_48-96	TATGGTAGAAGGAGTTATTGGAGTTTGGTTAGGAACCTTGAATCGTTCG	74,2	49	0,984	1	0,996	1	0,992	0,852	random
15	5	O20	**pc1907**	unknown protein	-	270	pc1907_7-60	CTTCTAGACCCTAAAGAGTTACCAAAAGACCCCCGTTCAAATGATTTTCTAGTT	74,3	54	0,962	1	0,996	1	0,871	0,775	mid
15	5	C24	**pc1908**	unknown protein	-	192	pc1908_52-103	TTATTAGTGATTCAGAGCGGGAAAAATTCAACGAGGAAAACGGTTAAATTAT	74,2	52	0,628	0,118	0,999	1	0,955	0,754	mid
15	5	G24	**pc1909**	hypothetical protein	-	795	pc1909_331-379	AAAGCCGATTTGGTTCAAAGAAGTCATGATGAAATCAGTGTAAATTTTG	74,2	49	0,964	1	0,999	1	0,933	0,708	mid
15	5	K24	**pc1910**	unknown protein	-	957	pc1910_541-591	AAAATCCATAGAGTGTATACGGGAAGTCTAAATCGGCTTCATGACTTGAAA	74,2	51	0,979	1	0,995	1	0,938	0,867	mid
15	5	O24	**pc1911**	unknown protein	-	222	pc1911_114-167	TAACCCTCATCTATGTTCCAAATTAGAGTCTACAAACCCAAACAATTACTTGGC	74,2	54	0,98	1	0,996	1	0,998	0,795	mid
15	6	C04	**pc1912**	conserved hypothetical protein	-	267	pc1912_133-179	CGCGATCATAATTTGACTGGTAATTGGGTAGCTTACAGAGAATGTCA	74,2	47	0,985	1	0,999	1	0,998	0,844	mid
15	6	G04	**pc1913**	unknown protein	-	267	pc1913_117-164	CATGTCATACGTTAGACCAAATATTCCCCATAATGAGCCTAATGCTGA	74,2	48	0,986	1	0,998	1	0,983	0,871	mid
15	6	K04	**pc1914**	conserved hypothetical protein	-	1587	pc1914_727-778	TTAAAGGGTTTGCAGCATCTAGATCTAAGCTACTGTGAGAATCTCACTGATG	74,1	52	0,6	0,058	0,991	1	0,932	0,758	mid
15	6	O04	**pc1915**	conserved hypothetical protein	-	2052	pc1915_989-1038	ATTTAAGGGTTTGTAAGAATATCACTGATGCAGGACTAGCGCATTTAGCA	74,2	50	0,623	0,094	0,999	1	0,962	0,795	mid
15	6	C08	**pc1916**	conserved hypothetical protein	-	933	pc1916_463-516	CATCTAAAGCTGAATGCATGCTATAATCTTACCGATGATGGATTAGTCCATTTA	74,2	54	0,619	0,076	0,994	1	0,995	0,796	mid
15	6	G08	**pc1917**	conserved hypothetical protein	-	249	pc1917_68-112	AAAAACATTCATTCTCAGGACATAGCTTACGGGCTGGATTTGCTA	74,2	45	0,612	0,05	0,996	1	0,987	0,838	random
15	6	K08	**pc1918**	conserved hypothetical protein	-	1659	pc1918_883-935	TTGCAGAATCTAGCTCTAACTAGCTGCAAAAATCTCACCGATAGAGGATTATC	74,1	53	0,618	0,099	0,986	1	0,948	0,777	mid
15	6	O08	**pc1919**	conserved hypothetical protein	-	294	pc1919_136-181	CTAGATCTAAGCTTGTGCGAGAAATTCACTGATGATGGATTAGCCC	74	46	0,614	0,084	0,98	1	0,988	0,759	mid
15	6	C12	**pc1920**	conserved hypothetical protein	-	1554	pc1920_754-799	TTAAAAGTGCTTCATTTAGAGGCGTGTCAAGCTATTACGGACGATG	74,3	46	0,628	0,109	0,994	1	0,976	0,776	mid
15	6	G12	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
16	1	D04	**Cont**	Cont				GGAAGGAAGGAAGGAAG									
16	1	H04	**pc1921**	hypothetical protein	-	291	pc1921_114-167	TGATTCCGACATCGTGTATTTAGATAAGGACGGATACTCTGTTTTTCATTATTG	74,2	54	0,977	1	0,998	1	0,967	0,802	mid
16	1	L04	**pc1922**	unknown protein	-	315	pc1922_65-110	AACAGCGAAAAGCTATTAGAATGTTGGCTGCGCAAGAAGATAAAAG	74,2	46	0,975	1	0,997	0,99	0,999	0,753	random
16	1	P04	**pc1923**	conserved hypothetical protein	-	279	pc1923_109-153	GAACAAGTTTTGCCTAATCAATACCGCGATCATGCTCTACTAGGC	74,3	45	0,976	1	0,997	0,974	0,968	0,825	mid
16	1	D08	**pc1924**	unknown protein	-	1527	pc1924_874-924	GCATATTTGAAAGCTCATCGAGGCCAGGTGTTATCTAACGAAATAATTCTA	74,2	51	0,961	1	0,995	1	0,891	0,738	mid
16	1	H08	**pc1925**	strongly similar to endonuclease G, mitochondrial precursor	-	453	pc1925_158-207	TAGTTATACAAGTGTATCTTTCTCATGACGGATGCGACGGGAAACGTTAT	74,8	50	0,718	0,341	0,945	1	0,999	0,878	random
16	1	L08	**pc1926**	conserved hypothetical protein	-	2286	pc1926_1457-1502	GATTTGCCCATCTGACACCTTTAACGGGCTTACAGTATCTTGATTT	74,2	46	0,64	0,133	0,998	1	0,973	0,797	random
16	1	P08	**pc1927**	conserved hypothetical protein	-	330	pc1927_103-148	CTAGATTTAAGCTCTTGTAAGGAAATCACTGATGCGGGATTAGCGC	74,1	46	0,626	0,109	0,986	1	0,999	0,749	random
16	1	D12	**pc1928**	conserved hypothetical protein	-	1587	pc1928_872-922	CATCTTTAACCGCTTTGCAATATCTAGCTCTAATGGGCTGTAAAAATCTCA	74,2	51	0,6	0,061	0,996	1	0,923	0,75	mid
16	1	H12	**pc1929**	conserved hypothetical protein	-	360	pc1929_1-47	ATGGGATCAAACATTCTCACTTGTCCTGTCAGAACCTTAAATGATTG	74,1	47	0,615	0,08	0,991	0,958	0,996	0,799	random
16	1	L12	**pc1930**	conserved hypothetical protein	-	330	pc1930_15-61	AAATAGCATTATGGAAAGGCTTCTAGAGCATATTGGCGGGAGAAAAG	74,2	47	0,622	0,07	0,999	1	0,998	0,831	random
16	1	P12	**pc1931**	conserved hypothetical protein	-	591	pc1931_18-64	AATCATTGATCCGCTTCTCTCATCTACTTTGGAAACCTATGAACAGG	74,1	47	0,977	1	0,983	1	0,985	0,821	random
16	1	D16	**pc1932**	unknown protein	-	249	pc1932_89-135	AAAATCAGAAAGCACATGAAGAGCCGATTGAAATCAAGAAAACAACT	74,2	47	0,973	1	0,998	1	0,975	0,744	random
16	1	H16	**pc1933**	unknown protein	-	249	pc1933_34-79	AATGCTAAAGTAATTGACAGTCATGATGAACAAATGGCTAAGCGCC	74,3	46	0,979	1	0,991	1	0,996	0,803	random
16	1	L16	**pc1934**	conserved hypothetical protein	-	786	pc1934_320-368	ATCTAAGCAACTGTATGAATCTCACTGACGATGGTTTGGTGCATTTAAC	74,2	49	0,616	0,086	0,996	1	0,926	0,814	mid
16	1	P16	**pc1935**	conserved hypothetical protein	-	1515	pc1935_1139-1183	AACATTTAAATCTGAGTGGATGTGGCGGCATAGGTGCTGGATTAG	76	45	0,654	0,416	0,824	1	0,619	0,745	mid
16	1	D20	**pc1936**	conserved hypothetical protein	-	1131	pc1936_822-866	ATCGAAACAGGTGTTCTCAAAAGTCGAACTAGGTGGTCATGAAAA	74,3	45	0,949	1	0,996	1	0,745	0,818	mid
16	1	H20	**pc1937**	unknown protein	-	690	pc1937_386-438	ATAAAGCCCTCTATATGGCTAACTGTATGGAATTTGATTTACCTTACCACGCC	74,3	53	0,975	1	0,991	1	0,96	0,811	mid
16	1	L20	**pc1938**	unknown protein	-	300	pc1938_132-180	TCATCCCTCATTAAATACTCACAAATTTGGGGCTATTTCCTCTCCTTTT	74,2	49	0,604	0,05	0,997	1	0,983	0,749	random
16	1	P20	**pc1939**	unknown protein	-	285	pc1939_146-199	TGCAACAAGGTTGGCCTATGAGAAAATATATTAATCAAAAACAAGTTAAGCTTCA	74,2	54	0,609	0,04	0,999	1	0,998	0,82	mid
16	1	D24	**pc1940**	unknown protein	-	204	pc1940_56-100	ATATTTTGTTTTGGAAAGAAATGCACGATTTGAAAGGAACGCAGA	74,4	45	0,602	0,083	0,982	1	0,96	0,657	random
16	1	H24	**pc1941**	unknown protein	-	198	pc1941_52-106	TTATGGCGATACGGACTAATTATATCTAAAAGGTTTTTGCTCATTCTTCTTGGGT	74,3	55	0,627	0,119	0,997	1	0,952	0,754	mid
16	1	L24	**pc1942**	unknown protein	-	210	pc1942_37-83	GCCTTATCAAATGAAAGTTTATCAACGCCGTCCAAAAAAACCATAAA	74,3	47	0,617	0,11	0,997	1	0,982	0,631	random
16	1	P24	**pc1943**	unknown protein	-	216	pc1943_4-58	AGTTATAATGTTACCAGATTCATGGGATATAGAGATTTGGATTCCATTCAATTGC	73,5	55	0,807	0,64	0,925	1	0,895	0,788	mid
16	2	D04	**pc1944**	unknown protein	-	3009	pc1944_2661-2707	AACTCGAATCAGTGGATTCGAGGGATTTAACTCAGTTCTTTCTGTTG	74,3	47	0,983	1	0,997	1	0,996	0,829	random
16	2	H04	**pc1945**	unknown protein	-	294	pc1945_80-126	GGTTATCATGGGGTTCTGGGCTAGGAAGGATGATTAATATTTGTGAA	74,3	47	0,981	1	0,998	1	0,998	0,801	random
16	2	L04	**pc1946**	conserved hypothetical protein	-	1389	pc1946_660-704	AAATGGCTTAAAATGTTACGAATCTCCCTTTTTCCGCTCTTCCAT	74,3	45	0,609	0,06	0,998	1	0,965	0,778	mid
16	2	P04	**pc1947**	unknown protein	-	2544	pc1947_1262-1315	TTCCAATACATACAAGATAGGAAAAGGCTAACGGAAGAGATGATAGGCAAACT	74,3	54	0,624	0,09	0,993	1	0,989	0,804	mid
16	2	D08	**pc1948**	unknown protein	-	252	pc1948_61-105	TTTGTTATTCATCGGCCAGGTTATTCTTTACACTATGATGCACGC	74,2	45	0,977	1	0,999	1	0,934	0,844	mid
16	2	H08	**pc1949**	unknown protein	-	219	pc1949_9-63	CTTACCAATTTTCCAGTTTCAATACCTTAAAAAAACGTGTGAGGACTGCTACTTC	74,3	55	0,637	0,145	0,992	1	0,994	0,704	random
16	2	L08	**pc1950**	unknown protein	-	183	pc1950_7-51	TTGTCGGTGCTTGTCATCCCAAAATTACCACCTTTTTTAAATTGT	74,2	45	0,597	0,07	0,998	1	0,982	0,586	random
16	2	P08	**pc1951**	strongly similar to metalloproteinase	-	336	pc1951_21-70	AAATCATAATCGACTTGGTAATCAAGAAGAAACAGGGGCGTTAAATGAAG	74,3	50	0,641	0,15	0,994	1	0,99	0,723	5´preference

16	2	D12	**pc1952**	unknown protein	-	1110	pc1952_631-683	GGAAATTCTTATATTGAACAATTTGGACATCGTGCGACTACAGAGATTACAATC	74,2	53	0,594	0,04	0,993	1	0,925	0,777	mid
16	2	H12	**pc1953**	conserved hypothetical protein	-	420	pc1953_173-217	CGAGATTTGGAAAGCCTGTGATGATCAATCAAGTCACTATGACAT	74,2	45	0,617	0,08	0,998	1	0,962	0,787	mid
16	2	L12	**pc1954**	conserved hypothetical protein	-	2115	pc1954_976-1022	CTAAGCTACTGTAAAAATCTTACCAATGTCGGATTGTCGCATTTGGC	74,2	47	0,605	0,063	0,992	0,998	0,917	0,812	mid
16	2	P12	**pc1955**	conserved hypothetical protein	-	1365	pc1955_498-551	CTATTTAGAATTGACTGTTGTGAGCGCCTTATTAAACCAGGCTTCTCAGTTAAC	74,2	54	0,619	0,13	0,998	1	0,814	0,806	mid
16	2	D16	**pc1956**	conserved hypothetical protein	-	1980	pc1956_1011-1057	ACTCACCGATACAGGATTAGTCCGTTTAAGTCCCTTAACAGCTTTGC	74,3	47	0,652	0,157	0,998	1	0,98	0,816	mid
16	2	H16	**pc1957**	hypothetical protein	-	3435	pc1957_1879-1923	TTATCTCAGGAGTTACGAAATCGCCGCAAAAAAGCAATAGGCTAT	74,3	45	0,957	1	0,991	1	0,84	0,776	mid
16	2	L16	**pc1958**	similar to metalloproteinase	-	1461	pc1958_734-786	TTCGAAAGACAAATAATCACGAAATTCAAGAGTTAAATAAGCGTGGTTTTCTG	74,3	53	0,975	1	0,992	1	0,998	0,753	mid
16	2	P16	**pc1959**	unknown protein	-	258	pc1959_161-207	GCATCTTTAAATCGATAGTTTTTCATCATGCGTTAGCACAAATTCGC	74,5	47	0,952	1	0,97	0,927	0,969	0,708	mid
16	2	D20	**pc1960**	unknown protein	-	1077	pc1960_444-498	TACTTCTGAGAGTAAACCTTATGCTATGCCAGGAAATTTTGTCTTTTCTCAAACA	74,2	55	0,965	1	0,998	0,997	0,904	0,757	mid
16	2	H20	**pc1961**	unknown protein	-	1104	pc1961_524-578	TGTTAAATGCTATCCAAAACCTTAAGCATGAAGAAGAGGTAAGCTATAGTTCAGG	73,3	55	0,949	1	0,91	0,959	0,971	0,794	mid
16	2	L20	**pc1962**	conserved hypothetical protein	-	378	pc1962_166-210	ATGGAACAAGGAGCACTACAAGGAATTAGCAGCCGAGAAGAACTA	74,2	45	0,981	1	0,998	1	0,976	0,833	mid
16	2	P20	**pc1963**	conserved hypothetical protein	-	813	pc1963_378-424	CTCGTTGGATACATGTGACAGAGAAGTCATGCGTTATATTGCCTCTA	74,2	47	0,984	1	0,997	1	0,97	0,871	mid
16	2	D24	**pc1964**	unknown protein	-	222	pc1964_96-146	ACTTACTAGCAGAACTTCAGTTCTATCTATTGCCCCATATCCCATGCCATA	74,2	51	0,978	1	0,997	1	0,922	0,881	random
16	2	H24	**pc1965**	similar to metalloproteinase	-	981	pc1965_594-645	TCCATCGTCTATGCAGCAATACCAAGAAGATCTTAATAAACAAGGTTTACCT	73,5	52	0,948	1	0,93	1	0,897	0,778	mid
16	2	L24	**pc1966**	conserved hypothetical protein	-	3849	pc1966_1907-1951	TCCAAGTGATTATGACAACCCATAATCCGACAACGGTTAGTTTTG	74,3	45	0,982	1	0,994	1	0,981	0,844	mid
16	2	P24	**pc1967**	unknown protein	-	186	pc1967_1-52	GTGATTAACCACGCAGATGGATTAGAGAAATTAAAATTAATGTTTTTCCGCA	74,5	52	0,739	0,47	0,97	1	0,907	0,621	mid
16	3	D04	**pc1968**	conserved hypothetical protein	-	1278	pc1968_1090-1143	ATATACGATGATGCACAAGGTAACAACAGCCTAGAGGGTACTTCTTTCTCTCTT	74,2	54	0,985	1	0,996	1	0,993	0,861	random
16	3	H04	**pc1969**	unknown protein	-	228	pc1969_1-51	TTGATTAACTCCATAGGTGATTCAGAGGAATTAAAATTAATGTTTTGCCGC	73,9	51	0,773	0,518	0,966	1	0,996	0,669	random
16	3	L04	**pc1970**	conserved hypothetical protein	-	1302	pc1970_173-219	CAGCCTCAGTCACAATGGACCTACATACAAGTCCGATTTGTTTAAAG	74,2	47	0,922	1	0,999	1	0,521	0,828	mid
16	3	P04	**pc1971**	unknown protein	-	672	pc1971_290-335	TCCAAGAATGCATTCAGAAAGGCATATCAAGTAATGAACTATGGCA	74,2	46	0,977	1	0,995	1	0,953	0,825	mid
16	3	D08	**pc1972**	hypothetical protein	-	1944	pc1972_986-1030	CTATTTGTGACACGTTATCCATTCGTCTTTTTGATGCCAGAACAG	74	45	0,969	1	0,975	1	0,987	0,749	mid
16	3	H08	**pc1973**	unknown protein	-	216	pc1973_6-52	GAGGCTAAATCTCGGCAAGCGCATAAAACATTCAGCTATAGCTAAAG	74,2	47	0,98	1	0,995	1	0,993	0,807	random
16	3	L08	**pc1974**	unknown protein	-	687	pc1974_250-295	CAATTTACGTCTGGATACATTGGATTGGGTCAATACATTCCTGTGA	74,3	46	0,974	1	0,992	1	0,905	0,87	mid
16	3	P08	**pc1975**	strongly similar to coproporphyrinogen oxidase III, aerobic	**hemF**	801	pc1975_404-453	ATTTTCACACTATTGCAGAGCAAGCCTTACTTCCTTTTGGTTCTCACTTA	74,2	50	0,983	1	0,995	1	0,997	0,831	mid
16	3	D12	**pc1976**	unknown protein	-	294	pc1976_92-145	AAATACCTAGATTTCTGGTTTGGACTTATTGGATTTTACCTTTTTGGGGCATTA	74,2	54	0,974	1	0,993	1	0,955	0,795	5´preference
16	3	H12	**pc1977**	similar to cytochrome-c oxidase fixO chain	**fixO**	1248	pc1977_593-646	AGCCTTATCATCGAGATTATGGGGTCATTTATTCACTTAATCCTCAAGAATTTC	74,2	54	0,975	1	0,997	1	0,968	0,782	mid
16	3	L12	**pc1978**	similar to cytochrome-c oxidase fixN chain	**fixN**	1416	pc1978_663-707	AATAGCGGGTACACCCATATATAGCCACCGCCTATCAATGATAGG	74,2	45	0,98	1	0,999	0,982	0,954	0,872	mid
16	3	P12	**pc1979**	unknown protein	-	234	pc1979_15-68	AATGCTTGGAGCTTCTCAGTTAGGTTTCTTATACCCTAATGCATTGAAAGTTCT	74,3	54	0,983	1	0,994	1	0,995	0,836	random
16	3	D16	**pc1980**	unknown protein	-	222	pc1980_142-190	TATAGCATTGTAGACATCGATTTGCTTGTTCACAGACCACTTAAACGGT	74,3	49	0,98	1	0,995	1	0,97	0,833	mid
16	3	H16	**pc1981**	conserved hypothetical protein	-	561	pc1981_37-82	TTAGGGACGGGGGAAACAATCTATTGCTGAACATAGCTATCGAGTCT	74,2	46	0,982	1	0,997	1	0,982	0,84	5´preference
16	3	L16	**pc1982**	conserved hypothetical protein	-	1116	pc1982_666-712	TTTCAATATTCACCAACCAGTGGATTTTGTCATTTCGTTACATGCTT	74,2	47	0,967	1	0,999	0,985	0,893	0,816	mid
16	3	P16	**pc1983**	similar to transaldolase	**talB**	660	pc1983_346-392	TTGATGGCTGCTCTTGCTGGAGCTAATTATGTGGCTCCTTATATTAG	74,2	47	0,978	1	0,995	0,959	0,985	0,852	mid
16	3	D20	**pc1984**	hypothetical protein	-	2355	pc1984_1213-1258	GTTCCTCAAATAGTAGATGGTGGACATGCCCCTTCAAAGCTTTTAA	74,3	46	0,973	1	0,997	1	0,966	0,758	mid
16	3	H20	**pc1985**	conserved hypothetical protein	-	1605	pc1985_706-759	CCAAAGTTATCACCTCAAGAATCGCATAACATAGGTCAAGAACGTAGACTAGAC	74,1	54	0,974	1	0,99	1	0,902	0,883	mid
16	3	L20	**pc1986**	hypothetical protein	-	663	pc1986_338-383	TTCGAAACTCTGAGAAGTCTACTTTGATGGTTCACCAAGAGAAGCA	74,2	46	0,984	1	0,992	1	0,995	0,854	mid
16	3	P20	**pc1987**	conserved hypothetical protein	-	894	pc1987_449-502	AATTAGCCGCTAAATCGATTAAGATTATTGGAAATGGTGATGTTTTAGATGGTC	74,2	54	0,978	1	0,994	1	0,999	0,775	mid
16	3	D24	**pc1988**	conserved hypothetical protein	-	276	pc1988_54-98	TACTCTTATGCTATTTGCTCGCATTATTGCCTCATGGTTTCCTCA	74,2	45	0,985	1	0,999	1	0,998	0,84	random
16	3	H24	**pc1989**	hypothetical protein	-	1578	pc1989_902-951	CTTATCCTCATCCCTGGAGAAGACTTAAACTTCCTATCGCGCTTTACTTT	74,2	50	0,968	1	0,997	0,989	0,888	0,833	mid
16	3	L24	**pc1990**	unknown protein	-	624	pc1990_388-432	ACATTTCCTCTCTTTCAAGAAACGATTGAAACACTTGTTCACCCC	74,4	45	0,964	1	0,98	1	0,925	0,767	mid
16	3	P24	**pc1991**	conserved hypothetical protein	-	1275	pc1991_604-648	CAACAAATCAATTACGTTCAAGGACAAAAACATGGACCATCGTTT	74,3	45	0,974	1	0,994	1	0,965	0,783	mid
16	4	D04	**pc1992**	conserved hypothetical protein	-	1614	pc1992_637-684	GAATTTACCATTGTGAGCGCCTTATTAAACCAGACTTCTCAGTTAGCG	74,2	48	0,611	0,1	0,996	1	0,829	0,832	mid
16	4	H04	**pc1993**	conserved hypothetical protein	-	390	pc1993_51-100	CCATTTGAAACCCTTAGTCACTTTAACGCATTTGAGACTAAGTGAGTGTG	74,2	50	0,602	0,034	0,999	1	0,975	0,797	5´preference
16	4	L04	**pc1994**	unknown protein	-	303	pc1994_28-73	TTTTTTGGATCAATAGGTGTTTGCATTTTGGTTCATTCATTTGTGA	74,3	46	0,97	1	0,998	1	0,999	0,68	random
16	4	P04	**pc1995**	strongly similar to recombination protein recA	**recA**	1086	pc1995_528-	GATGTCACAAGCATTAAGAAAATTAACGGCCTCTCTCTCAAAAAGCAATAC	74,3	51	0,97	1	0,995	1	0,984	0,709	mid

							578										
16	4	D08	**pc1996**	similar to geranyltranstransferase	**ispA**	810	pc1996_400-449	ATTTTAGGGGCAACGGGGGGACAATATTTAGATTTAAATCCTCCTAATCT	74,2	50	0,968	1	0,999	1	0,994	0,658	mid
16	4	H08	**pc1997**	similar to UDP-N-acetylglucosamine diphosphorylase	**glmU**	681	pc1997_361-408	CATGCAGCTCACTTTGCTTACGTGGGAGATACTATTTTAGGACATGAT	74,3	48	0,982	1	0,996	1	0,981	0,843	mid
16	4	L08	**pc1998**	similar to 23S rRNA (Uracil-5-)-methyltransferase	**rumA**	1152	pc1998_560-604	TTTTTACAGACAAATGGGAGAAAGTGTGGGGTGAGCCTTATTTGT	74,2	45	0,979	1	0,999	0,984	0,983	0,817	mid
16	4	P08	**pc1999**	strongly similar to mgtC protein	**mgtC**	690	pc1999_293-339	ATACGATTAAAGGATTAACGACTGCAGCTAGCTTATGGGCTGTTGCT	74,3	47	0,977	1	0,995	1	0,947	0,834	mid
16	4	D12	**pc2000**	unknown protein	**-**	249	pc2000_115-169	GCCTTATTAGCAAAAACAACGATAGTTTTAAGAATAGACGTCAGGGAAGAAAGGT	74	55	0,856	0,709	0,972	1	0,989	0,758	mid
16	4	H12	**pc2001**	conserved hypothetical protein	**-**	870	pc2001_370-424	GAAATTTCTATAATGGCTTATTTTGGGCGTACTCGATTTAAGGTCGCAATAGATA	74,2	55	0,971	1	0,999	1	0,934	0,778	mid
16	4	L12	**pc2002**	conserved hypothetical protein	**-**	594	pc2002_294-348	TTGGATAGCTATTCCTCATGAATCTTATGCTCCTAAAAGACCGAATACAAAAGTC	74,2	55	0,981	1	0,998	1	0,996	0,805	mid
16	4	P12	**pc2003**	unknown protein	**-**	564	pc2003_254-303	TTGTTGAAGGAGCTGGTCTTTACGCAAATACTACTTGGATAGAATTGTCC	74,3	50	0,98	1	0,996	1	0,971	0,83	mid
16	4	D16	**pc2004**	hypothetical protein	**cbbY**	786	pc2004_478-532	ATTGGTTTAGATAATGCCTTTGACTTGGTAATTTCTGGTTCTGATGACCTAGAAG	74,3	55	0,971	1	0,995	1	0,916	0,82	mid
16	4	H16	**pc2005**	unknown protein	**-**	192	pc2005_3-47	GAACTCGTTAAGAAGAGCATATGGTCTCTCTTTTGCGATTCCTGC	74,3	45	0,949	1	0,99	0,857	0,906	0,811	mid
16	4	L16	**pc2006**	hypothetical protein	**-**	528	pc2006_215-264	TTCAAACAGCTAATCTAGCTCATTATGGTCATGTGACTCATCTTGAAGGA	74,2	50	0,978	1	0,995	0,996	0,95	0,846	mid
16	4	P16	**pc2007**	conserved hypothetical protein	**-**	303	pc2007_137-184	AAGTACGCAAAACAGAAGAAGGGCAAGCGACTGAAAATAGTCCTTATT	74,2	48	0,977	1	0,999	0,986	0,981	0,797	random
16	4	D20	**pc2008**	conserved hypothetical protein	**-**	249	pc2008_52-96	AAAGATGGTATGTTCGCTAATTTCCGCGTAAAAGGAATGAAAGGA	74,2	45	0,981	1	0,998	1	0,993	0,809	random
16	4	H20	**pc2009**	unknown protein	**-**	600	pc2009_271-317	TGGGGTACAGCTATCGACTTATTTGATATTGATAATCGCCTCATTGG	74,3	47	0,972	1	0,994	1	0,97	0,751	mid
16	4	L20	**pc2010**	unknown protein	**-**	375	pc2010_16-63	GAAGGAAGTGGAATCCAGATCCCAGTCGAAGGATCGGATATTAATATA	74,4	48	0,982	1	0,985	1	0,996	0,851	random
16	4	P20	**pc2011**	unknown protein	**-**	333	pc2011_78-122	TTTTATTGATCGCAATCTCCAAATTCAACTTCCTGGTGTCACTTC	74,2	45	0,973	1	0,999	1	0,999	0,705	random
16	4	D24	**pc2012**	strongly similar to uracil-DNA glycosylase	**ung**	711	pc2012_331-375	TTACCAATTCCTTCCCATGGTTGTTTGTTAAAGTGGGCTAAACAA	74,2	45	0,976	1	0,995	1	0,975	0,781	mid
16	4	H24	**pc2013**	conserved hypothetical protein	**-**	738	pc2013_372-426	ACCCTACAACCTCATGCAATATTATGAATTTTATGAGTCTATGCCAAAACCTCTT	74,2	55	0,979	1	0,994	1	0,998	0,787	mid
16	4	L24	**pc2014**	similar to partition protein	**parA;minD**	753	pc2014_414-459	TGCTGCTCAACACACACTCGTTTGCATTACACCAGAGTTTTATAGT	74,2	46	0,982	1	0,998	1	0,964	0,864	mid
16	4	P24	**pc2015**	strongly similar to threonine-tRNA ligase	**thrS**	1953	pc2015_976-1022	GAAGATCGTGATTTTGCCATTAAACCAATGAATTGTCCAGGTTGTAT	74,4	47	0,974	1	0,98	1	0,999	0,775	mid
16	5	D04	**pc2016**	conserved hypothetical protein	**-**	201	pc2016_49-96	CCTCCAGTACTTTTAGCAGGGATTGCACAGTTTCAACTCGTTCATATA	74,2	48	0,981	1	0,997	1	0,965	0,853	random
16	5	H04	**pc2017**	hypothetical protein	**-**	1218	pc2017_752-799	AAGTAGCATGTGCTCAAATAGCACAAAGATTAGACCAAACTCGACATG	74	48	0,96	1	0,975	0,991	0,858	0,847	mid
16	5	L04	**pc2018**	unknown protein	**-**	201	pc2018_12-56	GAGGATGAAATTACTAGCTTGCATGTTGCCACCAAAAATCTGCAT	75,1	45	0,662	0,244	0,916	1	0,988	0,781	random
16	5	P04	**pc2019**	hypothetical protein	**-**	2880	pc2019_1173-1222	AGATTTAACGCAGTTGGGACTGGCTAAATGTCATAACATTACAGACAATG	74,2	50	0,946	1	0,992	1	0,732	0,813	mid
16	5	D08	**pc2020**	unknown protein	**-**	318	pc2020_150-203	GTTTTGTATTGTACCGCTCATGTTAACAACTTTTAGTTTTCCTGGAATTGTTCC	74,3	54	0,979	1	0,997	1	0,99	0,789	mid
16	5	H08	**pc2021**	unknown protein	**-**	192	pc2021_6-52	ATTCCAGCTACAGAATGCTTACATTGCGCCATCAAAAATTCACTATT	74,2	47	0,972	1	0,998	0,978	0,987	0,753	random
16	5	L08	**pc2022**	hypothetical protein	**-**	1437	pc2022_728-772	AGCTTCGAGAAGATAACGAACAGCTTGCACAAGGTTTAGAAGAGC	74,2	45	0,977	1	0,996	1	0,992	0,765	mid
16	5	P08	**pc2023**	hypothetical protein	**-**	1452	pc2023_750-803	ATTAGTTGAAACGGAAAAAGACCGAGATGAAGCTAAACACAAATTGAGTTTAGA	74,2	54	0,974	1	0,996	1	0,977	0,763	mid
16	5	D12	**pc2024**	unknown protein	**-**	840	pc2024_411-456	CCTTGCTCGAGAAATGATCAGTTTTGTCCCGACTTTTATATTCGAT	74,3	46	0,969	1	0,989	0,978	0,99	0,741	mid
16	5	H12	**pc2025**	unknown protein	**-**	360	pc2025_74-122	CAATTTCTTGTGAAAATCCTCACTATGTAATCGTGAAAGCTCCTCAACA	74,2	49	0,977	1	0,999	0,999	0,999	0,756	random
16	5	L12	**pc2026**	unknown protein	**-**	192	pc2026_39-91	GATAAATCCCTTTCAGTTAAACTTACACTCAGTACAGTACCCAGGAAAGCGTG	74,1	53	0,966	1	0,982	0,919	0,942	0,875	mid
16	5	P12	**pc2027**	unknown protein	**-**	1281	pc2027_552-599	GTTTGAAGGATGTGACTTTGGAGAAGGGGTTGATGTTGATAAGCTAAT	74,2	48	0,969	1	0,999	1	0,911	0,786	mid
16	5	D16	**pc2028**	unknown protein	**-**	663	pc2028_323-368	TACCGAAAATTGAAACAACCGCTACTGATTATGCCTTAGAAATGGC	74,3	46	0,974	1	0,993	1	0,99	0,746	mid
16	5	H16	**pc2029**	conserved hypothetical protein	**-**	300	pc2029_79-133	ACCCTTAAATCAGAAATAATTGAAATATCCGATTCTCTAGCTGATTACAAAGCCC	73,8	55	0,586	0,057	0,96	1	0,928	0,707	mid
16	5	L16	**pc2030**	unknown protein	**-**	258	pc2030_134-179	AAATGTTAGAATATGAACAAGACTGCAAGGATGCAGAAGCAGCTCA	74,2	46	0,983	1	0,999	1	0,996	0,824	mid
16	5	P16	**pc2031**	unknown protein	**-**	219	pc2031_79-132	ATGTTCATCTTACTTTACTGTATTTTCGCTAAGACGTGGCATGAAGTAGTGACC	74,2	54	0,984	1	0,999	1	0,968	0,871	mid
16	5	D20	**pcr02**	23S ribosomal RNA	**23S rRNA**	2300	pcr02_1953-1998	CCCTGGTGAATGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAA	79,8	46	0,985	1	0,999	1	0,965	0,893	random
16	5	H20	**pcr03**	16S ribosomal RNA	**16S rRNA**	1600	pcr03_941-991	ACGCGAAGAACCTTACCCAGACTTGACATGTAGTAGACCGGTCTAGAAATA	75.5	51	0,989	1	0,998	1	0,987	0,902	random
16	5	L20	**NON**	NONSENSE	**NON**		NON	AGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG									
16	5	P20	**18S**	18S ribosomal RNA	**18S rRNA**		C1_18S_1793-1837	CAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCGCACGCGC	82,3	45	0,991	1	0,995	1	0,992	0,923	
16	5	D24	**p_folA**	plasmid_folA	**p_folA**	519	p_folA_239-284	ATTTCTCAACTTCATTCGGCTGGAGTTAAACATATCTGGATCGATG	74,1	46	0,983	1	0,991	1	0,997	0,844	random
16	5	H24	**Dth**	internal control 1) Dth	**Dth**	~1600	Dth	GTAGTCCACACCGTAAACGATGGGTGCTAGGTGTTGGGGGATGTA	78,5	45	0,87	1	0,645	0,82	0,939	0,927	
16	5	L24	**Dpr**	internal control 2) Dpr	**Dpr**	~1600	Dpr	GAAGAAACTGTTGGAGTCGAATAGGCTCTTTCACTGACGGTACCTC	74,9	46	0,944	1	0,99	1	0,676	0,873	
16	5	P24	**Thi**	internal control 3) Thi	**Thi**	~1600	Thi	GCGTAGGTGGTTTTGTAAGTCTAAGGTGGAATTCCACAGCTTAACTGTG	75,2	49	0,961	1	0,982	1	0,817	0,883	
16	6	D04	**Tth**	internal control 4) Tth	**Tth**	~1600	Tth	ATAGGTTAAAGCCCGGAGCTCAACTCCGGAAAAGCCTATGATACT	75	45	0,932	1	0,998	0,739	0,813	0,894	

Table S2. Unexpressed predicted coding sequences (<500 bp)

Index	ID CDS	Description	CDS (bp)	CDS (aa)	Mean SNR≥3
1	pc0001	unknown protein	216	71	0,39
2	pc0002	unknown protein	285	94	0,95
3	pc0006	unknown protein	213	70	0,52
4	pc0070	unknown protein	240	79	0,21
5	pc0074	unknown protein	246	81	0,51
6	pc0080	unknown protein	225	74	0,27
7	pc0090	unknown protein	198	65	0,89
8	pc0105	unknown protein	210	69	2,32
9	pc0112	unknown protein	213	70	1,05
10	pc0122	unknown protein	201	66	1,00
11	pc0147	unknown protein	225	74	1,00
12	pc0157	unknown protein	204	67	0,94
13	pc0167	unknown protein	486	161	1,00
14	pc0183	unknown protein	186	61	0,08
15	pc0197	unknown protein	216	71	1,39
16	pc0212	unknown protein	186	61	0,62
17	pc0213	unknown protein	216	71	0,25
18	pc0215	unknown protein	183	60	0,92
19	pc0216	unknown protein	183	60	0,68
20	pc0285	unknown protein	387	128	1,31
21	pc0291	unknown protein	186	61	0,32
22	pc0292	unknown protein	201	66	0,26
23	pc0342	unknown protein	186	61	1,33
24	pc0360	unknown protein	234	77	0,44
25	pc0377	unknown protein	258	85	1,34
26	pc0380	unknown protein	222	73	0,71
27	pc0406	unknown protein	186	61	0,75
28	pc0407	unknown protein	186	61	0,20
29	pc0439	unknown protein	195	64	0,75
30	pc0457	unknown protein	198	65	0,99
31	pc0492	unknown protein	345	114	0,70
32	pc0493	unknown protein	204	67	2,65
33	pc0507	unknown protein	351	116	2,97
34	pc0508	unknown protein	378	125	0,82
35	pc0511	unknown protein	198	65	0,94
36	pc0513	unknown protein	270	89	0,97
37	pc0515	unknown protein	213	70	1,56
38	pc0521	unknown protein	225	74	0,51
39	pc0523	unknown protein	216	71	0,46
40	pc0524	unknown protein	195	64	0,36
41	pc0525	unknown protein	186	61	0,53
42	pc0526	unknown protein	291	96	0,72
43	pc0529	unknown protein	237	78	1,31
44	pc0533	unknown protein	201	66	1,63
45	pc0535	unknown protein	234	77	0,79
46	pc0539	unknown protein	240	79	0,93
47	pc0547	unknown protein	198	65	0,82
48	pc0556	unknown protein	183	60	0,14
49	pc0557	unknown protein	216	71	0,31
50	pc0558	unknown protein	270	89	0,23
51	pc0608	unknown protein	183	60	0,72
52	pc0611	unknown protein	297	98	2,90
53	pc0612	unknown protein	258	85	0,30
54	pc0613	unknown protein	201	66	0,31
55	pc0614	unknown protein	309	102	0,92
56	pc0624	unknown protein	192	63	0,32
57	pc0629	unknown protein	231	76	0,27
58	pc0661	unknown protein	201	66	0,25
59	pc0712	unknown protein	219	72	1,49
60	pc0730	unknown protein	192	63	0,76
61	pc0731	unknown protein	243	80	0,74

62	pc0744	unknown protein	216	71	0,62
63	pc0755	unknown protein	210	69	0,28
64	pc0763	unknown protein	183	60	0,31
65	pc0788	unknown protein	267	88	1,62
66	pc0831	unknown protein	201	66	0,30
67	pc0832	unknown protein	186	61	0,20
68	pc0833	unknown protein	366	121	1,66
69	pc0834	unknown protein	252	83	1,20
70	pc0841	unknown protein	279	92	2,71
71	pc0844	unknown protein	291	96	1,57
72	pc0849	unknown protein	288	95	0,50
73	pc0854	unknown protein	255	84	2,00
74	pc0866	unknown protein	186	61	1,38
75	pc0875	unknown protein	186	61	1,06
76	pc0897	unknown protein	183	60	0,19
77	pc0910	unknown protein	192	63	2,93
78	pc0917	unknown protein	192	63	0,73
79	pc0940	unknown protein	183	60	0,10
80	pc0941	unknown protein	219	72	2,13
81	pc0965	unknown protein	291	96	0,28
82	pc0966	unknown protein	255	84	0,76
83	pc0972	unknown protein	222	73	1,92
84	pc0997	unknown protein	198	65	1,08
85	pc1008	unknown protein	186	61	0,28
86	pc1012	unknown protein	228	75	0,33
87	pc1020	unknown protein	282	93	0,17
88	pc1027	unknown protein	204	67	0,46
89	pc1030	unknown protein	210	69	0,51
90	pc1034	unknown protein	432	143	0,80
91	pc1036	unknown protein	201	66	1,49
92	pc1037	unknown protein	285	94	0,51
93	pc1040	unknown protein	231	76	0,60
94	pc1101	unknown protein	255	84	0,98
95	pc1122	unknown protein	216	71	0,43
96	pc1130	unknown protein	183	60	0,17
97	pc1170	unknown protein	243	80	0,40
98	pc1185	unknown protein	216	71	0,53
99	pc1232	unknown protein	357	118	2,67
100	pc1258	unknown protein	198	65	2,16
101	pc1283	unknown protein	282	93	1,06
102	pc1284	unknown protein	255	84	0,97
103	pc1294	unknown protein	228	75	2,38
104	pc1303	unknown protein	192	63	0,07
105	pc1339	unknown protein	192	63	0,24
106	pc1340	unknown protein	222	73	1,80
107	pc1357	unknown protein	195	64	0,58
108	pc1366	unknown protein	219	72	0,28
109	pc1406	unknown protein	297	98	1,91
110	pc1407	unknown protein	348	115	1,18
111	pc1409	unknown protein	261	86	0,27
112	pc1416	unknown protein	186	61	0,39
113	pc1428	unknown protein	474	157	1,27
114	pc1436	unknown protein	186	61	-0,05
115	pc1450	unknown protein	195	64	1,12
116	pc1454	unknown protein	192	63	0,80
117	pc1460	unknown protein	201	66	1,21
118	pc1463	unknown protein	189	62	2,14
119	pc1479	unknown protein	198	65	1,59
120	pc1482	unknown protein	201	66	0,17
121	pc1493	unknown protein	210	69	0,34
122	pc1494	unknown protein	186	61	0,59
123	pc1522	unknown protein	198	65	0,05
124	pc1523	unknown protein	252	83	0,18
125	pc1532	unknown protein	231	76	1,34
126	pc1538	unknown protein	258	85	0,92

127	pc1539	unknown protein	225	74	1,31
128	pc1550	unknown protein	249	82	1,59
129	pc1551	unknown protein	288	95	0,31
130	pc1552	unknown protein	294	97	0,94
131	pc1586	unknown protein	258	85	0,31
132	pc1609	unknown protein	528	175	2,94
133	pc1610	unknown protein	207	68	0,64
134	pc1612	unknown protein	207	68	1,05
135	pc1613	unknown protein	213	70	0,74
136	pc1622	unknown protein	309	102	0,34
137	pc1648	unknown protein	189	62	0,25
138	pc1662	unknown protein	183	60	0,31
139	pc1714	unknown protein	498	165	2,50
140	pc1721	unknown protein	228	75	2,19
141	pc1723	unknown protein	189	62	0,28
142	pc1725	unknown protein	231	76	1,44
143	pc1747	unknown protein	183	60	0,19
144	pc1776	unknown protein	210	69	2,33
145	pc1777	unknown protein	246	81	0,87
146	pc1780	unknown protein	249	82	0,53
147	pc1781	unknown protein	453	150	0,67
148	pc1795	unknown protein	291	96	1,81
149	pc1811	unknown protein	462	153	0,43
150	pc1818	unknown protein	183	60	0,53
151	pc1872	unknown protein	240	79	1,60
152	pc1902	unknown protein	240	79	2,91
153	pc1904	unknown protein	261	86	0,18
154	pc1905	unknown protein	207	68	1,24
155	pc1908	unknown protein	192	63	0,19
156	pc1932	unknown protein	249	82	2,34
157	pc1933	unknown protein	249	82	1,24
158	pc1941	unknown protein	198	65	0,71
159	pc1942	unknown protein	210	69	0,47
160	pc1949	unknown protein	219	72	0,16
161	pc1959	unknown protein	258	85	0,37
162	pc1973	unknown protein	216	71	0,51
163	pc1979	unknown protein	234	77	2,47
164	pc1980	unknown protein	222	73	0,21
165	pc1994	unknown protein	303	100	-0,08
166	pc2000	unknown protein	249	82	0,70
167	pc2005	unknown protein	192	63	0,44
168	pc2026	unknown protein	192	63	0,73
169	pc2031	unknown protein	219	72	0,47

Table S3. Predicted genes of *P. amoebophila*. Genes which were expressed during intracellular growth are marked in grey.

ID CDS	Gene name	Gene Description	Length	Mean SNR≥3
pc0001	-	unknown protein	216	0,39
pc0002	-	unknown protein	285	0,95
pc0003	-	hypothetical protein	2970	1,31
pc0004	-	hypothetical protein	1413	14,91
pc0005	-	conserved hypothetical protein	2397	5,07
pc0006	-	unknown protein	213	0,52
pc0007	-	conserved hypothetical protein	1704	2,61
pc0008	**recC**	similar to exodeoxyribonuclease V gamma chain	3588	1,31
pc0009	**recB**	similar to exodeoxyribonuclease V beta chain	3501	2,20
pc0010	**recD**	similar to exodeoxyribonuclease V alpha chain recD	1869	2,12
pc0011	-	unknown protein	195	8,23
pc0012	-	unknown protein	1983	0,55
pc0013	**ssuA**	similar to substrate-binding protein of aliphatic sulfonate ABC transporter	1095	3,70
pc0014	**ssuB**	strongly similar to ATP-binding component of ABC transporters	792	4,43
pc0015	**ssuC**	similar to integral membrane components of the ABC transporters	777	2,05
pc0016	**glmU**	similar to UDP-N-acetylglucosamine pyrophosphorylase	1332	1,47
pc0017	**rfaF;waaF**	similar to ADP-heptose--lipopolysaccharide heptosyltransferase II	1050	2,05
pc0018	-	hypothetical protein	1623	2,06
pc0019	**ruvC**	strongly similar to Holliday junction endodeoxyribonuclease	507	1,69
pc0020	**ruvA**	strongly similar to Holliday junction DNA helicase	606	2,99
pc0021	**nth**	strongly similar to endonuclease III (UV endonuclease)	642	2,05
pc0022	**thdF;trmE**	strongly similar to GTP-binding protein in thiophene and furan oxidation	1377	1,69
pc0023	**psdD**	similar to phosphatidylserine decarboxylase proenzyme	918	3,89
pc0024	**ahpC**	strongly similar to alkylhydroperoxide reductase	558	16,18
pc0025	-	conserved hypothetical protein	633	3,72
pc0026	-	conserved hypothetical protein	4536	4,40
pc0027	**prmA**	similar to ribosomal protein L11 methyltransferase	795	2,60
pc0028	-	unknown protein	363	12,80
pc0029	-	conserved hypothetical protein	252	6,75
pc0030	**groEL, hsp60**	strongly similar to 60 kDa chaperonin (GroEL)	1674	71,36
pc0031	**groES, cpn10**	strongly similar to chaperonin groES	348	82,93
pc0032	-	conserved hypothetical protein	1236	1,03
pc0033	**putA, poaA**	similar to bifunctional protein (proline dehydrogenase and delta-1-pyrroline-5-carboxylate dehydrogenase)	3648	1,90
pc0034	**mutD, uvrD, recL**	strongly similar to ATP-dependent DNA helicase	2286	4,02
pc0035	-	conserved hypothetical protein	300	3,05
pc0036	-	unknown protein	582	22,80
pc0037	-	similar to metalloprotease	942	1,14
pc0038	-	conserved hypothetical protein	2862	2,23
pc0039	-	unknown protein	348	3,57
pc0040	-	hypothetical protein	3423	3,86
pc0041	-	hypothetical protein	3432	1,37
pc0042	-	hypothetical protein	3438	3,27
pc0043	-	unknown protein	1329	15,34
pc0044	-	hypothetical protein	3429	0,96
pc0045	-	hypothetical protein	3462	5,53
pc0046	-	hypothetical protein	3282	4,62
pc0047	-	unknown protein	306	3,19
pc0048	-	hypothetical protein	1596	3,41
pc0049	-	unknown protein	858	65,67
pc0050	-	unknown protein	1053	8,87
pc0051	-	hypothetical protein	3456	2,37
pc0052	-	hypothetical protein	1140	1,66
pc0053	-	hypothetical protein	2127	1,22
pc0054	-	hypothetical protein	2916	1,09
pc0055	-	unknown protein	510	2,09
pc0056	-	unknown protein	1350	12,21
pc0057	-	hypothetical protein	3435	1,77

pc0058	-	hypothetical protein	3042	6,39
pc0059	-	hypothetical protein	3444	4,92
pc0060	-	similarity to extracellular metalloproteinase	855	5,16
pc0061	-	hypothetical protein	663	1,33
pc0062	-	unknown protein	711	2,06
pc0063	-	hypothetical protein	888	2,34
pc0064	-	unknown protein	1584	0,96
pc0065	-	hypothetical protein	549	1,69
pc0066	-	conserved hypothetical protein	909	1,21
pc0067	-	hypothetical protein	1173	0,92
pc0068	-	hypothetical protein	183	7,67
pc0069	**aspC**	strongly similar to aspartate transaminase	1221	2,04
pc0070	-	unknown protein	240	0,21
pc0071	**topA, top1**	similar to DNA topoisomerase I	2604	4,52
pc0072	**dprA**	similar to protein required for chromosomal DNA transformation	1092	1,05
pc0073	**aroB**	similar to 3-dehydroquinate synthase	1059	0,90
pc0074	-	unknown protein	246	0,51
pc0075	-	unknown protein	246	46,79
pc0076	-	unknown protein	753	6,04
pc0077	**parB**	similarity to chromosome partitioning protein	783	0,96
pc0078	**copA, zntA**	similar to copper-transporting ATPase	2190	4,14
pc0079	-	strongly similar to UDP-glucuronat epimerase	984	1,10
pc0080	-	unknown protein	225	0,27
pc0081	-	unknown protein	651	6,40
pc0082	-	conserved hypothetical protein	1500	1,89
pc0083	**gpsA**	stongly similar to NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1002	5,77
pc0084	-	unknown protein	669	2,56
pc0085	-	conserved hypothetical protein	600	2,83
pc0086	-	conserved hypothetical protein	2172	16,70
pc0087	-	unknown protein	441	29,60
pc0088	-	hypothetical protein	1194	11,57
pc0089	**mutY**	similar to A/G-specific adenine glycosylase, mutY	1059	1,40
pc0090	-	unknown protein	198	0,89
pc0091	**bcp**	similar to bacterioferritin comigratory protein (BCP)	489	2,40
pc0092	**hemB**	strongly similar to porphobilinogen synthase (delta-aminolevulinic acid dehydratase, (ALAD)), hemB	1035	12,53
pc0093	-	hypothetical protein	2163	1,13
pc0094	**napA**	similar to Na(+)/H(+) antiporter	1233	4,13
pc0095	**nqrA, nqr1**	similar to component of alpha subunit of Na+-translocating NADH-quinone reductase (NQR)	1401	6,78
pc0096	**oppF**	strongly similar to ATP binding protein, component of oligopeptide permease, oppF	825	2,21
pc0097	**oppD**	strongly similar to ATP binding protein, component of oligopeptide permease, oppD	1026	2,17
pc0098	-	conserved hypothetical protein	732	5,87
pc0099	-	conserved hypothetical protein	1416	12,67
pc0100	-	unknown protein	579	15,87
pc0101	**oppC**	similar to oligopeptide transport system permease protein, oppC	1764	2,11
pc0102	**dppB**	similar to dipeptide transport system permease protein, dppB	1497	2,72
pc0103	**oppA**	similar to substrate binding proteins, component of oligopeptide permease, oppA	2148	4,19
pc0104	-	hypothetical protein	693	1,99
pc0105	-	unknown protein	210	2,32
pc0106	**glgP**	strongly similar to glycogen phosphorylase	2604	4,52
pc0107	-	unknown protein	2052	11,68
pc0108	**fliY**	similar to amino acid ABC transporter, periplasmic amino acid-binding protein	837	1,98
pc0109	**glgC**	strongly similar to glucose-1-phosphate adenylyltransferase	1419	9,10
pc0110	-	conserved hypothetical protein	768	2,46
pc0111	**nrdD**	similar to ribonucleoside triphosphate reductase	2013	22,98
pc0112	-	unknown protein	213	1,05
pc0113	-	hypothetical protein	984	4,42
pc0114	**batE**	similar to batE protein	756	0,53
pc0115	-	hypothetical protein	378	2,93
pc0116	-	unknown protein	1773	0,61
pc0117	-	unknown protein	1677	1,12
pc0118	-	unknown protein	1071	1,70

pc0119	**batA**	similar to batA protein	1089	0,92
pc0120	**cicA**	similar to protein involved in cell wall biosynthesis, morphogenesis and cell division	618	2,22
pc0121	**-**	conserved hypothetical protein	2658	2,07
pc0122	**-**	unknown protein	201	1,00
pc0123	**rfbA, rmlA**	strongly similar to glucose-1-phosphate thymidylyltransferase (dTDP-glucose synthase),rfbA	888	5,21
pc0124	**rfbC, rmlC**	strongly similar to dTDP-4-dehydrorhamnose 3,5-epimerase, rfbC	555	8,76
pc0125	**rfbD, rmlD**	similar to dTDP-4-keto-L-rhamnose reductase, (TDP-rhamnose synthetase), rfbD	885	9,07
pc0126	**rfbB, rmlB**	strongly similar to dTDP-glucose 4,6-dehydratase, rfbB	1059	7,10
pc0127	**emrB**	similar to multidrug resistance membrane translocase protein, emrB	1542	2,93
pc0128	**emrA**	strongly similar to multidrug resistance protein, emrA	1200	2,18
pc0129	**-**	unknown protein	882	7,97
pc0130	**-**	unknown protein	450	1,22
pc0131	**rluA**	similar to ribosomal large subunit pseudouridine synthase (pseudouridylate synthase), rluA	732	4,65
pc0132	**rpsT**	similar to 30S ribosomal protein S20	291	25,48
pc0133	**-**	similar to acylase and diesterase	1686	11,75
pc0134	**-**	conserved hypothetical protein	744	16,11
pc0135	**-**	conserved hypothetical protein	3465	1,63
pc0136	**rpsB**	strongly similar to 30S ribosomal protein S2	819	51,71
pc0137	**tsf**	similar to elongation factor Ts (EF-Ts)	975	30,82
pc0138	**-**	conserved hypothetical protein	1077	39,71
pc0139	**mutL**	similar to methyl-directed mismatch repair (MMR) protein, mutL	1959	3,50
pc0140	**pcnB**	similar to poly A polymerase	1239	1,92
pc0141	**-**	conserved hypothetical protein	750	4,92
pc0142	**-**	hypothetical protein	1065	10,12
pc0143	**eno**	strongly similar to phosphopyruvate hydratase (enolase)	1305	4,34
pc0144	**-**	conserved hypothetical protein	396	4,89
pc0145	**-**	conserved hypothetical protein	747	22,18
pc0146	**secA**	similar to preprotein translocase SecA	3063	5,21
pc0147	**-**	unknown protein	225	1,00
pc0148	**aspH**	similar to aspartyl/asparaginyl beta-hydroxylase (= peptide-aspartate beta-dioxygenase)	612	7,75
pc0149	**arsAB**	similar to arsenical pump membrane protein	1260	2,10
pc0150	**-**	hypothetical protein	474	18,11
pc0151	**lpdA**	strongly similar to dihydrolipoamide dehydrogenase	1410	11,78
pc0152	**lipA**	strongly similar to lipoate synthetase	972	7,18
pc0153	**-**	unknown protein	921	4,83
pc0154	**-**	conserved hypothetical protein	900	5,88
pc0155	**-**	strongly similar to thymidylate synthase	1647	15,58
pc0156	**-**	hypothetical protein	903	2,21
pc0157	**-**	unknown protein	204	0,94
pc0158	**-**	unknown protein	1791	3,28
pc0159	**-**	hypothetical protein	1179	5,24
pc0160	**yjbC**	similar to ribosomal large chain pseudouridine synthase B	705	3,18
pc0161	**pgmA**	similar to phosphoglycerate mutase	681	4,98
pc0162	**nifS**	similar to iron-sulfur cofactor synthesis protein/cysteine desulfurase nifS	1182	4,31
pc0163	**-**	similar to iron-sulfur cluster assembly protein nifU	792	4,97
pc0164	**-**	unknown protein	465	4,44
pc0165	**birA**	similar to biotin-[acetyl-CoA-carboxylase] ligase/biotin repressor (bifunctional)	681	0,91
pc0166	**rodA**	strongly similar to cell shape (rod)-determining protein	1137	0,76
pc0167	**-**	unknown protein	486	1,00
pc0168	**tyrP_1**	similar to tyrosine/tryptophan transport protein	1191	0,97
pc0169	**tyrP_1**	similar to tyrosine/tryptophan transport protein	1200	0,87
pc0170	**trpS**	similar to tryptophanyl-tRNA synthetase (=tryptophan-tRNA ligase)	1062	3,32
pc0171	**-**	similar to O-linked N-acetylglucosamine transferase	2481	8,50
pc0172	**-**	similar to O-linked N-acetylglucosamine transferase	3414	3,23
pc0173	**-**	similar to O-linked N-acetylglucosamine transferase	3591	1,82
pc0174	**uvrB**	strongly similar to Helicase subunit B of the DNA excision repair complex (excinuclease ABC)	2022	5,65

pc0175	-	hyopthetical protein	1074	2,48
pc0176	**dinG, yoaA**	similar to ATP-dependent DNA helicase dinG	2262	1,83
pc0177	**sigA, rpoD**	strongly similar to transcription initiation factor sigma 70	1665	7,25
pc0178	-	hypothetical protein	867	1,62
pc0179	-	hypothetical protein	867	2,29
pc0180	-	hypothetical protein	1131	2,22
pc0181	**wzt**	strongly similar to ABC transporter ATP-binding protein wzt	1257	4,49
pc0182	**wzm**	strongly similar to ABC transporter protein wzm	834	2,46
pc0183	-	unknown protein	186	0,08
pc0184	-	hypothetical protein	1308	4,77
pc0185	-	unknown protein	1365	1,67
pc0186	**wza**	similar to polysaccharide export protein wza	1050	2,83
pc0187	**wzc**	similar to Tyrosine-protein kinase	2946	2,66
pc0188	-	hypothetical protein	849	5,86
pc0189	**sufB**	strongly similar to ABC transporter protein sufB	1446	10,88
pc0190	**sufC**	strongly similar to ABC transporter ATP-binding protein sufC	765	10,80
pc0191	**sufD, ynhC**	similar to sufD	1353	11,57
pc0192	**sufS, nifS, csdB**	strongly similar to L-selenocysteine lyase	1233	6,36
pc0193		conserved hypothetical protein	936	2,32
pc0194	-	unknown protein	1206	8,53
pc0195	**npr**	similar to metalloendopeptidase	813	1,48
pc0196	**glpQ;ugpQ**	similar to glycerophosphoryl diester phosphodiesterase	891	1,32
pc0197	-	unknown protein	216	1,39
pc0198	**ppaB**	similar to F-box protein	990	1,60
pc0199	**ppaA**	similar to F-box protein	1014	1,94
pc0200	**yscT, sctT**	similar to type III secretion inner membrane protein SctT	843	4,57
pc0201	**sctS**	strongly similar to type III secretion inner membrane protein SctS	237	9,97
pc0202	**yscR, sctR; fliP**	similar to type III secretion inner membrane protein SctR	972	15,22
pc0203	**yscL, sctL**	similar to type III secretion protein SctL	672	17,84
pc0204	-	hypothetical protein	846	10,58
pc0205	**yscJ, sctJ**	similar to type III secretion protein SctJ	1014	8,06
pc0206	**rs10**	strong similarity to 30S ribosomal protein S10	336	77,66
pc0207	**fusA**	strongly similar to translation elongation factor EF-G	2088	93,16
pc0208	**rpsG; rs7**	strong similarity to 30S ribosomal protein S7	474	133,55
pc0209	**rs12**	strong similarity to 30S ribosomal protein S12	381	139,22
pc0210	-	conserved hypothetical protein	705	4,59
pc0211	-	conserved hypothetical protein	732	2,44
pc0212	-	unknown protein	186	0,62
pc0213	-	unknown protein	216	0,25
pc0214	**tsp**	similar to carboxy-terminal (= tail-specific) proteinase	2016	5,88
pc0215	-	unknown protein	183	0,92
pc0216	-	unknown protein	183	0,68
pc0217	**rplU**	strong similarity to 50S ribosomal protein L21	345	41,53
pc0218	**r(p)l27**	strongly similar to 50S ribosomal protein L27	252	16,49
pc0219	**yhbZ;obg**	strong similarity to GTP binding protein	1014	3,84
pc0220	-	hypothetical protein	750	8,23
pc0221	**rho**	strongly similar to transcription termination factor Rho	1386	24,28
pc0222	**yacE**	similar to Dephospho-CoA kinase	612	11,49
pc0223	**polA**	strongly similar to DNA polymerase I	2676	3,79
pc0224	**sohB**	similar to proteinase IV	1038	6,72
pc0225	-	conserved hypothetical protein	1950	9,70
pc0226	**yvgR, cysJ, sirA**	similar to sulfite reductase (NADPH) flavoprotein	1155	11,57
pc0227	**ipsF, ygbB**	similar to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECDP-synthase)	480	3,24
pc0228	-	hypotetical protein	1089	2,76
pc0229	**murA, murZ**	similar to UDP-N-acetylglucosamine 1-carboxyvinyl transferase (= UDP-N-acetylglucosamine enolpyruvyl transferase)	1398	15,63
pc0230	**yodO, kamA, yjeK**	simlar to L-lysine 2,3-aminomutase	1044	2,48
pc0231	**argS**	strong similarity to arginyl-tRNA synthetase (=arginine-tRNA-ligase)	1755	2,61
pc0232	**clpB**	similar to endopeptidase Clp ATP-binding chain B (heat shock protein)	1125	6,28
pc0233	-	conserved hypothetical protein	735	11,98
pc0234	**yjeE**	strongly similar to YjeE protein	441	11,42

pc0235	**-**	conserved hypothetical protein	621	3,68
pc0236	**dnaQ_2**	similar to DNA polymerase III epsilon chain	750	8,05
pc0237	**-**	conserved hypothetical protein	900	18,05
pc0238	**hisH**	similar to glutamine amidotransferase	594	3,79
pc0239	**pgk**	strongly similar to 3-phosphoglycerate kinase	1209	18,74
pc0240	**ntt_3**	strongly similar to ATP/ADP translocase	1611	11,02
pc0241	**ntt_2**	Nucleotide triphosphate/H+ symporter	1551	7,55
pc0242	**pgsA**	similar to Phosphatidylglycerophosphate synthase (= CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase)	426	3,90
pc0243	**-**	hypothetical protein	1146	9,57
pc0244	**gltX**	strongly similar to glutamate-tRNA ligase (= glutamyl-tRNA synthetase)	1509	4,63
pc0245	**-**	unknown protein	366	5,70
pc0246	**tsp**	similar to carboxy-terminal (= tail-specific) proteinase	1962	6,76
pc0247	**euo**	strongly similar to lysine-rich histone-specific protease	420	13,00
pc0248	**-**	similar to RNA methyl transferase	1305	1,01
pc0249	**recJ**	similar to ssDNA-specific exonuclease	1785	4,90
pc0250	**ntt_1**	ATP/ADP translocase	1542	84,85
pc0251	**secDF**	similar to fusion protein export proteins SecD/SecF	4533	19,33
pc0252	**-**	unknown protein	444	3,00
pc0253	**-**	conserved hypothetical protein	498	95,73
pc0254	**-**	conserved hypothetical protein	861	6,63
pc0255	**-**	hypothetical protein	324	2,27
pc0256	**ytgA**	similar to ABC transporter periplasmic substrate-binding protein TroA	1011	5,36
pc0257	**ytgB**	similar to ABC transporter ATP-binding protein troB	843	4,09
pc0258	**ytgC**	similar to ABC transporter permease TroC	1353	3,84
pc0259	**ytgD**	similar to ABC transporter permease TroD	1011	1,86
pc0260	**dxr**	strongly similar to 1-deoxy-D-xylulose 5-phosphate reductoisomerase	1155	6,77
pc0261	**-**	conserved hypothetical protein	1962	6,29
pc0262	**-**	hypothetical protein	1710	3,68
pc0263	**-**	unknown protein	285	0,73
pc0264	**-**	hypothetical protein	5418	4,41
pc0265	**-**	conserved hypothetical protein	327	0,47
pc0266	**ptsN;rpoP**	similar to nitrogen regulatory IIA protein (enzyme IIA-ntr) (phosphotransferase enzyme II, A component)	720	46,11
pc0267	**ptsN;rpoP**	similar to nitrogen regulatory IIA protein (enzyme IIA-ntr) (phosphotransferase enzyme II, A component)	339	2,76
pc0268	**dut**	strongly similar to Deoxyuridine 5'-triphosphate nucleotidohydrolase	453	9,01
pc0269	**accD**	strongly similar to acetyl-CoA carboxylase, carboxyltransferase beta chain	918	6,45
pc0270	**sodM**	strongly similar to superoxide dismutase (Mn) precursor	627	9,34
pc0271	**-**	conserved hypothetical protein	654	0,88
pc0272	**hemC;gmc**	similar to Porphobilinogen deaminase	702	2,36
pc0273	**sms**	strongly similar to DNA repair	1371	1,43
pc0274	**rnc**	similar to Ribonuclease III	729	2,88
pc0275	**-**	unknown protein	675	3,29
pc0276	**-**	conserved hypothetical protein	666	1,22
pc0277	**-**	unknown protein	1218	0,89
pc0278	**-**	hypothetical protein	1038	9,00
pc0279	**-**	hypothetical protein	1518	1,61
pc0280	**-**	unknown protein	639	4,01
pc0281	**gcvT**	strongly similar to glycine cleavage system T protein	1035	2,28
pc0282	**gcvH;gcsH**	strongly similar to glycine cleavage system H protein	369	7,69
pc0283	**gcvP1**	strongly similar to glycine dehydrogenase P protein subunit 1	1341	2,54
pc0284	**gcvP2**	strongly similar to glycine dehydrogenase (decarboxylating) P protein subunit 2	1443	4,08
pc0285	**-**	unknown protein	387	1,31
pc0286	**alkB**	strongly similar to alkylated DNA repair protein	669	1,61
pc0287	**cadA**	similar to cadmium-transporting ATPase	1926	3,96
pc0288	**czcA**	strongly similar to cation efflux system membrane protein A	3216	2,93
pc0289	**czcB**	similar to cation efflux system membrane protein B	1143	1,48
pc0290	**czcC**	similar to cation efflux system membrane protein C	1155	0,80
pc0291	**-**	unknown protein	186	0,32
pc0292	**-**	unknown protein	201	0,26

pc0293	-	unknown protein	432	14,39
pc0294	-	unknown protein	804	6,56
pc0295	-	conserved hypothetical protein	348	6,65
pc0296	-	unknown protein	387	8,03
pc0297	-	unknown protein	762	5,24
pc0298	**nqrE**	strongly similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain E	744	3,79
pc0299	**nqrD**	strongly similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain D	636	2,93
pc0300	**nqrC**	similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain C	933	9,93
pc0301	**nqrB**	similar to sodium-translocating NADH dehydrogenase (ubiquinone) chain B	1530	7,45
pc0302	-	unknown protein	477	3,05
pc0303	-	unknown protein	5115	1,18
pc0304	-	unknown protein	978	3,22
pc0305	**comF**	similar to competence-related protein comF	726	1,66
pc0306	**corA**	similar to divalent cation transport protein	1134	7,96
pc0307	**dnaA**	similar to replication initiation protein dnaA	1386	6,69
pc0308		hypothetical protein	1173	4,33
pc0309	-	conserved hypothetical protein	396	7,65
pc0310	-	hypothetical protein	450	33,78
pc0311	**mraW;yabC**	strongly similar to S-adenosyl-methyltransferase	951	4,99
pc0312	-	conserved hypothetical protein	294	3,27
pc0313	**pbp2**	similar to penicillin-binding protein 2 (transglycolase/transpeptidase)	2031	1,77
pc0314	**murE**	similar to UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1479	1,16
pc0315	**amiA, cwlC**	similar to N-acetylmuramoyl-L-alanine amidase	843	3,73
pc0316	-	hypothetical protein	891	1,34
pc0317	**pgd**	strongly similar to phosphogluconate dehydrogenase (decarboxylating)	1455	14,66
pc0318	**plsC**	similar to 1-acylglycerol-3-phosphate O-acyltransferase	633	5,74
pc0319	**cmk**	strongly similar to cytidylate kinase	687	5,28
pc0320	**cdsA**	similar to phosphatidate cytidylyltransferase	939	3,55
pc0321	**uppS**	strongly similar to undecaprenyl pyrophosphate synthetase	777	5,56
pc0322	**lepA**	strongly similar to GTP-binding protein lepA	1809	7,26
pc0323	-	unknown protein	1056	4,42
pc0324	-	hypothetical protein	2196	1,14
pc0325	-	conserved hypothetical protein	297	7,90
pc0326	**ykuE, yaeI**	conserved hypothetical protein	966	1,49
pc0327	**ispD**	similar to 4-diphosphocytidyl-2C-methyl-D-erythritol synthase	693	0,88
pc0328	**truA**	similar to tRNA pseudouridylate synthase I	771	2,85
pc0329	-	hypothetical protein	684	9,01
pc0330	-	unknown protein	927	1,15
pc0331	-	hypothetical protein	369	34,22
pc0332	-	hypothetical protein	987	1,72
pc0333	-	conserved hypothetical protein	261	0,95
pc0334	**ppaA**	hypothetical protein	1851	2,52
pc0335	**ppaA**	hypothetical protein	1929	1,32
pc0336	**ppa**	hypothetical protein	1809	5,23
pc0337	-	hypothetical protein	444	3,70
pc0338	-	hypothetical protein	636	35,66
pc0339	-	hypothetical protein	1077	0,39
pc0340	-	hypothetical protein	696	2,64
pc0341	-	conserved hypothetical protein	801	3,62
pc0342	-	unknown protein	186	1,33
pc0343	-	unknown protein	978	45,04
pc0344	-	hypothetical protein	1608	1,48
pc0345	**nfo**	strongly similar to endonuclease IV	849	2,44
pc0346	**asnS**	strongly similar to asparagine-tRNA ligase	1404	3,94
pc0347	**hemA**	similar to glutamyl tRNA reductase	1023	4,15
pc0348	-	conserved hypothetical protein	1851	0,65
pc0349	-	conserved hypothetical protein	1029	2,80
pc0350	**gyrB**	similar to DNA gyrase (topoisomerase) chain B	1821	8,95
pc0351	**gyrA**	similar to DNA gyrase (topoisomerase) chain A	1902	2,29
pc0352	-	hypothetical protein	624	4,00
pc0353	-	unknown protein	267	65,18
pc0354	-	unknown protein	306	6,33

pc0355	**rluD**	strongly similar to 23S RNA-specific pseudouridine synthase D	957	10,77
pc0356	**dtd**	strongly similar to D-tyrosyl-tRNA(Tyr) deacylase	456	2,97
pc0357	**-**	conserved hypothetical protein	249	30,32
pc0358	**-**	unknown protein	2658	5,28
pc0359	**-**	unknown protein	405	25,28
pc0360	**-**	unknown protein	234	0,44
pc0361	**folK**	similar to multifunctional folic acid synthesis protein	516	1,71
pc0362	**kdsA**	strongly similar to 2-dehydro-3-deoxyphosphooctonate aldolase (KDO synthetase)	828	2,25
pc0363	**-**	unknown protein	633	1,46
pc0364	**-**	unknown protein	1524	1,71
pc0365	**-**	conserved hypothetical protein	741	5,40
pc0366	**ndk**	strongly similar to nucleoside-diphosphate kinase	729	11,30
pc0367	**pabA**	strongly similar to p-aminobenzoate synthase	579	1,84
pc0368	**ndk**	strongly similar to nucleoside-diphosphate kinase	432	6,86
pc0369	**pheT**	similar to phenylalanine-tRNA ligase beta chain	2409	6,98
pc0370	**-**	hypothetical protein	966	12,35
pc0371	**fdxC**	similar to ferredoxin [2Fe-2S] IV	276	0,64
pc0372	**-**	unknown protein	552	2,30
pc0373	**-**	conserved hypothetical protein	228	1,66
pc0374	**-**	unknown protein	213	5,73
pc0375	**rapA**	similar to rapA, a bacterial member of the swi/snf helicase family	2682	1,08
pc0376	**-**	hypothetical protein	819	6,69
pc0377	**-**	unknown protein	258	1,34
pc0378	**-**	conserved hypothetical protein	963	9,74
pc0379	**trxA**	strongly similar to thioredoxin	321	32,76
pc0380	**-**	unknown protein	222	0,71
pc0381	**kefC**	similar to glutathione-regulated potassium-efflux system protein	1680	6,89
pc0382	**-**	similar to tRNA (guanosine-2'-O-)-methyltransferase	447	2,93
pc0383	**mip**	similar to macrophage infectivity potentiator (fkbp-type peptidyl-prolyl cis-trans isomerase)	873	51,88
pc0384	**aspS**	strongly similar to aspartate-tRNA ligase	1800	9,19
pc0385	**hisS**	strongly similar to histidine-tRNA ligase	1275	3,45
pc0386	**-**	unknown protein	2472	15,15
pc0387	**uhpC, glpT**	strongly similar to regulatory protein uhpC	1383	12,91
pc0388	**-**	unknown protein	483	59,96
pc0389	**dnaE**	similar to DNA polymerase III, alpha chain	3759	2,84
pc0390	**-**	hypothetical protein	1407	11,11
pc0391	**-**	hypothetical protein	558	6,11
pc0392	**rsbW**	similar to rsbW, negative regulator of sigma-B activity (switch protein/serine kinase)	423	1,60
pc0393	**-**	hypothetical protein	498	4,90
pc0394	**dac**	similar to serine-type D-Ala-D-Ala carboxypeptidase (penicillin binding protein)	1371	3,99
pc0395	**ksgA**	similar to dimethyladenosine transferase	771	5,52
pc0396	**-**	hypothetical protein	1128	4,58
pc0397	**rsmB, fmu, fmv, sun**	similar to 16S rRNA m5C967 SAM-dependent methyltransferase	1134	5,67
pc0398	**ddlA**	similar to D-alanine--D-alanine ligase	2397	2,00
pc0399	**zip**	similar to inclusion protein IncA	2523	3,15
pc0400	**cutE**	similar to apolipoprotein N-acyltransferase	1590	1,28
pc0401	**envA, lpxC**	similar to UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	879	4,54
pc0402	**fabZ**	strongly similar to myristoyl-acyl carrier dehydratase	465	16,62
pc0403	**lpxA**	strongly similar to acyl-(acyl-carrier-protein)-UDP-N-acetylglucosamine o-acyltransferase	849	4,88
pc0404	**fmt**	strongly similar to methionyl-tRNA formyltransferase	957	1,99
pc0405	**-**	hypothetical protein	828	25,28
pc0406	**-**	unknown protein	186	0,75
pc0407	**-**	unknown protein	186	0,20
pc0408	**-**	unknown protein	1005	88,48
pc0409	**-**	unknown protein	897	112,72
pc0410	**-**	unknown protein	1083	5,66
pc0411	**-**	unknown protein	558	0,99
pc0412	**rplC**	strongly similar to 50S ribosomal protein L3	708	36,71
pc0413	**rplD**	similar to 50S ribosomal protein L4	591	50,55
pc0414	**rplW**	strongly similar to 50S ribosomal protein L23	336	53,70
pc0415	**rplB**	strongly similar to 50S ribosomal protein L2	846	39,55
pc0416	**rpsS**	strongly similar to 30S ribosomal protein S19	264	53,72

pc0417	**rplV**	strongly similar to 50S ribosomal protein L22	336	23,61
pc0418	**rpsC**	strongly similar to 30S ribosomal protein S3	645	42,09
pc0419	**rplP**	strongly similar to 50S ribosomal protein L16	420	97,29
pc0420	**rpmC**	similar to 50S ribosomal protein L29	222	30,92
pc0421	**rpsQ**	strongly similar to 30S ribosomal protein S17	246	52,34
pc0422	**rplN**	strongly similar to 50S ribosomal protein L14	369	52,73
pc0423	**rplX**	strongly similar to 50S ribosomal protein L24	351	64,98
pc0424	**rplE**	strongly similar to 50S ribosomal protein L5	558	95,75
pc0425	**rpsH**	strongly similar to 30S ribosomal protein S8	402	48,44
pc0426	**rplF**	strongly similar to 50S ribosomal protein L6	549	63,94
pc0427	**rplR**	strongly similar to 50S ribosomal protein L18	372	98,21
pc0428	**rpsE**	strongly similar to 30S ribosomal protein S5	504	30,67
pc0429	**rplO**	strongly similar to 50S ribosomal protein L15	453	37,10
pc0430	**secY**	similar to preprotein translocase SecY	1482	31,26
pc0431	**rpsM**	strongly similar to 30S ribosomal protein S13	369	47,89
pc0432	**rpsK**	strongly similar to 30S ribosomal protein S11	408	50,79
pc0433	**rpoA**	similar to DNA-directed RNA polymerase alpha chain	1116	25,63
pc0434	**rplQ**	strongly similar to 50S ribosomal protein L17	429	32,64
pc0435	**gapA**	strongly similar to Glyceraldehyde 3-P dehydrogenase A	1020	9,33
pc0436	**-**	unknown protein	351	1,25
pc0437	**-**	hypothetical protein	1131	4,95
pc0438	**-**	unknown protein	1992	4,99
pc0439	**-**	unknown protein	195	0,75
pc0440	**-**	unknown protein	759	6,07
pc0441	**-**	conserved hypothetical protein	1167	50,66
pc0442	**dapF**	similar to diaminopimelate epimerase	810	7,72
pc0443	**clpP**	strongly similar to ATP-dependent Clp protease proteolytic subunit	621	25,35
pc0444	**glyA**	strongly similar to glycine hydroxymethyltransferase	1476	11,39
pc0445	**-**	unknown protein	441	21,36
pc0446	**-**	conserved hypothetical protein	771	18,82
pc0447	**-**	conserved hypothetical protein	285	1,20
pc0448	**-**	unknown protein	675	4,89
pc0449	**folE**	strongly similar to GTP cyclohydrolase I	675	2,68
pc0450	**trmH**	similar to tRNA (Guanosine-2'-O-)-methyltransferase	741	1,98
pc0451	**-**	conserved hypothetical protein	1587	11,23
pc0452	**-**	hypothetical protein	1317	2,58
pc0453	**yaeC, metQ**	similar to ABC transporter substrate binding protein yaeC	807	16,59
pc0454	**yaeE, metI**	strongly similar to ABC transporter permease yaeE	621	4,32
pc0455	**abc**	strongly similar to ABC transporter ATP-binding protein abc	1026	3,48
pc0456	**-**	unknown protein	1485	11,49
pc0457	**-**	unknown protein	198	0,99
pc0458	**xerC**	similar to XerC Protein	990	3,58
pc0459	**elaC**	similar to RNase Z (tRNA 3 endonuclease)	921	2,86
pc0460	**glpG**	similar to glpG protein	1176	4,40
pc0461	**rfaE**	strongly similar to ADP-heptose synthase	513	7,08
pc0462	**lon**	similar to endopeptidase (ATP-dependent serine protease) La	2508	12,52
pc0463	**-**	unknown protein	2139	8,41
pc0464	**-**	unknown protein	2229	6,05
pc0465	**dgt**	similar to deoxyguanosinetriphosphate triphosphohydrolase (dGTPase)	1149	4,88
pc0466	**-**	similar to O-sialoglycoprotein endopeptidase	669	3,19
pc0467	**rpsU**	strongly similar to 30S ribosomal protein S21	180	10,86
pc0468	**dnaJ**	strongly similar to heat shock protein dnaJ	1161	27,48
pc0469		conserved hypothetical protein	780	6,14
pc0470	**ftsK**	similar to multifunctional cell division protein ftsK	2628	4,30
pc0471	**bacA**	similar to bacitracin resistance protein (probable undecaprenol kinase)	774	4,16
pc0472		hypothetical protein	1554	1,94
pc0473	**-**	hypothetical protein	807	4,33
pc0474	**hprK;ptsK**	strongly similar to HPr(Ser) kinase/phosphatase	948	7,25
pc0475	**ptsH**	similar to phosphocarrier protein hpr (histidine-containing phosphocarrier protein of the PTS)	267	4,08
pc0476	**ptsI**	similar to phosphoenolpyruvate-protein phosphotransferase (PTS enzyme I)	1779	1,99
pc0477	**-**	hypothetical protein	297	5,33
pc0478	**dnaX, dnaX, dnaZX**	strongly similar to DNA-directed DNA polymerase III subunits gamma/tau dnaX	1569	7,90

pc0479	-	hypothetical protein	1410	2,80
pc0480	-	conserved hypothetical protein	1518	4,78
pc0481	-	hypothetical protein	684	2,31
pc0482	-	conserved hypothetical protein	1296	18,70
pc0483	-	conserved hypothetical protein	702	24,67
pc0484	**phoH, psiH**	similiar to phosphate starvation-inducible protein (phoH)	1302	7,61
pc0485	**ntt_4**	NAD+/ADP antiporter	1296	9,65
pc0486	-	hypothetical protein	501	3,48
pc0487	**mutT**	similar to dGTP pyrophosphohydrolase, mutT	459	12,98
pc0488	-	conserved hypothetical protein	321	1,27
pc0489	-	conserved hypothetical protein	1023	2,82
pc0490	-	conserved hypothetical protein	630	2,11
pc0491	-	unknown protein	276	1,24
pc0492	-	unknown protein	345	0,70
pc0493	-	unknown protein	204	2,65
pc0494	**ileS, ilvS**	similar to isoleucyl-tRNA synthetase	3117	6,40
pc0495	-	conserved hypothetical protein	225	6,27
pc0496	**lepB**	similar to signal peptidase I	1965	2,51
pc0497	-	hypothetical protein	738	5,64
pc0498	-	unknown protein	327	8,02
pc0499	-	unknown protein	330	9,62
pc0500	-	conserved hypothetical protein	279	0,93
pc0501	-	conserved hypothetical protein	1560	5,96
pc0502	-	conserved hypothetical protein	234	0,29
pc0503	**alkA**	similarity to DNA-3-methyladenine glycosylase II	414	0,34
pc0504	-	unknown protein	201	3,73
pc0505	-	conserved hypothetical protein	357	1,40
pc0506	-	unknown protein	249	3,11
pc0507	-	unknown protein	351	2,97
pc0508	-	unknown protein	378	0,82
pc0509	-	unknown protein	189	1,19
pc0510	-	unknown protein	624	0,55
pc0511	-	unknown protein	198	0,94
pc0512	-	similar to antibiotic resistance protein	339	0,11
pc0513	-	unknown protein	270	0,97
pc0514	-	conserved hypothetical protein	1626	0,98
pc0515	-	unknown protein	213	1,56
pc0516	-	hypothetical protein	600	4,83
pc0517	-	conserved hypothetical protein	849	4,18
pc0518	**ada**	strongly similar to DNA-6-O-methylguanine[protein]-L-cysteine S-methyltransferase	375	0,57
pc0519	**vatB, satG**	strongly similar to streptogramin A acetyltransferase	639	0,56
pc0520	-	conserved hypothetical protein	219	0,40
pc0521	-	unknown protein	225	0,51
pc0522	-	unknown protein	981	18,31
pc0523	-	unknown protein	216	0,46
pc0524	-	unknown protein	195	0,36
pc0525	-	unknown protein	186	0,53
pc0526	-	unknown protein	291	0,72
pc0527	-	conserved hypothetical protein	213	8,87
pc0528	-	conserved hypothetical protein	723	3,67
pc0529	-	unknown protein	237	1,31
pc0530	-	unknown protein	756	4,65
pc0531	**cpt**	similar to chloramphenicol 3-O phosphotransferase	279	1,45
pc0532	-	unknown protein	678	2,18
pc0533	-	unknown protein	201	1,63
pc0534	-	unknown protein	468	4,51
pc0535	-	unknown protein	234	0,79
pc0536	-	unknown protein	1245	5,32
pc0537	-	hypothetical protein	1593	1,99
pc0538	**rtxA**	similar to RTX-toxin, partial length	1089	3,33
pc0539	-	unknown protein	240	0,93
pc0540	-	hypothetical protein	309	0,77
pc0541	**def, fms**	similar to Peptide deformylase	471	7,66
pc0542	-	conserved hypothetical protein	432	1,92
pc0543	**mocA**	strongly similar to oxidoreductase MocA family	1032	12,86
pc0544	**nasA**	similarity to nasA protein	1224	5,01
pc0545	-	unknown protein	918	1,56
pc0546	**map**	similar to methionine aminopeptidase	897	5,27
pc0547	-	unknown protein	198	0,82
pc0548	**rf-2, prfB**	similar to peptide chain release factor 2	357	1,24

pc0549	-	conserved hypothetical protein	756	1,43
pc0550	**acrA;mexA**	similar to multidrug-efflux transport protein acrA	1188	3,23
pc0551	**acrB;mexB**	strongly similar to multidrug-efflux transport protein, acrB	3114	3,52
pc0552	**oprK**	similar to outer membrane protein, componenet of multidrug efflux systems	1470	5,88
pc0553	-	hypothetical protein	738	2,89
pc0554	-	conserved hypothetical protein	2073	4,54
pc0555	**rfbB, rmlB**	similar to dTDP-glucose 4,6-dehydratase, rfbB	918	1,82
pc0556	-	unknown protein	183	0,14
pc0557	-	unknown protein	216	0,31
pc0558	-	unknown protein	270	0,23
pc0559	**nuoA, nuo1**	similar to NADH-ubiquinone oxidoreductase chain A	363	8,27
pc0560	**nuoB, nuo2**	strongly similar to NADH-ubiquinone oxidoreductase chain B	495	7,57
pc0561	**nuoC, nuoCD, nuo3nuo4**	similar to NADH-ubiquinone oxidoreductase chain C/D	525	6,86
pc0562	**nuoD, nuoCD, nuo3nuo4**	similar to NADH-ubiquinone oxidoreductase chain C/D	1209	8,83
pc0563	**nuoE, nuo5**	similar to NADH-ubiquinone oxidoreductase chain E	480	10,48
pc0564	**nuoF, nuo6**	strongly similar to NADH-ubiquinone oxidoreductase chain F	1299	5,48
pc0565	**nuoG, nuo7**	similar to NADH-ubiquinone oxidoreductase chain G	2322	36,04
pc0566	**nuoH, nuo8**	strongly similar to NADH-ubiquinone oxidoreductase chain H	978	6,43
pc0567	**nuoI, nuo9**	strongly similar to NADH-ubiquinone oxidoreductase chain I	432	6,23
pc0568	**nuoJ, nuo10**	similar to NADH-ubiquinone oxidoreductase chain J	513	3,92
pc0569	**nuoK, nuo11**	similar to NADH-ubiquinone oxidoreductase chain K	300	7,62
pc0570	**nuoL, nuo12**	similar to NADH-ubiquinone oxidoreductase chain L	1887	3,19
pc0571	**nuoM, nuo13**	similar to NADH-ubiquinone oxidoreductase chain M	1446	3,39
pc0572	**nuoN, nuo14**	similar to NADH-ubiquinone oxidoreductase chain N	1443	4,36
pc0573	-	conserved hypothetical protein	855	1,39
pc0574	-	unknown protein	207	5,12
pc0575	-	conserved hypothetical protein	1029	16,64
pc0576	-	unknown protein	963	13,58
pc0577	-	unknown protein	606	14,65
pc0578	-	unknown protein	1029	2,88
pc0579	-	unknown protein	606	50,27
pc0580	-	unknown protein	1005	5,03
pc0581	-	conserved hypothetical protein	2223	6,25
pc0582	-	conserved hypothetical protein	873	2,71
pc0583	**PCKI 1**	similar to protein kinase C inhibitor 1	339	5,68
pc0584	-	conserved hypothetical protein	570	1,72
pc0585	-	hypothetical protein	1743	0,64
pc0586	-	hypothetical protein	1674	4,97
pc0587	-	hypothetical protein	1194	4,09
pc0588	**nasD**	similar to ATP-binding cassette protein	741	2,83
pc0589	**tyrP**	similar to aromatic amino acid-specific transport protein	1284	3,84
pc0590	-	hypothetical protein	480	8,46
pc0591	**dnaK, grpF, groP, seg**	similar to heat shock protein 70 (chaperone protein dnaK)	1836	4,13
pc0592	-	hypothetical protein	441	17,13
pc0593	-	unknown protein	1593	1,37
pc0594	**infA**	strongly similar to translation initiation factor IF-1	270	14,82
pc0595	**tufA**	strongly similar to translation elongation factor Tu (EF-Tu)	1185	83,99
pc0596	-	unknown protein	192	3,65
pc0597	**secE**	similar to preprotein translocase SecE	288	19,95
pc0598	**nusG**	similar to transcription antitermination factor NusG	204	20,70
pc0599	**nusG**	strongly similar to transcription antitermination factor NusG	375	18,23
pc0600	**rplK**	strongly similar to 50S ribosomal protein L11	429	161,45
pc0601	**rplA**	strongly similar to 50S ribosomal protein L1	711	109,70
pc0602	**rplJ;rl10**	similar to 50S ribosomal protein L10	546	80,12
pc0603	**rplL;rl7**	strongly similar to 50S ribosomal protein L7/L12	390	39,15
pc0604	**rpoB**	strongly similar to DNA-directed RNA polymerase, beta chain	3765	38,86
pc0605	**rpoC;tabB**	strongly similar to DNA-directed RNA polymerase, beta' chain	4167	21,12
pc0606	**pal**	strongly similar to peptidoglycan-associated	468	10,09

		lipoprotein precursor (pal)		
pc0607	-	hypothetical protein	2163	2,88
pc0608	-	unknown protein	183	0,72
pc0609	-	hypothetical protein	1686	4,64
pc0610	**maf**	strongly similar to septum formation protein	585	2,73
pc0611	-	unknown protein	297	2,90
pc0612	-	unknown protein	258	0,30
pc0613	-	unknown protein	201	0,31
pc0614	-	unknown protein	309	0,92
pc0615	-	unknown protein	1380	1,10
pc0616	**omcB**	similar to 60 kDa cysteine-rich outer membrane protein	1677	337,33
pc0617	**omcA**	similar to 9 kDa cysteine-rich outer membrane protein	270	278,41
pc0618	-	similar to NAD+ kinase	840	6,26
pc0619	**dxs**	similar to 1-deoxy-D-xylulose 5-phosphate synthase	1908	6,69
pc0620	**xseB**	similar to exodeoxyribonuclease VII, small chain	279	5,25
pc0621	**xseA**	similar to exodeoxyribonuclease VII, large chain	1449	4,69
pc0622	**dagA**	similar to D-alanine/glycine transport protein, sodium-dependent	1380	11,27
pc0623	**nfi**	strongly similar to endonuclease V (deoxyinosine 3'endonuclease)	708	4,80
pc0624	-	unknown protein	192	0,32
pc0625	-	hypothetical protein	492	37,46
pc0626	-	conserved hypothetical protein	675	50,06
pc0627	-	unknown protein	354	41,02
pc0628	-	unknown protein	618	2,73
pc0629	-	unknown protein	231	0,27
pc0630	-	similar to Thermostable carboxypeptidase 1	1521	2,36
pc0631	**alr**	similar to alanine racemase	2526	3,66
pc0632	-	conserved hypothetical protein	201	35,47
pc0633	**acrD**	similar to acriflavin resistance protein D	3078	3,31
pc0634	-	hypothetical protein	813	5,49
pc0635	**tolC**	similar to outer membrane protein TolC	1269	4,31
pc0636	-	hypothetical protein	1083	1,05
pc0637	-	conserved hypothetical protein	1152	2,12
pc0638	-	unknown protein	336	2,39
pc0639	-	conserved hypothetical protein	1377	4,10
pc0640	**ftsH;hflB**	strongly similar to cell division protein FtsH	2751	20,90
pc0641	-	hypothetical protein	747	3,68
pc0642	**cps**	similar to beta-1,4-galactosyltransferase	810	5,76
pc0643	**pnp**	strongly similar to polyribonucleotide nucleotidyltransferase	2109	8,54
pc0644	**rpsO;rs15**	strongly similar to 30S ribosomal protein S15	270	22,96
pc0645	-	conserved hypothetical protein	276	1,47
pc0646	-	conserved hypothetical protein	369	9,51
pc0647	-	unknown protein	684	17,87
pc0648	-	conserved hypothetical protein	501	11,13
pc0649	-	conserved hypothetical protein	258	15,96
pc0650	-	unknown protein	1188	3,60
pc0651	**rpmE;rl31**	similar to 50S ribosomal protein L31	354	54,12
pc0652	**prfA**	strongly similar to translation releasing factor RF-1	1080	5,95
pc0653	**hemK**	strongly similar to methyltransferase for peptide chain release factors RF-1 and RF-2	840	1,66
pc0654	**ffh**	strongly similar to signal recognition particle chain ffh	1365	17,00
pc0655	**rpsP;rs16**	similar to 30S ribosomal protein S16	321	53,56
pc0656	**trmD**	strongly similar to tRNA (guanine N-1)-methyltransferase	669	27,73
pc0657	**rplS**	strongly similar to ribosomal protein L19	408	27,64
pc0658	**rnh**	strongly similar to ribonuclease HII	669	14,43
pc0659	-	unknown protein	525	7,87
pc0660	-	conserved hypothetical protein	885	5,56
pc0661	-	unknown protein	201	0,25
pc0662	**gmk**	similar to guanylate kinase	594	1,66
pc0663	-	conserved hypothetical protein	324	10,52
pc0664	-	unknown protein	594	8,18
pc0665	**metG**	similar to methionine-tRNA ligase	2097	4,63
pc0666	**rpmB**	similar to ribosomal protein L28	276	12,04
pc0667	-	unknown protein	216	5,16
pc0668	-	unknown protein	327	9,65
pc0669	**gatB**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain B	1485	10,55

pc0670	**gatA**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain A	1470	6,13
pc0671	**gatC**	similar to glutamyl-tRNA(Gln) amidotransferase chain C	300	6,23
pc0672	**phrB**	similar to photolyase	1416	4,76
pc0673	**-**	conserved hypothetical protein	852	2,35
pc0674	**-**	hypothetical protein	3465	5,11
pc0675	**-**	hypothetical protein	963	19,85
pc0676	**-**	conserved hypothetical protein	1914	5,82
pc0677	**recN**	similar to DNA repair protein RecN	1626	7,15
pc0678	**-**	unknown protein	441	6,67
pc0679	**rnhB**	strongly similar to ribonuclease HII	906	2,95
pc0680	**-**	conserved hypothetical protein	489	4,85
pc0681	**-**	conserved hypothetical protein	1170	2,12
pc0682	**truA**	similar to tRNA-pseudouridine synthase I	789	0,82
pc0683	**-**	conserved hypothetical protein	600	6,83
pc0684	**-**	similar to multiple antibiotic resistance protein	597	5,27
pc0685	**aspC**	LL-DAP aminotransferase	1263	2,00
pc0686	**dapA**	similar to dihydrodipicolinate synthase	903	1,46
pc0687	**dapB**	similar to dihydrodipicolinate reductase	657	3,15
pc0688	**-**	similar to phospholipase D (PLD)	1125	1,71
pc0689	**recD**	similar to exodeoxyribonuclease V	2166	3,84
pc0690	**dnaG**	similar to DNA primase	1779	5,53
pc0691	**-**	conserved hypothetical protein	417	3,19
pc0692	**-**	unknown protein	294	0,52
pc0693	**glyS**	strongly similar to glycyl-tRNA synthetase	3054	7,80
pc0694	**-**	unknown protein	228	10,00
pc0695	**-**	conserved hypothetical protein	993	6,33
pc0696	**-**	unknown protein	393	7,91
pc0697	**uvrC**	similar to Excinuclease ABC subunit C	1833	8,29
pc0698	**-**	unknown protein	534	18,60
pc0699	**-**	unknown protein	1344	17,21
pc0700	**-**	unknown protein	411	20,19
pc0701	**thrS**	similar to threonine-tRNA ligase	1662	3,74
pc0702	**infC**	strongly similar to translation initiation factor IF-3	555	91,12
pc0703	**rpmI**	strongly similar to 50S ribosomal protein L35	195	112,87
pc0704	**rplT**	strongly similar to ribosomal protein L20	357	28,03
pc0705	**pheS**	strongly similar to phenylalanine-tRNA ligase alpha chain	1041	40,68
pc0706	**-**	similar to ribosomal large subunit pseudouridine synthase D	897	4,65
pc0707	**waaC;rfaC**	similar to heptosyltransferase I	1089	3,56
pc0708	**-**	conserved hypothetical protein	477	3,42
pc0709	**-**	conserved hypothetical protein	930	7,75
pc0710	**-**	conserved hypothetical protein	1140	4,29
pc0711	**-**	conserved hypothetical protein	1239	3,92
pc0712	**-**	unknown protein	219	1,49
pc0713	**-**	conserved hypothetical protein	1344	1,13
pc0714	**-**	conserved hypothetical protein	1338	3,00
pc0715	**sugE**	strongly similar to sugE protein	333	2,63
pc0716	**-**	conserved hypothetical protein	438	2,60
pc0717	**-**	conserved hypothetical protein	654	4,47
pc0718	**-**	hypothetical protein	876	2,87
pc0719	**-**	similar to serine protease	1233	2,89
pc0720	**-**	similar to serine/threonine phosphoprotein phosphatase	780	7,46
pc0721	**nifS**	similar to cysteine sulfinate desulfinase	1170	4,51
pc0722	**-**	conserved hypothetical protein	324	1,75
pc0723	**-**	conserved hypothetical protein	507	1,43
pc0724	**-**	unknown protein	255	9,89
pc0725	**udhA**	strongly similar to soluble pyridine nucleotide transhydrogenase	1398	5,29
pc0726	**-**	unknown protein	495	3,67
pc0727	**-**	unknown protein	1209	2,79
pc0728	**clpB**	strongly similar to endopeptidase Clp ATP-binding chain	2607	11,71
pc0729	**-**	conserved hypothetical protein	2748	2,36
pc0730	**-**	unknown protein	192	0,76
pc0731	**-**	unknown protein	243	0,74
pc0732	**-**	unknown protein	186	0,59
pc0733	**-**	unknown protein	2826	4,11
pc0734	**-**	hypothetical protein	2847	1,72

pc0735	-	unknown protein	3228	21,26
pc0736	-	conserved hypothetical protein	2598	2,06
pc0737	-	conserved hypothetical protein	879	2,35
pc0738	-	unknown protein	474	9,33
pc0739	**rhs**	similar to rhs core protein with extension	5508	4,03
pc0740	**gcpE**	strongly similar to gcpE protein	1965	7,19
pc0741	-	conserved hypothetical protein	585	6,41
pc0742	-	conserved hypothetical protein	1536	4,59
pc0743	-	conserved hypothetical protein	2298	11,96
pc0744	-	unknown protein	216	0,62
pc0745	**malQ**	similar to 4-alpha-glucanotransferase	1671	4,61
pc0746	**scc1, sycE**	strongly similar to type III secretion chaperone sycE	459	8,19
pc0747	-	hypothetical protein	351	5,37
pc0748	-	unknown protein	1086	12,20
pc0749	**sctV;lcrD**	strongly similar to type III secretion pathway protein SctV	2181	4,84
pc0750	**sctU;yscU**	similar to type III secretion pathway protein sctU	1074	7,58
pc0751	-	unknown protein	1815	6,04
pc0752	-	strongly similar to GTP-binding protein YchF	1098	7,12
pc0753	-	conserved hypothetical protein	1143	4,49
pc0754	-	hypothetical protein	1506	4,54
pc0755	-	unknown protein	210	0,28
pc0756	-	unknown protein	186	0,22
pc0757	-	unknown protein	228	0,48
pc0758	**ribF**	similar to riboflavin kinase/FMN adenylyltransferase	942	2,79
pc0759	**truB**	strongly similar to tRNA pseudouridine synthase B	789	8,83
pc0760	**rbfA**	similar to ribosome binding factor A	396	6,92
pc0761	-	similar to translation initiation factor IF-2	2763	19,41
pc0762	**nusA**	similar to transcription termination-antitermination factor nusA	1275	12,51
pc0763	-	unknown protein	183	0,31
pc0764	**rpsA**	strongly similar to ribosomal protein S1	1764	34,57
pc0765	**lysC**	strongly similar to aspartate kinase II precursor	801	1,85
pc0766	-	unknown protein	1908	0,58
pc0767	**braB**	similar to branched-chain amino acid transport system II carrier protein	1182	1,27
pc0768	**rpe**	similar to ribulose-phosphate 3-epimerase	732	5,49
pc0769	**efp**	similar to elongation factor P	555	19,00
pc0770	-	unknown protein	342	15,33
pc0771	**accB, BCCP**	similar to biotin carboxyl carrier protein of acetyl-CoA carboxylase	513	17,14
pc0772	**accC**	strongly similar to biotin carboxylase	1362	13,56
pc0773	-	unknown protein	711	2,23
pc0774	-	unknown protein	678	4,27
pc0775	-	conserved hypothetical protein	693	3,87
pc0776	-	conserved hypothetical protein	957	15,12
pc0777	-	unknown protein	411	3,68
pc0778	**exoD**	similar to exopolysaccharide synthesis protein	627	3,14
pc0779	-	hypothetical protein	1968	3,89
pc0780	**map1**	strongly similar to methionyl aminopeptidase	888	4,75
pc0781	**pgi**	similarity to Glucose-6-phosphate isomerase (GPI), (Phosphoglucoseisomerase, PGI), (Phosphohexose isomerase, PHI)	1614	12,24
pc0782	-	unknown protein	453	7,69
pc0783	**XerD**	strongly similar to site-specific recombinases XerD	876	3,66
pc0784	-	unknown protein	432	16,23
pc0785	-	unknown protein	219	21,40
pc0786	-	unknown protein	318	21,76
pc0787	**lcrH**	similar to regulatory protein, involved in type III secretion lcrH, sycD	501	9,60
pc0788	-	unknown protein	267	1,62
pc0789	**adh3**	similar to alcohol dehydrogenase class III	1128	15,19
pc0790	-	hypothetical protein	738	23,08
pc0791	-	hypothetical protein	1452	2,96
pc0792	-	hypothetical protein	1299	1,65
pc0793	**mscL**	similar to mechanosensitive channel of large conductance	402	3,24
pc0794	-	strongly similar to queuine tRNA-ribosyltransferase (guanine insertion enzyme)	1164	3,32
pc0795	-	conserved hypothetical protein	654	2,09
pc0796	-	similar to tonoplast intrinsic protein (Aquaporin)	699	8,51
pc0797	-	hypothetical protein	630	3,38

pc0798	-	unknown protein	222	2,03
pc0799	-	unknown protein	243	0,29
pc0800	-	hypothetical protein	942	1,68
pc0801	**tpiA**	strongly similar to triose-phosphate isomerase	795	8,87
pc0802	**secG**	similar to integral membrane component of the sec protein-translocation machinery, secG	294	8,99
pc0803	**def**	similar to polypeptide deformylase	531	4,77
pc0804	-	unknown protein	189	0,33
pc0805	-	unknown protein	1857	11,65
pc0806	-	unknown protein	408	57,48
pc0807	-	unknown protein	270	0,97
pc0808	-	hypothetical protein	366	7,02
pc0809	**copB**	similar to copper-transporting ATPase	2295	1,59
pc0810	**tdh**	strongly similar to threonine 3-dehydrogenase	1029	4,56
pc0811	-	strongly similar to 2-amino-3-ketobutyrate coenzyme A ligase (Glycine acetyltransferase)	1191	7,44
pc0812	-	unknown protein	1083	28,91
pc0813	-	unknown protein	831	3,76
pc0814	-	unknown protein	696	2,33
pc0815	**lolD**	strongly similar to lipoprotein releasing system ATP-binding protein	687	1,86
pc0816	-	conserved hypothetical protein	2133	9,81
pc0817	**rpmG**	strongly similar to 50S ribosomal protein L33	156	14,66
pc0818	-	strong similarity to O-sialoglycoprotein endopeptidase	1032	6,01
pc0819	**devB;pgl**	similar to 6-phosphogluconolactonase (6PGL).	639	8,92
pc0820	-	hypothetical protein	1077	5,48
pc0821	**zwf**	similarity to glucose-6-phosphate 1-dehydrogenase (G6PD)	1551	8,41
pc0822	-	similarity to bumetanide-sensitive Na-K-Cl cotransporter	2295	9,59
pc0823	-	conserved hypothetical protein	405	3,51
pc0824	**pyrG**	strongly similar to CTP synthase	1635	5,01
pc0825	**kdsB**	strongly similar to 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)	780	4,44
pc0826	-	conserved hypothetical protein	951	8,69
pc0827	**gseA;kdtA**	similarity to 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO transferase)	1254	2,72
pc0828	-	unknown protein	189	6,68
pc0829	-	unknown protein	1311	1,96
pc0830	-	unknown protein	696	7,12
pc0831	-	unknown protein	201	0,30
pc0832	-	unknown protein	186	0,20
pc0833	-	unknown protein	366	1,66
pc0834	-	unknown protein	252	1,20
pc0835	-	hypothetical protein	1149	2,78
pc0836	-	unknown protein	267	1,63
pc0837	-	unknown protein	423	1,39
pc0838	-	unknown protein	1239	1,59
pc0839	-	unknown protein	1020	3,03
pc0840	-	unknown protein	759	13,94
pc0841	-	unknown protein	279	2,71
pc0842	-	unknown protein	444	35,77
pc0843	-	hypothetical protein	1164	3,13
pc0844	-	unknown protein	291	1,57
pc0845	-	conserved hypothetical protein	366	1,46
pc0846	-	hypothetical protein	618	0,24
pc0847	-	unknown protein	219	0,04
pc0848	-	hypothetical protein	492	0,30
pc0849	-	unknown protein	288	0,50
pc0850	-	hypothetical protein	747	5,88
pc0851	-	conserved hypothetical protein	1371	2,54
pc0852	-	conserved hypothetical protein	684	0,51
pc0853	-	conserved hypothetical protein	192	0,61
pc0854	-	unknown protein	255	2,00
pc0855	-	conserved hypothetical protein	432	3,38
pc0856	**pcm**	strongly similar to L-isoaspartyl protein carboxyl methyltransferase	633	8,28
pc0857	-	conserved hypothetical protein	246	2,89
pc0858	-	unknown protein	411	0,52
pc0859	-	conserved hypothetical protein	333	20,41
pc0860	-	conserved hypothetical protein	741	3,82

pc0861	-	hypothetical protein	855	4,32
pc0862	-	unknown protein	1827	4,15
pc0863	-	hypothetical protein	1014	2,48
pc0864	**surE**	similar to acid phosphatase	786	2,60
pc0865	**acnB**	strongly similar to aconitate hydratase	2847	3,82
pc0866	-	unknown protein	186	1,38
pc0867	-	conserved hypothetical protein	699	4,21
pc0868	-	conserved hypothetical protein	390	0,17
pc0869	-	unknown protein	960	2,41
pc0870	-	unknown protein	891	3,01
pc0871	**potA**	strongly similar to spermidin/putrescin transport ATP-binding protein, component of ATP-transporter system	1122	7,69
pc0872	**potB**	strongly similar to spermidine/putrescine transport system permease, component of ATP-transporter system	915	6,24
pc0873	**potC**	strongly similar to spermidine/putrescine transport system permease, component of ATP-transporter system	768	7,31
pc0874	**potD**	similar to spermidine/putrescine-binding protein precursor, component of ABC transporter system	1038	2,33
pc0875	-	unknown protein	186	1,06
pc0876	-	unknown protein	201	8,95
pc0877	**mgtE**	similar to Mg2+ transporter	1365	4,18
pc0878	**sdaB**	strongly similar to L-serine ammonia-lyase	1392	9,05
pc0879	-	conserved hypothetical protein	792	4,27
pc0880	**pfkA**	similar to 6-phosphofructokinase 1	1662	8,68
pc0881	-	hypothetical protein	603	7,46
pc0882	**aroA**	similar to 3-phosphoshikimate 1-carboxyvinyltransferase(5-enolpyruvylshikimate-3-phosphate synthase, EPSP synthase)	2820	1,83
pc0883	**aroL**	similar to shikimate kinase precursor	612	6,00
pc0884	**aroC**	strongly similar to chorismate synthase	1104	1,63
pc0885	-	unknown protein	738	0,12
pc0886	-	unknown protein	702	18,41
pc0887	-	unknown protein	387	6,73
pc0888	-	conserved hypothetical protein	1962	3,57
pc0889	**ribH;ribE**	strongly similar to riboflavin synthase beta chain	519	3,68
pc0890	**ribA;ribB**	strongly similar to 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	1239	2,35
pc0891	**ribC**	strongly similar top riboflavin synthase alpha chain	606	4,31
pc0892	**mutM, fpg**	similar to formamidopyrimidine-DNA glycosidase	831	2,65
pc0893	**rbp**	strongly similar to nucleic acid-binding protein	339	85,87
pc0894	-	unknown protein	4047	7,09
pc0895	-	similar to outer membrane protein	1614	3,67
pc0896	-	hypothetical protein	1422	2,96
pc0897	-	unknown protein	183	0,19
pc0898	**rbn**	similar to RNase BN, tRNA processing enzyme	1170	6,08
pc0899	-	unknown protein	2406	16,63
pc0900	-	conserved hypothetical protein	606	6,41
pc0901	-	hypothetical protein	981	8,00
pc0902	-	conserved hypothetical protein	369	5,76
pc0903	-	conserved hypothetical protein	516	6,15
pc0904	**rgpB**	strongly similar to rhamnosyltransferase	939	3,01
pc0905	-	unknown protein	1650	22,45
pc0906	-	conserved hypothetical protein	1317	2,84
pc0907	-	hypothetical protein	1815	1,20
pc0908	-	hypothetical protein	468	4,26
pc0909	-	conserved hypothetical protein	729	3,92
pc0910	-	unknown protein	192	2,93
pc0911	-	unknown protein	2232	4,79
pc0912	-	conserved hypothetical protein	558	2,68
pc0913	-	hypothetical protein	594	5,26
pc0914	**czcD**	similar to cation efflux system protein	942	2,17
pc0915	**kefC**	similar to glutathione-regulated potassium-efflux system protein	2016	0,77
pc0916	-	similar to CPAF (chlamydia protease-like activity factor)	1713	9,93
pc0917	-	unknown protein	192	0,73
pc0918	-	hypothetical protein	954	0,70
pc0919	-	conserved hypothetical protein	825	0,67
pc0920	-	conserved hypothetical protein	312	4,16

pc0921	-	hypothetical protein	441	20,18
pc0922	-	unknown protein	1509	2,59
pc0923	-	hypothetical protein	858	1,51
pc0924	-	unknown protein	471	39,35
pc0925	-	unknown protein	435	10,95
pc0926	-	unknown protein	675	8,63
pc0927	-	similar to cationic amino acid transport protein	1308	2,25
pc0928	**trpD**	similar to anthranilate synthase component II	804	1,30
pc0929	-	conserved hypothetical protein	459	3,45
pc0930	**cynT**	similar to carbonic anhydrase	651	4,15
pc0931	-	hypothetical protein	1014	1,97
pc0932	-	unknown protein	207	8,94
pc0933	**dhnA;fbaB**	strongly similar to fructose-bisphosphate aldolase class I	1056	19,48
pc0934	-	conserved hypothetical protein	630	8,69
pc0935	**glk**	similar to glucokinase	984	7,73
pc0936	-	unknown protein	291	2,16
pc0937	-	unknown protein	372	3,18
pc0938	-	hypothetical protein	9546	2,98
pc0939	-	hypothetical protein	546	4,79
pc0940	-	unknown protein	183	0,10
pc0941	-	unknown protein	219	2,13
pc0942	-	conserved hypothetical protein	1407	2,78
pc0943	**blc**	similar to outer membrane lipoprotein	579	4,04
pc0944	-	hypothetical protein	723	15,04
pc0945	-	unknown protein	786	5,53
pc0946	-	unknown protein	534	3,90
pc0947	**trxA**	similar to thioredoxin	435	2,03
pc0948	-	conserved hypothetical protein	648	1,16
pc0949	-	conserved hypothetical protein	2415	2,33
pc0950	**lig**	similar to DNA ligase	1593	4,42
pc0951	-	conserved hypothetical protein	1005	18,24
pc0952	-	strongly similar to putative oxidoreductases	867	8,33
pc0953	**yciF**	strongly similar to yciF protein	525	53,30
pc0954	-	unknown protein	357	85,80
pc0955	**ftn**	strongly similar to ferritin	489	9,03
pc0956	-	conserved hypothetical protein	618	1,74
pc0957	-	conserved hypothetical protein	1002	1,50
pc0958	**dcd**	strongly similar to dctp deaminase	567	2,23
pc0959	-	conserved hypothetical protein	276	0,72
pc0960	-	unknown protein	1005	2,40
pc0961	-	unknown protein	195	0,54
pc0962	-	unknown protein	201	3,87
pc0963	-	conserved hypothetical protein	288	24,35
pc0964	**msrA**	strongly similar to protein-methionine-s-oxide reductase	855	5,43
pc0965	-	unknown protein	291	0,28
pc0966	-	unknown protein	255	0,76
pc0967	-	unknown protein	366	14,19
pc0968	-	unknown protein	771	17,29
pc0969	-	conserved hypothetical protein	198	1,76
pc0970	-	conserved hypothetical protein	4818	4,05
pc0971	-	conserved hypothetical protein	210	0,10
pc0972	-	unknown protein	222	1,92
pc0973	-	conserved hypothetical protein	597	6,01
pc0974	-	conserved hypothetical protein	2265	4,53
pc0975	**umuC**	similar to SOS mutagenesis and repair protein UmuC	1182	5,79
pc0976	**umuD**	strongly similar to SOS mutagenesis and repair protein UmuD	432	2,74
pc0977	-	unknown protein	552	15,98
pc0978	-	unknown protein	444	38,61
pc0979	-	conserved hypothetical protein	441	5,98
pc0980	-	conserved hypothetical protein	339	5,91
pc0981	-	hypothetical protein	1404	5,33
pc0982	-	unknown protein	282	0,29
pc0983	-	unknown protein	243	1,44
pc0984	-	unknown protein	378	0,31
pc0985	-	unknown protein	264	9,62
pc0986	-	conserved hypothetical protein	261	0,86
pc0987	-	conserved hypothetical protein	336	1,78
pc0988	-	unknown protein	276	0,23
pc0989	-	unknown protein	249	10,64

pc0990	-	conserved hypothetical protein	258	6,56
pc0991	-	unknown protein	186	1,64
pc0992	-	conserved hypothetical protein	1752	46,61
pc0993	-	conserved hypothetical protein	1437	5,85
pc0994	-	conserved hypothetical protein	306	8,10
pc0995	-	conserved hypothetical protein	303	5,12
pc0996	-	conserved hypothetical protein	342	8,88
pc0997	-	unknown protein	198	1,08
pc0998	-	unknown protein	219	5,49
pc0999	-	conserved hypothetical protein	270	81,07
pc1000	-	conserved hypothetical protein	813	4,06
pc1001	-	conserved hypothetical protein	378	2,43
pc1002	-	unknown protein	717	2,47
pc1003	-	hypothetical protein	366	1,77
pc1004	-	conserved hypothetical protein	264	1,78
pc1005	-	conserved hypothetical protein	846	2,26
pc1006	-	unknown protein	2874	1,67
pc1007	-	unknown protein	264	1,65
pc1008	-	unknown protein	186	0,28
pc1009	-	unknown protein	2811	9,18
pc1010	-	conserved hypothetical protein	1251	1,97
pc1011	-	conserved hypothetical protein	1941	3,71
pc1012	-	unknown protein	228	0,33
pc1013	-	unknown protein	276	0,41
pc1014	-	hypothetical protein	339	0,46
pc1015	-	hypothetical protein	366	3,40
pc1016	-	unknown protein	216	1,43
pc1017	-	conserved hypothetical protein	210	5,41
pc1018	-	conserved hypothetical protein	357	13,24
pc1019	-	unknown protein	270	1,24
pc1020	-	unknown protein	282	0,17
pc1021	**doc**	similar to death on curing protein	378	8,13
pc1022	-	conserved hypothetical protein	231	10,46
pc1023	-	unknown protein	186	4,84
pc1024	-	unknown protein	186	1,48
pc1025	-	conserved hypothetical protein	2088	11,92
pc1026	-	conserved hypothetical protein	249	0,76
pc1027	-	unknown protein	204	0,46
pc1028	-	conserved hypothetical protein	378	7,13
pc1029	-	conserved hypothetical protein	813	5,27
pc1030	-	unknown protein	210	0,51
pc1031	-	conserved hypothetical protein	1662	8,11
pc1032	-	conserved hypothetical protein	2205	10,12
pc1033	-	hypothetical protein	1989	30,03
pc1034	-	unknown protein	432	0,80
pc1035	**soj, parA**	similar to sporulation initiation inhibitor protein	597	0,66
pc1036	-	unknown protein	201	1,49
pc1037	-	unknown protein	285	0,51
pc1038	-	unknown protein	2598	5,82
pc1039	-	unknown protein	2607	13,83
pc1040	-	unknown protein	231	0,60
pc1041	**adk**	strongly similar to adenylate kinase (EC 2.7.4.3)	696	8,56
pc1042	**ribD, ribG**	strongly similar to diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	1107	2,26
pc1043	-	conserved hypothetical protein	1173	3,72
pc1044	-	conserved hypothetical protein	441	4,13
pc1045	-	unknown protein	441	3,97
pc1046	-	conserved hypothetical protein	771	3,31
pc1047	**leuS**	strongly similar to leucyl-tRNA synthetase	2538	7,22
pc1048	**vacB, rnr**	similar to ribonuclease R	2328	3,24
pc1049	-	conserved hypothetical protein	708	5,56
pc1050	-	conserved hypothetical protein	657	3,09
pc1051	-	unknown protein	453	2,42
pc1052	-	unknown protein	1506	3,88
pc1053	-	conserved hypothetical protein	159	9,70
pc1054	-	conserved hypothetical protein	453	1,33
pc1055	-	similar to hemolysin	1374	2,80
pc1056	-	conserved hypothetical protein	1560	2,41
pc1057	-	conserved hypothetical protein	1998	7,88
pc1058	**cynT**	similar to carbonate dehydratase, cynT	786	8,74

pc1059	-	unknown protein	270	16,19
pc1060	**ubiE**	similar to ubiquinone/menaquinone biosynthesis methyltransferase, ubiE	729	18,75
pc1061	-	conserved hypothetical protein	414	2,22
pc1062	**menE**	similar to o-succinylbenzoate-CoA ligase, menE	1134	3,48
pc1063	**menA**	similar to 1,4-dihydroxy-2-naphthoate octaprenyltransferase, menA	903	2,26
pc1064	**menB**	strongly similar to naphthoate synthase, menB	828	3,70
pc1065	-	conserved hypothetical protein	4518	8,16
pc1066	-	conserved hypothetical protein	306	0,26
pc1067	-	conserved hypothetical protein	711	0,62
pc1068	**menD, menCF**	similar to menaquinone biosynthesis protein, menD	1563	1,08
pc1069	**menF**	similar to menaquinone-specific isochorismate synthase, menF	1056	1,82
pc1070	-	hypothetical protein	1095	7,46
pc1071	-	hypothetical protein	1428	5,14
pc1072	**holB**	similar to DNA polymerase III, delta' subunit, holB	1110	1,52
pc1073	**tmk**	similar to thymidylate kinase, tmk	678	7,60
pc1074	**gyrA**	strongly similar to DNA gyrase subunit A	2571	10,36
pc1075	**gyrB**	strongly similar to DNA gyrase subunit B	2508	18,47
pc1076	-	conserved hypothetical protein	339	5,76
pc1077	-	unknown protein	1038	269,00
pc1078	**lytB, ispH**	strongly similar to protein involved in isoprenoid biosynthesis and penicillin tolerance	942	13,09
pc1079	**wzb**	similar to low molecular weight protein-tyrosine-phosphatase	483	5,94
pc1080	-	conserved hypothetical protein	1968	18,42
pc1081	**yidC**	similar to 60 kDa inner-membrane protein	2601	6,41
pc1082	**dnaA**	similar to chromosomal replication initiator protein, dnaA	1356	1,75
pc1083	**lgt**	similar to prolipoprotein diacylglycerol transferase	1125	3,19
pc1084	**fdlV**	similar to ferredoxin [2Fe-2S] 4	267	8,09
pc1085	-	conserved hypothetical protein	705	25,53
pc1086	-	hypothetical protein	1098	83,35
pc1087	-	hypothetical protein	1146	43,33
pc1088	**dld1, pdhD, aceD, citL**	strongly similar to dihydrolipoamide dehydrogenase precursor (E3 component of pyruvate dehydrogenase multi-enzyme complex)	1398	8,96
pc1089	**sucB, odo2, E2o**	strongly similar to dihydrolipoamide S-succinyltransferase, (2-oxogluturate dehydrogenase complex E2 component), sucB	1215	3,40
pc1090	**sucA, odo1, E1o**	strongly similar to 2-oxoglutarate dehydrogenase E1 component, sucA	2673	4,23
pc1091	-	unknown protein	663	1,22
pc1092	-	unknown protein	2376	2,42
pc1093	**ysgA**	similar to carboxymethylenebutenolidase	732	7,86
pc1094	-	hypothetical protein	1905	2,17
pc1095	-	conserved hypothetical protein	468	9,39
pc1096	**hemN**	similar to oxygen-independent coproporphyrinogen III oxidase, hemN	1158	2,86
pc1097	-	unknown protein	2091	1,03
pc1098	-	unknown protein	387	22,57
pc1099	-	conserved hypothetical protein	726	13,04
pc1100	-	hypothetical protein	1032	5,72
pc1101	-	unknown protein	255	0,98
pc1102	**asd**	similar to aspartate-semialdehyde dehydrogenase	1068	9,65
pc1103	**pepA, xerB, carP**	similar to aminopeptidase A, pepA	1500	11,87
pc1104	**ssb, lexC, exrB**	similar to Single-strand binding protein	477	42,69
pc1105	-	conserved hypothetical protein	504	63,86
pc1106	-	strongly similar to isoamylase	2013	3,45
pc1107	-	hypothetical protein	864	15,31
pc1108	**ruvB**	strongly similar to holliday junction DNA helicase, ruvB	999	6,45
pc1109	-	unknown protein	540	29,64
pc1110	**lcrH, ycD**	similar to low calcium response protein lcrH	387	31,78
pc1111	-	unknown protein	963	26,17
pc1112	-	unknown protein	579	34,23
pc1113	-	conserved hypothetical protein	633	3,12
pc1114	-	unknown protein	963	7,63
pc1115	**mgtE**	similar to Mg2+ transporter	1473	4,97
pc1116	**fusA**	similar to Elongation factor G (EF-G), fusA	1821	9,42
pc1117	-	hypothetical protein	2049	20,10

pc1118	-	conserved hypothetical protein	2157	14,50
pc1119	-	conserved hypothetical protein	966	5,88
pc1120	-	conserved hypothetical protein	1260	1,69
pc1121	**yedO**	similar to 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase)	1008	2,17
pc1122	-	unknown protein	216	0,43
pc1123	-	unknown protein	909	5,25
pc1124	-	similar to calcium-dependent protein kinase 9	1395	1,03
pc1125	**hlyE;hly3**	strongly similar to hemolysin III	585	2,06
pc1126	-	unknown protein	291	4,11
pc1127	-	unknown protein	207	10,56
pc1128	-	unknown protein	2325	8,17
pc1129	-	unknown protein	3321	4,60
pc1130	-	unknown protein	183	0,17
pc1131	-	hypothetical protein	969	1,84
pc1132	**proC,**	similar to pyrroline-5-carboxylate reductase, proC	795	9,60
pc1133	**ppiB**	strongly similar to peptidylprolyl isomerase II (cyclophilin A)	480	28,74
pc1134	-	unknown protein	675	9,59
pc1135	-	unknown protein	2256	11,92
pc1136	-	unknown protein	1242	26,36
pc1137	-	unknown protein	1233	56,95
pc1138	-	unknown protein	1119	1,47
pc1139	-	unknown protein	186	4,80
pc1140	-	conserved hypothetical protein	186	0,26
pc1141	-	conserved hypothetical protein	585	0,71
pc1142	-	conserved hypothetical protein	1773	10,50
pc1143	-	conserved hypothetical protein	1011	1,16
pc1144	-	unknown protein	219	5,67
pc1145	-	conserved hypothetical protein	264	0,51
pc1146	-	conserved hypothetical protein	273	0,84
pc1147	-	conserved hypothetical protein	543	11,79
pc1148	-	conserved hypothetical protein	540	39,85
pc1149	-	similar to DNA protection during starvation protein	465	28,61
pc1150	-	unknown protein	240	17,76
pc1151	-	unknown protein	936	2,63
pc1152	**fabI**	strongly similar to NADH-dependent enoyl-ACP reductase	912	10,09
pc1153	-	unknown protein	873	1,48
pc1154	-	unknown protein	1110	1,20
pc1155	-	unknown protein	276	1,06
pc1156	**fabG**	similar to 3-ketoacyl-acyl carrier protein reductase, fabG	708	4,27
pc1157	**folB, mutT**	similar to dGTP pyrophosphohydrolase/dihydroneopterin aldolase (mutT/folB, fusion protein)	789	1,16
pc1158	-	hypothetical protein	879	5,13
pc1159	-	conserved hypothetical protein	573	11,52
pc1160	-	conserved hypothetical protein	480	2,84
pc1161	**dnaQ, mutD**	similar to DNA polymerase III, epsilon chain, mutD	651	3,59
pc1162	-	conserved hypothetical protein	810	1,04
pc1163	**msbA**	similar to transport ATP binding protein	1941	3,02
pc1164	**accA**	strongly similar to acetyl-CoA carboxylase	951	4,94
pc1165	-	hypothetical protein	978	7,61
pc1166	-	unknown protein	297	2,36
pc1167	-	hypothetical protein	1497	5,44
pc1168	**himD; ihfB**	similar to integration host factor	363	21,44
pc1169	**tyrS**	strongly similar to tyrosine-tRNA ligase	1278	6,28
pc1170	-	unknown protein	243	0,40
pc1171	**osmY**	similar to hyperosmotically inducible periplasmic protein	393	147,57
pc1172	-	hypothetical protein	627	72,37
pc1173	-	conserved hypothetical protein	759	5,07
pc1174	-	unknown protein	855	5,04
pc1175	**rpiA**	similar to ribose 5-phosphate isomerase A	699	5,77
pc1176	-	conserved hypothetical protein	414	4,43
pc1177	**ptsH**	strongly similar to PTS phosphocarrier protein HPr	294	6,72
pc1178	**pepF**	similar to oligoendopeptidase F	1845	25,37
pc1179	**groES**	strongly similar to chlamydial heat shock protein groES	321	134,35
pc1180	**groEL**	strongly similar to 60 kDa chaperonin GroEL	1623	47,15
pc1181	-	hypothetical protein	963	2,87

pc1182	**topI**	similar to DNA topoisomerase I	1077	0,48
pc1183	**wbdA**	similar to mannosyltransferase	1086	4,88
pc1184		hypothetical protein	1644	0,81
pc1185	**-**	unknown protein	216	0,53
pc1186	**-**	unknown protein	423	71,03
pc1187	**-**	unknown protein	420	6,33
pc1188	**tspO**	similar to outer membrane protein tspO	465	3,48
pc1189	**cyoA**	strongly similar to cytochrome o ubiquinol oxidase chain II cyoA	888	6,86
pc1190	**cyoB**	strongly similar to cytochrome o ubiquinol oxidase chain I cyoB	1962	11,48
pc1191	**cyoC**	strongly similar to cytochrome o ubiquinol oxidase chain III cyoC	636	10,03
pc1192	**cyoD**	similar to cytochrome O ubiquinol oxidase chain IV cyoD	363	12,72
pc1193	**cyoE**	strongly similar to heme O synthase (=protoheme IX farnesyltransferase) cyoE	852	7,67
pc1194	**-**	unknown protein	5046	3,02
pc1195	**-**	conserved hypothetical protein	231	9,72
pc1196	**-**	conserved hypothetical protein	309	5,71
pc1197	**-**	hypothetical protein	2001	11,79
pc1198	**-**	conserved hypothetical protein	360	1,15
pc1199	**-**	conserved hypothetical protein	333	2,22
pc1200	**-**	conserved hypothetical protein	357	0,94
pc1201	**-**	conserved hypothetical protein	711	5,37
pc1202	**-**	conserved hypothetical protein (chlamydia plasmid)	417	1,39
pc1203	**-**	conserved hypothetical protein (chlamydia plasmid)	483	2,05
pc1204	**-**	unknown protein	783	7,56
pc1205	**-**	unknown protein	726	2,68
pc1206	**-**	unknown protein	234	0,40
pc1207	**-**	unknown protein	1404	5,78
pc1208	**-**	unknown protein	2523	1,20
pc1209	**-**	conserved hypothetical protein	183	0,61
pc1210	**-**	unknown protein	183	0,20
pc1211	**cnp; nprC**	similar to metalloprotease	831	46,92
pc1212	**-**	unknown protein	1110	10,07
pc1213	**-**	conserved hypothetical protein	267	0,31
pc1214	**-**	conserved hypothetical protein	336	1,44
pc1215	**-**	conserved hypothetical protein	381	6,71
pc1216		hypothetical protein	1152	4,04
pc1217	**glnQ**	similar to ABC transporter, ATP-binding protein	690	0,77
pc1218	**-**	hypothetical protein	1065	0,55
pc1219	**oprM**	similar to outer membrane protein of AcrAB(MexAB)-OprM multidrug efflux pump	1461	3,01
pc1220	**DHCR7**	similar to 7-dehydrocholesterol reductase	1308	9,07
pc1221	**mutS**	similar to DNA mismatch repair protein mutS	2577	7,69
pc1222	**-**	unknown protein	201	377,20
pc1223	**-**	unknown protein	723	4,06
pc1224	**-**	unknown protein	945	7,91
pc1225	**priA**	similar to primosomal protein N'	2238	7,15
pc1226	**-**	conserved hypothetical protein	1428	4,50
pc1227	**-**	unknown protein	243	9,01
pc1228	**lysS**	strongly similar to lysyl-tRNA synthetase	1590	8,63
pc1229	**-**	unknown protein	276	10,01
pc1230	**-**	unknown protein	1266	27,08
pc1231	**-**	unknown protein	1065	6,26
pc1232	**-**	unknown protein	357	2,67
pc1233	**-**	unknown protein	1308	3,64
pc1234	**-**	unknown protein	252	4,89
pc1235	**cysS**	similar cysteinyl tRNA synthetase	1437	2,57
pc1236	**aas**	similar to bifunctional AAS protein	2718	7,42
pc1237	**mutT**	similar to dGTP pyrophosphohydrolase, mutT	354	1,81
pc1238	**fabF**	strongly similar to beta-ketoacyl-ACP synthetase	1257	13,85
pc1239	**-**	conserved hypothetical protein	381	13,56
pc1240	**glnA**	similar to glutamate-ammonia ligase (=glutamine synthetase) type III	2178	1,02
pc1241	**-**	hypothetical protein	642	3,34
pc1242	**-**	hypothetical protein	1722	7,91
pc1243	**MiaA**	similar to tRNA delta-2-isopentenylpyrophosphate transferase	1035	4,54
pc1244	**spoIIAA**	similar to sigma regulatory factor	354	17,35
pc1245	**uvrA**	similar to excinuclease ABC chain A	2814	1,35

pc1246	-	hypothetical protein	771	5,81
pc1247	**murC**	similar to UDP-N-acetylmuramate-alanine ligase murC	1365	3,59
pc1248	**murG**	similar to UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase MurG	1131	6,56
pc1249	**ftsW**	similar to cell division protein ftsW	1110	2,61
pc1250	**lytF**	similar to muropeptidase (autolysin)	735	6,91
pc1251	**murD**	similar to UDP-N-acetylmuramoylalanine-D-glutamate ligase murD	1335	2,23
pc1252	**mraY**	similar to phospho-N-acetylmuramoyl-pentapeptide-transferase mraY	1233	3,17
pc1253	**murF**	similar to UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate -D-alanyl-D-alanine-ligase murF	1338	5,12
pc1254	-	unknown protein	237	2,31
pc1255	-	similar to eucaryotic stearoyl-CoA 9-desaturase	1146	5,00
pc1256	**ipgD**	similar to virulence protein ipgD (Shigella flexneri plasmid pINV)	1818	3,22
pc1257	-	conserved hypothetical protein	816	1,22
pc1258	-	unknown protein	198	2,16
pc1259	**groEL**	strongly similar to heat shock protein GroEL	1605	40,03
pc1260	-	conserved hypothetical protein	1401	1,41
pc1261	-	conserved hypothetical protein	447	16,91
pc1262	**pgm**	similar to phosphoglucomutase/phosphomannomutase	1779	11,47
pc1263	-	hypothetical protein	828	24,47
pc1264	**neuB**	similar to sialic acid synthase	1056	5,03
pc1265	**deaD**	similar to ATP-dependent RNA helicase	1224	7,86
pc1266	-	conserved hypothetical protein	834	9,18
pc1267	-	conserved hypothetical protein	2076	13,06
pc1268	-	hypothetical protein	678	6,83
pc1269	**lexA;dinR**	similar to SOS response regulator lexA	612	3,06
pc1270	**pssA**	similar to CDPdiacylglycerol-serine O-phosphatidyltransferase	864	3,51
pc1271	-	conserved hypothetical protein	2976	5,53
pc1272	-	conserved hypothetical protein	1857	6,51
pc1273	-	hypothetical protein	1245	2,93
pc1274	-	conserved hypothetical protein	417	1,51
pc1275	-	unknown protein	222	0,43
pc1276	-	conserved hypothetical protein	2004	17,14
pc1277	-	conserved hypothetical protein	426	2,10
pc1278	-	conserved hypothetical protein	2196	2,76
pc1279	-	conserved hypothetical protein	276	2,73
pc1280	-	conserved hypothetical protein	303	14,20
pc1281	-	conserved hypothetical protein	222	0,17
pc1282	-	conserved hypothetical protein	3249	5,57
pc1283	-	unknown protein	282	1,06
pc1284	-	unknown protein	255	0,97
pc1285	-	conserved hypothetical protein	678	1,74
pc1286	-	unknown protein	1059	2,64
pc1287	-	unknown protein	198	0,47
pc1288	-	conserved hypothetical protein	990	1,60
pc1289	-	conserved hypothetical protein	1443	0,84
pc1290	-	unknown protein	864	11,15
pc1291	**htrA, degP**	similar to serine proteinase	1455	15,33
pc1292	-	unknown protein	1635	5,32
pc1293	-	conserved hypothetical protein	990	0,81
pc1294	-	unknown protein	228	2,38
pc1295	-	unknown protein	600	3,99
pc1296	-	hypothetical protein	1146	3,33
pc1297	**sucD**	strongly similar to succinate-CoA ligase (ADP-forming) alpha chain	906	3,94
pc1298	**sucC**	strongly similar to succinate-CoA ligase (ADP-forming) beta chain	1170	4,02
pc1299	**ftsY**	strongly similar to signal recognition particle	930	3,93
pc1300	-	unknown protein	516	11,85
pc1301	-	unknown protein	552	4,59
pc1302	**galE**	similar to UDP-glucose 4-epimerase	969	2,08
pc1303	-	unknown protein	192	0,07
pc1304	-	unknown protein	405	11,77
pc1305	**tyrP**	similar to tyrosine-specific transport protein	1215	2,34

pc1306	**glmS**	strongly similar to glutamine-fructose-6-phosphate transaminase (isomerizing)	1824	3,85
pc1307	**pgm**	strongly similar to phosphoglucomutase	1464	6,16
pc1308	**pcnB**	similar to Poly(A) polymerase	1275	1,51
pc1309	**-**	unknown protein	771	5,08
pc1310	**dpm1**	similar to dolichol-phosphate mannosyltransferase	642	6,43
pc1311	**-**	conserved hypothetical protein	684	3,21
pc1312	**lpxB**	similar to lipid A-disaccharide synthase	1128	4,10
pc1313	**-**	conserved hypothetical protein	654	1,74
pc1314	**plsX**	similar to fatty acid/phospholipid synthesis protein PlsX	1020	2,35
pc1315	**rpmF**	similar to 50S ribosomal protein L32	222	8,54
pc1316	**-**	hypothetical protein	477	2,80
pc1317	**cafA;rng**	similar to ribonuclease G (axial filament protein)	1539	6,19
pc1318	**ats1**	similar to glycerol-3-phosphate acyltransferase	999	6,83
pc1319	**-**	conserved hypothetical protein	336	1,84
pc1320	**-**	hypothetical protein	750	7,77
pc1321	**-**	conserved hypothetical protein	819	4,52
pc1322	**-**	unknown protein	333	10,21
pc1323	**-**	conserved hypothetical protein	879	1,34
pc1324	**proS**	similar to prolyl-tRNA synthetase	1524	5,39
pc1325	**pabC**	similar to 4-amino-4-deoxychorismate lyase	843	3,21
pc1326	**-**	unknown protein	492	6,35
pc1327	**pabB**	similar to para-aminobenzoate synthase component I	1305	2,57
pc1328	**-**	conserved hypothetical protein	738	6,79
pc1329	**-**	conserved hypothetical protein	708	5,78
pc1330	**-**	conserved hypothetical protein	513	15,61
pc1331	**prfB**	strongly similar to peptide chain release factor RF-2	981	7,47
pc1332	**-**	conserved hypothetical protein	846	0,30
pc1333	**-**	similar to ABC transporter ATP-binding protein	1824	4,08
pc1334	**tpx**	similar to thioredoxin peroxidase	288	0,13
pc1335	**-**	hypothetical protein	528	1,44
pc1336	**aac**	similar to aminoglycoside N6'-acetyltransferase	501	2,35
pc1337	**-**	conserved hypothetical protein	606	10,16
pc1338	**tag**	strongly similar to 3-methyladenine-DNA glycosylase I	567	3,16
pc1339	**-**	unknown protein	192	0,24
pc1340	**-**	unknown protein	222	1,80
pc1341	**-**	conserved hypothetical protein	5295	6,29
pc1342	**-**	unknown protein	204	0,22
pc1343	**ntt_5**	similar to ADP/ATP translocase	1470	4,00
pc1344	**arsC;arsG**	similar to arsenate reductase	348	1,67
pc1345	**-**	unknown protein	672	1,06
pc1346	**-**	unknown protein	2448	0,52
pc1347	**-**	conserved hypothetical protein	1368	3,32
pc1348	**nrdA**	strongly similar to ribonucleoside-diphosphate reductase large chain	2322	18,31
pc1349	**nrdB**	strongly similar to ribonucleoside-diphosphate reductase small chain	972	8,04
pc1350	**-**	unknown protein	186	20,51
pc1351	**-**	unknown protein	249	2,85
pc1352	**-**	unknown protein	228	4,29
pc1353	**-**	conserved hypothetical protein (possible outer surface protein wsp)	438	0,93
pc1354	**-**	unknown protein	1410	3,83
pc1355	**-**	unknown protein	2604	0,72
pc1356	**-**	unknown protein	186	0,25
pc1357	**-**	unknown protein	195	0,58
pc1358	**-**	unknown protein	435	5,90
pc1359	**-**	hypothetical protein	2166	2,03
pc1360	**-**	hypothetical protein	2832	5,81
pc1361	**-**	hypothetical protein	1896	5,58
pc1362	**ackA**	strongly similar to acetate kinase	1188	2,69
pc1363	**-**	hypothetical protein	3366	1,01
pc1364	**-**	strongly similar to two-component response regulator	1326	8,02
pc1365	**-**	similar to two-component sensor histidine kinase	1233	2,60
pc1366	**-**	unknown protein	219	0,28
pc1367	**rpsD**	strongly similar to 30S ribosomal protein S4	621	119,63
pc1368	**-**	conserved hypothetical protein	249	2,03
pc1369	**-**	similar to glycosyltransferase	1131	2,08
pc1370	**-**	hypothetical protein	1449	2,35
pc1371	**pckG**	strongly similar to Phosphoenolpyruvate	1776	4,70

		carboxykinase [GTP]		
pc1372	**mreB;envB**	strongly similar to rod shape-determining protein mreB	1092	2,83
pc1373	**-**	unknown protein	186	5,93
pc1374	**-**	conserved hypothetical protein	3486	3,83
pc1375	**tig**	similar to trigger factor	1308	12,85
pc1376	**clpP;lopP**	strongly similar to ATP-dependent Clp protease proteolytic subunit P	624	26,57
pc1377	**clpX**	strongly similar to ATP-dependent Clp protease ATP-binding subunit X	1242	10,49
pc1378	**-**	hypothetical protein	750	2,02
pc1379	**-**	hypothetical protein	924	3,01
pc1380	**-**	unknown protein	2610	1,95
pc1381	**-**	unknown protein	1245	8,89
pc1382	**-**	unknown protein	1449	12,17
pc1383	**-**	unknown protein	1308	21,02
pc1384	**lcrH;sycD**	similar to low calcium response protein H	573	25,93
pc1385	**-**	unknown protein	2250	16,40
pc1386	**lcrH;sycD**	similar to low calcium response protein H	594	17,35
pc1387	**-**	unknown protein	675	30,63
pc1388	**-**	unknown protein	951	8,67
pc1389	**-**	unknown protein	1083	36,99
pc1390	**-**	hypothetical protein	387	5,22
pc1391	**-**	conserved hypothetical protein	1830	15,92
pc1392	**-**	conserved hypothetical protein	243	7,78
pc1393	**-**	conserved hypothetical protein	465	17,28
pc1394	**-**	similar to UDPgalactose-glucose galactosyltransferase	684	6,00
pc1395	**-**	unknown protein	279	67,12
pc1396	**-**	unknown protein	852	37,63
pc1397	**sctN;yscN**	strongly similar to type III secretion pathway protein sctN	1365	19,31
pc1398	**-**	conserved hypothetical protein	498	7,36
pc1399	**-**	unknown protein	993	11,14
pc1400	**sctQ**	similar to flagellar motor switch protein (= type III secretion translocase SctQ)	1338	13,82
pc1401	**pkn**	similar to serine/threonine protein kinase	1590	6,38
pc1402	**-**	conserved hypothetical protein	477	2,82
pc1403	**-**	unknown protein	402	1,36
pc1404	**-**	unknown protein	873	1,92
pc1405	**-**	conserved hypothetical protein	321	0,74
pc1406	**-**	unknown protein	297	1,91
pc1407	**-**	unknown protein	348	1,18
pc1408	**-**	unknown protein	552	1,99
pc1409	**-**	unknown protein	261	0,27
pc1410	**-**	conserved hypothetical protein	1119	4,80
pc1411	**-**	unknown protein	201	1,45
pc1412	**-**	unknown protein	204	4,11
pc1413	**-**	unknown protein	300	1,39
pc1414	**-**	unknown protein	315	4,27
pc1415	**-**	unknown protein	1497	7,14
pc1416	**-**	unknown protein	186	0,39
pc1417	**-**	unknown protein	1473	7,45
pc1418	**-**	unknown protein	1104	5,98
pc1419	**-**	hypothetical protein	828	23,01
pc1420	**-**	unknown protein	405	1,42
pc1421	**-**	unknown protein	318	3,05
pc1422	**-**	unknown protein	306	0,37
pc1423	**traE**	similar to F pilus assembly protein traE	570	0,38
pc1424	**-**	unknown protein	693	0,09
pc1425	**traB**	similar to F pilus assembly protein traB	1227	0,16
pc1426	**-**	conserved hypothetical protein	495	0,44
pc1427	**-**	conserved hypothetical protein	441	0,30
pc1428	**-**	unknown protein	474	1,27
pc1429	**-**	unknown protein	375	0,04
pc1430	**traC**	similar to inner-membrane protein traC	2487	0,19
pc1431	**traF**	similar to F pilus assembly protein traF	483	1,44
pc1432	**traW**	similar to F pilus assembly protein traW	633	3,19
pc1433	**trbC**	similar to F pilus assembly protein trbC	597	0,21
pc1434	**traU**	similar to F pilus assembly protein traU	936	0,71
pc1435	**-**	unknown protein	768	0,39
pc1436	**-**	unknown protein	186	-0,05

pc1437	**traN**	similar to conjugative transfer protein traN precursor	555	0,17
pc1438	**traF**	similar to F pilus assembly protein traF	792	0,66
pc1439	**traH**	similar to F pilus assembly protein traH	1359	0,63
pc1440	**traG**	similar to conjugative transfer protein traG	2784	1,30
pc1441	**traD**	similar to conjugative transfer protein traD	1671	11,31
pc1442	**-**	conserved hypothetical protein	354	19,21
pc1443	**-**	conserved hypothetical protein	357	15,08
pc1444	**-**	unknown protein	264	2,06
pc1445	**-**	unknown protein	282	0,88
pc1446	**-**	conserved hypothetical protein	681	0,30
pc1447	**-**	unknown protein	333	3,18
pc1448	**-**	unknown protein	774	0,42
pc1449	**-**	hypothetical protein	2094	2,36
pc1450	**-**	unknown protein	195	1,12
pc1451	**-**	hypothetical protein	336	7,49
pc1452	**-**	unknown protein	1035	1,60
pc1453	**-**	conserved hypothetical protein	324	2,01
pc1454	**-**	unknown protein	192	0,80
pc1455	**-**	conserved hypothetical protein	5601	14,00
pc1456	**doc**	strongly similar to doc (death on cure) protein of bacteriophage P1	378	11,56
pc1457	**-**	conserved hypothetical protein	231	10,47
pc1458	**-**	unknown protein	186	7,52
pc1459	**-**	unknown protein	726	9,91
pc1460	**-**	unknown protein	201	1,21
pc1461	**-**	conserved hypothetical protein	321	7,08
pc1462	**-**	conserved hypothetical protein	2613	4,51
pc1463	**-**	unknown protein	189	2,14
pc1464	**-**	unknown protein	222	1,98
pc1465	**-**	hypothetical protein	828	20,22
pc1466	**-**	unknown protein	795	1,68
pc1467	**-**	unknown protein	2103	4,03
pc1468	**-**	unknown protein	390	1,18
pc1469	**tnpR**	strongly similar to resolvase	558	0,60
pc1470	**tnpA**	strongly similar to transposase, partial length	531	0,18
pc1471	**tnpA**	strongly similar to transposase, partial length	321	0,39
pc1472	**-**	unknown protein	246	7,12
pc1473	**doc**	strongly similar to doc (death on cure) protein of bacteriophage P1	378	10,41
pc1474	**-**	unknown protein	192	1,99
pc1475	**gspD;sctC;pulD**	similar to component D of type II secretion pathway	2862	14,47
pc1476	**-**	unknown protein	969	10,15
pc1477	**-**	conserved hypothetical protein, partial length	381	3,19
pc1478	**HVST1**	similar to sulfate transport protein	1923	1,52
pc1479	**-**	unknown protein	198	1,59
pc1480	**-**	conserved hypothetical protein	1464	4,51
pc1481	**-**	hypothetical protein	915	3,13
pc1482	**-**	unknown protein	201	0,17
pc1483	**-**	conserved hypothetical protein	1029	1,07
pc1484	**-**	conserved hypothetical protein	3771	1,87
pc1485	**dnaK, grpF, groP, seg**	similar to heat shock protein 70, dnaK	2838	4,21
pc1486	**ald**	strongly similar to alanine dehydrogenase	1113	3,66
pc1487	**smc**	similar to chromosome segregation SMC protein	3540	7,74
pc1488	**serS**	strongly similar to seryl-tRNA synthetase	1362	8,76
pc1489	**-**	unknown protein	954	280,89
pc1490	**-**	similarity to aspartyl aminopeptidase (metalloprotease)	1305	5,62
pc1491	**-**	unknown protein	1221	40,11
pc1492	**-**	conserved hypothetical protein	879	2,15
pc1493	**-**	unknown protein	210	0,34
pc1494	**-**	unknown protein	186	0,59
pc1495	**-**	hypothetical protein	1680	2,85
pc1496	**gdhB**	similar to eucaryotic NAD-specific glutamate dehydrogenase	3075	1,95
pc1497	**hrcA**	similar to Heat-inducible transcription repressor hrcA	1158	5,39
pc1498	**grpE**	strongly similar to heat shock protein GrpE	636	17,53
pc1499	**dnaK**	strongly similar to chaperone protein dnaK (heat shock protein 70)	1965	88,22
pc1500	**-**	unknown protein	702	11,27
pc1501	**-**	hypothetical protein	804	1,64
pc1502	**oppA, dppA, spo0KA**	strongly similar to oligo/dipeptide-binding protein oppA	1584	6,43

pc1503	**oppB, dppB, spo0KB**	strongly similar to oligo/dipeptide ABC transporter (permease) oppB	936	2,85
pc1504	**oppC, dppC, spo0KC**	strongly similar to oligo/dipeptide ABC transporter (permease) oppC	903	6,51
pc1505	**oppD, dppD, spo0KD**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppD	987	4,35
pc1506	**dppF, oppF, spoOKF**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppF	945	2,52
pc1507	**-**	hypothetical protein	1872	10,20
pc1508	**-**	hypothetical protein	1974	0,73
pc1509	**-**	hypothetical protein	297	0,41
pc1510	**-**	hypothetical protein	2013	9,26
pc1511	**clpC**	strongly similar to endopeptidase ATP-binding chain clpC	2544	12,03
pc1512	**hemG**	similar to protoporphyrinogen oxidase	1374	2,47
pc1513	**hemE**	strongly similar to uroporphyrinogen decarboxylase	1095	2,53
pc1514	**tkt**	strongly similar to transketolase	2034	12,17
pc1515	**-**	hypothetical protein	312	1,63
pc1516	**-**	unknown protein	2385	37,31
pc1517	**-**	unknown protein	1215	64,04
pc1518	**-**	unknown protein	1233	56,21
pc1519	**alaS**	strongly similar to alanyl-tRNA synthetase	2637	4,64
pc1520	**-**	similar to periplasmic immunogenic protein	732	3,23
pc1521	**mfd, tcrF**	strongly similar to transcription-repair coupling factor mfd	3306	3,60
pc1522	**-**	unknown protein	198	0,05
pc1523	**-**	unknown protein	252	0,18
pc1524	**-**	hypothetical protein	1146	8,29
pc1525	**lcrH, sycD**	similar to regulatory protein lcrH and chaperone sycD	540	7,94
pc1526	**-**	unknown protein	1494	4,75
pc1527	**amn**	similar to AMP nucleosidase	846	3,29
pc1528	**-**	unknown protein	243	3,09
pc1529	**efp**	strongly similar to translation elongation factor EF-P	573	7,00
pc1530	**lysS**	similar to lysyl-tRNA synthetase	903	5,01
pc1531	**-**	unknown protein	462	3,06
pc1532	**-**	unknown protein	231	1,34
pc1533	**nqrF**	strongly similar to Na(+)-translocating NADH-quinone reductase, chain F	1398	11,85
pc1534	**yabJ, yjgF**	strongly similar to yabJ	390	9,55
pc1535	**htpG**	similar to heat shock protein HtpG	1848	10,26
pc1536	**-**	hypothetical protein	1365	2,94
pc1537	**-**	unknown protein	810	2,20
pc1538	**-**	unknown protein	258	0,92
pc1539	**-**	unknown protein	225	1,31
pc1540	**-**	unknown protein	2571	0,97
pc1541	**-**	hypothetical protein	531	3,07
pc1542	**-**	unknown protein	2214	20,82
pc1543	**yajC**	similar to preprotein translocase YajC subunit	399	9,67
pc1544	**ygcA, rumA**	similar to rRNA methyltransferse	1329	6,69
pc1545	**hctA**	strongly similar to histone H1-like protein	396	214,12
pc1546	**-**	unknown protein	2691	2,83
pc1547	**exbB, tolQ**	similar to biopolymer transport protein exbB	726	4,52
pc1548	**exbD, tolR**	similar to biopolymer transport protein exbD	441	4,03
pc1549	**-**	unknown protein	705	3,00
pc1550	**-**	unknown protein	249	1,59
pc1551	**-**	unknown protein	288	0,31
pc1552	**-**	unknown protein	294	0,94
pc1553	**-**	unknown protein	201	2,74
pc1554	**-**	conserved hypothetical protein	837	35,08
pc1555	**-**	unknown protein	561	222,54
pc1556	**-**	conserved hypothetical protein	2871	1,33
pc1557	**hemH**	similar to ferrochelatase (heme synthetase), hemH	1044	2,90
pc1558	**clpB**	similar to heat shock protein ClpB	1944	1,88
pc1559	**deaD**	similar to ATP-dependent RNA helicase	1548	6,32
pc1560	**-**	unknown protein	276	31,21
pc1561	**-**	conserved hypothetical protein	336	5,79
pc1562	**-**	conserved hypothetical protein	333	0,56
pc1563	**-**	hypothetical protein	1143	0,52
pc1564	**-**	unknown protein	186	5,14
pc1565	**-**	hypothetical protein	3432	16,45
pc1566	**-**	conserved hypothetical protein	735	3,88
pc1567	**-**	hypothetical protein	678	1,48

pc1568	-	hypothetical protein	1794	2,59
pc1569	**rimL**	similar to ribosomal-protein-serine acetyltransferase	573	2,93
pc1570	-	conserved hypothetical protein	2763	3,19
pc1571	**rnr, vacB**	similar to ribonuclease R	1569	4,81
pc1572	-	similar to tylosin resistance protein	1866	9,53
pc1573	**rf-3, prfC**	strongly similar to peptide chain release factor 3	1602	9,45
pc1574	-	hypothetical protein	549	3,66
pc1575	-	unknown protein	390	59,54
pc1576	**suhB**	similar to inositol-1(or 4)-monophosphatase	798	1,63
pc1577	-	unknown protein	1206	16,78
pc1578	-	similar to blue fluorescent protein	792	3,51
pc1579	**yohI, dusC**	similar to protein involved in tRNA-dihydrouridine synthesis	981	4,36
pc1580	-	hypothetical protein	1236	2,66
pc1581	-	unknown protein	906	3,89
pc1582	-	unknown protein	828	1,09
pc1583	-	unknown protein	777	2,22
pc1584	-	conserved hypthetical protein	186	4,40
pc1585	-	conserved hypothetical protein	258	17,99
pc1586	-	unknown protein	258	0,31
pc1587	**hldE,rfaE**	similar to bifunctional protein involved in LPS core biosynthesis, hdlE	1362	2,04
pc1588	**hldD, waaD, rfaD**	similar to ADP-D-beta-D-heptose epimerase, hldD	987	3,42
pc1589	-	strongly similar to isopentenyl monophosphate kinase (IPK)	867	1,57
pc1590	-	similar to ribosomal protein L9	486	33,93
pc1591	**rpsR**	strongly similar to ribosomal protein S18	261	51,50
pc1592	**rpsF**	similar to ribosomal protein S6 (BS9)	345	44,31
pc1593	**spoVC**	similar to peptidyl-tRNA hydrolase	597	26,72
pc1594	**ctc**	similar to general stress protein ctc	555	31,05
pc1595	**prsA, prs**	strongly similar to phosphoribosyl pyrophosphate synthetase (PRPP)	942	20,96
pc1596	**glgA**	similar to starch synthase, precursor, glgA	1503	5,26
pc1597	**pgsA**	similar to phosphatidylglycerophosphate synthase (PGP synthase)	618	2,18
pc1598	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	1362	4,09
pc1599	-	unknown protein	537	2,41
pc1600	-	hypothetical protein	624	18,41
pc1601	**pcrA, mutU, recL**	strongly similar to ATP-dependent DNA helicase, mutU	2007	7,24
pc1602	-	unknown protein	1875	8,61
pc1603	-	similar to ribonuclease P protein component	336	5,44
pc1604	**rpmH**	strongly similar to 50S ribosomal protein L34	138	19,80
pc1605	**rpmJ**	strongly similar to 50S ribosomal protein L36	138	70,90
pc1606	-	strongly similar to ribosomal protein S14	306	14,92
pc1607	-	hypothetical protein	477	6,92
pc1608	-	conserved hypothetical protein	480	10,95
pc1609	-	unknown protein	528	2,94
pc1610	-	unknown protein	207	0,64
pc1611	-	conserved hypothetical protein	4785	2,75
pc1612	-	unknown protein	207	1,05
pc1613	-	unknown protein	213	0,74
pc1614	-	conserved hypothetical protein	1512	27,08
pc1615	-	unknown protein	213	0,53
pc1616	-	conserved hypothetical protein	2442	4,01
pc1617	-	unknown protein	216	0,50
pc1618	-	unknown protein	2781	3,31
pc1619	-	unknown protein	252	1,09
pc1620	-	conserved hypothetical protein	549	2,88
pc1621	-	unknown protein	582	3,69
pc1622	-	unknown protein	309	0,34
pc1623	**nusB, groNB**	similar to transcription termination factor, nusB	465	4,65
pc1624	**murB**	similar to UDP-N-acetylmuramate dehydrogenase	900	3,95
pc1625	-	conserved hypothetical protein	843	1,75
pc1626	**folC**	similar to folylpolyglutamate synthase	1233	6,81
pc1627	-	unknown protein	462	10,07
pc1628	-	unknown protein	597	163,71
pc1629	**cydB, cyd-2**	similar to cytochrome bd-I oxidase subunit II	933	3,06
pc1630	**cydA, cyd-1**	similar to cytochrome bd-I oxidase subunit I	1398	5,45
pc1631	-	unknown protein	189	3,23
pc1632	**folP, dhpS**	similar to dihydropteroate synthase	780	1,56

pc1633	-	conserved hypothetical protein	1338	1,72
pc1634	-	hypothetical protein	723	7,81
pc1635	-	unknown protein	2793	1,89
pc1636	**pyk**	strongly similar to pyruvate kinase	1797	4,21
pc1637	-	conserved hypothetical protein	453	0,48
pc1638	-	unknown protein	279	0,85
pc1639	-	conserved hypothetical protein	4602	14,61
pc1640	-	conserved hypothetical protein	291	0,39
pc1641	**uvrA**	strongly similar to excinuclease ABC subunit A, uvrA	5703	4,00
pc1642	-	unknown protein	1176	3,59
pc1643	-	unknown protein	702	6,56
pc1644	-	unknown protein	342	6,84
pc1645	-	similar to serine/threonine-protein kinase	2949	1,53
pc1646	**mutT**	similar to dGTP pyrophosphohydrolase, mutT	564	1,15
pc1647	-	unknown protein	243	0,50
pc1648	-	unknown protein	189	0,25
pc1649	-	conserved hypothetical protein	1566	5,24
pc1650	-	conserved hypothetical protein	273	0,75
pc1651	-	conserved hypothetical protein	339	1,80
pc1652	-	unknown protein	960	53,56
pc1653	-	conserved hypothetical protein	213	2,30
pc1654	**valS**	strongly similar to valyl-tRNA synthetase	2850	6,59
pc1655	-	unknown protein	3312	2,19
pc1656	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	1398	4,06
pc1657	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	1386	3,67
pc1658	**aroF**	strongly similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (tyrosine-sensitive), aroF	1092	4,44
pc1659	-	hypothetical protein	534	3,81
pc1660	**fumC**	stongly similar to fumarate hydratase class II, fumC	1392	3,55
pc1661	-	conserved hypothetical protein	972	2,49
pc1662	-	unknown protein	183	0,31
pc1663	**menC**	similar to o-succinylbenzoate synthase II, menC	939	0,42
pc1664	-	conserved hypothetical protein	333	2,08
pc1665	-	unknown protein	237	3,69
pc1666	-	hypothetical protein	1557	9,39
pc1667	**atpC**	similar to H+-transporting two-sector ATPase (epsilon chain, atpC)	444	1,55
pc1668	**atpD**	strongly similar to H+-transporting two-sector ATPase (beta chain, atpD)	1461	10,18
pc1669	**atpG**	similar to H+-transporting two-sector ATPase (gamma chain, atpG)	858	16,57
pc1670	**atpA**	strongly similar to H+-transporting ATP synthase (alpha chain, atpA)	1527	9,47
pc1671	**atpH**	similar to H+-transporting two-sector ATPase (delta chain, atpH)	546	6,67
pc1672	**atpF; uncF**	similar to H+-transporting two-sector ATPase (chain b, atpF)	483	11,84
pc1673	**atpE**	strongly similar to H+-transporting two-sector ATPase lipid-binding protein (chainC, atpE)	297	18,65
pc1674	**atpB**	similar to H+-transporting two-sector ATPase (chain a, atpB)	816	9,50
pc1675	-	unknown protein	396	5,34
pc1676	**ntpK**	similar to V-type sodium ATP synthase subunit K (ntpK)	423	39,92
pc1677	**ntpI**	similar to V-type sodium ATP synthase subunit I (ntpI)	1917	7,83
pc1678	**ntpD**	similar to V-type sodium ATP synthase (subunit D, ntpD)	648	10,20
pc1679	**atpB**	similar to H+-transporting two-sector ATPase (chain B, atpB)	1317	8,80
pc1680	**ntpA**	strongly similar to V-type sodium ATP synthase (subunit A, ntpA)	1782	11,73
pc1681	-	hypothetical protein	792	7,08
pc1682	**ntpE**	similar to V-type sodium ATP synthase (subunit E, ntpE)	513	14,14
pc1683	-	hypothetical protein	816	23,73
pc1684	-	unknown protein	297	28,07
pc1685	-	unknown protein	477	3,62
pc1686	-	unknown protein	366	36,57
pc1687	-	unknown protein	297	20,02
pc1688	-	hypothetical protein	828	27,93

pc1689	-	unknown protein	1776	3,64
pc1690	-	hypothetical protein	393	3,74
pc1691	**talB**	strongly similar to transaldolase B	969	19,23
pc1692	-	hypothetical protein	1296	2,09
pc1693	-	unknown protein	942	4,10
pc1694	-	unknown protein	1857	2,97
pc1695	**rkpK**	strongly similar to UDPglucose 6-dehydrogenase	1410	7,96
pc1696	**crtE**	strongly similar to farnesyltranstransferase	885	5,88
pc1697	**exoY**	strongly similar to exopolysaccharide production protein	654	7,14
pc1698	-	conserved hypothetical protein	519	2,10
pc1699	-	conserved hypothetical protein	1269	3,32
pc1700	-	unknown protein	504	12,59
pc1701	**folD**	strongly similar to bifunctional protein folD	879	3,05
pc1702	**apbE**	similar to Thiamine biosynthesis lipoprotein apbE precursor	1074	2,29
pc1703	-	unknown protein	261	3,34
pc1704	-	unknown protein	1359	1,91
pc1705	**dnaN**	similar to DNA polymerase III, beta chain	1212	12,51
pc1706	**recF, uvrF**	similar to DNA replication and repair protein recF	1080	3,34
pc1707	-	strongly similar to small protein B	462	7,38
pc1708	-	conserved hypothetical protein	423	3,41
pc1709	-	unknown protein	399	5,94
pc1710	-	conserved hypothetical protein	1095	11,00
pc1711	**acpS**	strongly similar to holo-(acyl carrier protein) synthase	369	2,84
pc1712	-	unknown protein	822	6,20
pc1713	**trxB**	strongly similar to thioredoxin-disulfide reductase 2	951	9,10
pc1714	-	unknown protein	498	2,50
pc1715	**putP**	strongly similar to sodium/proline symporter	1431	2,78
pc1716	-	unknown protein	1794	8,27
pc1717	**acpP**	strongly similar to acyl carrier protein	234	6,09
pc1718	**fabG**	strongly similar to 3-oxoacyl-[acyl-carrier protein] reductase, fabG	756	5,18
pc1719	**fabD**	similar to malonyl CoA-acyl carrier protein transacylase, fabD	990	4,53
pc1720	**fabH**	strongly similar to 3-oxoacyl-[acyl-carrier-protein] synthase III, fabH	999	11,74
pc1721	-	unknown protein	228	2,19
pc1722	-	unknown protein	237	0,79
pc1723	-	unknown protein	189	0,28
pc1724	**recR**	strongly similar to recombination protein RecR	597	9,19
pc1725	-	unknown protein	231	1,44
pc1726	-	similar to outer membrane protein Omp85	2448	9,25
pc1727	-	similar to outer membrane protein OmpH	573	30,08
pc1728	**lpxD;firA**	similar to UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	1050	4,11
pc1729	**ptc1**	similar to phosphoprotein phosphatase	1461	2,84
pc1730	-	unknown protein	774	19,97
pc1731	**pdhC;aceF**	strongly similar to pyruvate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	1302	11,83
pc1732	**pdhB**	strongly similar to pyruvate dehydrogenase (lipoamide), E1 component, beta chain	993	10,07
pc1733	**pdhA**	similar to pyruvate dehydrogenase (lipoamide), E1 component, alpha chain	1029	6,47
pc1734	**aaaT**	similar to neutral amino acid (glutamate) transporter	1260	5,82
pc1735	-	conserved hypothetical protein	633	2,95
pc1736	-	unknown protein	474	5,52
pc1737	-	conserved hypothetical protein	1029	8,97
pc1738	-	hypothetical protein	480	7,88
pc1739	-	hypothetical protein	2232	1,57
pc1740	-	unknown protein	423	16,99
pc1741	-	unknown protein	603	13,07
pc1742	-	unknown protein	846	5,97
pc1743	-	unknown protein	330	84,37
pc1744	-	unknown protein	276	8,11
pc1745	-	unknown protein	834	3,24
pc1746	-	unknown protein	222	1,07
pc1747	-	unknown protein	183	0,19
pc1748	**hemL**	strongly similar to glutamate-1-semialdehyde 2,1-aminomutase	1299	2,98
pc1749	-	hypothetical protein	1953	2,00
pc1750	-	hypothetical protein	3867	2,72

pc1751	-	unknown protein	363	13,38
pc1752	-	conserved hypothetical protein	723	2,18
pc1753	-	conserved hypothetical protein	714	4,26
pc1754	-	hypothetical protein	1230	5,13
pc1755	-	conserved hypothetical protein	570	10,11
pc1756	**rpsI, rs9**	strong similarity to small subunit ribosomal protein S9	390	25,77
pc1757	**rl13, rplM**	strongly similar to large subunit ribosomal protein L13	432	29,47
pc1758	**miaB**	strongly similar to 2-methylthioadenine synthetase	1353	4,95
pc1759	**sodC**	similar to Superoxide dismutase (Cu-Zn)	618	28,99
pc1760	**dnlJ, ligA**	strongly similar to DNA ligase	1998	2,15
pc1761	**glgB**	strongly similar to 1,4-alpha-glucan branching enzyme (= Glycogen branching enzyme)	2184	6,63
pc1762	-	hypothetical protein	1059	1,06
pc1763	**yqeV, miaB, yleA**	similar to 2-methylthioadenine synthetase	1305	9,58
pc1764	-	unknown protein	7209	4,06
pc1765	**radC**	similar to DNA repair protein radC	696	3,06
pc1766	-	conserved hypothetical protein	1335	8,33
pc1767	**phnP**	similar to phnP protein	717	1,91
pc1768	-	unknown protein	555	4,62
pc1769	-	hypothetical protein	1005	2,49
pc1770	-	unknown protein	750	6,24
pc1771	**gltA**	similar to citrate (si)-synthase	1161	15,34
pc1772	**mdh**	strongly similar to NADP-dependent malate dehydrogenase	993	4,54
pc1773	-	unknown protein	894	5,23
pc1774	-	unknown protein	822	4,03
pc1775	-	unknown protein	324	4,98
pc1776	-	unknown protein	210	2,33
pc1777	-	unknown protein	246	0,87
pc1778	-	hypothetical protein	993	15,88
pc1779	-	unknown protein	357	17,52
pc1780	-	unknown protein	249	0,53
pc1781	-	unknown protein	453	0,67
pc1782	**gutQ**	similar to Gut Q protein	960	2,45
pc1783	**icd**	strongly similar to isocitrate dehydrogenase (NADP)	1452	8,61
pc1784	-	unknown protein	804	2,05
pc1785	**gltT**	similar to proton/sodium-glutamate symporter	1230	3,30
pc1786	**lpxK**	similar to tetraacyldisaccharide (lipid A) 4'-kinase	1107	7,93
pc1787	**gmhA, lpcA**	strongly similar to phosphoheptose isomerase	645	3,91
pc1788	-	hypothetical protein	594	5,84
pc1789	-	unknown protein	270	1,22
pc1790	-	unknown protein	1233	11,65
pc1791	**rlu**	similar to 23S rRNA pseudouridine synthase	660	3,67
pc1792	**rlmB, yjfH**	similar to tRNA (Gm18) methyltransferase	798	6,26
pc1793	-	hypothetical protein	864	8,11
pc1794	**ppx**	similar to exopolyphosphatase	1029	1,59
pc1795	-	unknown protein	291	1,81
pc1796	-	unknown protein	702	2,90
pc1797	**lspA**	similar to signal peptidase II (prolipoprotein signal peptidase)	528	10,23
pc1798	**dksA**	similar to dnaK suppressor	366	28,18
pc1799	-	conserved hypothetical protein	489	8,24
pc1800	**ycfB, trmU, mnmA, asuE**	strongly similar to tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase/ Antisuppressor	1131	4,18
pc1801	**fur**	similar to ferric uptake regulator protein	393	0,39
pc1802	-	unknown protein	819	1,64
pc1803	-	conserved hypothetical protein	1071	2,52
pc1804	**sHsp**	similar to small heat shock protein	447	41,89
pc1805	**znuA, ycdH**	similar to zinc ABC transporter periplasmic binding protein	858	4,64
pc1806	**znuC**	strongly similar to zinc ABC transporter ATP-binding protein	738	3,77
pc1807	**znuB**	similar to zinc ABC transporter membrane protein	1056	2,30
pc1808	-	unknown protein	354	4,41
pc1809	**ndh**	similar to NADH2 dehydrogenase	1245	3,12
pc1810	**dnaB**	similar to replicative DNA helicase	1446	2,05
pc1811	-	unknown protein	462	0,43
pc1812	-	hypothetical protein	1092	4,73
pc1813	-	hypothetical protein	792	2,30
pc1814	-	unknown protein	654	0,57
pc1815	**fbp**	similar to fibronectin/fibrinogen binding protein	1416	1,46

pc1816	-	hypothetical protein	2199	3,10
pc1817	-	unknown protein	261	0,27
pc1818	-	unknown protein	183	0,53
pc1819	-	unknown protein	279	3,07
pc1820	**dinP;dinB**	strongly similar to DNA polymerase IV	1053	1,89
pc1821	-	unknown protein	438	5,66
pc1822	**panF**	similar to sodium/pantothenate symporter (pantothenate permease)	1368	3,77
pc1823	-	conserved hypothetical protein	570	8,81
pc1824	-	unknown protein	819	3,40
pc1825	**nagA**	similar to beta-N-acetylglucosaminidase	1653	0,70
pc1826	-	unknown protein	681	2,74
pc1827	-	unknown protein	1209	1,80
pc1828	-	conserved hypothetical protein	936	6,72
pc1829	-	conserved hypothetical protein	471	5,99
pc1830	-	conserved hypothetical protein	855	2,18
pc1831	-	conserved hypothetical protein	678	1,74
pc1832	-	hypothetical protein	1371	2,12
pc1833	-	conserved hypothetical protein	2487	2,78
pc1834	**alkA**	similar to DNA-3-methyladenine glycosidase II	1431	3,09
pc1835	**ada**	similar to methylated-DNA-[protein]-cysteine S-methyltransferase	522	2,60
pc1836	**hctB**	similar to histone H1-like protein	636	86,44
pc1837	-	hypothetical protein	417	16,27
pc1838	**lplA**	similar to lipoate-protein ligase	702	2,50
pc1839	**gidA**	similar to glucose-inhibited division protein	1878	3,70
pc1840	-	hypothetical protein	1554	5,05
pc1841	**sdhB**	strongly similar to succinate dehydrogenase iron-sulfur protein	774	4,36
pc1842	**sdhA**	strongly similar to succinate dehydrogenase flavoprotein	1884	3,32
pc1843	**sdhC**	similar to succinate dehydrogenase cytochrome b558	963	2,70
pc1844	**tatD;mttC**	similar to deoxyribonuclease TatD	798	4,36
pc1845	-	similar to thiol-disulfide interchange protein	2244	0,90
pc1846	**dsbD**	unknown protein	198	6,96
pc1847	**tolQ**	similar to TolQ protein	753	8,28
pc1848	**tolR**	similar to TolR protein	429	3,53
pc1849	**tolA**	similar to tolA protein of Tol-Pal system	1068	3,56
pc1850	**tolB**	similar to TolB protein	1410	3,22
pc1851	**pal;excC**	strongly similar to peptidoglycan-associated lipoprotein precursor (pal)	741	28,66
pc1852	-	hypothetical protein	720	8,59
pc1853	**murI**	strongly similar to glutamate racemase	750	1,44
pc1854	-	unknown protein	351	0,46
pc1855	**phoB**	similar to two-component response regulator phoP	690	9,96
pc1856	-	conserved hypothetical protein	933	3,56
pc1857	-	conserved hypothetical protein	1032	5,02
pc1858	-	unknown protein	1272	5,83
pc1859	-	similar to N-6 Adenine-specific DNA methylase	597	4,54
pc1860	-	unknown protein	978	16,08
pc1861	-	hypothetical protein	1203	4,13
pc1862	-	unknown protein	495	7,75
pc1863	-	unknown protein	441	84,02
pc1864	-	unknown protein	633	31,13
pc1865	-	conserved hypothetical protein	861	6,75
pc1866	-	unknown protein	897	3,15
pc1867	-	unknown protein	648	17,04
pc1868	-	conserved hypothetical protein	771	0,56
pc1869	-	similar to phosphoglycerate mutase	648	1,15
pc1870	-	unknown protein	1551	14,67
pc1871	-	unknown protein	492	17,89
pc1872	-	unknown protein	240	1,60
pc1873	-	hypothetical protein	1095	5,16
pc1874	-	similar to arginine kinase	990	3,21
pc1875	-	conserved hypothetical protein	579	7,35
pc1876	**rrf**	similar to ribosome recycling factor (ribosome releasing factor)	552	12,87
pc1877	**pyrH;smbA**	strongly similar to uridylate kinase	756	9,19
pc1878	-	similar to procollagen-lysine 5-dioxygenase	888	6,62
pc1879	-	hypothetical protein	1086	12,24
pc1880	-	similar to X-Pro dipeptidase	999	2,17
pc1881	**phoR**	similar to two-component sensor histidine kinase	1770	2,88

		phoR		
pc1882	-	conserved hypothetical protein	996	6,83
pc1883	-	conserved hypothetical protein	879	1,59
pc1884	-	unknown protein	1095	3,91
pc1885	-	hypothetical protein	654	76,82
pc1886	-	conserved hypothetical protein	1110	1,63
pc1887	-	conserved hypothetical protein	1128	2,23
pc1888	-	conserved hypothetical protein	1731	1,64
pc1889	-	conserved hypothetical protein	849	2,86
pc1890	-	conserved hypothetical protein	972	2,37
pc1891	-	unknown protein	885	0,84
pc1892	-	unknown protein	798	0,83
pc1893	-	unknown protein	567	2,85
pc1894	-	unknown protein	588	5,57
pc1895	-	similar to general secretion pathway protein G	405	6,25
pc1896	**gspF;xcpS**	similar to protein of the general secretion pathway	1188	3,89
pc1897	**gspE;xcpR**	strongly similar to protein of the general secretion pathway	1632	9,64
pc1898	**gspD;xcpQ**	similar to protein of the general secretion pathway	2490	6,37
pc1899	-	conserved hypothetical protein	1419	7,58
pc1900	-	unknown protein	525	7,42
pc1901	**rpoN**	similar to RNA polymerase sigma-54 factor (sigma-N)	1479	2,52
pc1902	-	unknown protein	240	2,91
pc1903	-	unknown protein	429	0,95
pc1904	-	unknown protein	261	0,18
pc1905	-	unknown protein	207	1,24
pc1906	-	conserved hypothetical protein	486	0,13
pc1907	-	unknown protein	270	0,60
pc1908	-	unknown protein	192	0,19
pc1909	-	hypothetical protein	795	13,94
pc1910	-	unknown protein	957	12,26
pc1911	-	unknown protein	222	4,07
pc1912	-	conserved hypothetical protein	267	8,55
pc1913	-	unknown protein	267	9,02
pc1914	-	conserved hypothetical protein	1587	43,97
pc1915	-	conserved hypothetical protein	2052	3,40
pc1916	-	conserved hypothetical protein	933	0,78
pc1917	-	conserved hypothetical protein	249	2,70
pc1918	-	conserved hypothetical protein	1659	4,16
pc1919	-	conserved hypothetical protein	294	6,80
pc1920	-	conserved hypothetical protein	1554	5,98
pc1921	-	hypothetical protein	291	0,29
pc1922	-	unknown protein	315	14,89
pc1923	-	conserved hypothetical protein	279	11,07
pc1924	-	unknown protein	1527	1,25
pc1925	-	strongly similar to endonuclease G, mitochondrial precursor	453	0,46
pc1926	-	conserved hypothetical protein	2286	8,89
pc1927	-	conserved hypothetical protein	330	6,04
pc1928	-	conserved hypothetical protein	1587	2,28
pc1929	-	conserved hypothetical protein	360	1,33
pc1930	-	conserved hypothetical protein	330	2,64
pc1931	-	conserved hypothetical protein	591	1,92
pc1932	-	unknown protein	249	2,34
pc1933	-	unknown protein	249	1,24
pc1934	-	conserved hypothetical protein	786	5,40
pc1935	-	conserved hypothetical protein	1515	6,98
pc1936	-	conserved hypothetical protein	1131	0,21
pc1937	-	unknown protein	690	6,88
pc1938	-	unknown protein	300	0,16
pc1939	-	unknown protein	285	0,48
pc1940	-	unknown protein	204	5,04
pc1941	-	unknown protein	198	0,71
pc1942	-	unknown protein	210	0,47
pc1943	-	unknown protein	216	0,85
pc1944	-	unknown protein	3009	2,89
pc1945	-	unknown protein	294	1,18
pc1946	-	conserved hypothetical protein	1389	11,41
pc1947	-	unknown protein	2544	0,41
pc1948	-	unknown protein	252	0,25
pc1949	-	unknown protein	219	0,16
pc1950	-	unknown protein	183	0,22

pc1951	-	strongly similar to metalloproteinase	336	2,88
pc1952	-	unknown protein	1110	6,88
pc1953	-	conserved hypothetical protein	420	0,80
pc1954	-	conserved hypothetical protein	2115	3,82
pc1955	-	conserved hypothetical protein	1365	9,67
pc1956	-	conserved hypothetical protein	1980	5,56
pc1957	-	hypothetical protein	3435	1,23
pc1958	-	similar to metalloproteinase	1461	2,72
pc1959	-	unknown protein	258	0,37
pc1960	-	unknown protein	1077	3,19
pc1961	-	unknown protein	1104	0,48
pc1962	-	conserved hypothetical protein	378	7,66
pc1963	-	conserved hypothetical protein	813	6,18
pc1964	-	unknown protein	222	7,13
pc1965	-	similar to metalloproteinase	981	13,50
pc1966	-	conserved hypothetical protein	3849	9,66
pc1967	-	unknown protein	186	0,42
pc1968	-	conserved hypothetical protein	1278	1,58
pc1969	-	unknown protein	228	0,16
pc1970	-	conserved hypothetical protein	1302	1,51
pc1971	-	unknown protein	672	0,86
pc1972	-	hypothetical protein	1944	1,79
pc1973	-	unknown protein	216	0,51
pc1974	-	unknown protein	687	7,07
pc1975	**hemF**	strongly similar to coproporphyrinogen oxidase III, aerobic	801	6,73
pc1976	-	unknown protein	294	7,75
pc1977	**fixO**	similar to cytochrome-c oxidase fixO chain	1248	6,77
pc1978	**fixN**	similar to cytochrome-c oxidase fixN chain	1416	8,83
pc1979	-	unknown protein	234	2,47
pc1980	-	unknown protein	222	0,21
pc1981	-	conserved hypothetical protein	561	4,34
pc1982	-	conserved hypothetical protein	1116	3,61
pc1983	**talB**	similar to transaldolase	660	5,28
pc1984	-	hypothetical protein	2355	3,28
pc1985	-	conserved hypothetical protein	1605	3,15
pc1986	-	hypothetical protein	663	0,76
pc1987	-	conserved hypothetical protein	894	4,85
pc1988	-	conserved hypothetical protein	276	5,40
pc1989	-	hypothetical protein	1578	2,03
pc1990	-	unknown protein	624	3,55
pc1991	-	conserved hypothetical protein	1275	2,79
pc1992	-	conserved hypothetical protein	1614	9,95
pc1993	-	conserved hypothetical protein	390	4,32
pc1994	-	unknown protein	303	-0,08
pc1995	**recA**	strongly similar to recombination protein recA	1086	43,41
pc1996	**ispA**	similar to geranyltranstransferase	810	5,90
pc1997	**glmU**	similar to UDP-N-acetylglucosamine diphosphorylase	681	0,84
pc1998	**rumA**	similar to 23S rRNA (Uracil-5-)-methyltransferase	1152	0,90
pc1999	**mgtC**	strongly similar to mgtC protein	690	11,97
pc2000	-	unknown protein	249	0,70
pc2001	-	conserved hypothetical protein	870	1,42
pc2002	-	conserved hypothetical protein	594	0,71
pc2003	-	unknown protein	564	0,68
pc2004	**cbbY**	hypothetical protein	786	0,25
pc2005	-	unknown protein	192	0,44
pc2006	-	hypothetical protein	528	0,11
pc2007	-	conserved hypothetical protein	303	1,18
pc2008	-	conserved hypothetical protein	249	2,95
pc2009	-	unknown protein	600	8,30
pc2010	-	unknown protein	375	5,05
pc2011	-	unknown protein	333	3,18
pc2012	**ung**	strongly similar to uracil-DNA glycosylase	711	6,39
pc2013	-	conserved hypothetical protein	738	8,44
pc2014	**parA;minD**	similar to partition protein	753	9,01
pc2015	**thrS**	strongly similar to threonine-tRNA ligase	1953	5,93
pc2016	-	conserved hypothetical protein	201	4,32
pc2017	-	hypothetical protein	1218	21,02
pc2018	-	unknown protein	201	3,18
pc2019	-	hypothetical protein	2880	8,00
pc2020	-	unknown protein	318	5,54
pc2021	-	unknown protein	192	5,65

pc2022	-	hypothetical protein	1437	274,45
pc2023	-	hypothetical protein	1452	207,34
pc2024	-	unknown protein	840	292,52
pc2025	-	unknown protein	360	205,63
pc2026	-	unknown protein	192	0,73
pc2027	-	unknown protein	1281	2,56
pc2028	-	unknown protein	663	27,76
pc2029	-	conserved hypothetical protein	300	2,69
pc2030	-	unknown protein	258	2,76
pc2031	-	unknown protein	219	0,47
2036		p_folA		5,40

Table S4. Predicted genes during energy metabolism. Genes which were expressed during intracellular growth are marked in grey.

Glycolysis

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0143	**eno**	strongly similar to phosphopyruvate hydratase (enolase)	4,34
pc0161	**pgmA**	similar to phosphoglycerate mutase	4,98
pc0239	**pgk**	strongly similar to 3-phosphoglycerate kinase	18,74
pc0387	**uhpC, glpT**	glycose-6-phosphate transporter	12,91
pc0435	**gapA**	strongly similar to Glyceraldehyde 3-P dehydrogenase A	9,33
pc0781	**pgi**	similarity to Glucose-6-phosphate isomerase (GPI)	12,24
pc0789	**adh3**	similar to alcohol dehydrogenase class III	15,19
pc0880	**pfkA**	pyrophosphate-dependent phospofructokinase	8,68
pc0933	**dhnA;fbaB**	strongly similar to fructose-bisphosphate aldolase class I	19,48
pc0935	**glk**	glucokinase	7,73
pc1262	**pgm**	similar to phosphoglucomutase/phosphomannomutase	11,47
pc1307	**pgm**	strongly similar to phosphoglucomutase	6,16
pc1636	**pyk**	strongly similar to pyruvate kinase	4,21
pc1731	**pdhC;aceF**	strongly similar to pyruvate dehydrogenase	11,83
pc1732	**pdhB**	strongly similar to pyruvate dehydrogenase (lipoamide), E1 component, beta chain	10,07
pc1733	**pdhA**	similar to pyruvate dehydrogenase (lipoamide), E1 component, alpha chain	6,47

Citrat Cycle (TCA cycle)

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0151	**lpdA**	strongly similar to dihydrolipoamide dehydrogenase	11,78
pc0865	**acnB**	strongly similar to aconitate hydratase	3,82
pc1089	**sucB, odo2, E2o**	strongly similar to dihydrolipoamide S-succinyltransferase	3,40
pc1090	**sucA, odo1, E1o**	strongly similar to 2-oxoglutarate dehydrogenase E1 component, sucA	4,23
pc1298	**sucC**	strongly similar to succinate-CoA ligase (ADP-forming) beta chain	4,02
pc1371	**pckG**	strongly similar to Phosphoenolpyruvate carboxykinase [GTP]	4,70
pc1660	**fumC**	stongly similar to fumarate hydratase class II, fumC	3,55
pc1771	**gltA**	similar to citrate (si)-synthase	15,34
pc1772	**mdh**	strongly similar to NADP-dependent malate dehydrogenase	4,54
pc1783	**icd**	strongly similar to isocitrate dehydrogenase (NADP)	8,61
pc1843	**sdhC**	similar to succinate dehydrogenase cytochrome b558	2,70

Pentose Phosphate Way

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0317	**pgd**	strongly similar to phosphogluconate dehydrogenase (decarboxylating)	14,66
pc0768	**rpe**	similar to ribulose-phosphate 3-epimerase	5,49
pc0781	**pgi**	similarity to Glucose-6-phosphate isomerase (GPI)	12,24
pc0819	**devB;pgl**	similar to 6-phosphogluconolactonase (6PGL)	8,92
pc0821	**zwf**	similarity to glucose-6-phosphate 1-dehydrogenase (G6PD)	8,41
pc0880	**pfkA**	similar to 6-phosphofructokinase 1	8,68
pc0933	**dhnA;fbaB**	strongly similar to fructose-bisphosphate aldolase class I	19,48
pc1175	**rpiA**	similar to ribose 5-phosphate isomerase A	5,77
pc1262	**pgm**	similar to phosphoglucomutase/phosphomannomutase	11,47
pc1302	**galE**	similar to UDP-glucose 4-epimerase	2,08
pc1514	**tkt**	strongly similar to transketolase	12,17
pc1691	**talB**	strongly similar to transaldolase B	19,23
pc1983	**talB**	similar to transaldolase	5,28

Oxidative Phosphorylation

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0559	**nuoA, nuo1**	similar to NADH-ubiquinone oxidoreductase chain A	8,27
pc0560	**nuoB, nuo2**	strongly similar to NADH-ubiquinone oxidoreductase chain B	7,57
pc0561	**nuoC, nuoCD, nuo3nuo4**	similar to NADH-ubiquinone oxidoreductase chain C/D	6,86
pc0562	**nuoD, nuoCD, nuo3nuo4**	similar to NADH-ubiquinone oxidoreductase chain C/D	8,83
pc0563	**nuoE, nuo5**	similar to NADH-ubiquinone oxidoreductase chain E	10,48
pc0564	**nuoF, nuo6**	strongly similar to NADH-ubiquinone oxidoreductase chain F	5,48
pc0565	**nuoG, nuo7**	similar to NADH-ubiquinone oxidoreductase chain G	36,04
pc0566	**nuoH, nuo8**	strongly similar to NADH-ubiquinone oxidoreductase chain H	6,43
pc0567	**nuoI, nuo9**	strongly similar to NADH-ubiquinone oxidoreductase chain I	6,23
pc0568	**nuoJ, nuo10**	similar to NADH-ubiquinone oxidoreductase chain J	3,92
pc0569	**nuoK, nuo11**	similar to NADH-ubiquinone oxidoreductase chain K	7,62
pc0570	**nuoL, nuo12**	similar to NADH-ubiquinone oxidoreductase chain L	3,19
pc0571	**nuoM, nuo13**	similar to NADH-ubiquinone oxidoreductase chain M	3,39
pc0572	**nuoN, nuo14**	similar to NADH-ubiquinone oxidoreductase chain N	4,36

pc0909	**-**	conserved hypothetical protein	3,92
pc1189	**cyoA**	strongly similar to cytochrome o ubiquinol oxidase chain II cyoA	6,86
pc1190	**cyoB**	strongly similar to cytochrome o ubiquinol oxidase chain I cyoB	11,48
pc1191	**cyoC**	strongly similar to cytochrome o ubiquinol oxidase chain III cyoC	10,03
pc1192	**cyoD**	similar to cytochrome O ubiquinol oxidase chain IV cyoD	12,72
pc1193	**cyoE**	strongly similar to heme O synthase (=protoheme IX farnesyltransferase) cyoE	7,67
pc1629	**cydB, cyd-2**	similar to cytochrome bd-I oxidase subunit II	3,06
pc1630	**cydA, cyd-1**	similar to cytochrome bd-I oxidase subunit I	5,45
pc1667	**atpC**	similar to H+-transporting two-sector ATPase (epsilon chain, atpC)	1,55
pc1668	**atpD**	strongly similar to H+-transporting two-sector ATPase (beta chain, atpD)	10,18
pc1669	**atpG**	similar to H+-transporting two-sector ATPase (gamma chain, atpG)	16,57
pc1670	**atpA**	strongly similar to H+-transporting ATP synthase (alpha chain, atpA)	9,47
pc1671	**atpH**	similar to H+-transporting two-sector ATPase (delta chain, atpH)	6,67
pc1672	**atpF; uncF**	similar to H+-transporting two-sector ATPase (chain b, atpF)	11,84
pc1673	**atpE**	strongly similar to H+-transporting two-sector ATPase lipid-binding protein (chainC, atpE)	18,65
pc1674	**atpB**	similar to H+-transporting two-sector ATPase (chain a, atpB)	9,50
pc1676	**ntpK**	similar to V-type sodium ATP synthase subunit K (ntpK)	39,92
pc1677	**ntpI**	similar to V-type sodium ATP synthase subunit I (ntpI)	7,83
pc1678	**ntpD**	similar to V-type sodium ATP synthase (subunit D, ntpD)	10,20
pc1679	**atpB**	similar to H+-transporting two-sector ATPase (chain B, atpB)	8,80
pc1680	**ntpA**	strongly similar to V-type sodium ATP synthase (subunit A, ntpA)	11,73
pc1682	**ntpE**	similar to V-type sodium ATP synthase (subunit E, ntpE)	14,14

Table S5. Predicted genes involved in amino acid metabolism. Genes which were expressed during intracellular growth are marked in grey.

Glutamate Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0033	**poaA, putA**	similar to bifunctional protein (proline dehydrogenase and delta-1-pyrroline-5-carboxylate dehydrogenase)	L-glutamate - L-1-pyrroline 5-carboxylate	1,90
pc0069	**aspC**	strongly similar to aspartate transaminase	2-oxoglutarate - L-glutamate	2,04
pc0244	**gltX**	strongly similar to glutamate-tRNA ligase (= glutamyl-tRNA synthetase)	L-glutamate to L-glutamyl-tRNA (Glu)	4,63
pc0669	**gatB**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain B	L-glutamyl-tRNA (Gln) to L-glutaminyl-tRNA (gln)	10,55
pc0670	**gatA**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain A	L-glutamyl-tRNA (Gln) to L-glutaminyl-tRNA (Gln)	6,13
pc0671	**gatC**	similar to glutamyl-tRNA(Gln) amidotransferase chain C	L-glutamyl-tRNA (Gln) to L-glutaminyl-tRNA (Gln)	6,23
pc0685	**aspC**	LL-DAP aminotransferase	2-oxoglutarate - L-glutamate	2,00
pc1240	**glnA**	similar to glutamate-ammonia ligase (=glutamine synthetase) type III	L-glutamine - L-glutamate	1,02
pc1306	**glmS**	strongly similar to glutamine-fructose-6-phosphate transaminase (isomerizing)	L-glutamine to glucosamine-6P	3,85
pc1496	**gdhB**	similar to eucaryotic NAD-specific glutamate dehydrogenase	2-oxoglutarate - L-glutamate	1,95
pc1853	**murI**	strongly similar to glutamate racemase	L-glutamate - D-glutamate	1,44

Glycin, Serin, Threonine Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0023	**psdD**	similar to phosphatidylserine decarboxylase proenzyme	O-phosphatidyl-L-serine to (3-phosphatidyl)-ethanolamine	3,89
pc0151	**lpdA**	strongly similar to dihydrolipoamide dehydrogenase	diihydrolipoylprotein to lipoylprotein	11,78
pc0281	**gcvT**	strongly similar to glycine cleavage system T protein	S-amino-methyldihydrolipoylprotein to dihydrolipoylprotein	2,28
pc0283	**gcvP1**	strongly similar to glycine dehydrogenase P protein subunit 1	lipoylprotein to S-amino-methyldihydrolipoylprotein	2,54
pc0284	**gcvP2**	strongly similar to glycine dehydrogenase (decarboxylating) P protein subunit 2	lipoylprotein to S-amino-methyldihydrolipoylprotein	4,08
pc0444	**glyA**	strongly similar to glycine hydroxymethyltransferase	serine - glycine	11,39
pc0693	**glyS**	strongly similar to glycyl-tRNA synthetase	glycine zu glycyl-tRNA (Gly)	7,80
pc0701	**thrS**	similar to threonine-tRNA ligase	threonine to L-threonyl-tRNA (Thr)	3,74
pc0765	**lysC**	strongly similar to aspartate kinase II precursor	L-aspartate to L-4-aspartylphosphate	1,85
pc0810	**tdh**	strongly similar to threonine 3-dehydrogenase	threonine to L-2-amino-acetate	4,56
pc0878	**sdaB**	strongly similar to L-serine ammonia-lyase	pyruvate - serine	9,05
pc1102	**asd**	similar to aspartate-semialdehyde dehydrogenase	L-4-aspartyl phosphate zu L-aspartate 4-semialdehyde	9,65
pc1270	**pssA**	similar to CDPdiacylglycerol-serine O-phosphatidyltransferase	serin zu O-phosphatidyl-L-serine	3,51
pc1488	**serS**	strongly similar to seryl-tRNA synthetase	serine to L-seryl-tRNA (Ser)	8,76
pc2015	**thrS**	strongly similar to threonine-tRNA ligase	threonine to L-threonyl-tRNA Thr)	5,93

Arginine, Proline Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0033	**putA, poaA**	similar to bifunctional protein (proline dehydrogenase and delta-1-pyrroline-5-carboxylate dehydrogenase)	L-proline to L-1-pyrroline 5-carboxylate	1,90
pc0069	**aspC**	strongly similar to aspartate transaminase	L-erytrho-4-hydroxy-glutamate to D-4-hydroxy-2-oxoglutarate	2,04
pc0685	**aspC**	LL-DAP aminotransferase	L-erytrho-4-hydroxy-glutamate to D-4-hydroxy-2-oxoglutarate	2,00
pc1132	**proC**	similar to pyrroline-5-carboxylate reductase, proC	Glutamate - L-Proline	9,60
pc1324	**proS**	similar to prolyl-tRNA synthetase	L-Proline zu L-prolyl-tRNA (Pro)	5,39

Phenylalanine, Tyrosine, Tryptophan Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0069	**aspC**	strongly similar to aspartate transaminase	tyrosine - 4-hydroxyphenylpyruvate	2,04
pc0073	**aroB**	similar to 3-dehydroquinate synthase	7P-2-dehydro-3-deoxy-D-arabino-heptonate to 3-	0,90

			dehydroquinate	
pc0143	**eno**	strongly similar to phosphopyruvate hydratase (enolase)	3-dehydroquinate - 3-dehydroshikimate	4,34
pc0685	**aspC**	LL-DAP aminotransferase	tyrosine - 4-hydroxyphenylpyruvate	2,00
pc0705	**pheS**	strongly similar to phenylalanine-tRNA ligase alpha chain	phenylalanine to phe-tRNA	40,68
pc0882	**aroA**	similar to 3-phosphoshikimate 1-carboxyvinyltransferase(5-enolpyruvylshikimate-3-phosphate synthase, EPSP synthase)	shikimate 3-phosphate - 3-phosphoshikimate	1,83
pc0883	**aroL**	similar to shikimate kinase precursor	shikimate to shikimate 3-phosphate	6,00
pc0884	**aroC**	strongly similar to chorismate synthase	3-phosphoshikimate - chorismate	1,63
pc0928	**trpD**	similar to anthranilate synthase component II	chorismate to anthranilate	1,30
pc1169	**tyrS**	strongly similar to tyrosine-tRNA ligase	tyrosine to tyr-tRNA	6,28
pc1658	**aroF**	strongly similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (tyrosine-sensitive), aroF	phosphoenolpyruvate to 7P-2-dehydro-3-deoxy-D-arabino-heptonate	4,44

Lysine Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0314	**murE**	similar to UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	meso-2,6-diaminopimelate to UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate	1,16
pc0400	**cutE**	similar to apolipoprotein N-acyltransferase	2,3,4,5-tetrahydrodipicolinate to N-acetyl-L-2-amino-6-oxopimelate	1,28
pc0442	**dapF**	similar to diaminopimelate epimerase	2,6-diaminopimelate - meso-2,6-diaminopimelate	7,72
pc0686	**dapA**	similar to dihydrodipicolinate synthase	L-aspartate 4-semialdehyde to 2,3-dihydrodipicolinate	1,46
pc0687	**dapB**	similar to dihydrodipicolinate reductase	2,3-dihydrodipicolinate - 2,3,4,5-tetrahydrodipicolinate	3,15
pc0765	**lysC**	strongly similar to aspartate kinase II precursor	L-aspartate to L-4-aspartylphosphate	1,85
pc1102	**asd**	similar to aspartate-semialdehyde dehydrogenase	L-4-aspartylphosphate to L-aspartate 4-semialdehyde	9,65
pc1228	**lysS**	strongly similar to lysyl-tRNA synthetase	L-lysine to L-lys-tRNA (Lys)	8,63
pc1253	**murF**	similar to UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate -D-alanyl-D-alanine-ligase murF	DP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate to DP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine	5,12
pc1530	**lysS**	similar to lysyl-tRNA synthetase	L-lysine to L-lys-tRNA (Lys)	5,01
pc1569	**rimL**	similar to ribosomal-protein-serine acetyltransferase	2,3,4,5-tetrahydrodipicolinate to N-acetyl-L-2-amino-6-oxopimelate	2,93

Cystein Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0069	**aspC**	strongly similar to aspartate transaminase	L-cysteate - 3-sulfopyruvate	2,04
pc0685	**aspC**	LL-DAP aminotransferase	L-cysteate - 3-sulfopyruvate	2,00
pc0878	**sdaB**	strongly similar to L-serine ammonia-lyase	L-serine to 2-aminoacrylate	9,05
pc1235	**cysS**	similar cysteinyl tRNA synthetase	L-cysteine to L-cysteinyl-tRNA (Cys)	2,57

Valine, Leucine, Isoleucine Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0494	**ileS, ilvS**	similar to isoleucyl-tRNA synthetase	L-isoleucine to L-Ile-tRNA (Ile)	6,40
pc1047	**leuS**	strongly similar to leucyl-tRNA synthetase	L-leucine to L-leu-tRNA (Leu)	7,22
pc1654	**valS**	strongly similar to valyl-tRNA synthetase	L-valine to L-val-tRNA (Val)	6,59
pc1732	**pdhB**	strongly similar to pyruvate dehydrogenase (lipoamide), E1 component, beta chain	pyruvate to 2-hydroxyethyl-ThPP	10,07
pc1733	**pdhA**	similar to pyruvate dehydrogenase (lipoamide), E1 component, alpha chain	pyruvate to 2-hydroxyethyl-ThPP	6,47

Alanine, Aspartate Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0069	**aspC**	strongly similar to aspartate transaminase	oxaloacetate - L-aspartate	2,04
pc0151	**lpdA**	strongly similar to dihydrolipoamide dehydrogenase	lipoamide-E - dihydrolipoamide-E	11,78
pc0346	**asnS**	strongly similar to asparagine-tRNA ligase	L-asparagine to L-asparaginyl-tRNA (Asn)	3,94
pc0384	**aspS**	strongly similar to aspartate-tRNA ligase	L-aspartate to L-aspartyl-tRNA (Asp)	9,19
pc0631	**alr**	similar to alanine racemase	L-alanine - D-alanine	3,66
pc0669	**gatB**	strongly similar to glutamyl-tRNA(Gln) amidotransferase chain B	L-aspartyl-tRNA (asn) to L-asparaginyl-tRNA (Asn)	10,55
pc1519	**alaS**	strongly similar to alanyl-tRNA synthetase	L-alanine - L-alanyl-tRNA (Ala)	4,64

pc1731	**pdhC;aceF**	strongly similar to pyruvate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	dihydrolipoamide-E, acetyl-CoA to S-acetyldihydrolipoamide-E	11,83
pc1732	**pdhB**	strongly similar to pyruvate dehydrogenase (lipoamide), E1 component, beta chain	pyruvate to 2-hydroxy-ethyl-ThPP	10,07

Methionine Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0404	**fmt**	strongly similar to methionyl-tRNA formyltransferase	L-methionyl-tRNA to N-formylmethionyl-tRNA	1,99
pc0665	**metG**	similar to methionine-tRNA ligase	L-methionine to L-methionyl-tRNA	4,63

Histidine Metabolism

ID CDS	Gene name	Gene description	Enzyme activity	Mean SNR≥3
pc0248	**-**	similar to RNA methyl transferase	L-histidinal to L-histidine	1,01
pc0385	**hisS**	strongly similar to histidine-tRNA ligase	L-histidine to L-histidyl-tRNA (His)	3,45

Table S6. Predicted amino acid and nucleotide transporter genes. Genes which were expressed during continuous growth are marked in grey.

Di-/Oligopeptide transporter

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0096	**oppF**	strongly similar to ATP binding protein, component of oligopeptide permease, oppF	2,21
pc0097	**oppD**	strongly similar to ATP binding protein, component of oligopeptide permease, oppD	2,17
pc0101	**oppC**	similar to oligopeptide transport system permease protein, oppC	2,11
pc0102	**dppB**	similar to dipeptide transport system permease protein, dppB	2,72
pc0103	**oppA**	similar to substrate binding proteins, component of oligopeptide permease, oppA	4,19
pc1502	**oppA, dppA, spo0KA**	strongly similar to oligo/dipeptide-binding protein oppA	6,43
pc1503	**oppB, dppB, spo0KB**	strongly similar to oligo/dipeptide ABC transporter (permease) oppB	2,85
pc1504	**oppC, dppC, spo0KC**	strongly similar to oligo/dipeptide ABC transporter (permease) oppC	6,51
pc1505	**oppD, dppD, spo0KD**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppD	4,35
pc1506	**dppF, oppF, spoOKF**	strongly similar to oligo/dipeptide abc transporter, ATP-binding protein oppF	2,52

D-methionine

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0453	**yaeC, metQ**	similar to ABC transporter substrate binding protein yaeC	16,59
pc0454	**yaeE, metI**	strongly similar to ABC transporter permease yaeE	4,32

Glutamine

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0108	**fliY**	similar to amino acid ABC transporter, periplasmic amino acid-binding protein	1,98
pc1217	**glnQ**	similar to ABC transporter, ATP-binding protein	0,77

Sodium ion/alanine

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0622	**dagA**	similar to D-alanine/glycine transport protein, sodium-dependent	11,27
pc1598	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	4,09
pc1656	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	4,06
pc1657	**dagA, cycA**	similar to D-alanine/glycine transport protein, sodium-dependent	3,67

Amino acid general

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0927	**-**	similar to cationic amino acid transport protein	2,25

Proton/sodium ion/glutamate

ID CDS	Gene name	Gene description	Mean SNR≥3
pc1734	**aaaT**	similar to neutral amino acid (glutamate) transporter	5,82
pc1785	**gltT**	similar to proton/sodium-glutamate symporter	3,30

Cationic amino acid

ID CDS	Gene name	Gene description	Mean SNR≥3
pc1332	**-**	conserved hypothetical protein	0,30

Tyrosine/tryptophan

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0168	**tyrP_1**	similar to tyrosine/tryptophan transport protein	0,97
pc0169	**tyrP_1**	similar to tyrosine/tryptophan transport protein	0,87
pc0589	**tyrP**	similar to aromatic amino acid-specific transport protein	3,84
pc1305	**tyrP**	similar to tyrosine-specific transport protein	2,34

Branched amino acids

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0767	**braB**	similar to branched-chain amino acid transport system II carrier protein	1,27

Sodium ion/proline

ID CDS	Gene name	Gene description	Mean SNR≥3
pc1715	**putP**	strongly similar to sodium/proline symporter	2,78

Sodium ion/amino acid

ID CDS	Gene name	Gene description	Mean SNR≥3
pc1260	**-**	conserved hypothetical protein	1,41

Nucleotide transporter

ID CDS	Gene name	Gene description	Mean SNR≥3

pc0240	**ntt_3**	strongly similar to ATP/ADP translocase	11,02
pc0241	**ntt_2**	Nucleotide triphosphate/H+ symporter	7,55
pc0250	**ntt_1**	ATP/ADP translocase	84,85
pc1343	**ntt_5**	similar to ADP/ATP translocase	4,00
pc0485	**ntt_4**	NAD+/ADP antiporter	9,65

Table S7. Predicted TTSS, TFSS and putative Inc genes. Genes which were expressed during intracellular growth are marked in grey.

Type III secretion system

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0200	**yscT, sctT**	similar to type III secretion inner membrane protein SctT	4,57
pc0201	**sctS**	strongly similar to type III secretion inner membrane protein SctS	9,97
pc0202	**yscR, sctR; fliP**	similar to type III secretion inner membrane protein SctR	15,22
pc0203	**yscL, sctL**	similar to type III secretion protein SctL	17,84
pc0205	**yscJ, sctJ**	similar to type III secretion protein SctJ	8,06
pc0749	**sctV;lcrD**	strongly similar to type III secretion pathway protein SctV	4,84
pc0750	**sctU;yscU**	similar to type III secretion pathway protein sctU	7,58
pc1397	**sctN;yscN**	strongly similar to type III secretion pathway protein sctN	19,31
pc1400	**sctQ**	similar to flagellar motor switch protein (= type III secretion translocase SctQ)	13,82
pc1475	**gspD;sctC;pulD**	similar to component D of type II secretion pathway	14,47

Type IV secretion system

ID CDS	Gene name	Gene description	Mean SNR≥3
pc1423	**traE**	similar to F pilus assembly protein traE	0,38
pc1425	**traB**	similar to F pilus assembly protein traB	0,16
pc1430	**traC**	similar to inner-membrane protein traC	0,19
pc1431	**traF**	similar to F pilus assembly protein traF	1,44
pc1432	**traW**	similar to F pilus assembly protein traW	3,19
pc1433	**trbC**	similar to F pilus assembly protein trbC	0,21
pc1434	**traU**	similar to F pilus assembly protein traU	0,71
pc1437	**traN**	similar to conjugative transfer protein traN precursor	0,17
pc1438	**traF**	similar to F pilus assembly protein traF	0,66
pc1439	**traH**	similar to F pilus assembly protein traH	0,63
pc1440	**traG**	similar to conjugative transfer protein traG	1,30
pc1441	**traD**	similar to conjugative transfer protein traD	11,31

Putative Incs

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0063	-	hypothetical protein	2,34
pc0156	-	hypothetical protein	2,21
pc0164	-	unknown protein	4,44
pc0184	-	hypothetical protein	4,77
pc0399	-	similar to inclusion protein IncA	3,15
pc0508	-	unknown protein	0,82
pc0530	-	unknown protein	4,65
pc0577	-	unknown protein	14,65
pc0579	-	unknown protein	50,27
pc0699	-	unknown protein	17,21
pc0726	-	unknown protein	3,67
pc0791	-	hypothetical protein	2,96
pc0922	-	unknown protein	2,59
pc1111	-	unknown protein	26,17
pc1114	-	unknown protein	7,63
pc1290	-	unknown protein	11,15
pc1422	-	unknown protein	0,37
pc1540	-	unknown protein	0,97
pc1549	-	unknown protein	3,00
pc1730	-	unknown protein	19,97
pc1737	-	conserved hypothetical protein	8,97
pc1857	-	conserved hypothetical protein	5,02
pc1910	-	unknown protein	12,26

Table S8. Predicted plant homologues in *P. amoebophila*. Genes which were expressed during intracellular growth are marked in grey.

Plant homologues

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0048		hypothetical protein	3,41
pc0079	-	strongly similar to UDP-glucuronat epimerase	1,10
pc0099	-	conserved hypothetical protein	12,67
pc0141	-	conserved hypothetical protein	4,92
pc0160	**yjbC**	similar to ribosomal large chain pseudouridine synthase B	3,18
pc0161	**pgmA**	similar to phosphoglycerate mutase	4,98
pc0175	-	hyopthetical protein	2,48
pc0199	**ppaA**	similar to F-box protein	1,94
pc0324	-	hypothetical protein	1,14
pc0325	-	conserved hypothetical protein	7,90
pc0327	**ispD**	similar to 4-diphosphocytidyl-2C-methyl-D-erythritol synthase	0,88
pc0334	**ppaA**	hypothetical protein	2,52
pc0346	**asnS**	strongly similar to asparagine-tRNA ligase	3,94
pc0395	**ksgA**	similar to dimethyladenosine transferase	5,52
pc0398	**ddlA**	similar to D-alanine--D-alanine ligase	2,00
pc0527	-	conserved hypothetical protein	8,87
pc0643	**pnp**	strongly similar to polyribonucleotide nucleotidyltransferase	8,54
pc0648	-	conserved hypothetical protein	11,13
pc0674	-	hypothetical protein	5,11
pc0685	**aspC**	LL-DAP aminotransferase	2,00
pc0693	**glyS**	strongly similar to glycyl-tRNA synthetase	7,80
pc0718	-	hypothetical protein	2,87
pc0740	**gcpE**	strongly similar to gcpE protein	7,19
pc0743	-	conserved hypothetical protein	11,96
pc0745	**malQ**	similar to 4-alpha-glucanotransferase	4,61
pc0754	-	hypothetical protein	4,54
pc0796	-	similar to tonoplast intrinsic protein (Aquaporin)	8,51
pc0798	-	unknown protein	2,03
pc0825	**kdsB**	strongly similar to 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)	4,44
pc0850	-	hypothetical protein	5,88
pc0888	-	conserved hypothetical protein	3,57
pc0890	**ribA;ribB**	strongly similar to 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	2,35
pc0893	**rbp**	strongly similar to nucleic acid-binding protein	85,87
pc0992	-	conserved hypothetical protein	46,61
pc1025	-	conserved hypothetical protein	11,92
pc1031	-	conserved hypothetical protein	8,11
pc1032	-	conserved hypothetical protein	10,12
pc1033	-	hypothetical protein	30,03
pc1106	-	strongly similar to isoamylase	3,45
pc1131	-	hypothetical protein	1,84
pc1142	-	conserved hypothetical protein	10,50
pc1152	**fabI**	strongly similar to NADH-dependent enoyl-ACP reductase	10,09
pc1161	**dnaQ, mutD**	similar to DNA polymerase III, epsilon chain, mutD	3,59
pc1169	**tyrS**	strongly similar to tyrosine-tRNA ligase	6,28
pc1197	-	hypothetical protein	11,79
pc1238	**fabF**	strongly similar to beta-ketoacyl-ACP synthetase	13,85
pc1272	-	conserved hypothetical protein	6,51
pc1276	-	conserved hypothetical protein	17,14
pc1278	-	conserved hypothetical protein	2,76
pc1282	-	conserved hypothetical protein	5,57
pc1297	**sucD**	strongly similar to succinate-CoA ligase (ADP-forming) alpha chain	3,94
pc1318	**ats1**	similar to glycerol-3-phosphate acyltransferase	6,83
pc1343	**ntt_5**	similar to ADP/ATP translocase	4,00
pc1462	-	conserved hypothetical protein	4,51
pc1495	-	hypothetical protein	2,85
pc1507	-	hypothetical protein	10,20
pc1508	-	hypothetical protein	0,73
pc1510	-	hypothetical protein	9,26
pc1565	-	hypothetical protein	16,45
pc1589	-	strongly similar to isopentenyl monophosphate kinase (IPK)	1,57
pc1596	**glgA**	similar to starch synthase, precursor, glgA	5,26
pc1607	-	hypothetical protein	6,92

pc1616	-	conserved hypothetical protein	4,01
pc1620	-	conserved hypothetical protein	2,88
pc1652	-	unknown protein	53,56
pc1666	-	hypothetical protein	9,39
pc1673	**atpE**	strongly similar to H+-transporting two-sector ATPase lipid-binding protein (chainC, atpE)	18,65
pc1713	**trxB**	strongly similar to thioredoxin-disulfide reductase 2	9,10
pc1769	-	hypothetical protein	2,49
pc1772	**mdh**	strongly similar to NADP-dependent malate dehydrogenase	4,54
pc1782	**gutQ**	similar to Gut Q protein	2,45
pc1832	-	hypothetical protein	2,12
pc1838	**lplA**	similar to lipoate-protein ligase	2,50
pc1909	-	hypothetical protein	13,94
pc1914	-	conserved hypothetical protein	43,97
pc1915	-	conserved hypothetical protein	3,40
pc1918	-	conserved hypothetical protein	4,16
pc1920	-	conserved hypothetical protein	5,98
pc1926	-	conserved hypothetical protein	8,89
pc1928	-	conserved hypothetical protein	2,28
pc1935	-	conserved hypothetical protein	6,98
pc1954	-	conserved hypothetical protein	3,82
pc1956	-	conserved hypothetical protein	5,56
pc1981	-	conserved hypothetical protein	4,34
pc1996	**ispA**	similar to geranyltranstransferase	5,90
pc1998	**rumA**	similar to 23S rRNA (Uracil-5-)-methyltransferase	0,90
pc2012	**ung**	strongly similar to uracil-DNA glycosylase	6,39
pc2019	-	hypothetical protein	8,00

Table S9. Predicted cyanobacterial gene homologues. Genes which were expressed during continuous growth are marked in grey.

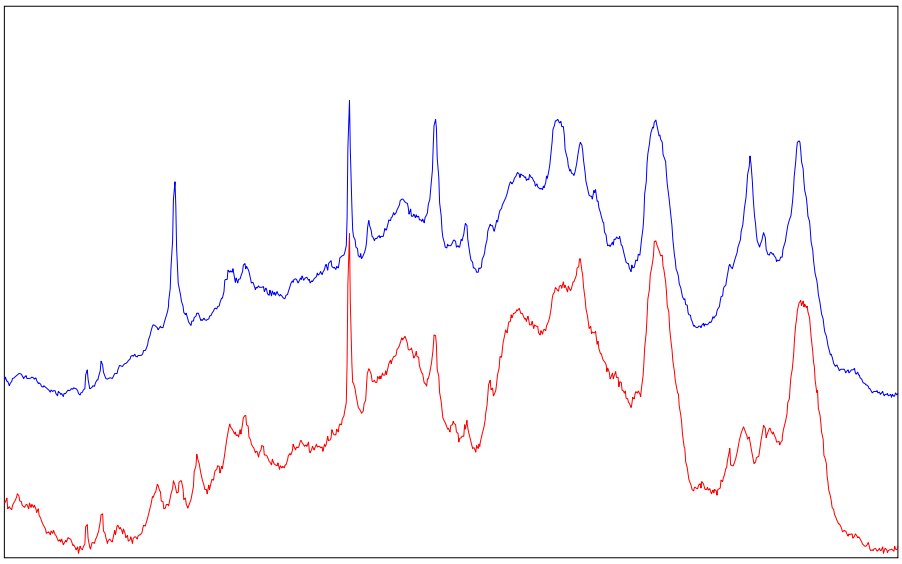
Cyanobacterial gene homologues

ID CDS	Gene name	Gene description	Mean SNR≥3
pc0005	-	conserved hypothetical protein	5,07
pc0040	-	hypothetical protein	3,86
pc0041	-	hypothetical protein	1,37
pc0042	-	hypothetical protein	3,27
pc0044	-	hypothetical protein	0,96
pc0045	-	hypothetical protein	5,53
pc0046	-	hypothetical protein	4,62
pc0051	-	hypothetical protein	2,37
pc0052	-	hypothetical protein	1,66
pc0053	-	hypothetical protein	1,22
pc0054	-	hypothetical protein	1,09
pc0057	-	hypothetical protein	1,77
pc0058	-	hypothetical protein	6,39
pc0059	-	hypothetical protein	4,92
pc0061	-	hypothetical protein	1,33
pc0072	**dprA**	similar to protein required for chromosomal DNA transformation	1,05
pc0106	**glgP**	strongly similar to glycogen phosphorylase	4,52
pc0108	**fliY**	similar to amino acid ABC transporter, periplasmic amino acid-binding protein	1,98
pc0109	**glgC**	strongly similar to glucose-1-phosphate adenylyltransferase	9,10
pc0115	-	hypothetical protein	2,93
pc0181	**wzt**	strongly similar to ABC transporter ATP-binding protein wzt	4,49
pc0182	**wzm**	strongly similar to ABC transporter protein wzm	2,46
pc0189	**sufB**	strongly similar to ABC transporter protein sufB	10,88
pc0190	**sufC**	strongly similar to ABC transporter ATP-binding protein sufC	10,80
pc0227	**ipsF, ygbB**	similar to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECDP-synthase)	3,24
pc0231	**argS**	strong similarity to arginyl-tRNA synthetase (=arginine-tRNA-ligase)	2,61
pc0232	**clpB**	similar to endopeptidase Clp ATP-binding chain B (heat shock protein)	6,28
pc0311	**mraW;yabC**	strongly similar to S-adenosyl-methyltransferase	4,99
pc0315	**amiA, cwlC**	similar to N-acetylmuramoyl-L-alanine amidase	3,73
pc0320	**cdsA**	similar to phosphatidate cytidylyltransferase	3,55
pc0321	**uppS**	strongly similar to undecaprenyl pyrophosphate synthetase	5,56
pc0371	**fdxC**	similar to ferredoxin [2Fe-2S] IV	0,64
pc0390	-	hypothetical protein	11,11
pc0392	**rsbW**	similar to rsbW, negative regulator of sigma-B activity (switch protein/serine kinase)	1,60
pc0442	**dapF**	similar to diaminopimelate epimerase	7,72
pc0480	-	conserved hypothetical protein	4,78
pc0538	**rtxA**	similar to RTX-toxin, partial length	3,33
pc0623	**nfi**	strongly similar to endonuclease V (deoxyinosine 3'endonuclease)	4,80
pc0641	-	hypothetical protein	3,68
pc0644	**rpsO;rs15**	strongly similar to 30S ribosomal protein S15	22,96
pc0645	-	conserved hypothetical protein	1,47
pc0729	-	conserved hypothetical protein	2,36
pc0733	-	unknown protein	4,11
pc0734	-	hypothetical protein	1,72
pc0736	-	conserved hypothetical protein	2,06
pc0742	-	conserved hypothetical protein	4,59
pc0753	-	conserved hypothetical protein	4,49
pc0769	**efp**	similar to elongation factor P	19,00
pc0772	**accC**	strongly similar to biotin carboxylase	13,56
pc0820	-	hypothetical protein	5,48
pc0821	**zwf**	similarity to glucose-6-phosphate 1-dehydrogenase (G6PD)	8,41
pc0868	-	conserved hypothetical protein	0,17
pc0903	-	conserved hypothetical protein	6,15
pc0952	-	strongly similar to putative oxidoreductases	8,33
pc0971	-	conserved hypothetical protein	0,10
pc0980	-	conserved hypothetical protein	5,91
pc0990	-	conserved hypothetical protein	6,56
pc0996	-	conserved hypothetical protein	8,88
pc1010	-	conserved hypothetical protein	1,97
pc1044	-	conserved hypothetical protein	4,13
pc1066	-	conserved hypothetical protein	0,26
pc1079	**wzb**	similar to low molecular weight protein-tyrosine-phosphatase	5,94
pc1107	-	hypothetical protein	15,31
pc1113	-	conserved hypothetical protein	3,12
pc1120	-	conserved hypothetical protein	1,69

pc1146	-	conserved hypothetical protein	0,84
pc1157	**folB, mutT**	similar to dGTP pyrophosphohydrolase/dihydroneopterin aldolase (mutT/folB, fusion protein)	1,16
pc1158	-	hypothetical protein	5,13
pc1162	-	conserved hypothetical protein	1,04
pc1195	-	conserved hypothetical protein	9,72
pc1196	-	conserved hypothetical protein	5,71
pc1214	-	conserved hypothetical protein	1,44
pc1215	-	conserved hypothetical protein	6,71
pc1226	-	conserved hypothetical protein	4,50
pc1266	-	conserved hypothetical protein	9,18
pc1277	-	conserved hypothetical protein	2,10
pc1279	-	conserved hypothetical protein	2,73
pc1362	**ackA**	strongly similar to acetate kinase	2,69
pc1369	-	similar to glycosyltransferase	2,08
pc1378	-	hypothetical protein	2,02
pc1379	-	hypothetical protein	3,01
pc1391	-	conserved hypothetical protein	15,92
pc1402	-	conserved hypothetical protein	2,82
pc1453	-	conserved hypothetical protein	2,01
pc1484	-	conserved hypothetical protein	1,87
pc1534	**yabJ, yjgF**	strongly similar to yabJ	9,55
pc1535	**htpG**	similar to heat shock protein HtpG	10,26
pc1554	-	conserved hypothetical protein	35,08
pc1556	-	conserved hypothetical protein	1,33
pc1570	-	conserved hypothetical protein	3,19
pc1573	**rf-3, prfC**	strongly similar to peptide chain release factor 3	9,45
pc1624	**murB**	similar to UDP-N-acetylmuramate dehydrogenase	3,95
pc1637	-	conserved hypothetical protein	0,48
pc1640	-	conserved hypothetical protein	0,39
pc1696	**crtE**	strongly similar to farnesyltranstransferase	5,88
pc1697	**exoY**	strongly similar to exopolysaccharide production protein	7,14
pc1724	**recR**	strongly similar to recombination protein RecR	9,19
pc1728	**lpxD;firA**	similar to UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	4,11
pc1761	**glgB**	strongly similar to 1,4-alpha-glucan branching enzyme (= Glycogen branching enzyme)	6,63
pc1803	-	conserved hypothetical protein	2,52
pc1879	-	hypothetical protein	12,24
pc1910	-	unknown protein	12,26
pc1957	-	hypothetical protein	1,23
pc1988	-	conserved hypothetical protein	5,40

Chapter VI

Raman microspectroscopy reveals long-term extracellular activity of a member of the *Chlamydiae*



Mean Raman spectra of *Protochlamydia amoebophila* RBs (blue) and EBs (red) obtained by Raman microspectroscopy.

Raman microspectroscopy reveals long-term extracellular activity of a member of the *Chlamydiae*

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M.W., M.H and S.H. planned the experiments and wrote the manuscript. S.H. performed the Raman experiments, S.H. and A.M. made the incubation experiments and B.S.S. prepared RB and EB fractions, J.M. and E.R.T. made the transmission electron microscopy, C.B. performed the statistical analysis.

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ABSTRACT

The phylum *Chlamydiae* consists exclusively of obligate intracellular bacteria which can infect a wide range of host species including amoebae and humans. These bacteria possess a unique biphasic life cycle consisting of replicative reticulate bodies and infectious elementary bodies, which are believed to be physiologically inactive. According to their genome sequences, all chlamydiae have incomplete key biosynthetic pathways including those for most amino acids, indicating that these compounds are taken up from the host.

In this study, Raman microspectroscopy was applied to differentiate between reticulate and elementary bodies of *Protochlamydia amoebophila* and to monitor *in situ* the uptake of stable isotope labelled phenylalanine into this amoeba symbiont on a single cell level. Not only reticulate but also elementary bodies were labelled with phenylalanine within amoebal host cells. Unexpectedly, uptake of this amino acid was also observed for both growth stages, if incubated extracellularly with labelled phenylalanine, even if the amino acid was added three weeks after mechanical lysis of the host cells. Extracellular uptake was inhibited by ionophore addition, but this effect was reversible, showing that elementary bodies of *P. amoebophila* are able to energize their cytoplasmic membrane outside of the host. Furthermore, infection experiments revealed that *P. amoebophila* cells remain infective even after three weeks of host-free incubation.

Overall, we show for a chlamydial symbiont intra- and extracellular metabolic activity of elementary bodies and reveal that not all chlamydial species rapidly cease their activity after being released from the host cell. This previously not recognized feature might contribute to infectivity and ecological success of these bacteria. More generally, our results demonstrate a new experimental single-cell approach to investigate specific functions of obligate intracellular bacteria.

INTRODUCTION

Chlamydiae are a phylogenetically well separated group of bacteria that live exclusively as pathogens and symbionts inside eukaryotic cells. The chlamydial host range spans large parts of the animal kingdom and also includes protozoa (Horn, 2008). For humans, chlamydiae are important pathogens causing a variety of severe diseases such as pneumonia, trachoma (with over 90 million cases per year worldwide), and urogenital tract infections which are a major cause of female infertility and make *Chlamydia trachomatis* the most frequently sexually transmitted bacterial pathogen (Schachter, 1999; WHO, 2001; WHO, 2008). In the environment, some chlamydiae are found as symbionts of ubiquitous, free-living amoebae (Corsaro *et al.*, 2003; Fritsche *et al.*, 2000; Horn *et al.*, 2000; Horn, 2008; Schmitz-Esser *et al.*, 2008; Thomas *et al.*, 2008). A hallmark of chlamydiae is the unique intracellular developmental cycle, which consists of reticulate bodies (RBs), elementary bodies (EBs), and intermediate bodies (IBs) (Abdelrahman & Belland, 2005; Greub & Raoult, 2002; Hatch, 1999; Horn, 2008; Kahane *et al.*, 2002; Ward, 1988). RBs represent the intracellular life stage; they are metabolically active and multiply inside host-derived vacuoles. The EB is a spore-like stage, which is considered to be metabolically inert and adapted for extracellular survival and infection of new host cells. IBs represent the transition stages between both life stages. All chlamydiae possess reduced biosynthetic capabilities compared to free-living bacteria and rely on the import of essential compounds such as nucleotides and amino acids from their host cells (Al-Younes *et al.*, 2006; Grieshaber *et al.*, 2002; Hatch, 1975; McClarty, 1994; Tipples & McClarty, 1993). These interactions were generally inferred by comparative genomics (Kalman *et al.*, 1999; Read *et al.*, 2000; Read *et al.*, 2003; Stephens *et al.*, 1998; Stephens, 1999), heterologous expression of transporters (Haferkamp *et al.*, 2004; Haferkamp *et al.*, 2006; Schmitz-Esser *et al.*, 2004; Trentmann *et al.*, 2007) or by labelling studies with host-free chlamydial cells immediately after host cell lysis (Hatch *et al.*, 1982; Hatch *et al.*, 1985; Sarov & Becker, 1971), but direct observation of intracellular substrate uptake of chlamydial cells was not yet achieved. Because of the metabolic dependency on their hosts and their obligate intracellular developmental cycle, chlamydiae have been referred to as the ultimate auxotroph (Hatch, 1988).

In this study we used Raman microspectroscopy to investigate the intra- and extracellular metabolic activity of *Protochlamydia amoebophila* UWE25, a model organism for symbiotic chlamydiae and the only non-pathogenic chlamydia for which a genome sequence is available (Horn *et al.*, 2004). Raman microspectroscopy is commonly used in chemistry for the identification of molecules and the characterization of materials (Baena & Lendl, 2004;

De Gelder *et al.*, 2007). Raman spectra provide fingerprints of the chemical composition of the analyzed samples and can thus also be used for the characterization and differentiation of bacteria (Buijtels *et al.*, 2008; Maquelin *et al.*, 2002; Schuster, 2002). The great potential of Raman microspectroscopy for biologists, however, lies in the observation that incorporation of heavy isotopes into cell compounds leads to pronounced changes (peak shifts) in the respective parts of the whole cell Raman spectrum (Huang *et al.*, 2004). This effect has recently been exploited by microbial ecologists to analyze the uptake and incorporation of labelled substrates into free-living bacteria on a single-cell level, without the need for cultivation (Huang & Gogarten, 2007). Here we asked, whether this approach could also be useful for the analysis of metabolic interactions between intracellular bacteria and their eukaryotic host cells and successfully used Raman microspectroscopy to monitor uptake of the amino acid phenylalanine by intracellular *P. amoebophila*. Furthermore, our experiments revealed an unexpected long-term extracellular activity and resilience of *P. amoebophila* EBs, challenging our current perception of chlamydial EBs as metabolically inert life stages.

RESULTS

Raman microspectroscopy-based identification of chlamydial life stages

Identification of the two different life stages of chlamydiae is a fundamental prerequisite for investigating functional differences between them and for understanding the life cycle of these microorganisms. Traditionally this differentiation is based on morphological criteria observed by transmission electron microscopy (Matsumoto, 1988; Rake, 1957; Ward, 1983; Ward, 1988). To test whether this task can also be achieved by Raman microspectroscopy, RBs and EBs of *P. amoebophila* were separated by density gradient centrifugation and subsequently aliquots of the respective fractions were analyzed by transmission electron microscopy and Raman microspectroscopy, respectively. According to transmission electron microscopy 61% RBs, 34% IBs and 5% EBs were found in the RB fraction (n = 1106 cells), and 76% EBs, 16% IBs and 8% RBs were detected in the EB fraction (n = 530 cells). Raman spectra of cells from the EB fraction (n = 44) could be clustered in two groups. 95% of the spectra were highly similar with each other and were thus considered to represent EBs (including IBs with an EB-like chemical composition), while 5% of the spectra were clearly different and were thus assigned to the RBs (including IBs with a RB-like chemical composition). The same two groups of spectra were retrieved from the RB fraction (n = 93 cells), but in this case 76% were RB spectra while only 24% were EB spectra. Generally, Raman spectra of RBs were clearly different from EB spectra (Figure 1) and principal component analysis revealed that this discrimination is statistically significant and can be mainly attributed to three peaks at wavelengths of 746, 1127, and 1585 cm^{-1} (Figure S1).

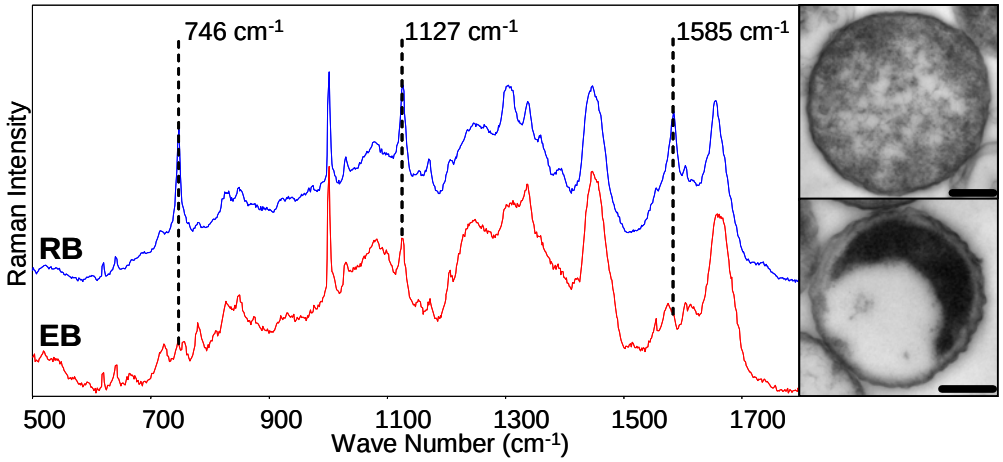

Figure 1. Differentiation of chlamydial RBs and EBs by Raman microspectroscopy. Left panel, mean Raman spectra of RBs and EBs. Comparison of mean Raman spectra of RBs (blue) and EBs (red). For each developmental stage 12 spectra were merged. The wave numbers of three peaks which are more pronounced in RB spectra than in EB spectra are indicated. Right panel, electron microscopic images of *P. amoebophila* RB and an EB. Scale bars represent 200 nm.

Intracellular uptake of phenylalanine

To explore the suitability of Raman microspectroscopy to monitor metabolic interactions between intracellular bacteria and their hosts, we investigated whether *P. amoebophila* is able to take up phenylalanine from its amoeba host. An unsynchronised amoeba culture infected with *P. amoebophila* was grown for different time periods in a defined medium containing ^{13}C9-^{15}N-phenylalanine as only source of this amino acid. Subsequently the amoeba host cells were lysed and the released symbionts were immediately monitored for uptake of the labelled amino acid by Raman microspectroscopy.

After 264h of incubation with labelled phenylalanine, the spectra of *P. amoebophila* showed a marked decrease of three peaks known to originate from unlabelled phenylalanine in bacterial biomass (Huang *et al.*, 2004; Notingher *et al.*, 2004), while three new peaks with a shifted wave number appeared representing the uptake/incorporation of labelled phenylalanine (Figure 2). Almost identical peak shifts were observed when Raman spectra recorded with pure labelled or unlabelled phenylalanine were compared (Figure S2). For all subsequent analyses, the most pronounced peak shift from 1003 cm^{-1} to 967 cm^{-1}, representing the unlabelled and labelled aromatic ring (Wei *et al.*, 2008), respectively, was used as indicator for phenylalanine uptake.

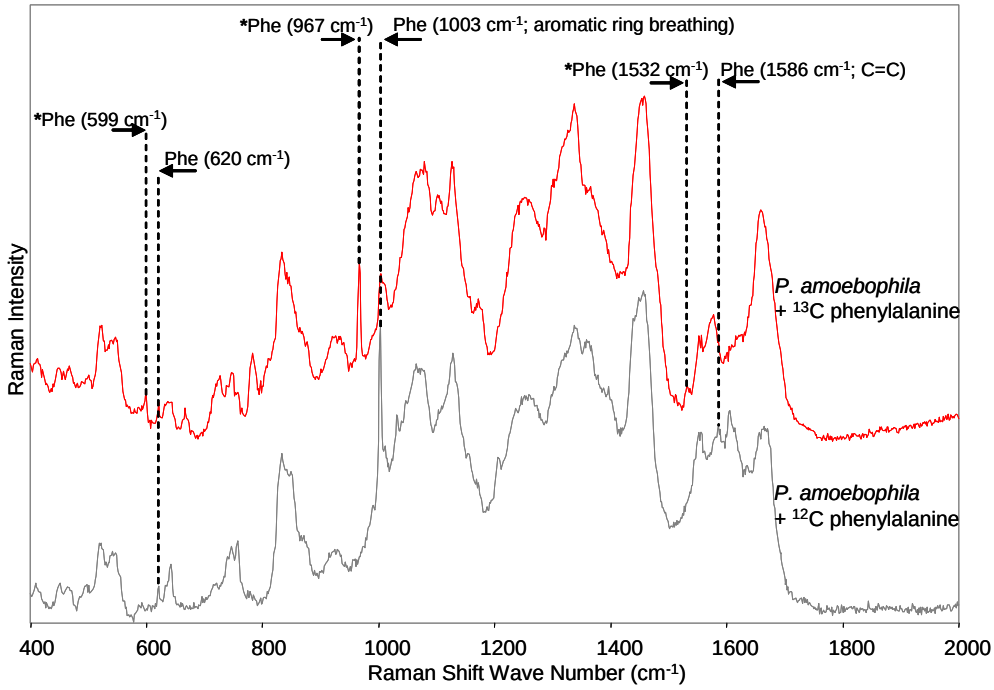

Figure 2. Peak shifts induced by labelled phenylalanine in the Raman spectrum of *P. amoebophila*. Mean Raman spectra of *P. amoebophila* after incubation of the amoebal host in medium for 264h with unlabelled (lower spectrum) and labelled phenylalanine (upper spectrum), respectively. For each analysis 12 spectra were merged. Phenylalanine peaks are indicated. It should be noted that the peak at 1003 cm^{-1} does not completely disappear in fully labelled symbiont cells because labelled phenylalanine also has a minor peak at this wave number (Figure S2).

Already after 24h of incubation, the spectra of 50% of the *P. amoebophila* cells demonstrated phenylalanine uptake, while no peak shift was observed in the spectra of all cells in the corresponding control experiment with unlabelled phenylalanine in the medium (Figure 3). With longer incubation times in the medium supplemented with ^{13}C-phenylalanine, the number of labelled cells increased, and after 120h all chlamydial cells were labelled. Interestingly, in some cells the ^{12}C-phenylalanine peak almost disappeared compared to spectra from unlabelled cells of the control experiment, unambiguously demonstrating that the observed peak shift was due to incorporation of the labelled amino acid into the biomass of the symbionts (Figure S3). Unexpectedly, phenylalanine uptake was not only observed for cells which were identified as RBs by their Raman spectra, but was also measured for cells which had EB spectra (Figure 3). Generally, more EBs than RBs were detected within the released cells. This finding is consistent with corresponding transmission electron

microscopy analyses which showed that the experimental lysis step did not only destroy the host cells but also lysed some RBs, therefore increasing the relative abundance of EBs in the lysate. In detail, 46% RBs, 31% IBs and 23% EBs were detected by transmission electron microscopy within the amoebal host cell (data not shown), while 20% RBs, 23% IBs and 57% EBs were counted after host cell lysis (Figure S4).

In addition to *P. amoebophila*, we also investigated two other bacterial symbionts of acanthamoebae, '*Candidatus* Amoebophilus asiaticus 5a2' (*Bacteroidetes*; (Horn *et al.*, 2001; Schmitz-Esser *et al.*, 2008)), and the rickettsial symbiont UWC36 (*Alphaproteobacteria*; (Fritsche *et al.*, 1999)), which are only distantly related to the *Chlamydiae*. Interestingly, uptake of labelled phenylalanine was also observed for both symbionts within 96h (Figure 3).

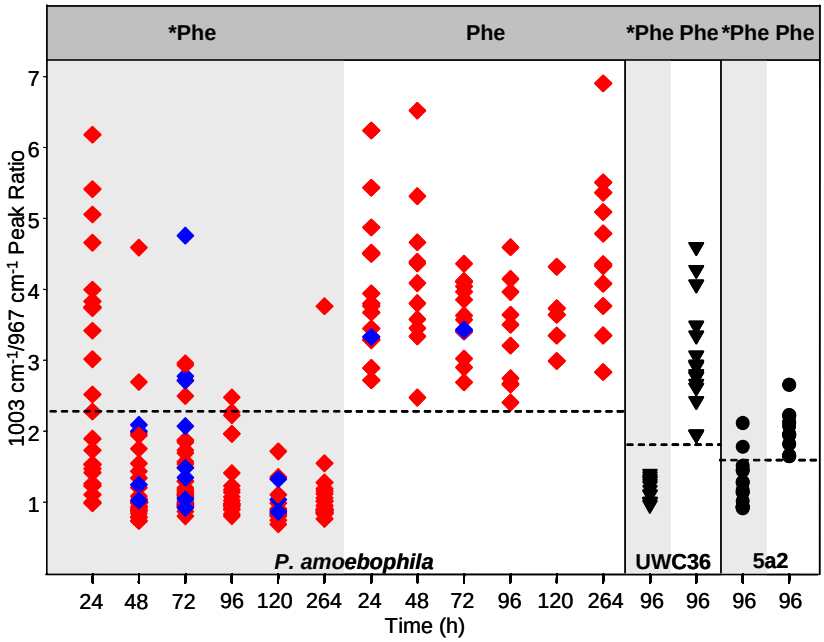

Figure 3. Phenylalanine uptake by intracellular *P. amoebophila* and other amoebal endosymbionts. Endosymbionts were incubated inside their host cells in medium containing labelled phenylalanine (*Phe). In parallel, control experiments with medium containing unlabelled phenylalanine were performed (Phe). The ratio of the 1003 cm^{-1} peak intensity (representing unlabelled phenylalanine) to the 967 cm^{-1} peak intensity (representing labelled phenylalanine) is indicated for individual cells. The lower the ratio the higher the labelling of the cells. Red diamonds represent EBs and blue diamonds RBs. Empty circles represent the obligate *Rickettsia*-like endosymbiont UWC36, and filled circles the amoeba endosymbiont '*Candidatus* Amoebophilus strain 5a2'. The dashed line represents the threshold below which no values were observed for cells of the respective endosymbiont in the control

experiment. The difference between ratios of labelled (n = 147) and unlabelled (n = 67) cells is highly significant (Mann-Whitney-U test, Mann-Whitney-U = 644, asymptotic 2-tailed significance $p < 0.001$).

Host-free uptake of phenylalanine

The observed intracellular activity of *P. amoebophila* EBs was surprising and prompted us to also investigate the metabolic activity of *P. amoebophila* outside of its host. Chlamydial cells were released by lysis of the amoeba host cells, and the absence of intact amoebae in the lysate was confirmed by light microscopy. Subsequently, the host-free chlamydial cells were incubated in defined medium containing unlabelled phenylalanine. Live/dead staining of the released bacteria showed that immediately after host cell lysis 89% (SD±5.7) of the chlamydiae were alive, and this number decreased to 15% (SD±16.8) after 15 days of extracellular incubation. After incubation periods from 24h to 21 days the medium was replaced by a medium containing ^{13}C9-^{15}N-phenylalanine and after another 24h of incubation, phenylalanine uptake was measured by Raman microspectroscopy. Interestingly, in all experiments the host-free chlamydial cells became labelled and the percentage of labelled cells after 24h of incubation with the labelled amino acid was always much higher than in the intracellular uptake experiments. Unexpectedly, even after host-free incubation for 21 days, living *P. amoebophila* cells were still able to take up phenylalanine (Figure 4) while cells which were dead according to the live/dead assay gave no analyzable Raman spectra (data not shown). Surprisingly, almost all of the active cells were EBs according to their Raman spectra.

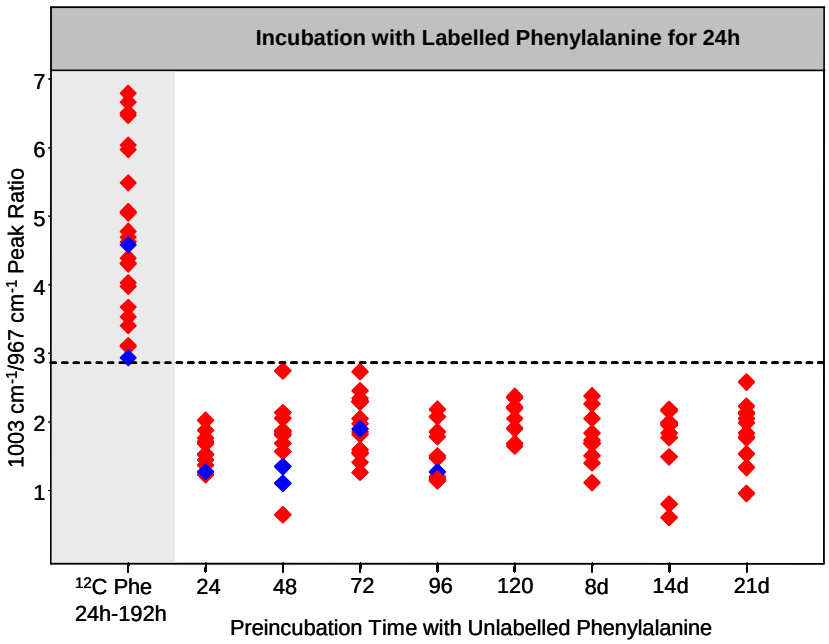

Figure 4. Phenylalanine uptake by host-free *P. amoebophila.* After lysis of amoeba host cells, chlamydial cells were incubated extracellularly for the indicated time periods in medium containing unlabelled phenylalanine. Subsequently, the medium was removed and medium with labelled phenylalanine was added for 24h before Raman spectra were recorded. In parallel, control experiments with medium containing unlabelled phenylalanine were performed (Phe). The ratio of the 1003 cm^{-1} peak intensity (representing unlabelled phenylalanine) to the 967 cm^{-1} peak intensity (representing labelled phenylalanine) is indicated for individual cells. The lower the ratio the higher the labelling of the cells. Red diamonds represent EBs and blue diamonds RBs. The dashed line represents the threshold below which no values were observed for cells in the control experiment. The difference between ratios of labelled (n=94) and unlabelled (n=21) cells is highly significant (Mann-Whitney-U test, Mann-Whitney-U = 0, asymptotic 2-tailed significance $p < 0.001$).

Destruction of H^+ and Na^+ concentration gradients across the membrane of *P. amoebophila* by addition of 10 µM of the ionophore carbonylcyanide m-chlorophenylhydrazone (CCCP) blocked the uptake of the labelled amino acid in almost all cells. Interestingly, this effect was reversible. Cells, which were treated with CCCP and subsequently washed to remove the ionophore, regained the capability to take up labelled phenylalanine demonstrating their ability to re-energize their membrane outside of their host (Figure 5).

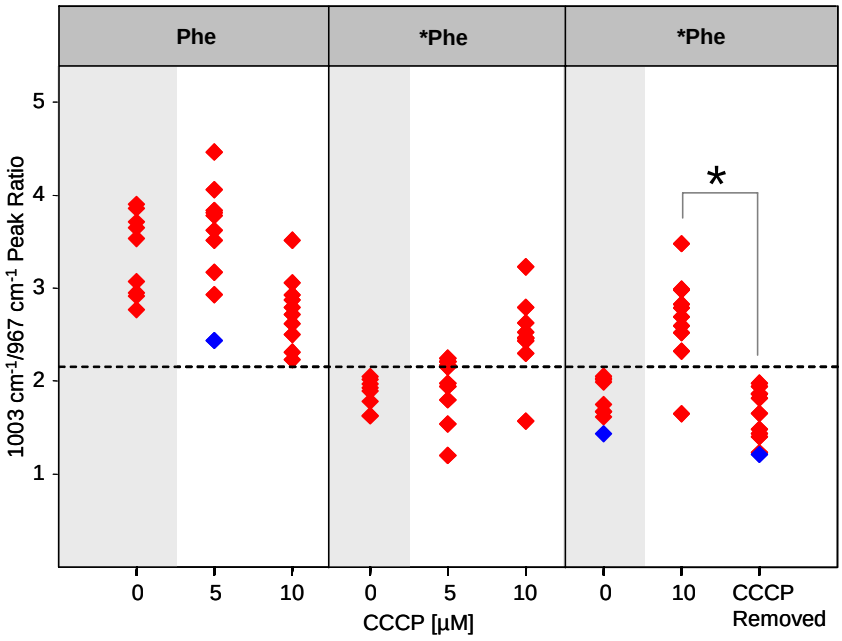

Figure 5. Extracellular phenylalanine uptake by *P. amoebophila* is reversibly inhibited by the inonophore CCCP. Left panel, after amoebal cell lysis, chlamydial cells were incubated extracellularly for 24h in medium with unlabelled phenylalanine in the absence or

presence (5 µM, 10 µM) of CCCP. Middle panel, the same experiment was performed with medium containing labelled phenylalanine. Right Panel, after amoebal cell lysis, the chlamydial cells were incubated for 24h without or with 10 µM CCCP with medium containing labelled phenylalanine. An aliquot of those cells which were exposed to CCCP for 24h were washed to remove the CCCP and were subsequently incubated again with medium containing labelled phenylalanine for 24h. For all experiments the ratio of the 1003 cm^{-1} peak intensity (representing unlabelled phenylalanine) to the 967 cm^{-1} peak intensity (representing labelled phenylalanine) is indicated for individual cells. The lower the ratio the higher the labelling of the cells. Red diamonds represent EBs and blue diamonds RBs. The dashed line represents the threshold below which no values were observed for cells in the control experiment. The difference between ratios of CCCP-inhibited samples (n=10) and samples where CCCP was removed (n=11) is highly significant (labelled by an asterisk; Mann-Whitney-U test, Mann-Whitney-U = 5.5, asymptotic 2-tailed significance $p < 0.001$).

To investigate whether extracellular *P. amoebophila* cells are still infectious after prolonged incubation periods, we performed co-incubation experiments with symbiont-free amoeba host cells. Extracellular *P. amoebophila* remained infective for amoebae over the complete experimental period of 21 days.

DISCUSSION

A detailed understanding of the biology of members of the phylum *Chlamydiae* requires methods which allow researchers to assign specific traits to RBs and EBs, representing the different life stages of these bacteria. Traditionally, RBs and EBs are differentiated by transmission electron microscopy based on their morphological differences like the presence of condensed chromatin in EBs (Barry *et al.*, 1992; Rake, 1957). RBs and EBs can be physically separated by density gradient centrifugation (Howard *et al.*, 1974; Knudsen *et al.*, 1999), but it should be noticed that this separation is not perfect (Caldwell *et al.*, 1981; Yong, 1979) and that intermediate forms exist. Using cell fractions from *P. amoebophila* prepared by this approach we showed that RBs and EBs of this organism can also be reliably identified by analyzing their chemical composition with Raman microspectroscopy (Figure S1). The numbers of RBs and EBs determined in the two fractions were comparable but not identical between Raman and transmission electron microscopic analyses. The differences most likely reflect that intermediate stages between both developmental forms exist (Chi *et al.*, 1987; Friis, 1972; Kahane *et al.*, 2002; Ward, 1988), and that some of these IBs have a chemical composition more similar to RBs while others resemble more EBs. RB and EB Raman spectra possessed several conspicuous differences which were statistically

significant. In detail, RB spectra contained three peaks (at 746, 1585, and 1126cm^{-1}) of which the former two are absent and the latter is much less pronounced in EB spectra (Figure 1). These peaks resemble three of the four peaks known to represent cytochrome *c* (Pätzold R., 2008), but apparently do not originate from this compound as the fourth peak at 1311 cm^{-1}, described for cytochrome *c*, does not vary significantly between RB and EB spectra. We did not find any unambiguous correlation between the three peaks and reported spectra of other biological molecules, but noticed that the peaks might represent nucleobases (De Gelder *et al.*, 2007) and thus might reflect a higher DNA/RNA content in RBs. This is further supported by the observation of an increased RNA content in RBs compared to EBs, when *P. amoebophila* cell fractions were stained with the nucleic acid dye acridine orange (Figure S5).

Raman microspectroscopy analysis was subsequently used to test whether *P. amoebophila* takes up phenylalanine from its amoeba host during intracellular growth in an unsynchronized culture containing RBs, EBs, and intermediate stages. Phenylalanine was selected as model substrate, because according to the annotation of the *P. amoebophila* genome the biosynthesis pathway for this amino acid is incomplete and the organism uses a proton/sodium neutral amino acid symporter for uptake of this essential amino acid from the host (Horn *et al.*, 2004; Horn *et al.*, 2006). However, as 62% of the genes of *P. amoebophila* lack homology to genes with recognized function in public data bases, *in silico* genome analysis is insufficient to prove absence of a certain pathway and the inferred host-symbiont interaction. We investigated this interaction, by combining EB and RB differentiation by Raman microspectroscopy with the recently documented capability of this technique to detect labelling of individual microbial cells with ^{13}C-tagged compounds (Huang & Gogarten, 2007; Huang *et al.*, 2004). Phenylalanine is ideally suited for such analysis as its Raman peak at 1003 cm^{-1}, which is caused by the symmetric aromatic ring breathing mode (Wei *et al.*, 2008), is easily detectable in EB and RB spectra of *P. amoebophila* and shows a pronounced shift to 967 cm^{-1} if the aromatic ring is fully ^{13}C-labelled (Figure 2). Furthermore, the *Acanthamoeba* host strain is auxotrophic for phenylalanine and thus cannot dilute the isotope signal of the amino acid (Adam, 1964; Anderson *et al.*, 2005). Raman microspectroscopy demonstrated a time-dependent uptake of ^{13}C9-^{15}N-phenylalanine by intracellular *P. amoebophila*. Interestingly, the Raman spectra of labelled *P. amoebophila* cells showed characteristics of RBs and EBs, respectively, and 120h after the addition, labelled phenylalanine could be detected in virtually all chlamydial cells (Figure 3). This finding was unexpected as not only RBs, the replicative forms of the symbionts, but also the proposed spore-like and physiologically inert EBs (Abdelrahman & Belland, 2005; Hatch,

1999) were metabolically active within the host cell and took up phenylalanine from the amoeba host.

The capability to import phenylalanine from the amoeba host is not restricted to symbiotic chlamydiae but seems to be widespread among obligate intracellular bacteria thriving in these free-living protozoa. Using the Raman microspectroscopy approach, we demonstrated this metabolic interaction also for the alphaproteobacterial *Rickettsia*-like symbiont UWC36 and '*Candidatus* Amoebophilus asiaticus 5a2' (a member of the *Bacteroidetes*) when living in *Acanthamoeba castellanii* Neff (Figure 3). It is tempting to speculate, that acanthamoebae as predators of bacteria and small eukaryotes (Rodriguez-Zaragoza, 1994), are generally well supplied with amino acids. The availability of these compounds in their host cells might have made *de novo* synthesis dispensable, and the respective biosynthetic pathways were thus lost from the genomes of these amoeba symbionts during genome streamlining and reduction. Particularly, the outsourcing of biosynthesis of aromatic amino acids including phenylalanine provides a selective advantage for the symbionts, as these amino acids are metabolically very costly to synthesize (Akashi & Gojobori, 2002). Consistent with this consideration, phenylalanine is also an important metabolic exchange product between other symbiotic partners like *Ignicoccus hospitalis* and *Nanoarchaeum equitans* (Jahn *et al.*, 2008) and the bacterial symbionts of various aphids and ants (Baumann *et al.*, 1995; Moran & Degnan, 2006; Zientz *et al.*, 2004).

The surprising activity of *P. amoebophila* EBs was not limited to the intracellular environment. Indeed, both extracellular RBs and extracellular EBs took up phenylalanine in a host-free medium, and this activity was observed for EBs even after 21 days of host-free incubation (Figure 4). Already after an incubation period of 24h with labelled phenylalanine all extracellular *P. amoebophila* cells were labelled, while complete labelling of the *P. amoebophila* population took 120h in the intracellular labelling experiment, reflecting that host-free cells have more direct access to the added amino acid and that the intracellular symbionts compete with the host for incorporation of the added amino acid. Inferred from the 1003 cm^{-1} to 967 cm^{-1} phenylalanine peak ratios, the amount of maximally incorporated labelled phenylalanine in intracellular and host-free cells was comparable even if the intracellular bacteria were exposed for as long as 11 days to the labelled amino acid (Figures 3 and 4). This finding shows that host-free *P. amoebophila* cells can incorporate within 24h (the incubation time with labelled phenylalanine used for all host-free experiments) significant amounts of phenylalanine. Furthermore, extracellular RBs and EBs were capable to re-energize their membrane after destruction of the H^+ and Na^+-gradient by transient exposure to the ionophore CCCP (Figure 5), demonstrating respiratory activity and/or H^+/Na^+ translocation via the F and/or V-type ATPase of *P. amoebophila*. These findings contradict

the dogma that chlamydial EBs are metabolically inactive outside of their host cells. This dogma is based on studies with host-free EBs of *C. trachomatis* and *C. psittaci* which showed that these cells were unable to incorporate radioactively labelled amino acids into protein (Hatch *et al.*, 1985). Furthermore, host free EBs of *C. psittaci* also did not take up ATP although this organism is an intracellular ATP parasite (Hatch *et al.*, 1982). Only after addition of 2-mercaptoethanol or dithiothreitol to host-free EBs of *C. trachomatis* in order to increase cell wall permeability, these cells could take up and incorporate UTP into their RNA and oxidatively decarboxylate externally added glutamate (Hackstadt *et al.*, 1985; Sarov & Becker, 1971), but not all of these findings could be reproduced by others (Hatch, 1988). In contrast, host-free RBs of clinically relevant chlamydiae show a wider spectrum of metabolic activities including lysine uptake, but to the best of our knowledge such activities have only been reported for RBs, which were exposed to extracellular conditions for no longer than 2-4 hours (Crenshaw *et al.*, 1990; Hatch *et al.*, 1982; Hatch *et al.*, 1985; Tamura, 1967; Weiss & Wilson, 1969).

The long-term extracellular metabolic activity of *P. amoebophila* EBs might reflect that these cell types possess a more permeable cell wall than EBs of clinically relevant chlamydiae, facilitating uptake of exogenous compounds. This speculation is in line with the absence of the chlamydial major outer membrane protein (MOMP) in *P. amoebophila* (Horn *et al.*, 2004) as MOMP is contributing to the rigidity of the EB cell wall through extensive disulfide cross-linking (Bavoil *et al.*, 1984). Additional major differences in the outer membrane composition of *P. amoebophila* and clinical chlamydiae were revealed by bioinformatic and proteomic analyses (Heinz, unpublished data). More generally, genome analysis of *P. amoebophila* has revealed that this organism is a living chlamydial fossil which maintained in its relatively large genome many features of the last chlamydial ancestor which were lost by genome reduction in the clinical chlamydiae (Horn *et al.*, 2004; Horn, 2008). Although *P. amoebophila* is dependent on uptake of nucleotides and NAD^+ from its host (Haferkamp *et al.*, 2004; Haferkamp *et al.*, 2006; Schmitz-Esser *et al.*, 2004; Trentmann *et al.*, 2007), other metabolic pathways like glycolysis and the oxidative pentose phosphate pathway are complete. In addition, *P. amoebophila* can synthesize more amino acids than clinical chlamydiae and uses a more complex respiratory chain which was postulated to generate a proton motive force more efficiently than in other *Chlamydiaceae* (Horn *et al.*, 2006). According to genome annotation, *P. amoebophila* can also synthesize glycogen and starch as storage products. Taken together, these features might enable *P. amoebophila* to maintain metabolically active over extended time periods outside of its host. It is tempting to speculate that the extracellular activity of *P. amoebophila* is contributing to the observed long-term survival and infectivity of the EBs of this organism after the release from the host cell and thus to its

ecological success in ecosystems with a relatively low abundance of suitable host organisms. This is consistent with reported enhanced resilience of chlamydiae which are transmitted environmentally, such as *Simkania negevensis* or the koala biovar of *Chlamydophila pneumoniae* (Kahane *et al.*, 2004; Rush & Timms, 1996), compared to *Chlamydia trachomatis*, which is spread by human-to-human transmission. From another perspective, the apparent partial autonomy of *P. amoebophila* from its host makes it a promising candidate organism for future host-free cultivation attempts and for the development of genetic manipulation systems for chlamydiae.

More generally, the findings reported in this study show that Raman microspectroscopy in combination with stable isotope labelling allows direct analysis of defined activities of obligate intracellular bacteria within their hosts. In comparison to the recently introduced NanoSIMS technology which is also suited to detect and quantify stable isotopes in bacterial symbionts on a single cell level with high sensitivity (Lechene *et al.*, 2007), the Raman microspectrometer is ten times cheaper, non-destructive (analyzed cells are available for downstream analysis) and enables microbiologists to assign the measured label to defined compound classes or as in the case of phenylalanine even to a specific compound.

MATERIAL AND METHODS

Separation of *P. amoebophila* RBs and EBs

Acanthamoeba sp. UWC1 harboring *P. amoebophila* was grown in trypticase soy broth with yeast extract (TSY; 30 g/l trypticase soy broth, 10 g/l yeast extract) (Visvesvara, 1999) at 20°C in culture flasks. Amoebae were harvested by centrifugation (3,214g, 10 min, 4°C), washed once in 1 x Page´s saline (Page, 1988), resuspended in 6.5 ml sucrose phosphate glutamic acid buffer (SPG; 750 g/l sucrose, 5.2 g/l KH_2PO_4, 23 g/l $NaHPO_4*7H_2O$, 7.5 g glutamic acid) per 1 g wet weight, and disrupted on ice by a dounce homogenizer (Wheaton). Released endosymbionts were harvested from the supernatant by centrifugation (5,500g, 20 min, 4°C), resuspended in 6 ml SPG, filtered (1.2 µm pore size), and 1 ml of the suspension was laid onto 6.5 ml 30% (v/v) Gastrografin (Schering). After ultracentrifugation (Optima^{TM} L-100 XP; Beckman Coulter, Inc) (40,000g, 1h, 4°C) pellets were resuspended in SPG and the suspension was homogenized by extruding it through needles (0.45 x 25 mm and 0.90 x 40 mm, respectively, Braun). 1 ml sample was laid onto a gradient consisting of 3 ml 30% (v/v) Gastrografin and 3 ml 50% (w/v) sucrose, and centrifuged (40,000g, 2h, 4°C). The pellet was resuspended in 0.75 ml SPG, supplemented with 32.5 µl DNase I (20 mg ml^{-1}), 32.5 µl RNase (20 mg ml^{-1}; both from Roche Diagnostics GmbH), and 37.5 µl $MgCl_2$ (1 M), and incubated for 1h at 37°C. The suspension was homogenized using needles as described above. Gradients consisting of 1.5 ml 34% (v/v), 2 ml 40% (v/v), 2 ml 46% (v/v), and 2.5 ml 52% (v/v) Gastrografin were built up and were overlaid with 1 ml sample. After centrifugation (40,000g, 2h, 4°C), bands that appeared at the 34/40% and 46/52% interfaces, corresponding to the RB- and EB-enriched fractions, respectively, were collected. Finally the collected fractions were diluted in SPG and centrifuged (40,000g, 1h, 4°C) to remove residual Gastrografin. Pellets were resuspended in 100-500 µl SPG. Aliquots were taken for Raman measurements and fixed immediately for TEM analyses.

Intracellular phenylalanine uptake experiments

P. amoebophila, the rickettsial endosymbiont of *Acanthamoeba* sp. UWC36 (Fritsche *et al.*, 1999) and '*Cand.* Amoebophilus asiaticus 5a2' (Horn *et al.*, 2001; Schmitz-Esser *et al.*, 2008) were grown in continuous culture with *Acanthamoeba castellanii* Neff as host cells. The cultures were grown in defined medium DGM-21A for *Acanthamoeba* spp. (Schuster, 2002) supplemented with unlabelled or $^{13}C9$-^{15}N-phenylalanine (Sigma) (11mM final concentration) at 20°C. At different time points cells were harvested by centrifugation (5,400g, 5 min) and resuspended in 500 µl 1 x Page´s saline. Amoebal cells were disrupted by freezing (-20°C) and thawing (room temperature). An equal volume of glass beads was added to the suspension which was subsequently vortexed for 15 sec. Then, the supernatant was

centrifuged (300g, 10 min, 20°C) to remove amoebal cell debris, and afterwards the supernatant was centrifuged to harvest the released chlamydial cells (20,800g, 15 min). The pellet was resuspended in 100 µl SPG and harvested again by centrifugation before it was finally resuspended in 20 µl SPG. For subsequent Raman microspectroscopy measurements, 2 µl of the chlamydial cell suspension was transferred to a CaF_2 slide (Crystran Ltd) and dried at RT. Spectra were collected immediately after sample preparation to avoid sample degradation.

Host-free phenylalanine uptake experiments

P. amoebophila was grown in *Acanthamoeba castellanii* Neff in peptone-yeast-glucose-medium (PYG; 20 g/l proteose peptone, 18 g/l glucose, 2 g/l yeast extract, 1 g/l sodium citrate-dihydrate, 980 mg/l $MgSO_4$*7 H_2O, 355 mg/l Na_2HPO_4*7 H_2O, 340 mg/l KH_2PO_4, 20 mg/l $Fe(NH_4)_2(SO_4)_2$* $6H_2O$) (Visvesvara, 1999) at 20°C. Cells were harvested by centrifugation (5,400g, 5 min) and resuspended in 1 x Page´s saline. Amoebal cells were disrupted and chlamydial cells were harvested as described for the intracellular uptake experiments. Chlamydial cells were then resuspended in 20 µl defined medium DGM-21A supplemented with unlabelled or $^{13}C9$-^{15}N-phenylalanine (11 mM final concentration) and were incubated for different time periods at 20°C. For Raman measurements 2 µl of the chlamydial cell suspension was transferred to a CaF_2 slide, dried at RT, and immediately analyzed.

For some samples the ionophor carbonylcyanide m-chlorophenylhydrazone (CCCP; Sigma) was added at a concentration of 5 or 10 µM during the incubation. In the next step, these samples were split in two, and one aliquot was analyzed by Raman microspectroscopy while the other was washed with 1 x Page´s saline and then incubated again with $^{13}C9$-^{15}N-phenylalanine.

Live/dead staining

At different time points after host-free incubation 2 µl of the chlamydial cell suspension were incubated for 1h at RT with 1 µg ml^{-1} 4', 6-diamidino-2-phenylindole (DAPI; Lactan) and 10 µg ml^{-1} propidium iodid (PI; Molecular Probes). Subsequently, 10 ml phosphate-buffered saline (PBS; NaCl 130 mM, Na_2PO_4 10mM; pH 7.2 - 7.4) was added, the suspension was filtered onto a 0.2 µm filter (Millipore) and live (DAPI stained) as well as dead (PI stained) cells were counted by epifluorescence microscopy. For some experiments an aliquot of the stained cells was dried onto CaF_2-slides and Raman spectra were recorded for live and dead cells after bleaching of the fluorescent dye using the protocol of Huang *et al.* 2007.

Confocal Raman microspectroscopy

Raman microspectroscopy was performed using a LabRAM HR800 confocal Raman microscope (Horiba Jobin-Yvon). Excitation for Raman scattering was provided by a 532-nm Nd:YAG Laser. For Raman spectral analysis of a chosen cell, the incident laser power was typically adjusted to 7 mW, to avoid damaging of the sample while still maintaining spectral sensitivity. The pinhole of the Peltier cooled CCD detector was set to 250 µm enabling a spatial resolution of approximately 2.5 µm.

Single cells were selected randomly using a 100x objective. Spectra were obtained from 8-40 cells per measurement. The signal acquisition time was 40-60s per measurement with a spectral resolution of 1.5 cm^{-1}. Initially, spectra were acquired from 381 to 2030 wave numbers (cm^{-1}). Visual inspection of these spectra showed that the most informative range was between 400 and 1800 cm^{-1}, and this was used for data analysis. Raman spectra were processed for baseline correction and normalization using the commercial Labspec software 5.25.15 (Jobin-Yvon). These data were exported to Microsoft Excel for further peak determinations and calculations. Calibration was periodically checked by recording the position of a known Raman line using a silicon Raman reference (520 cm^{-1}). The wave number accuracy was estimated to be ± 3 cm^{-1}.

Principal components analysis (PCA) was employed to reduce the dimensionality of the Raman data. Since homogeneity of variance was not given, the non-parametric Mann-Whitney-U test was performed to test for the significance of between group differences. All statistical analyses were performed using SPSS version 14.0 (SPSS Inc., Chicago, IL).

Transmission electron microscopy

Transmission electron microscopy was used as established method for distinguishing RBs and EBs of *P. amoebophila* in the intracellular and host-free uptake experiments and for assessing their relative proportions in density-gradient purified fractions. Density gradient purified cells were pelleted by centrifugation at 11,000g for 30 min and resuspended in fixative solution (2.5% glutaraldehyde in 3mM cacodylate-3mM sucrose buffer, pH 7.3 (Lindsay *et al.*, 1995)) and fixed overnight at 4°C. After washing in 0.1 M cacodylate buffer, fixed cells were encapsulated into 12% gelatine in 0.1 M cacodylate buffer. Post-fixation in 0.5% osmium tetroxide for 2h was followed by en-bloc staining with 2% aqueous uranyl acetate for 1h and a dehydration step in a graded ethanol series. Acetone incubation was used as an intermediate step before infiltration with low viscosity resin (Agar Scientific) overnight. The next day, cells were embedded in fresh resin and polymerised at 60°C for 12h. Ultra-thin sections were cut with a ultramicrotome, contrasted with uranyl acetate and lead citrate, and examined in the transmission electron microscope (Zeiss 902) at 80 kV accelerating voltage. Digital images were captured using an IK CCD camera (Sharpeye,

TRS). To assess the relative proportion of the different developmental stages of *P. amoebophila*, 20 to 40 randomly collected images at 7,000x magnification were recorded for each sample. The developmental stages were distinguished by chromatin morphology and staining intensity (Barry *et al.*, 1992; Rake, 1957). RBs stain less densely than EBs and RBs have a very open and even chromatin pattern without evidence for condensation while EBs possess condensed chromatin often contracting to one side of the cell wall. Relative numbers of RBs and EBs were determined by manual counting.

For the quantification of the proportion of RBs and EBs in the phenylalanine uptake experiments, amoebal cells infected with *P. amoebophila* were split into two fractions. One fraction was harvested by centrifugation (5,400g, 5 min) and fixed immediately in fixative solution (3 mM cacodylate buffer, 2.5% glutaraldehyde, 2% sucrose, pH 7.2) for 1h at RT. In the second fraction, the amoebal cells were lysed as described for the uptake experiments and the released cells were incubated in fixative solution. After another centrifugation step (amoebal cells at 5,400g for 3 min; host-free cells at 20,800g for 5 min) cells were washed in 0.1 M cacodylate buffer and fixed in 1% osmium tetroxide for 1h. After dehydration in a graded ethanol series, the samples were transferred to acetone followed by acetonitrile incubation. Subsequently, the cells were infiltrated in 1 volume of low viscosity resin and 1 volume acetonitrile overnight. The next day, cells were embedded in resin and ultra-thin sections were produced as described above.

Infection experiments

After different periods of host-free incubation, *P. amoebophila* was added to uninfected *A. castellanii* grown in multiwell plates (Iwaki) and centrifuged with 130g for 15 min at 20°C. The cells were left at 20°C for 48h and infection was visualized after DAPI staining by epifluorescence microscopy.

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Supporting Information

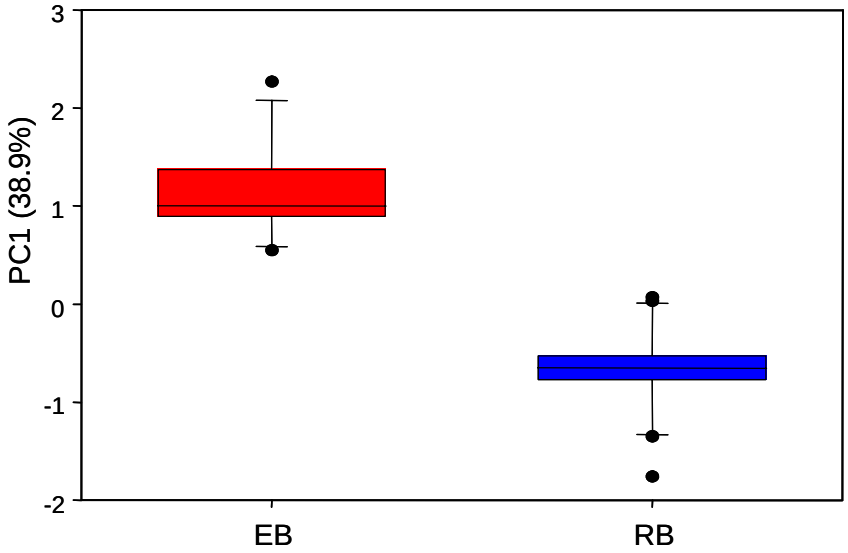

Figure S1. Box plot of principal component 1 (PC1) values which explained 38.9% of the total variance (RBs in blue and EBs in red). Differences between EBs (n = 12) and RBs (n = 20) proofed to be highly significant (Mann-Whitney-U test, Mann-Whitney-U = 0, asymptotic 2-tailed significance $p < 0.001$).

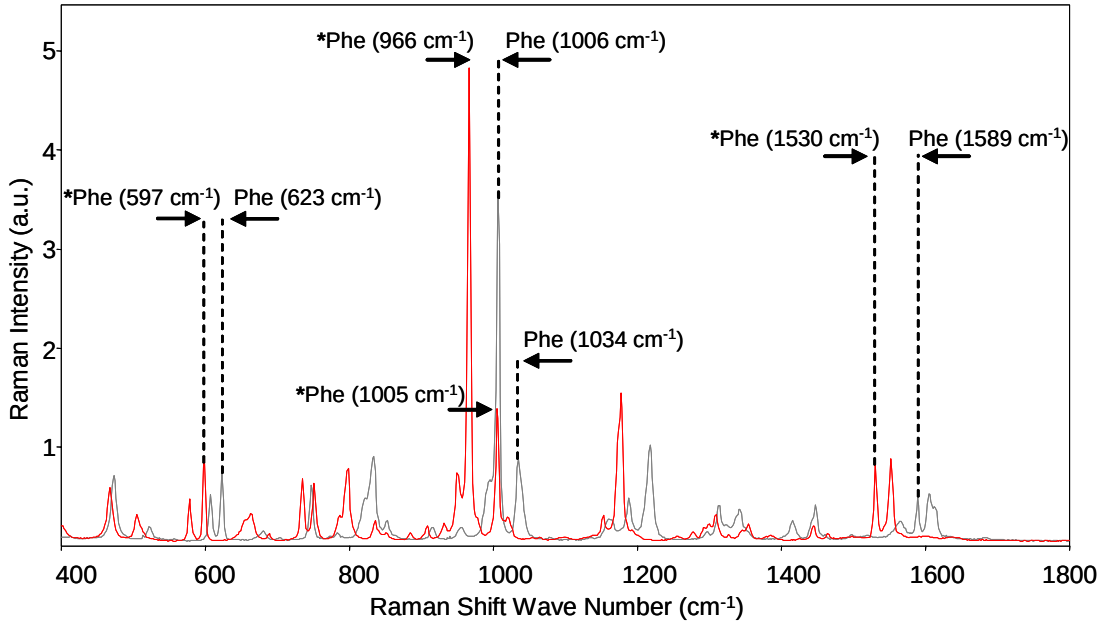

Figure S2. Comparison of Raman spectra obtained from unlabelled (lower spectrum) and labelled phenylalanine (upper spectrum), respectively. For each analysis five spectra were merged. Phenylalanine peak shifts also observed in biomass from *P. amoebophila* (Figure 2) are indicated.

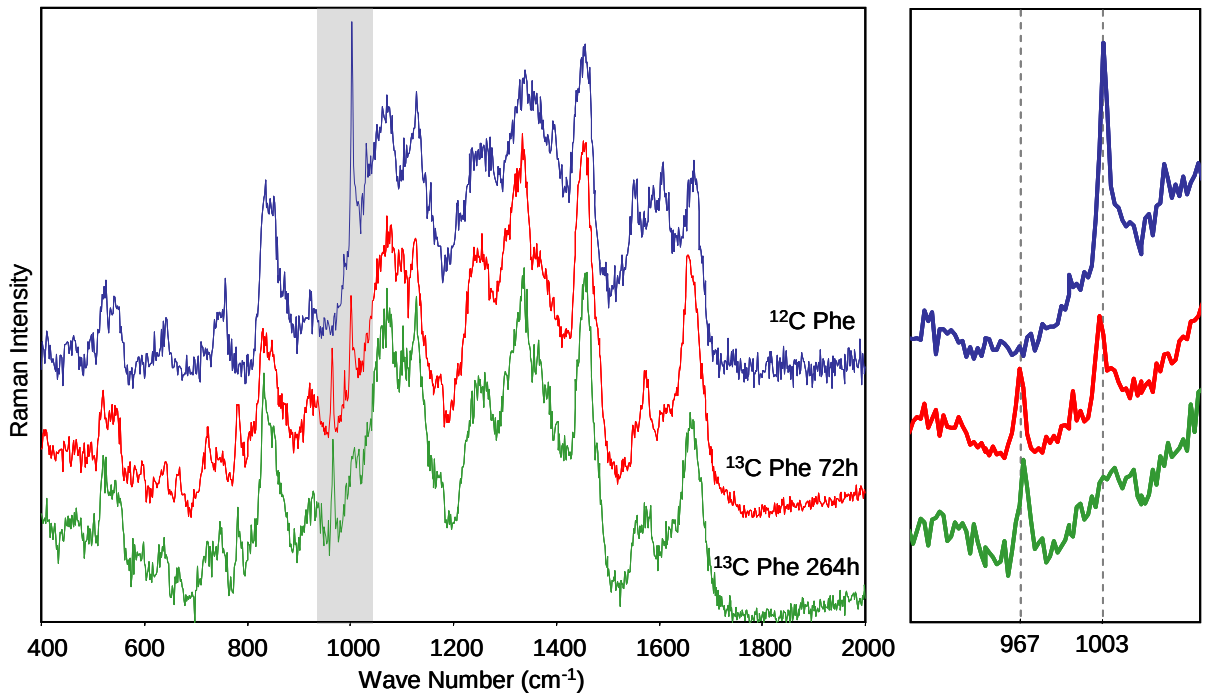

Figure S3. Comparison of three EB Raman spectra of labelled and unlabelled *P. amoebophila* cells. Spectra of EBs obtained from amoebae grown with unlabelled (blue) or labelled phenylalanine for 72h (red) or 264h (green) were recorded (left panel). The segment of the spectra shaded in grey contains the major peaks of unlabelled (1003 cm^{-1}) and labelled phenylalanine (967 cm^{-1}) and is magnified in the right panel.

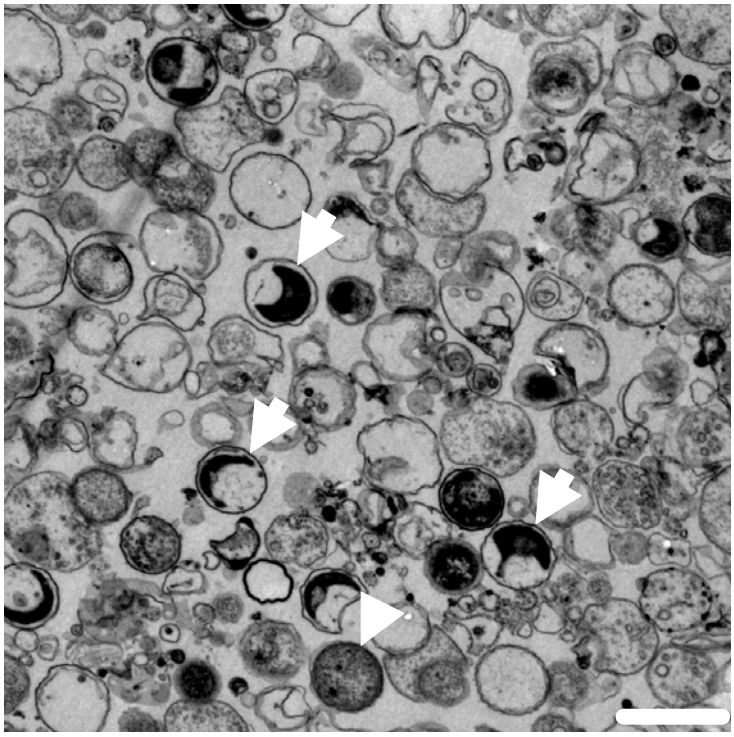

Figure S4. *P. amoebophila* immediately after mechanical host cell lysis. The relative abundance of EBs is significantly higher after host cell lysis, showing that the lysis step also destroys some RBs. White arrows point to EBs, the white arrowhead to a RB. Bar corresponds to 1 µm.

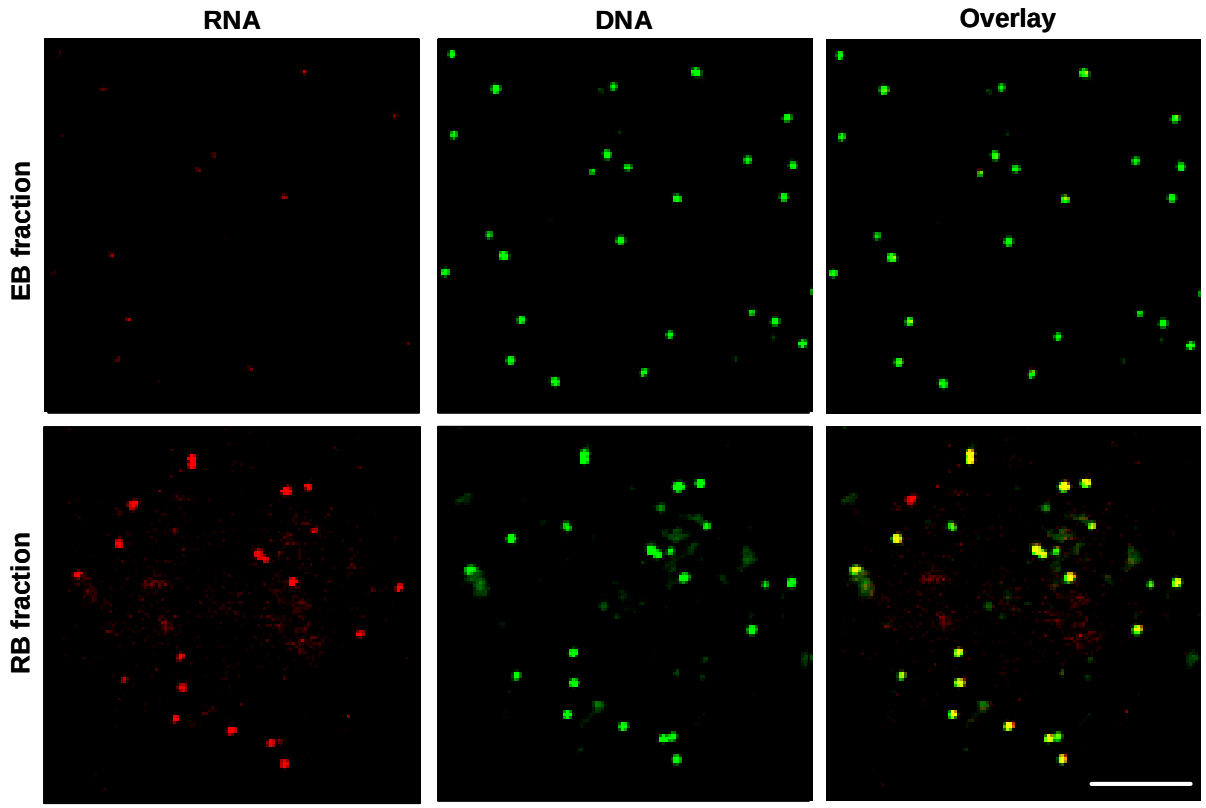

Figure S5. Differences in RNA content between *P. amoebophila* EBs and RBs. Acridine orange staining (1 mg l^{-1} for 5 min) of purified fractions of *P. amoebophila* EBs (upper panel) and RBs (lower panel). Intercalation of acridine orange with DNA leads to green fluorescence (525 nm), while RNA fluoresces red (650 nm). Identical microscopic fields are shown for each fraction. The yellow staining of RBs in the overlay images is indicative for a higher RNA content compared to EBs. Bar corresponds to 10 µm.

Chapter VII

Summary

Summary

Free-living amoebae of the genus *Acanthamoeba* are ubiquitous in nature and feed on various microorganisms including bacteria. However, a remarkably high number of bacteria can not only resist digestion by the amoebae, but proliferate within the amoebae and establish a stable symbiotic interaction with no obvious disadvantages for the host. In the framework of this study bacterial symbionts of several environmental *Acanthamoeba* strains isolated from different geographical locations were characterized. Phylogenetic analysis of the symbionts revealed their affiliation with four previously recognized evolutionary lineages of amoebal symbionts and confirmed that stable host-symbiont interactions have evolved only a few times during evolution. One of these phylogenetic lineages of amoebal symbionts comprises members of the *Chlamydiae* which were the main focus of this study. Interestingly, these *Chlamydia*-like bacteria are closely related to pathogenic chlamydiae, which include two of the most successful human and animal pathogens (*Chlamydia trachomatis* is responsible for trachoma and is a frequent cause of sexually transmitted genital infections as well as *Chlamydophila pneumoniae* which is the causative agent of pneumonia). This relationship raises the question whether these recently identified chlamydial symbionts can also cause disease in higher animals or humans. Consequently, a highly sensitive PCR-based screening of samples from patients with community-acquired pneumonia (CAP) was performed and DNA from three different *Chlamydia*-like bacteria was detected in some of the samples. However, whether these bacteria, which were detected for the first time in human respiratory specimens, were in fact agents of CAP has to be clarified in further studies.

Three additional studies were performed in the framework of this thesis in order to better understand the biology of the amoebal symbiont *P. amoebophila*. *P. amoebophila* serves as a model organism for *Chlamydia*-like organisms as it is the first representative of these bacteria for which a complete genome sequence is available. The first study reports on the developmental cycle of this amoebal symbiont. In contrast to the well-known pathogenic chlamydiae, little is known about the characteristic biphasic developmental cycle, with its spore-like, infectious elementary bodies (EBs) and the metabolically active, replicating reticulate bodies (RBs), of most *Chlamydia*-like bacteria. This thesis describes in detail the developmental cycle of *P. amoebophila* in two different *Acanthamoeba* hosts and provides evidence for a well-balanced symbiotic interaction between host and symbiont. Interestingly, iron depletion induced abnormal cell growth of *P. amoebophila* and the observed cellular morphology resembled the persistent forms known from members of the *Chlamydiaceae.* Formation of such life stages might reflect an ancient strategy of *P. amoebophila* to

overcome unfavourable conditions and represents an interesting topic for future investigations.

In a further study, a microarray consisting of more than 6,500 probes was developed for gene expression analyses of *P. amoebophila* during intracellular growth in acanthamoebae. Initial transcriptome analyses showed, that 61% of the *in silico* predicted *P. amoebophila* genes are transcribed *in vivo* and that the majority of enzyme transcripts are predicted to be involved in metabolism, protein synthesis, molecule uptake and host-cell manipulation. Interestingly, more than half of *P. amoebophila*-specific genes, which are absent in the genomes of pathogenic chlamydiae, are expressed. This finding indicates that these genes, which lack a functional annotation in most cases, might be of importance for adaptation and survival within the amoebal host cell.

In addition to the transcriptome analyses, the metabolic activity of *P. amoebophila* was also investigated on a single cell level by stable isotope Raman microspectroscopy using a ^{13}C-labelled amino acid. With this technique, which was used the first time to directly observe metabolic traits of intracellular bacteria, it could be demonstrated that reticulate bodies (RBs) and elementary bodies (EBs) of *P. amoebophila* take up phenylalanine within their amoebal host cells and also consume this amino acid extracellularly for several weeks. In addition, EBs were shown to be able to energize their cytoplasmic membrane outside of the host and remain infective even after three weeks of host-free incubation. This newly discovered feature is in contrast to textbook knowledge and proves that not all chlamydiae rapidly cease their activity outside their host cells. It is tempting to speculate that the extracellular activity of *Chlamydia*-like bacteria are linked with their infectivity and ecological success and represent an ancient trait of this phylum. More generally, stable isotope Raman microspectroscopy enables microbiologists to directly observe functional properties of the obligate intracellular and genetically intractable chlamydiae, and thus holds much promise for future investigations of these fascinating microorganisms.

Zusammenfassung

Frei lebende Amöben der Gattung *Acanthamoeba* sind ubiquitäre Protozoen, die sich von Mikroorganismen ernähren. Es gibt jedoch eine Reihe von Bakterien, die den Amöben nicht als Futter dienen, sondern die sich innerhalb der Amöben vermehren und dabei eine stabile symbiotische Interaktion mit ihren Wirtszellen eingehen. Eine Publikation, die Teil dieser Arbeit ist, beschreibt die Charakterisierung solcher obligat intrazellulärer Symbionten aus Akanthamöben, die aus verschiedenen geographischen Regionen isoliert wurden. Die untersuchten Symbionten konnten den vier Bakteriengruppen zugeordnet werden, für die bereits bekannt war, dass sie Amöbensymbionten enthalten. Diese Untersuchung lieferte somit einen weiteren Hinweis darauf, dass das stabile Zusammenleben zwischen Bakterien und Amöben nur wenige unabhängige Male während der Evolution “erfunden“ wurde. Eine dieser endosymbiontisch lebenden Bakterienlinien die im Stammbaum mit den *Chlamydiae* gruppiert, stand im Mittelpunkt der vorliegenden Arbeit. Die Mitglieder dieser Linie sind obligat intrazelluläre Bakterien und Verwandte der klinisch relevanten Chlamydien, die die sehr erfolgreichen humanen Krankheitserreger *Chlamydia trachomatis* (verantwortlich für das Trachom und sexuell übertragbare Infektionen des Urogenitaltrakts) und *Chlamydophila pneumoniae* (ein wichtiger Erreger von Lungenentzündungen) inkludieren. Aufgrund der weiten Verbreitung Chlamydien-ähnlicher Bakterien in frei lebenden Amöben (und vielen weiteren Wirten) und ihrer Verwandtschaft zu human pathogenen Bakterien, stellt sich die Frage, ob diese erst vor ca. zehn Jahren entdeckten Bakterien auch den Menschen infizieren können. In dieser Arbeit konnten im Rahmen eines umfangreichen Screenings von Proben aus Patienten mit Lungenentzündung mittels einer hochempfindlichen PCR-basierten Methode in einigen Proben DNA verschiedener Chlamydiensymbionten nachgewiesen werden. Ob diese Bakterien, die zum ersten Mal in humanen respiratorischen Proben detektiert wurden, tatsächlich krankheitsverursachend sind muss in weiteren Untersuchungen abgeklärt werden.

Im Rahmen dieser Doktorarbeit wurden neben den beiden oben angesprochenen Publikationen drei Studien zur Biologie des Amöbensymbionts *Protochlamydia amoebophila* durchgeführt. Dieser Mikroorganismus dient als Modellorganismus für Chlamydien-ähnliche Bakterien und ist der erste Vertreter dieser Gruppe für den ein vollständig sequenziertes Genom vorliegt. In der ersten Studie wurde der Entwicklungszyklus dieses Modellorganismus analysiert. Im Gegensatz zu den gut untersuchten pathogenen Chlamydien ist der Ablauf des charakteristischen zweiphasigen Entwicklungszyklus, mit seinen sporen-ähnlichen, infektiösen Elementarkörperchen (EBs) und den metabolisch aktiven, vegetativen Retikularkörperchen (RBs), für die meisten Chlamydien-ähnlichen

Bakterien noch nicht gezielt untersucht worden. Diese Arbeit beschreibt im Detail den viertägigen Entwicklungszyklus von *P. amoebophila* in zwei unterschiedlichen *Acanthamoeba* Wirts-Zellen und zeigt wie sich aus einer Infektion eine stabile symbiotische Beziehung zwischen Symbiont und Wirt entwickelt. Interessanterweise wurden zudem erste Hinweise auf eine Persistenz von *P. amoebophila* nach Eisenmangel erhalten. Persistente Formen, die bislang nur für pathogene Chlamydien beschrieben wurden, könnten eine mögliche Strategie zur Überdauerung von unwirtlichen Umweltbedingungen darstellen und bieten ein spannendes Thema für weiterführende Studien.

In einer weiteren Studie wurde ein Mikroarray für die Analyse der Genexpression von *P. amoebophila* während der Infektion von Amöben entwickelt. Erste Transkriptomanalysen zeigten, dass 61% aller *in silico* vorhergesagten *P. amoebophila*-Gene transkribiert werden und dass die Mehrzahl der abgelesenen Gene im zentralen Metabolismus, bei Transportvorgängen, bei der Proteinsynthese oder bei der Manipulation des Wirts eine große Rolle spielen. Interessanterweise konnte mit Hilfe des Mikroarrays auch nachgewiesen werden, dass mehr als die Hälfte der 52% *P. amoebophila*-spezifischen Gene, die im Genom pathogener Chlamydien nicht enthalten sind, transkribiert werden. Dieses Ergebnis deutet auf eine wichtige Funktion dieser größtenteils unbekannten Gene für das Leben des Symbionts innerhalb der Amöbe hin.

Neben Transkriptomanalysen wurde die Physiologie von *P. amoebophila* auch auf Einzelzellebene mittels konfokaler Raman-Mikrospektroskopie unter Verwendung einer ^{13}C-markierten Aminosäure untersucht. Mittels dieses neuartigen Verfahrens, das erstmals für die Analyse intrazellulärer Bakterien verwendet wurde, konnte gezeigt werden, dass EBs und RBs von *P. amoebophila* intrazellulär Phenylalanin aus dem Cytoplasma der Wirtszelle aufnehmen. Entgegen der herrschenden Lehrmeinung, konnte diese Aktivität mittels Raman-Mikrospektroskopie für beide Entwicklungsstadien auch außerhalb der Wirtszelle über einen Zeitraum von drei Wochen nachgewiesen werden. Zudem konnte gezeigt werden, dass extrazelluläre EBs über diesen Zeitraum infektiös bleiben und in der Lage sind außerhalb des Wirtes ihr Membranpotential neu aufzubauen. Diese Befunde widerlegen das Dogma, dass EBs generell außerhalb ihres Wirtes unmittelbar ihre Aktivität verlieren und stehen möglicherweise in direktem Zusammenhang mit dem großen ökologischen Erfolg Chlamydien-ähnlicher Bakterien. Da alle Chlamydien bislang genetisch nicht manipulierbar sind, stellt die Raman-Mikrospektroskopie generell eine faszinierende Methode für zukünftige physiologische Untersuchungen an diesen und anderen intrazellulären Bakterien dar.

Appendix

Publications

Schmitz-Esser S., Toenshoff E.R., Haider S., Heinz E., Hoenninger V.M., Wagner M., Horn M.

Diversity of bacterial endosymbionts of novel environmental *Acanthameobea* isolates. *Applied and Environmental Microbiology* (2008), Vol 74, P. 5822-5831

Haider S., Collingro A., Walochnik J., Wagner M., Horn M.

Chlamydia-like bacteria in respiratory samples of community-acquired pneumonia patients. *FEMS Microbiology Letters* (2008), 1-5

Haider S., Wagner M., Sixt B.S., Müller A., Baranyi C., Toenshoff E.R., Montanaro J., Horn M.

Raman microspectroscopy reveals long-term extracellular activity of a member of the *Chlamydiae. Submitted to Cell Host & Microbes.*

Haider S., König L., Müller A., Montanaro J., Wagner M., Horn M.

The developmental cycle of *Protochlamydia amoebophila* in amoebal hosts. *In preparation.*

Haider S., Müller A., Wagner M., Horn M.

First insights into the gene expression profile of *Protochlamydia amoebophila* during infection. *In preparation.*

Oral presentations

Haider S., Collingro A., Walochnik J., Wagner M., and Horn M.
Molecular evidence for chlamydia-like bacteria as agents of community acquired pneumonia (CAP). 3rd German Chlamydia Workshop (Deutscher Chlamydienworkshop DCW), May 2005, Jena, Germany.

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Curriculum vitae

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1998 – 2003	Studies of Biology at the University of Vienna, focus on Microbiology and Genetics
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