# Characterization of *Pseudomonas aeruginosa* phages for phage therapy

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Tiivistelmä — Referat — Abstract

Antibiotic-resistant bacteria are an increasing threat to global health, caused by the excessive use of antibiotics and the lack of new antimicrobial agents being introduced to the market. New approaches to prevent and cure bacterial infections are needed to halt the growing crisis. One of the most promising alternatives is phage therapy which utilizes bacteriophages to target and kill pathogens with specificity. *Pseudomonas aeruginosa* is a common opportunistic pathogen that is intrinsically resistant to antibiotics, making it one of the most heavily studied targets of phage therapy. In this study, I characterized four *P. aeruginosa* phages, fHo-PaeO1, PA1P1, PA8P1 and PA11P1, and evaluate their potency in therapeutic applications.

Bioinformatic analysis of the genomes revealed the phages to be genetically highly similar and belonging to the *Pbunavirus* genus of the *Myoviridae* family. No genes encoding harmful toxins, antibiotic-resistance, or lysogeny were predicted. On the other hand, many of the predicted genes had unknown functions. The host ranges of the phages were assessed using 47 clinical *P. aeruginosa* strains and predicted host receptor binding tail proteins were compared. Some correlation between the host ranges and mutations in the tail proteins were observed but this alone was not sufficient to explain the differences in the host ranges.

The recently isolated vB\_PaeM\_fHoPaeO1 (fHo-PaeO1) phage was further characterized by a one-step growth curve and imaged with a promising atomic force microscopy method that had not been used before in the Skurnik group. Though the imaging results failed to provide any further knowledge of the phage, the 70-minute-long latent period of infection could be determined from the growth curve. Anion-exchange chromatography was found inefficient in purifying the fHo-PaeO1 phage, so alternative methods such as endotoxin columns should be used when purifying these phages for patient use.

In conclusion, all four phages appeared to be safe for therapeutic use based on current knowledge, and PA1P1 and PA11P1 were the most promising candidates due to their broad host ranges.

 ${\sf Avainsanat-Nyckelord-Keywords}$ 

*Pseudomonas aeruginosa*, bacteriophage, phage therapy, *Pbunavirus*, vB\_PaeM\_fHoPae01, antibiotic-resistance

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Tiivistelmä — Referat — Abstract

Antibioottiresistentit bakteerikannat ovat kasvava uhka kansanterveydelle. Tämä johtuu antibioottien ylenpalttisesta käytöstä nyky-yhteiskunnassa ja uusien antimikrobisien yhdisteiden kehityksen huomattavasta hidastumisesta. Uusien bakteeri-infektioita parantavien ja ehkäisevien keinojen kehittäminen joko antibioottien tilalle tai rinnalle on välttämätöntä maailmanlaajuisen kriisin pysäyttämiseksi. Yksi lupaavimmista hoidoista on faagiterapia, jossa bakteeriofageja hyödynnetään patogeenisten bakteereiden hävityksessä.

*Pseudomonas aeruginosa* on yleinen opportunistinen patogeeni, joka on luontaisesti hyvin vastustuskykyinen antibiooteille. Tästä syystä sitä on tutkittu paljon faagiterapian kohteena. Tässä tutkielmassa karakterisoin neljä *P. aeruginosa* faagia - fHo-PaeO1, PA1P1, PA8P1 sekä PA11P1 – ja arvioin niiden käyttökelpoisuutta terapeuttisissa sovelluksissa.

Faagien genomit osoittautuivat hyvin samankaltaisiksi bioinformaattisessa analyysissä. Fylogeneettisesti samaa lajia edustavat neljä faagia luokiteltiin *Myoviridae*-perheen *Pbunavirus*-sukuun. Haitallisia toksiineja, antibioottiresistenttiyttä tai lysogeniaa koodaavia geenejä ei havaittu. Toisaalta vain osalla faagien oletetuista geeneistä oli tunnistettava tehtävä. Faagien isäntäkirjoja tutkittiin 47 kliinisellä *P. aeruginosa* kannalla ja oletettuja isännän reseptoriin sitoutuvia häntäproteiineja vertailtiin keskenään. Tulokset osittain korreloivat toisiaan, mutta erot häntäproteiineissa eivät riittäneet selittämään eroja isäntäkirjoissa.

Vastikään eristettyä faagia, fHo-Pae01, karakterisoitiin myös kasvukäyrän sekä AFM mikroskopoinnin (atomic force microscopy) avulla. Kyseistä mikroskooppia ei ollut aiemmin käytetty Skurnikin ryhmässä eikä sen resoluutio riittänyt pienille faagikapsideille. Sen sijaan kasvukäyrästä kyettiin määrittämään infektion latentin vaiheen pituudeksi 70 minuuttia. Puhdistuksessa havaittiin, että anioninvaihto-kromatografia ei ole riittävän tehokas keino puhdistaa fHo-Pae01 faagia. Vaihtoehtoisia keinoja kuten endotoksiinipylvästä on käytettävä, mikäli faagia halutaan puhdistaa terapiatuotteeksi.

Kaikki neljä faagia vaikuttivat olevan turvallisia käytettäväksi faagiterapiassa. PA1P1 ja PA11P1 olivat lupaavimmat kandidaatit niiden laajemman isäntäkirjon johdosta.

Avainsanat — Nyckelord — Keywords *Pseudomonas aeruginosa*, bakteriofagi, faagiterapia, *Pbunavirus*, vB\_PaeM\_fHoPae01, antibioottiresistenssi

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#### INTRODUCTION

*Pseudomonas aeruginosa* is a gram-negative, opportunistic pathogen occurring in the human intestine, on the skin, and in the environment. *P. aeruginosa* is pathogenic to humans only when introduced to an area lacking a natural defense mechanism or when a person's defenses are impaired due to an illness. Infection is often produced in damaged tissue such as wounds or burns [1], in the urinary tract after catheter introduction [2], or as a chronic respiratory infection in cystic fibrosis patients [3]. In addition, *P. aeruginosa* may in the most extreme cases cause fatal sepsis when invading the bloodstream. Among other *Pseudomonas* species, *P. aeruginosa* is naturally resistant to many antimicrobial agents [4] as well as to the immune system due to its biofilm formation [5,6].

Multidrug resistance of *P. aeruginosa* is occurring primarily in cystic fibrosis patients and patients hospitalized in intensive care units, and the proportion of isolates resistant to multiple drugs is rising rapidly [7]. The excessive use of antibiotics and the halt in the development of new antimicrobial drugs has caused the rise of antibiotic-resistance in bacteria and the selection for resistance genes [8].

Alternative ways to cure infections caused by antibiotic-resistant bacteria are being developed to replace or act alongside antibiotics. Phage therapy, a method which utilizes bacterial viruses (bacteriophages) to kill specific infectious bacteria, presents one possible way to battle the global threat caused by the spreading of antimicrobial-resistance [9,10]. Lytic phages lyse the bacterial cell at the end of their infection cycle, therefore killing the bacteria. This event lays the foundation for phage therapy [11]. The phages used for therapeutic purposes must meet strict criteria to be deemed safe to use. In addition to being free of any toxin or antibiotic-resistance coding genes they must be virulent, unable of lysogenic conversion [12]. A lysogenic phage integrates its genome into the host's chromosome becoming a prophage [11], usually making the host phage-resistant [11,12]. Lysogenic phages may convert back to a lytic cycle in certain conditions, but as a prophage, they do not cause cell lysis and thus would be ineffective in phage therapy [11]. Identifying lysogenic phages can often be carried out with genomic analysis, as the genomes of lysogenic phages usually code integrases, transposases or lytic phage repressors [13].

Over 94% of the known *Pseudomonas* phages found in the National Center for Biotechnology Information (NCBI) database are classified in three families of the *Caudovirales* order: *Podoviridae*, *Siphoviridae*, and *Myoviridae* with genome sizes ranging from 3.6 kb to 320 kb [14,15]. All phages in the order are double-stranded DNA viruses with differing tail structures, and approximately 60% of

them are lytic. The genome size is generally larger in *Myoviridae* than in *Podoviridae* or *Siphoviridae*, ranging from 64 kb to ~310 kb, whereas in the other two the size usually falls under 80 kb. It is characteristic of the phages in the *Myoviridae* family to have a long tail that contracts upon the phage injecting its genome into the host cell. [16]

This work aimed to study the genomic properties of four *P. aeruginosa* phages, in order to verify them safe to use for therapeutic purposes within the range of current knowledge. Additional experiments were conducted to determine the capsid structure and infection characteristics of one of the phages, vB\_PaeM\_fHoPae01 (fHo-Pae01, GenBank: MK318076.1), as it is a recent isolate of the Skurnik group.

#### MATERIALS AND METHODS

#### Phages, bacterial strains and growth conditions

All bacterial strains used in laboratory work were clinical *Pseudomonas aeruginosa* strains (HUSLAB, [17]) (Table S1).

The fHo-Pae01 phage was previously isolated in the Skurnik group by Tommi Patinen [18]. *P. aeruginosa* #5525 (HUSLAB) [18] was used as the standard host for this phage. Phages PA1P1, PA8P1 and PA11P1 were isolated elsewhere [17]. The standard hosts used were *P. aeruginosa* PA1 for PA1P1, PA8 for PA8P1, and PA11 for PA11P1 [17].

The bacterial cultures and phages were incubated at +37 °C using Luria broth (LB) liquid medium or soft agar medium (0.4% (w/v) agar) solidified on LB agar plates (1.5% (w/v) agar) [19]. The phage lysates were prepared from semiconfluent soft agar plates with the host bacteria from a culture incubated until the logarithmic growth phase. The amount of bacterial culture added was calculated from the equation:  $25.5\mu$ I OD<sub>600</sub><sup>-1</sup>. The same equation was used for the amount of bacterial culture when titrating phages on double layer plates [19].

#### In silico analysis of phage genomes

All phage genomes had previously been sequenced by next-generation sequencing (Eurofins GATC), assemblies of the over 12 million reads per genome had been made, and the contigs containing the phage genomes had been identified. In this work, PhageTerm program [20] was used to estimate the genome origins and packaging methods of the phages. The genomes were managed with Geneious 11.1.5 (https://www.geneious.com). The assembled genomes were also aligned in

Geneious 11.1.5 (https://www.geneious.com) with the original reads to ensure no mistakes were made in the assembly.

The preliminary annotations were automatically carried out with RAST 2.0 (Rapid Annotation using Subsystem Technology) [21-23]. Glimmer3 software [24,25] was used to make corrections to the annotations formed by RAST 2.0 [21-23]. Based on the RAST 2.0 [21-23] and Glimmer3 [24,25] results, the final, more detailed annotations were performed with BLASTp (Protein Basic Local Alignment Search Tool) [26], and the results were manually evaluated.

The phage genomes were screened for tRNA (tRNAscan-SE 2.0 [27], Aragorn [28]), virulence (VirulenceFinder 2.0 [29]), and antibiotic-resistance genes (ResFinder 3.1 [30]).

A comparative alignment between the phage genomes and the type phage PB1 (GenBank: NC\_011810.1) genome was conducted with Geneious 11.1.5 (https://www.geneious.com), Geneious alignment tool.

A phylogenetic tree was constructed with VICTOR software (Virus Classification and Tree Building Online Resource) [31] using Genome-BLAST Distance Phylogeny (GBDP) method. Genome-wide BLASTN runs were performed to the four phages and the type phage PB1. 22 of the best matches (query cover >90%) were chosen for the tree (Table S2). The open reading frame (ORF) of the first predicted gene in fHo-Pae01, FHP001, was identified in all phage genomes used for the tree. All the genomes were then set to start from that ORF, to yield a more reliable phylogenetic tree.

A protein corresponding to a predicted tail fiber protein (GenBank: BAU20669.1) of *Pseudomonas* phage KPP22 (GenBank: LC105987.1), assumed to affect the adsorption of the phage to the host cell [32], was identified in the genomes of fHo-Pae01 (FHP062), PA1P1 (PA1P1\_063), PA8P1 (PA8P1\_062), and PA11P1 (PA11P1\_062). The amino acid sequences of the predicted tail fiber proteins in fHo-Pae01, PA1P1, PA8P1, and PA11P1 were aligned with Clustal Omega 1.2.4 [33].

#### Host range screening

The host ranges for all four phages were screened with the 47 clinical, antibiotic-resistant *P. aeruginosa* strains available (Table S1). Screenings were performed in liquid cultures on a 96-well plate over 6 hours, by measuring the absorbance at 595 nm (Hidex Plate CHAMELEON Multilabel Detection Platform) at 60 min intervals. In each well, 190  $\mu$ l of 1:40 dilution of the host bacteria overnight culture was mixed with 10  $\mu$ l lysate (10<sup>9</sup> pfu/ml) of one of the phages. Wells with LB medium replacing the phage lysate were used as negative controls. As positive control, each phage

was also used to infect its standard host. The host range liquid culture screening method had previously been tested (Schaedig *et al.,* unpublished results) to yield results comparable to the more commonly used plating method [34].

#### One-step growth curve

The standard host of the phage fHo-PaeO1, *P. aeruginosa* #5525, was incubated in 10 ml LB medium until the absorbance, measured with Cell density meter DSM-Micro (Laxco) at 600 nm was 0.4 - 0.5. The phage was added to reach an MOI value of 0.0005 to ensure no more than one phage would infect a single host cell. A 150 µl sample at 0 min was taken immediately. The sample was treated by first harvesting the cells by centrifugation for 1 min at 11,000 x g. Then, the supernatant was discarded and replaced by fresh media so that only the phages adsorbed on the surface or inside the cells were taken into account. The sample was then titrated.

The phages were left to adsorb for 15 min with light shaking, after which the cells were harvested by centrifugation for 5 min at 4,500 x g, and the media was replaced to produce a synchronized infection. A dilution series was prepared until  $10^{-3}$  in 10 ml LB medium. The incubation was continued, and  $20 - 50 \mu$ l samples titrated every 10 - 30 min.

The growth curve was calculated using the mean values of three separate experiments by assigning the value 1 to correspond the phage titer at 0 min. [35,36]

#### Phage purification with anion-exchange chromatography

The phage lysate was concentrated to a volume of 1 ml and changed to buffer A (20 mM Tris-Cl, pH 8.5) by ultrafiltration with a Vivaspin 6 (100 kDa) centrifugal PES membrane concentrator (Sartorius). The sample was then filtered through a 0.2 µm pore filter. The anion-exchange chromatography was performed with Äkta Purifier (GE Healthcare), and a ClMmultus QA-1 tube advanced composite column with a 6-µm pore size (BIA Separations). The high pH of 8.5 for the buffers was selected to ensure the negative charge of the major capsid protein. The isoelectric point of the putative major structural protein of fHo-Pae01, FHP\_041, was determined using EMBOSS Pepstats software [37].

A linear gradient purification was made to determine the conditions for the two-step purification. The sample was injected to the column in buffer A, and the phage was eluted with buffer A and with a 0 mM – 550 mM gradient of NaCl. (Fig. S2)

In the step purification, the sample was injected to the column in buffer A, the column was washed with buffer A with 160 mM NaCl, and the phage was eluted with buffer A with 350 mM NaCl. The two fractions containing the phage were pooled, and the buffer was changed to gelatin-free SM buffer (100 mM NaCl, 10 mM MgSO<sub>4</sub>, 50mM Tris-HCl, pH 7.5) with a Vivaspin 6 centrifugal concentrator. (Fig. S3)

#### Atomic force microscopy

The purified phage was imaged a multimode 8 AFM connected to a Nanoscope V controller (Bruker). The images were taken in tapping mode in the air with an E scanner using NCHV-A probes (Bruker AFM probes). The images were taken at Aalto University, Department of Bioproducts and Biosystems.

#### RESULTS

#### Genome analyses

The genomic sequences of PA1P1, PA8P1, and PA11P1 were sequenced previously. PhageTerm [20] software was then used to determine the physical ends of the pre-assembled genomes. A headful packaging mechanism was predicted by the program as the method used by all three phages to package their genome into the phage capsid. The mechanism does not have a specific cleaving site for the C terminal end of the genome, but rather cleaves the DNA strand once the virion head is full, resulting in genomes of varying lengths in individual phage particles [38,39]. The annotation and PhageTerm analysis of fHo-PaeO1 was done by Pulkkinen *et al.* (manuscript under preparation).

All four phage genomes – fHo-PaeO1, PA1P1, PA8P1, and PA11P1 – were similar in length (65 – 67 kbp) and GC content (55 – 56%). Furthermore, the number of predicted genes was 92 – 93 in all genomes, of which 66 – 67 were hypothetical proteins with unknown functions (Tables S3 – S6). The scans performed using tRNAscan-SE 2.0 [27], and Aragorn [28] found no transfer RNA coding genes. The phages were expected to be strictly lytic as no lysogeny-associated genes or integrases were identified. Additionally, no virulence-associated, toxic or antibiotic-resistance genes were recognized in any of the four genomes. (Table 1)

All genomic sequences were constructed using over 12 million sequencing reads. The genomes were aligned with the original reads to find mistakes made during the assembly. One uncertain sequencing result was found in all four genomes: a 9 - 10 bp guanine repeat in *PA1P1\_61A*,

*PA8P1\_60A*, and *PA11P1\_60A*, and in between the predicted genes *FHP\_059* and *FHP\_060* in fHo-Pae01. The length of the repeat was nine bp in approximately half of the reads and ten bp in the other half. The final sequences have the sequence with nine guanine nucleotides in accordance to the sequence of PB1. The sequencing method may not have been sensitive enough to reliably be able to determine the length of unusually long one-nucleotide repeats.

#### Comparative genome analysis

Altogether, the genomes of fHo-PaeO1, PA1P1, PA8P1, and PA11P1 were highly similar, sharing over 90% identities with each other, and 85 – 86% with the *Pbunavirus* type phage PB1 (Table 1). The pattern of predicted genes is also highly similar in all four phages and the type phage (Fig. 1) with the most significant differences described in Table 2.

The phylogenetic tree (Fig. 2) clustered the 27 phage genomes as seven species, all belonging to the *Pbunavirus* genus and *Myoviridae* family. The phages fHo-Pae01, PA1P1, PA8P1, and PA11P1, were classified as the same species as *Pseudomonas* phages 14\_1, JG024, NP3, PII10A, SL1, and SN rather than the *Pbunavirus* type phage PB1.

**Table 1: Statistic of fHo-Pae01, PA1P1, PA8P1, PA11P1, and the type phage PB1 genome analyses.** Number of predicted genes and hypothetical proteins, GC content, genome length, and sequence identities of the phage genomes with each other.

	fHo-Pae01	PA1P1	PA8P1	PA11P1	PB1
Genome length (bp)	66,418	66,612	65,690	66,049	65,764
Predicted genes	92	93	92	92	94
Hypothetical proteins	66	67	67	67	80
GC%	55.7	55.8	55.7	55.7	54.9
Identity with fHo-Pae01 (%)	100	94.8	93.5	94.3	86.1
Identity with PA1P1 (%)	94.8	100	94.8	97.1	86.3
Identity with PA8P1 (%)	93.5	94.8	100	96.4	85.5
Identity with PA11P1 (%)	94.3	97.1	96.4	100	85.1

All statistics were calculated using Geneious 11.1.5 (https://www.geneious.com).



*Fig. 1. A genome-wide alignment created with Geneious 11.1.5 (https://www.geneious.com) software of the fHo-Pae01 (GenBank: MK318076.1), PA1P1, PA8P1, PA1P1 and PB1 (GenBank: NC\_011810.1) phage genomes.* The predicted genes are marked in yellow. The height and color of the identity bar indicates the mean pairwise identity over all pairs in the column (Green: 100% identity, yellow: 30% - 100% identity, red: below 30% identity). The PB1 type phage shared an overall 85-86% identity with the other phage genomes. The identities among phages fHo-Pae01, PA1P1, PA8P1 and PA11P1 were even higher: 93-97%. The genome of PB1 was adjusted to originate from the gene corresponding to the first predicted gene in the other phage genomes.

 Table 2: Major differences in the predicted genes of fHo-Pae01, PA1P1, PA8P1, PA11P1, and PB1.

fHo- Pae01	PA1P1	PA8P1	PA11P1	PB1	Description of the differences
FHP_003c	PA1P1_003c	PA8P1_003c	PA11P1_003c	PB1_gp81	PA1P1_003c, PA8P1_003c and PA11P1_003c are identical. FHP_003c and PB1_gp81 are similar to
FHP_006c	PA1P1_006c	no seq	PA11P1_006c	no seq	the previous three and to each other.
no seg	PA1P1 011c	no seg	no seg	PB1 qp88	
FHP_013c	PA1P1_014c	PA8P1_012c	PA11P1_013c	PB1_gp91, PB1_gp92	PB1_gp91 is a different protein than PB1_gp92, and both are different proteins than the others shown. FHP_013c is similar to PA1P1_014c.
FHP_015c	PA1P1_016c	PA8P1_014c	PA11P1_015c	PB1_gp94	PA8P1_014c and PA11P1_015c are identical but a different protein from the others shown. PB1_gp94 is approximately 90 amino acid residues shorter than FHP_015c and PA1P1_016c.
no ORF	PA1P1_018c	PA8P1_016c	PA11P1_017c	PB1_gp02	PB1_gp02 is a different protein from the others. A mutation in fHo-Pae01 leading to frameshift has caused a stop codon in the region.
FHP_017c	PA1P1_019c	PA8P1_017c	PA11P1_018c	PB1_gp03	PB1_gp03 is a different protein from the others.
no ORF	no ORF	PA8P1_018	no ORF	no ORF	Glimmer3 found a gene in this region of fHo-Pae01 and PA8P1. The gene predicted in fHo-Pae01 is similar to PA8P1_018, but it has not been annotated.
FHP_026c	PA1P1_028c	PA8P1_027c	PA11P1_027c	no ORF	Glimmer3 predicted a similar gene in PB1, but it has not been annotated. FHP_026c and PA1P1_030c are similar to the others shown and to one another.
FHP_028c	PA1P1_030c	PA8P1_029c	PA11P1_029c	no seq	
FHP_029	PA1P1_031c	PA8P1_030c	PA11P1_030c	PB1_gp13	PB1_gp13 is approximately 55 amino acid residues longer than the others shown, has a different predicted start codon, and is similar to PA1P1_031c, PA8P1_030c, and PA11P1_030c. FHP_029 is a different protein from the others shown.
FHP_038	no ORF	no ORF	no ORF	no ORF	Glimmer3 did not predict any genes. The DNA sequence has premature stop codons in all but FHP_038.

FHP_084c	PA1P1 085c	PA8P1_084c	PA11P1_084c	PB1_gp69	PA8P1_084c and PB1_gp69 are identical. The
	1111_00000				others are similar to them and to one another.
					PA8P1_088 and PB1_gp73 are different proteins
FHP_088	PA1P1_089	PA8P1_088	PA11P1_088	PB1_gp73	from the others and from one another. PA1P1_089
					and PA11P1_088 are identical, and FHP_088 is
					similar to them.

*Glimmer3* [24,25] and BLASTp [26] software were used to verify some of the genes predicted by RAST 2.0 [21-23]. No seq: a gap in the sequence on the site of the predicted gene. No ORF: no annotated predicted gene on the site. Identical: 95 - 100% pairwise amino acid identity. Similar: 60 - 95% pairwise amino acid identity. Low amino acid identity: 45 - 60% pairwise amino acid identity. Different protein: less than 45% pairwise amino acid identity.



0.003

**Fig. 2.** A phylogenetic tree of the 17 closest BLASTn matches to the fHo-Pae01, PA1P1, PA8P1, and PA11P1 phage genomes (highlighted in yellow) and 5 closest BLASTn matches to the type phage PB1 phage genome. The tree was constructed with VICTOR (Virus Classification and Tree Building Online Resource) [31]. All of the genomes in the tree belong to Pbunavirus genus of the Myoviridae family. The genomes were clustered in 7 species. The phages fHo-Pae01, PA1P1, PA8P1 and PA11P1 are classified as the same species as Pseudomonas phages 14\_1, JG024, NP3, PII10A, SL1, and SN, rather than Pseudomonas phage PB1 which is the type phage of the genus. S: species, G: genus, F: family.

#### Infection cycle

A one-step growth curve experiment was conducted to fHo-PaeO1 to determine the number of new phage progenies released by a single infected bacterial cell (burst size), as well as the duration of the latent period, i.e., the time from infection to the beginning of cell lysis. The latent period was determined to be 70 minutes long. However, the four repeated experiments deviated substantially from one another later during the infection cycle. Thus, the burst size could not be determined.

Experiments with longer incubation time did not reveal a new latent period (data not shown). (Fig. 3)

#### Host range

The host ranges of all four phages were assessed using 47 clinical *P. aeruginosa* strains (Table S7, Fig. S1). Of the four phages, fHo-Pae01 had the narrowest specificity, infecting only 14 clinical strains (30%). PA1P1 infected 33 (70%), PA8P1 infected 24 (51%) and, PA11P1 infected 31 (66%) of the strains. A comparative alignment of the possible host receptor recognizing tail fiber proteins was performed to elucidate the differences in host specificities. According to the alignment (Fig. 4), the predicted tail proteins PA1P1\_063 and PA11P1\_062 were 100.00% identical. Moreover, PA8P1\_062 was 97.40% identical to PA1P1\_063 and PA11P1\_062. However, the tail fiber protein of fHo-Pae01, FHP062, shared a sequence identity of 82.40% with PA1P1\_063 and PA11P1\_062, and 84.06% with PA8P1\_062. The variation between FHP062 and the others was concentrated in the C termini of the proteins with a pairwise identity of 54.0% in A670 – A963 determined by Geneious 11.1.5.



**Fig. 3: One-step growth curve of phage fHo-Pae01 in its standard host P. aeruginosa #5525 as PFU per infected cell at different timepoints.** The data points are averages of four experiments at time points 70 minutes, 90 minutes, and 110 minutes, and of three experiments for the other timepoints. The latent period was 70 minutes. The variation between the experiments did not allow for a reliable estimation of the burst size.

	1	100	200	300	400	500	600	700	800	900	967
Consensus Identity				Ü				, indial dat		ii <b>t</b> hi ka	1
1. fHo-Pae01 - FHP_062					putative tail fi	ber protei	n CDS				<b>_</b>
▷ 2. PA8P1 - PA8P1_062					Tail fib	er protein					
C+ 3. PA1P1 - PA1P1_063					Tail fib	er protein					5
🖙 4. PA11P1 - PA11P1_062					Tail fib	er protein					

**Fig. 4.** An alignment of the putative host recognizing tail proteins of fHo-Pae01, PA1P1, PA8P1, and PA11P1. Created with Geneious 11.1.5 (https://www.geneious.com) software. The height and color of the identity bar indicates the mean pairwise identity over all pairs in the column (Green: 100% identity, yellow: 30% - 100% identity, red: below 30% identity). PA1P1\_063 and PA11P1\_062 are 100.00% identical. PA8P1\_062 is 97.40% identical to the latter, with mutations spread evenly along the length of the protein. FHP\_062 is 84.06% identical to PA8P1\_062, and 82.40% identical to PA1P1\_063 and PA11P1\_062. The differences between FHP\_062 and the others are concentrated on the C terminal end of the protein.

#### Purification of phage fHo-Pae01

The phage fHo-PaeO1 was purified for atomic force microscopy using anion-exchange chromatography by determining the conditions for a step-gradient purification with a linear-gradient run (Fig. S2) before performing the step-gradient run (Fig. S3). The isoelectric point of the putative major structural protein, as determined by EMBOSS Pepstats [37] was 5.8560. The pH 8.5 of the buffers was chosen based on the isoelectric point and a previous unsuccessful purification with pH 7.0 (Patinen *et al.* unpublished results).

The amount of phage injected into the column in the step gradient purification,  $1.7 \times 10^{11}$  pfu, was determined by the titer of the lysate as measured before changing the buffer, filtration, or concentration of the sample. The purified phage yield was  $5.7 \times 10^9$  pfu, and the final yield after changing the buffer was  $4.7 \times 10^9$  pfu. Thus, the yield of purified phage was approximately 2.8% of the amount that was injected into the column, though a portion of the phages may have been lost during the sample preparation steps before injection.

#### Imaging

Atomic force microscopy was used to image the fHo-Pae01 virus particle. However, the resolution of the microscope was not optimized for biological samples. Although the objects in the images resemble bacteriophages by shape, no reliable conclusions can be made of them. (Fig. 5)



**Fig. 5. Image of the purified fHo-Pae01 phage particle taken using atomic force microscopy**. Although some particles resembling phages (indicated with red circles) could be found, the resolution of the microscope did not allow any conclusions to be made of the particle.

#### DISCUSSION

This study reports the fully annotated DNA sequences and infection characteristics of *P. aeruginosa* phages PA1P1, PA8P1 and PA11P1 as well as a new phage fHo-Pae01, isolated in the Skurnik group. All studied phages were predicted to belong to the same species with *Pseudomonas* phages 14\_1, JG024, NP3, PII10A, SL1, and SN of the *Pbunavirus* genus, but to a different species than the reference phage PB1. The phages all had genomes of 65 – 67 kbp. The small genome size is characteristic of *Pbunaviruses* unlike in many other members of the *Myoviridae* family [16]. The atomic force microscopy failed to produce further insight on the morphology of fHo-Pae01. This method of imaging phages has previously shown some promising results [40,41], but the atomic force microscope used may not have met the necessary standards for imaging particles on the nanometer scale. The phage has since been imaged by transmission electron microscopy (Pulkkinen *et al.,* manuscript under preparation), but that is beyond the scope of this thesis.

No tRNA-coding genes were identified, which indicates that phages are dependent on the host tRNA molecules and may use codon-optimization to exploit the translation machinery of the host [42]. Additionally, all four phages were concluded to likely be harmless to humans, as no potential virulence-associated, toxic, or antibiotic resistance genes were recognized. Moreover, no genes associated with a temperate infection cycle were identified, so all of the phages are assumed to be

strictly lytic. Still, more than 70% of the annotated genes had unknown functions, which is typical of bacteriophages (NCBI database) and demonstrates how much is still unknown about bacterial viruses. The annotated genomes of PA1P1, PA8P1, and PA11P1 will be submitted to the GenBank database shortly.

The GC content of approximately 56% in the studied phage genomes was similar to many other PB1like *P. aeruginosa* phages [43]. Often, the phage and host genomes are similar in GC content. However, it is common for *P. aeruginosa* phages to have a significantly lower GC content compared to the bacterial host [44]. No sequencing data of the bacterial hosts used in this study was available, but 186 of the 187 complete *P. aeruginosa* bacterial genomes on the NCBI database had a GC content of 65.08 – 66.84%. Therefore, these phages likely exhibit a similar difference in GC content to their hosts (approximately 10 percentage points lower) as previously reported for other *P. aeruginosa* phages [43].

The G-rich nucleotide sequence observed in all four phage genomes is a common feature of PB1like phages, as this stretch has been predicted to be a site for ribosomal frameshift [43]. This may also to be the case for the four phages studied here. It is possible that the slippery sequence of the repeated G nucleotide enables multiple proteins to be translated from the same mRNA sequence, depending on ribosomal frameshifts. Assuming the G repeat is nine nucleotides long in reality, a +1 frameshift is likely to take place, which would yield a merged form of PA1P1\_061A and PA1P1\_061B. In this case the same would be true for PA8P1\_060A and PA8P1\_060B as well as PA11P1\_060A and PA11P1\_060B.

A +1 shift is known to be common in dsDNA phages and has been well documented in many phages across multiple host organisms [45-47]. If a -1 frameshift took place on this site, a stop codon would form before the origin of the PA1P1\_061B (PA8P1\_060B, PA11P1\_060B) gene. Thus, two proteins originating from the same site may be produced: a short protein with no ribosomal frameshift (PA1P1\_061A, PA8P1\_060A, PA11P1\_060A), and a longer protein caused by a +1 frameshift (PA1P1\_061A + PA1P1\_061B, PA8P1\_060A + PA8P1\_060B, PA11P1\_060A + PA11P1\_060B). It would be interesting to analyze the protein production in an infected cell to find out which frameshift could be observed *in vivo*, and in what ratios the different products of this site are produced. Previous studies would suggest the shorter product with no frameshift to be the major product [46-48].

Of the four phages studied, PA1P1 and PA11P1 are the most promising candidates to be used for phage therapy as their host ranges are the broadest. This is a desirable property, as it indicates a higher probability of the phage being able to infect new host strains. Here, the tail fiber protein

predicted to mediate the adsorption of the phage to the host cell somewhat correlated with the observed host ranges. However, I assume this protein not to be the only factor mediating the phage attachment to its receptor as PA1P1\_063 and PA11P1\_062 were 100.00% identical, yet their host ranges differed marginally.

Phages are often applied as a cocktail, a mixture of two or more phages infecting the same host, to prevent the development of phage resistance and to improve the efficiency of the treatment [49,50]. For this purpose, phages with the widest host ranges are chosen to produce the broadest lytic range possible for the final cocktail. Therefore, it is exceedingly important for the establishment of efficient phage therapy to discover multiple phages infecting the same host species of bacteria. Phage resistance for therapy products develops when the receptor of the host bacteria is lost or mutated [11], so phages utilizing differing receptors should be prioritized. For that reason, it would be beneficial to determine the receptors of the phages in future studies. Often, phage resistance in these structures may even be beneficial, making the pathogen less virulent and more susceptible to the immune system [11].

The one-step growth curve characterizing the infection cycle of fHo-Pae01 revealed the latent period to be 70 minutes long. This result deviates from the 35 – 50 minutes previously reported for most PB1-like phages [35,51,52]. It has been documented that longer latent periods correlate with higher burst sizes at the lysis [53,54]. This is due to the phage having more time to utilize the resources of the host [53]. Thus, it would be reasonable to expect a large burst size in relation to other PB1-like phages. The optimization of the one-step growth curve method will be continued to determine the burst size of fHo-Pae01, although it is beyond the scope of this thesis. I hypothesize that the 15 minute adsorption time used before for *Pseudomonas* phage JG024 [35] was too long to produce a sufficiently synchronized infection for fHo-Pae01.

The optimization of the purification conditions must also be continued. When purifying the fHo-PaeO1 phage with anion-exchange chromatography, a significant number of the phages were lost, presumably caused by the weak attachment of the phage to the column. The yield 2.8% was merely a fraction of the >70% achieved for other phages in the Skurnik group. The bond could be tightened by raising the pH of the buffers used, but this would likely denature the phage capsids and render them unviable. For therapeutic use, an alternative approach for purification should be used. Promising results have recently been achieved by combining ultrafiltration with commercial

endotoxin binding columns. This method may even be faster and more efficient in separating bacterial LPS from the phage lysate than many of the other commonly used methods [55]. In conclusion, no indication of genes encoding antibiotic-resistance, toxins or lysogeny-associated was observed, suggesting the four phages – fHo-PaeO1, PA1P1, PA8P1, and PA11P1 – to be potentially safe to use in phage therapy to treat *P. aeruginosa* infections and in other possible applications such as biofilm prevention. The wide host ranges of PA1P1 and PA11P1 make them the most compelling candidates for treatment. In the future, clinical studies should be carried out to determine the *in vivo* efficiency of these phages in curing infections.

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#### Supplementary material

Table S1. Pseudomonas aeruginosa strains used in laboratory work.

Table S2. Phages used in the phylogenetic tree.

Table S3. Predicted genes of *P. aeruginosa* phage fHo-Pae01.

Table S4. Predicted genes of *P. aeruginosa* phage PA1P1.

Table S5. Predicted genes of *P. aeruginosa* phage PA8P1.

Table S6. Predicted genes of *P. aeruginosa* phage PA11P1.

Table S7. Detailed results of the host range screening.

Fig. S1. A demonstrative image of the evaluation of the host range screening results.

Fig. S2. Linear gradient purification of phage fHo-Pae01.

Fig. S3. Step-gradient purification of phage fHo-Pae01.

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Table S1.	Pseudomonas	aeruainosa	strains used	in	laboratory	work
TUDIE SI.	rseudonionus	ueruyinosu	strums useu		iubbiutbiy	VVOIN

	<b>1</b>		
Pseudomonas aeruginosa strain	Official	Notes	Reference/origin
access number in Skurnik lab	name		
5513			HUSLAB
5514			HUSLAB
5525			HUSLAB
5537			HUSLAB
5538		MDR	HUSLAB
5539		MDR	HUSLAB
5548			HUSLAB
5550			HUSLAB
5551			HUSLAB
5553			HUSLAB
5668			HUSLAB
5669			HUSLAB
5670			HUSLAB
5671			HUSLAB
5672			HUSLAB
5740			HUSLAB
5741			HUSLAB
5742			HUSLAB
5743			HUSLAB
5745			HUSLAB
5746			HUSLAB
5747			HUSLAB
5826			HUSLAB
5827		MDR	HUSLAB
5828			HUSLAB
5829			HUSLAB
5831			HUSLAB
5832			HUSLAB
5832		MDR	HUSLAB
5834		MDR	HUSLAB
5854 E92E		WIDK	
5855			
5850			
5857			
5838			
5839			HUSLAB
5840			HUSLAB
5841			HUSLAB
5842		MDR	HUSLAB
5844		MDR	HUSLAB
5845			HUSLAB
5846			HUSLAB
5847			HUSLAB
5848			HUSLAB
6327	PA1		(Mattila, Ruotsalainen & Jalasvuori 2015)
6329	PA8		(Mattila, Ruotsalainen & Jalasvuori 2015)
6331	PA11		(Mattila, Ruotsalainen & Jalasvuori 2015)
6663			HUSLAB

According to the GDPR law, official strain codes must not be presented for clinical strains from HUSLAB to protect patient identity.

MDR: strain confirmed to be multidrug resistant.

Table S2: Phages used in the phylogenetic tree.

Phage name	GenBank accession no.
Pseudomonas phage Kraken	KT372692.1
Pbunalikevirus phiVader	KT254130.1
Pseudomonas phage Poseidon	KT372696.1
Pseudomonas phage Kula	KT372693.1
Pseudomonas phage Nessie	KT372695.1
Pseudomonas aeruginosa isolate ph_PII10A	LT594786.1
Pseudomonas phage SN	FM887021.1
Pseudomonas phage JG024	GU815091.1
Pseudomonas phage NP3	KU198331.1
Pseudomonas phage 14-1	FM897211.1
Pseudomonas phage vB_Pae_PS44	KM434184.1
Pseudomonas phage vB_PaeM_E215	MF490241.1
Pseudomonas phage NH-4	JN254800.1
Pseudomonas phage SL1	MF768470.1
Pseudomonas phage phiKT28	KP340287.1
Pseudomonas phage KPP12 DNA	AB560486.1
Pseudomonas phage vB_PaeM_PAO1_Ab27	LN610579.1
Pseudomonas phage vB_PaeM_E217	MF490240.1
Pseudomonas phage vB_PaeM_CEB_DP1	KR869157.1
Pseudomonas phage BrSP1	MF623055.1
Pseudomonas phage S12-1 DNA	LC102730.1
Pseudomonas phage LMA2	FM201282.1

Table S3: Predicted genes of P. aeruginosa phage fHo-PaeO1. Annotations made by Elsi Pulkkinen. Homologs were achieved from BLASTp analyzes.

Locus	Position	GC	Protein	Amino acid sequence identity/similarity to best	E-value	Accession no
tag		(%)	length (aa)	homologs	(BLAST)	
				(% amino acid identity)		
FHP001	665 - 1234	59.5	570	hypothetical protein PPSN_gp77 [Pseudomonas	7e-138	YP_002418883.1
				phage SN]		
				hypothetical protein [Pseudomonas phage S12-1]	1e-137	BAU16489.1
FHP002c	1401 -	56.1	615	hypothetical protein PII10A_02 [Pseudomonas	1e-142	SBT96684.1
	2015			aeruginosa]		
				hypothetical protein PPSN_gp78 [Pseudomonas	4e-142	YP_002418884.1
				phage SN]		
FHP003c	2207 -	59.2	672	putative minor head protein [Pseudomonas	4e-157	SBT96685.1
	2878			aeruginosa]		
				hypothetical protein [Pseudomonas phage KPP12]	1e-143	YP_007238232.1
FHP004c	2889 -	55.7	312	hypothetical protein PP141_gp79 [Pseudomonas	1e-72	YP_002364387.1
	3200			phage 14-1]		
				hypothetical protein vBPaeME217_00082	7e-72	ASZ72466.1
				[Pseudomonas phage vB_PaeM_E217]		
FHP005c	3253-3474	51.4	222	hypothetical protein PP141_gp80 [Pseudomonas	3e-44	YP_002364388.1
				phage 14-1]		
				hypothetical protein I7A_082c [Pseudomonas	6e-44	YP_007002628.1
				phage NH-4]		
FHP006c	3484 -	56.9	255	hypothetical protein PP141_gp81 [Pseudomonas	2e-53	YP_002364389.1
	3738			phage 14-1]		
				hypothetical protein [Pseudomonas aeruginosa]	5e-50	WP_121332560.1

		1	I			
FHP007c	3792 -	55.6	225	hypothetical protein LBL3_gp79 [ <i>Pseudomonas</i>	3e-47	YP_002154224.1
	4016			phage LBL3 hypothetical protein PPSN_gp83 [ <i>Pseudomongs</i>	2e-46	YP 002418889.1
				phage SN]	20 40	11_002410005.1
FHP008c	4082 -	55.7	327	hypothetical protein [Pbunalikevirus phiVader]	2e-73	ALJ99257.1
	4408			hypothetical protein [Pseudomonas phage E79]	3e-73	AXF41825.1
FHP009c	4405 -	59.1	648	hypothetical protein [Pseudomonas phage PA5]	9e-149	APD20735.1
	5052			hypothetical protein PJG24_088 [Pseudomonas	5e-148	YP_006200852.1
				phage JG024]		
FHP010c	5084 -	58.1	210	hypothetical protein [ <i>Pseudomonas aeruginosa</i> ]	7e-45	WP_015994944.1
	3233			vB PaeM PAO1 Ab27]	86-40	1P_009124313.1
FHP011c	5290 -	51.9	216	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	2e-43	YP_009215142.1
	5505			hypothetical protein PJG24_090 [Pseudomonas	1e-42	YP_006200854.1
	5502	E4 2	201	phage JG024	Fo 41	414076209 1
FNF012C	5702	54.2	201	hypothetical protein PP141 gp87 [Pseudomonas	8e-41	YP 002364395.1
				phage 14-1]		
FHP013c	5699 -	51.2	252	hypothetical protein LMA2_gp89 [Pseudomonas	1e-53	YP_002154322.1
	5950			phage LMA2]	20.52	414076200 1
				hypothetical protein [Pseudomonds phage NPS]	20-55	AWIQ76209.1
FHP014c	6037 -	50.3	189	hypothetical protein PP141_gp89 [Pseudomonas	9e-40	YP_002364397.1
	6225			phage 14-1]		
				hypothetical protein PII10A_14 [ <i>Pseudomonas</i>	1e-37	SBT96696.1
FHP015c	6228 -	54.5	918	tail length tape-measure protein [ <i>Pseudomonas</i>	0	AXF41778.1
	7145			phage E79]		-
				tail length tape-measure protein [ <i>Pseudomonas</i>	0	AMQ76211.1
EHP016c	7192 -	53.8	303	phage NP3] hypothetical protein PPSN_gp01 [ <i>Pseudomongs</i>	5e-64	YP 002418807 1
1111 0100	7494	55.0	303	phage SN]	50 04	11_002410007.1
				hypothetical protein vBPaeMLS1_39 [Pseudomonas	4e-60	AVJ48808.1
FUD017a	7022	F2 1	1 47	phage vB_PaeM_LS1]	(a. 22	VD 003418800 1
FHP01/C	7822 - 7968	53.1	147	phage SN1	66-23	19_002418809.1
				hypothetical protein SAMN05216409_118116	6e-13	SER37912.1
				[Pseudomonas lutea]		
FHP018	8144 -	53.1	1383	terminase large subunit [ <i>Pseudomonas</i> phage	0	ANT44190.1
	5520			putative terminase large subunit [ <i>Pseudomonas</i>	0	YP 002154147.1
				phage LBL3]		-
FHP019c	9563 -	59.4	384	hypothetical protein PP141_gp04 [ <i>Pseudomonas</i>	5e-85	YP_002364312.1
	9946			pnage 14-1] hypothetical protein [ <i>Pseudomongs</i> phage NP3]	1e-84	AM076120.1
FHP020c	9943 -	58.0	219	hypothetical protein PPSN_gp06 [Pseudomonas	1e-44	YP_002418812.1
	10161			phage SN]		
				hypothetical protein BrSP1_22 [ <i>Pseudomonas</i>	3e-44	ATI16273.1
FHP021c	10161 -	61.8	351	hypothetical protein PPSN_gp07 [Pseudomongs	4e-78	YP 002418813.1
	10511	01.0	001	phage SN]		
				hypothetical protein SL1_06 [Pseudomonas phage	1e-75	AUS03281.1
ELIDODOC	10555	50.4	200	SL1] hypothetical protein [Regudemengs phage DL68]	80.86	VD 000215120 1
FHFUZZC	10353 -	55.4	333	hypothetical protein LBL3 gp06 [Pseudomonas	1e-84	YP_009215125.1 YP_002154151.1
				phage LBL3]		-
FHP023c	10956 -	55.6	780	hypothetical protein PP141_gp08 [ <i>Pseudomonas</i>	0	YP_002364316.1
	11/35			phage 14-1] hypothetical protein vB. Pae. PS44, 00009	0	YP 009211333 1
				[ <i>Pseudomonas</i> phage vB_Pae_PS44]	0	11_0002110000.1
FHP024c	11823 -	61.3	432	hypothetical protein BrSP1_26 [Pseudomonas	3e-82	ATI16277.1
	12254			phage BrSP1]	Co. 80	MD 121222544.1
FHP025c	12271 -	57.7	588	hypothetical protein [ <i>Pseudomonus</i> nhage NP3]	2e-143	AMQ76126.1
	12858	5717		hypothetical protein PP141_gp10 [Pseudomonas	1e-142	YP_002364318.1
	105			phage 14-1]		
FHP026c	12868 -	52.1	96	hypothetical protein vBPaeME215_00084	4e-11	ASZ72562.1
	12,000			hypothetical protein vB_Pae_PS44_00012	1e-10	YP_009211336.1
				[Pseudomonas phage vB_Pae_PS44]		
FHP027c	12960 -	56.8	933	hypothetical protein vBPaeME215_00085	0	ASZ72563.1
	13035			hypothetical protein PP141 gp12 [Pseudomongs	0	YP 002364320.1
				phage 14-1]		

FHP028c	13996 -	57.1	501	hypothetical protein vBPaeME215_00086	4e-120	ASZ72564.1
	14496			[Pseudomonas phage vB_PaeM_E215]		
				hypothetical protein PPSN_gp14 [Pseudomonas	1e-119	YP_002418820.1
				phage SN]		
FHP029	14519 -	49.4	168	ERROR: "No significant similarity found"		
	14686					
FHP030c	14987 -	52.6	312	hypothetical protein PII10A_31 [Pseudomonas	3e-68	SBT96713.1
	15298			aeruginosa]		
				hypothetical protein [Pseudomonas phage	3e-67	YP_009124336.1
				vB_PaeM_PAO1_Ab27]		
FHP031c	15304 -	58.2	213	hypothetical protein [Burkholderia vietnamiensis]	4e-41	WP_01605/510.1
	15510			Resendemends phage vB Page PS44_00018	20-40	1P_009211342.1
EHP032c	15504 -	56.5	324	hypothetical protein LMA2 gn15 [Pseudomongs	3e-75	YP 002154249 1
1111 0520	15827	50.5	524	phage LMA2]	50 / 5	11_002134245.1
				hypothetical protein vB Pae PS44 00019	2e-73	YP 009211343.1
				[ <i>Pseudomonas</i> phage vB_Pae_PS44]		-
FHP033c	15859 -	53.0	402	hypothetical protein LMA2_gp16 [Pseudomonas	2e-92	YP_002154250.1
	16260			phage LMA2]		
				hypothetical protein [ <i>Pseudomonas</i> phage	9e-92	YP_009124339.1
5110024	16111	56.0	2200	vB_PaeM_PAO1_Ab27]	0	CDT0C747.4
FHP034	16441 -	56.9	2298	putative portal protein [Pseudomonds deruginosd]	0	SB196/1/.1
	10/50			PB11	0	VP 002455948 1
EHP035	18738 -	53.6	837	putative minor head protein [ <i>Pseudomongs</i> phage	0	YP_002433348.1
	19574	5510		KPP12]	°	
				putative head protein [ <i>Pseudomonas</i> phage PB1]	0	YP_002455949.1
FHP036	19593 -	55.6	207	hypothetical protein PPSN_gp21 [Pseudomonas	2e-41	YP_002418827.1
	19799			phage SN]		
				hypothetical protein LBL3_gp17 [Pseudomonas	6e-40	YP_002154162.1
				phage LBL3]		
FHP037	19796 -	53.2	141	hypothetical protein PPSN_gp22 [ <i>Pseudomonas</i>	4e-23	YP_002418828.1
	19936			pnage SNJ hypothetical protein BIG24, 021 [ <i>Beaudomonae</i>	40.22	VD 006200786 1
				nbage IG024]	46-22	1P_000200780.1
FHP038	19936 -	42.9	126	No significant similarity found.		
	20061					
					-	
FHP039	20489 -	58.2	1383	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	0	YP_009215206.1
	218/1			hypothetical protein PP141_gp22 [Pseudomonus	0	1P_002364330.1
EHP040	21875 -	62.6	636	hypothetical protein PP141 gp23 [Pseudomongs	5e-148	YP 002364331 1
1111 040	22510	02.0	000	phage 14-1]	50 140	11_002004001.1
				structural protein [Pseudomonas phage SN]	2e-147	YP_002418830.1
FHP041	22520 -	61.0	1149	hypothetical protein PP141_gp24 [Pseudomonas	0	YP_002364332.1
	23668			phage 14-1]		
				putative major structural protein [Pseudomonas	0	YP_002154257.1
5110040	22770	55.2	420	phage LMA2]	6- 101	N/D 404000504.4
FHP042	23770 -	55.3	438	hypothetical protein [ <i>Pseudomonas deruginosa</i> ]	6e-104	WP_121332534.1
	24207			hypothetical protein [Pseudomonus phage KPP12]	20-105	1P_00/2581/9.1
FHP043	24222 -	59.4	468	DUF4054 domain-containing protein [Pseudomonas	5e-110	WP_016066139.1
	24689			aeruginosa]		
				putative structural protein [ <i>Pseudomonas</i> phage	2e-108	YP_002154259.1
ELIDOAA	24696	E2 1	200	LIVIAZ]	40.92	VD 007229191 1
FNF044	24000 - 25084	52.1	222	KPP12]	48-92	15_00/230101.1
	23004			structural protein [ <i>Pseudomonas</i> phage phiKTN6]	1e-91	AKJ71558.1
FHP045	25092 -	48.2	552	hypothetical protein vBPaeME215 00007	1e-133	ASZ72485.1
	25643			[Pseudomonas phage vB_PaeM_E215]		
				hypothetical protein [Pseudomonas phage	2e-133	YP_009124349.1
				vB_PaeM_PAO1_Ab27]		
FHP046	25640 -	54.8	582	hypothetical protein [Pseudomonas aeruginosa]	3e-137	WP_015981230.1
	26221			nypothetical protein [ <i>Pseudomonas</i> phage KPP12]	1e-136	YP_00/238183.1
FHP047	26237 -	59.8	1515	hypothetical protein vB Pae436M-8 30	0	ANT44216.1
-	27751	-		[Pseudomonas phage vB_Pae436M-8]		
				putative structural protein [Pseudomonas phage	0	YP_002154263.1
				LMA2]		
FHP048	27810 -	59.2	453	hypothetical protein [Pseudomonas aeruginosa]	2e-103	WP_015992745.1
	28262			structural protein [Pseudomonas phage phiKT28]	2e-102	AKJ71471.1
FHP049	28262 -	54.3	324	hypothetical protein [Pseudomonas aeruainosa]	2e-75	WP 015992746.1
-	28585	-		putative structural protein [Pseudomonas phage	6e-75	YP_006200797.1
				JG024]		

FHP050	28582 - 28932	52.4	351	hypothetical protein [ <i>Pseudomonas aeruginosa</i> ] structural protein [ <i>Pseudomonas</i> phage SL1]	3e-78 1e-77	WP_015992747.1 AUS03345.1
FHP051	28934 - 29365	63.9	432	hypothetical protein LMA2_gp33 [ <i>Pseudomonas</i>	6e-94	YP_002154267.1
	29303			hypothetical protein vBPaeMDP1_0034 [ <i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	4e-93	AKP24421.1
FHP052	29375 - 29878	51.6	504	hypothetical protein [ <i>Pseudomonas aeruginosa</i> ] structural protein [ <i>Pseudomonas</i> phage SN]	3e-114 6e-114	WP_015992749.1 YP_002418842.1
FHP053	29878 - 30417	51.1	540	putative structural protein [ <i>Pseudomonas</i> phage	6e-128	YP_002154269.1
				putative structural protein [ <i>Pseudomonas</i> phage LBL3]	2e-127	YP_002154178.1
FHP054	30426 - 31019	47.3	594	putative structural protein [ <i>Pseudomonas</i> phage KPP12]	4e-138	YP_007238190.1
				hypothetical protein vBPaeME217_00038 [Pseudomonas phage vB_PaeM_E217]	2e-137	ASZ72422.1
FHP055	31029 - 31457	56.6	429	hypothetical protein [ <i>Pseudomonas aeruginosa</i> ] hypothetical protein LMA2_gp37 [ <i>Pseudomonas</i> phage LMA2]	5e-101 2e-100	WP_121332529.1 YP_002154271.1
FHP056	31461 - 34037	58.1	2577	putative lytic tail protein [ <i>Pseudomonas</i> phage LMA2]	0	YP_002154272.1
500057	24027	51.0	0.54	internal (core) protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76156.1
FHP057	34037 - 34900	51.9	864	putative structural protein [ <i>Pseudomonas</i> phage	0	YP_002154273.1
	34300			putative structural protein [ <i>Pseudomonas</i> phage vB PaeM CEB DP1]	0	AKP24427.1
FHP058	34900 - 35433	48.1	534	hypothetical protein PP141_gp41 [ <i>Pseudomonas</i> phage 14-1]	2e-127	YP_002364349.1
				hypothetical protein [Pseudomonas phage DL68]	6e-127	YP_009215187.1
FHP059	35828 - 36154	53.2	327	putative baseplate protein [ <i>Pseudomonas</i> phage JG024]	1e-71	YP_006200807.1
				baseplate protein [ <i>Pseudomonas</i> phage phiKTN6]	1e-71	AKJ71573.1
FHP060	36211 - 37464	57.7	1254	putative structural protein [ <i>Pseudomonas</i> phage LMA2]	0	YP_002154276.1
				putative baseplate protein [ <i>Pseudomonas</i> phage SN]	0	YP_002418850.1
FHP061	37461 -	56.0	1515	hypothetical protein PP141_gp44 [Pseudomonas	0	YP_002364352.1
FHP061	37461 - 38975	56.0	1515	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage VB Pae436M-8]	0 0	YP_002364352.1 ANT44230.1
FHP061 FHP062	37461 - 38975 38980 -	56.0	1515 2895	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024	0 0 0	YP_002364352.1 ANT44230.1 ASZ72502.1
FHP061 FHP062	37461 - 38975 38980 - 41874	56.0	1515 2895	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruninosa]	0 0 0 0	YP_002364352.1 ANT44230.1 ASZ72502.1 SBT96745.1
FHP061 FHP062 FHP063	37461 - 38975 38980 - 41874 41876 -	56.0 57.1 58.5	1515 2895 429	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage	0 0 0 0 3e-99	YP_002364352.1 ANT44230.1 ASZ72502.1 SBT96745.1 AKJ71577.1
FHP061 FHP062 FHP063	37461 - 38975 38980 - 41874 41876 - 42304	56.0 57.1 58.5	1515 2895 429	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage	0 0 0 0 3e-99 3e-99	YP_002364352.1 ANT44230.1 ASZ72502.1 SBT96745.1 AKJ71577.1 YP_009124367.1
FHP061 FHP062 FHP063 FHP064	37461 - 38975 38980 - 41874 41876 - 42304 -	56.0 57.1 58.5 60	1515 2895 429 663	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage	0 0 0 0 3e-99 3e-99 3e-162	YP_002364352.1 ANT44230.1 ASZ72502.1 SBT96745.1 AKJ71577.1 YP_009124367.1 YP_009124368.1
FHP061 FHP062 FHP063 FHP064	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966	56.0           57.1           58.5           60	1515 2895 429 663	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27]	0 0 0 0 3e-99 3e-99 3e-99 3e-162	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1
FHP061 FHP062 FHP063 FHP064	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966	56.0 57.1 58.5 60	1515 2895 429 663	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage vB_PaeM_PA01_Ab27] endolysin [Pseudomonas phage PB1] herethetical protein [P14_0_10_partices	0 0 0 0 3e-99 3e-99 3e-162 9e-161	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1
FHP061           FHP062           FHP063           FHP064           FHP065c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241	56.0           57.1           58.5           60           51.2	1515 2895 429 663 252	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage vB_PaeM_PA01_Ab27] endolysin [Pseudomonas phage PB1] hypothetical protein PP141_gp48 [Pseudomonas phage 14-1]	0 0 0 0 0 3e-99 3e-99 3e-99 3e-162 9e-161 2e-50	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002364356.1
FHP061 FHP062 FHP063 FHP064 FHP065c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241	56.0           57.1           58.5           60           51.2	1515 2895 429 663 252	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage LMA2]	0 0 0 0 0 3e-99 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002364356.1         YP_002154281.1
FHP061           FHP062           FHP063           FHP064           FHP065c           FHP066c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241 43521 - 44432	56.0           57.1           58.5           60           51.2           57.2	1515 2895 429 663 252 912	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage LMA2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein PP141_gp49 [ <i>Pseudomonas</i> phage LMA2]	0 0 0 0 3e-99 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002364356.1         YP_002154281.1         SBT96752.1         YP_002364357.1
FHP061 FHP062 FHP063 FHP064 FHP065c FHP066c FHP067c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241 43521 - 44432 44487 -	56.0           57.1           58.5           60           51.2           57.2           53.7	1515 2895 429 663 252 912 555	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage vB_PaeM_PA01_Ab27] endolysin [Pseudomonas phage PB1] hypothetical protein PP141_gp48 [Pseudomonas phage 14-1] hypothetical protein LMA2_gp47 [Pseudomonas phage LMA2] putative DNA ligase [Pseudomonas aeruginosa] hypothetical protein PP141_gp49 [Pseudomonas phage 14-1] hypothetical protein ITA_051c [Pseudomonas	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002364356.1         YP_002154281.1         SBT96752.1         YP_002364357.1         YP_007002597.1
FHP061           FHP062           FHP063           FHP064           FHP065c           FHP066c           FHP067c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041	56.0       57.1         57.1       58.5         60       51.2         57.2       53.7	1515 2895 429 663 252 912 555	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage LMA2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein PP141_gp49 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage NH-4] hypothetical protein [ <i>Pseudomonas</i> phage KPP22]	0 0 0 0 3e-99 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002364356.1         YP_002364357.1         SBT96752.1         YP_007002597.1         BAU20664.1
FHP061 FHP062 FHP063 FHP064 FHP065c FHP066c FHP067c FHP068c	37461 - 38975 38980 - 41874 41876 - 42304 - 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646	56.0           57.1           58.5           60           51.2           57.2           53.7           60.6	1515 2895 429 663 252 912 555 609	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage 14-2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage NH-4] hypothetical protein [ <i>Pseudomonas</i> phage KPP22] hypothetical protein [ <i>Pseudomonas</i> phage KPP22] hypothetical protein vBPaeME215_0030	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002364356.1         YP_002154281.1         SBT96752.1         YP_002364357.1         YP_00202597.1         BAU20664.1         ASZ72508.1
FHP061           FHP062           FHP063           FHP064           FHP065c           FHP066c           FHP067c           FHP068c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646	56.0         57.1         58.5         60         51.2         53.7         60.6	1515 2895 429 663 252 912 555 609	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage vB_PaeM_PA01_Ab27] endolysin [Pseudomonas phage PB1] hypothetical protein PP141_gp48 [Pseudomonas phage 14-1] hypothetical protein ITA_051c [Pseudomonas phage 14-1] hypothetical protein I7A_051c [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage KPP22] hypothetical protein QS125_00030 [Pseudomonas phage vB_PaeM_E215] hypothetical protein ORF050 [Pseudomonas phage	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002154281.1         SBT96752.1         YP_002364357.1         YP_007002597.1         BAU20664.1         ASZ72508.1
FHP061 FHP062 FHP063 FHP064 FHP064 FHP065c FHP066c FHP067c FHP068c	37461 - 38975 38980 - 41874 41876 - 42304 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646	56.0         57.1         58.5         60         51.2         57.2         53.7         60.6	1515 2895 429 663 252 912 555 609	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein PP141_gp49 [ <i>Pseudomonas</i> phage 14-2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage KP22] hypothetical protein Reseudomonas phage KP22] hypothetical protein Reseudomonas phage KP22] hypothetical protein ORF050 [ <i>Pseudomonas</i> phage F8]	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139 1e-136	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002364356.1         YP_002154281.1         SBT96752.1         YP_002364357.1         YP_007002597.1         BAU20664.1         ASZ72508.1         YP_001294467.1
FHP061           FHP062           FHP063           FHP063           FHP064           FHP065c           FHP066c           FHP067c           FHP068c           FHP069c	37461 - 38975 38980 - 41874 41876 - 42304 - 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646	56.0       57.1         57.1       58.5         60       51.2         57.2       53.7         60.6       60.1	1515 2895 429 663 252 912 555 609 900	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage 14-2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage 14-1] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage NH-4] hypothetical protein IPseudomonas phage KP22] hypothetical protein ORF050 [ <i>Pseudomonas</i> phage F8] hypothetical protein ORF050 [ <i>Pseudomonas</i> phage F41]	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139 1e-136 0	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002364356.1         YP_002364356.1         YP_002364357.1         SBT96752.1         YP_007002597.1         BAU20664.1         ASZ72508.1         YP_002364360.1
FHP061           FHP062           FHP063           FHP064           FHP065c           FHP066c           FHP067c           FHP068c           FHP069c	37461 - 38975 38980 - 41874 41876 - 42304 - 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646 45700 - 46599	56.0         57.1         58.5         60         51.2         57.2         53.7         60.6         60.1	1515 2895 429 663 252 912 555 609 900	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage 14-2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage KP22] hypothetical protein ( <i>Pseudomonas</i> phage KP22] hypothetical protein ORF050 [ <i>Pseudomonas</i> phage F8] hypothetical protein PP141_gp52 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage KP22] hypothetical protein [ <i>Pseudomonas</i> phage F8] hypothetical protein PP141_gp52 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage KP22] hypothetical protein PP141_gp52 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage L68]	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139 1e-136 0 0 0	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124367.1         YP_009124368.1         YP_002364356.1         YP_002364356.1         YP_002364356.1         YP_002364357.1         SBT96752.1         YP_007002597.1         BAU20664.1         ASZ72508.1         YP_002364360.1         YP_009215176.1
FHP061           FHP062           FHP063           FHP063           FHP064           FHP065c           FHP066c           FHP067c           FHP068c           FHP069c           FHP069c           FHP070c	37461 - 38975 38980 - 41874 41876 - 42304 - 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646 45700 - 46599 46688 -	56.0         57.1         58.5         60         51.2         53.7         60.6         53.9	1515 2895 429 663 252 912 555 609 900 621	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14-1] structural protein [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [ <i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [ <i>Pseudomonas</i> <i>aeruginosa</i> ] tail fibers component [ <i>Pseudomonas</i> phage phiKTN6] hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] putative lytic enzyme [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27] endolysin [ <i>Pseudomonas</i> phage PB1] hypothetical protein PP141_gp48 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage LMA2] putative DNA ligase [ <i>Pseudomonas</i> aeruginosa] hypothetical protein I7A_051c [ <i>Pseudomonas</i> phage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage KPP22] hypothetical protein VBPaeME215_00030 [ <i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein ORF050 [ <i>Pseudomonas</i> phage F8] hypothetical protein [ <i>Pseudomonas</i> phage LMA2]	0 0 0 0 3e-99 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139 1e-136 0 0 0 3e-145	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124367.1         YP_002455978.1         YP_002364356.1         YP_002364356.1         YP_002364357.1         SBT96752.1         YP_002364357.1         PP_007002597.1         BAU20664.1         ASZ72508.1         YP_002364360.1         YP_002154286.1
FHP061           FHP062           FHP063           FHP064           FHP065c           FHP066c           FHP067c           FHP068c           FHP069c           FHP070c	37461 - 38975 38980 - 41874 41876 - 42304 - 42966 42990 - 43241 43521 - 44432 44487 - 45041 45038 - 45646 45700 - 46599 46688 - 47308	56.0         57.1         58.5         60         51.2         57.2         53.7         60.6         60.1         53.9	1515 2895 429 663 252 912 555 609 900 621	hypothetical protein PP141_gp44 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage vB_Pae436M-8] hypothetical protein vBPaeME215_00024 [Pseudomonas phage vB_PaeM_E215] putative tail fiber protein [Pseudomonas aeruginosa] tail fibers component [Pseudomonas phage phiKTN6] hypothetical protein [Pseudomonas phage vB_PaeM_PA01_Ab27] putative lytic enzyme [Pseudomonas phage vB_PaeM_PA01_Ab27] endolysin [Pseudomonas phage PB1] hypothetical protein PP141_gp48 [Pseudomonas phage 14-1] hypothetical protein ITA_051c [Pseudomonas phage 14-1] hypothetical protein ITA_051c [Pseudomonas phage 14-1] hypothetical protein ITA_051c [Pseudomonas phage NH-4] hypothetical protein RP500300 [Pseudomonas phage vB_PaeM_E215] hypothetical protein ORF050 [Pseudomonas phage 14-1] hypothetical protein PP141_gp52 [Pseudomonas phage 14-1] hypothetical protein ITA_0525 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage F8] hypothetical protein [Pseudomonas phage F8] hypothetical protein [Pseudomonas phage LMA2] phage 14-1] hypothetical protein PP141_gp52 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage LMA2] hypothetical protein [Pseudomonas phage LMA2]	0 0 0 0 3e-99 3e-99 3e-162 9e-161 2e-50 3e-50 0 0 2e-133 5e-133 9e-139 1e-136 0 0 0 3e-145 3e-145	YP_002364352.1         ANT44230.1         ASZ72502.1         SBT96745.1         AKJ71577.1         YP_009124367.1         YP_009124368.1         YP_002455978.1         YP_002364356.1         YP_002154281.1         SBT96752.1         YP_002364357.1         YP_0020264357.1         YP_0020264357.1         YP_0020264357.1         YP_002364360.1         YP_001294467.1         YP_002215176.1         YP_002154286.1         YP_00202600.1

48552         5.7         411         prophetical protein Pical gas2 [Pseudomones phage Pir2] parative DMA (Edseudomones Pir2] parative DMA (Edse	FHP071c	47403 -	54.6	1560	DNA helicase [ <i>Pseudomongs</i> phage DL68]	0	YP 009215174.1
FHIPTOR2         48859- 52.00         5.7         41.1         Psycholacia al potein Pseudomonas plage PP12] partitive DNA fielding Pseudomonas plage PP12] 52.463         28-94         VP_00023802.1           PHP073c         53.2         74.2		48962			hypothetical protein PP141_gp54 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364362.1
PHP07ac         apge/ 2269         So         So         PAP polymerase (II alpha subunit (Recordomons Parage & Parate SL1)         So         AV483841           PHP07ac         52.66         So         So         So         So         Parate & Parate SL1)         Personances phage         0         VP_007200201.1           PHP07ac         So         So         So         So         So         Personances phage         0         VP_007200200.1           PHP07ac         So         So         So         Parateve DNA polymerase III applion Subunit (Personances phage INAL)         2e-135         VP_0072154200.1           So         So         So         So         Parateve DNA polymerase III applion Subunit (Personances phage INAL)         2e-135         VP_0072154200.1           So         So         So         So         Parateve DNA polymerase III applion Parateve DNA polymerase III applion Parateve DNA polymerase III application Parateve DNA polymerase III applicati P	FHP072c	48959 - 49369	55.7	411	hypothetical protein [ <i>Pseudomonas</i> phage KPP12] putative DNA helicase [ <i>Pseudomonas</i> phage NH-4]	2e-94	YP_007238208.1
S2669         S2669         S2669         S2669         S2669         S2669         S2609         S260         S2609         S260         S2609         S	FHP073c	49362 -	55.2	3108	DNA polymerase III alpha subunit [Pseudomonas	3e-94 0	YP_007002602.1 AVJ48844.1
FHP074c         5340- 3023         530         555         plative DNA polymerase III epidin subuit (Peudomons phage NH-4) putative DNA polymerase III epidin subuit (Peudomons phage NLA]         2e-135         YP_00702604.1           FHP075c         5309- 54115         58.4         1017         Yp_0015in P1A1 gp58 [Peudomons phage 14:1] putative 3-pholynulectode kinase phage 14:1] putative 3-pholynulectode kinase phage 14:1] putative 3-pholynulectode kinase phage 200201         0         YP_002364365.1           FHP075c         54115         47.4         192         hypothetical protein P1A1 gp58 [Peudomons phage 14:1] putative symbol polynulectode kinase phage 200201         1e-35         AV7.05000828.1           FHP077c         54311         58.0         918         putative tymink/star symbase (Pseudomons) phage 200201         0         YP_00232631.1           FHP077c         55432         51.7         207         hypothetical protein (Pseudomons) phage 74.21         7e-40         YP_00232631.1           FHP077c         55432         51.7         207         hypothetical protein (Pseudomons) phage 74.21         7e-40         YP_002364370.1           FHP078c         5542.5         58.9         231         hypothetical protein P1A1 gp52 [Pseudomons         5e-46         YP_00214596.1           FHP080c         55195         53.9         219         hypothetical protein P1A1 gp52 [Pseudomons		52469			phage vB_PaeM_LS1] putative DNA polymerase [ <i>Pseudomonas</i> phage KPP12]	0	YP_007238209.1
JAND         Image in the protective DMA polymerase III epiden suburit performance phage MA3]         3e-135         VP_002154290.1           PHP075E         53099- 54115         58.4         1017         hypothetical protein PFALg058 [Pseudomonas phage field]         0         VP_002264366.1           PHP076E         54113- 54115         47.4         152         hypothetical protein pHR122_051 [Pseudomonas phage fiG23]         1e-35         AK71409.1           PHP076         54131- 54311         54.8         91.8         putative tymphylote PIG24_060 [Pseudomonas phage fiG23]         1e-35         AK71409.1           PHP077         54311         54.0         91.8         putative tymphylote PIG24_060 [Pseudomonas phage fiG23]         0         VP_007238213.1           PHP078         5522         56.7         21.1         phage fiG23         VP_00223417.1         VP_00223417.1           PHP078         55572         56.7         21.1         phage fiG23         VP_002241866.1         VP_002214260.1           PHP078         55572         57.7         21.1         phage filt Pseudomonas         Fig.462 [Pseudomonas phage filt Pseudomonas         Fig.463         VP_002214261.1           Fif40802         55927         57.3         21.9         this asemby protein [Pseudomonas         Fig.464         VP_002214263.1.1	FHP074c	52469 -	53.0	555	putative DNA polymerase III epsilon subunit	2e-135	YP_007002604.1
FIHP075c         5309- 54115         58.4         1017         hypothetical protein P141_gp58 [Pseudomonas page 14:1] putative 3".phosphatase 5".polynucleotide kinase         0         YP_002364366.1           PHP076c         54118-         47.4         192         hypothetical protein pNIG2_061 [Pseudomonas         16-35         AV71499.1           PHP076c         54118-         47.4         192         hypothetical protein pNIG2_060 [Pseudomonas         16-35         AV71499.1           PHP077c         54311         58.0         918         putative thymothetical protein pNIG2_060 [Pseudomonas         0         YP_00620025.1           PHP077c         54312         56.7         207         hypothetical protein [Pseudomonas phage KP12]         7e-40         YP_00723211.1           PHP077c         5542         56.7         231         hypothetical protein [Pseudomonas phage KP12]         7e-40         YP_0023621.1           PHP078c         5542         56.7         231         hypothetical protein PNK_gp63 [Pseudomonas         5e-49         YP_0024866.1           55923         53.3         219         hypothetical protein PNK_gp63 [Pseudomonas         5e-46         AV7159.1           FHP081c         55937         58.0         219         hypothetical protein PNK_gp63 [Pseudomonas         1e-43         YP_00236437.1 <td></td> <td>55025</td> <td></td> <td></td> <td>putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage LMA2]</td> <td>3e-135</td> <td>YP_002154290.1</td>		55025			putative DNA polymerase III epsilon subunit [ <i>Pseudomonas</i> phage LMA2]	3e-135	YP_002154290.1
Labor         Labor         putative 3*phosphatase 5*polynuclectide kinase         0         S8T96767.1           FHP076c         S4136         S414         192         Phypothetical protein phildT28_061 [Pseudomonas phage 6024]         1e-35         AK/T4499.1           FHP077c         S4311         S5.0         918         putative 1*phildT26_061 [Pseudomonas phage 6024]         0         YP_006200824.1           FHP077c         S4311         S5.0         918         putative 1*phildTylet synthase [Pseudomonas phage KP12]         0         YP_007238214.1           FHP077c         S5228         S1.7         207         Phypothetical protein [Pseudomonas phage KP12]         7e-40         YP_00238214.1           FHP078         S542- S5072         S5.7         231         Phypothetical protein [Pseudomonas phage SN]         7e-40         YP_002418869.1           FHP078         S542- S5072         S5.9         219         Phypothetical protein [Pseudomonas phage MA]         1e-48         YP_002418869.1           FHP078         S507         S5.0         219         Phypothetical protein [Pseudomonas phage MA]         1e-43         AK/1759.1           FHP088         S507         S5.0         219         Phypothetical protein Pictal gp62 [Pseudomonas phage MA]         1e-43         VP_00254373.1         Phypothetical prote	FHP075c	53099 - 54115	58.4	1017	hypothetical protein PP141_gp58 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364366.1
FHP076c         S413.9         S47.4         192         hypothetical protein philT22_061 [Pseudomonos phage [bit27]         1e-35         AV/7409.1           FHP077c         S431.1         S50.2         S40.0         918         putative thymidylate synthase [Pseudomonos phage [bit27]         0         YP_00728213.1           FHP077c         S523.8         S50.0         918         putative thymidylate synthase [Pseudomonos phage [bit27]         0         YP_00738214.1           FHP078c         S523.8         S1.7         207         hypothetical protein [Pseudomonos phage [PF31]         7e-40         YP_00738214.1           FHP078c         S527.8         S1.7         207         hypothetical protein [Pseudomonos phage [PF31]         7e-40         YP_002418869.1           FHP078c         S542.2         S6.7         23.1         hypothetical protein PI341_gp62 [Pseudomonos phage IA11]         7e-40         YP_002418869.1           FHP078c         S5705         S3.9         219         hypothetical protein PI341_gp62 [Pseudomonos phage IA11]         7e-40         YP_002154261.1           FHP080c         S5075         S8.0         219         hypothetical protein PI341_gp62 [Pseudomonos phage IA11]         7e-43         YP_00215427.1           FHP081c         S5037         S8.0         219         hypothetical protein					putative 3'-phosphatase 5'-polynucleotide kinase [Pseudomonas aeruginosa]	0	SBT96767.1
PHS09         Pringe Unit/20 pringe Unit/20 pring	FHP076c	54118 -	47.4	192	hypothetical protein phiKT28_061 [ <i>Pseudomonas</i>	1e-35	AKJ71499.1
FHP077c         54311 - 5228         58.0         918         putative thymidylate synthase [ <i>Pseudomonas</i> phage (PP21) putative thymidylate synthase [ <i>Pseudomonas</i> 0         VP_007282213.1           FHP078c         55228 - 55434         51.7         207         hypothetical protein [ <i>Pseudomonas</i> phage PA2] hypothetical protein [ <i>Pseudomonas</i> phage PA2]         1e-39         AP20762.1           FHP078c         55472         56.7         231         hypothetical protein [ <i>Pseudomonas</i> phage PA3]         1e-48         VP_002364370.1           FHP078c         55705         53.3         219         hypothetical protein PP3L gp52 [ <i>Pseudomonas</i> phage 141]         1e-48         VP_002364370.1           FHP081c         55907         58.0         219         hypothetical protein PP4L gp52 [ <i>Pseudomonas</i> phage 141]         1e-43         AK171595.1           FHP081c         55907         58.0         219         hypothetical protein P24L gp55 [ <i>Pseudomonas</i> phage 141]         1e-43         AK171595.1           FHP081c         55907         58.3         1002         hypothetical protein P14L gp56 [ <i>Pseudomonas</i> phage 141]         1e-43         VP_002364373.1           FHP084c         5752- 5837         58.3         1002         hypothetical protein P14L gp56 [ <i>Pseudomonas</i> phage 141]         1e-43         VP_002364375.1           FHP084c         5752- 59		54509			hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024]	3e-35	YP_006200824.1
Internation         Image Instance         Imputation through as phase (6024)         0         VP_006200825.1           FHP078c         \$5528 - \$1.7         207         httpothetical protein (Pseudomonas phage KP12)         7-40         XP_007282214.1           FHP078c         \$5574         \$6.7         213         httpothetical protein (Pseudomonas phage KP12)         7-40         XP_00238234.1           FHP078c         \$5575         \$6.7         213         httpothetical protein PSM_gp63 [Pseudomonas         5e-49         YP_00218869.1           FHP087c         \$5575         \$6.7         219         httpothetical protein PSM_gp63 [Pseudomonas         1e-48         YP_002154296.1           FHP087c         \$5507         \$5.8         219         httpothetical protein PSM_gp63 [Pseudomonas         1e-43         AK/71595.1           FHP087c         \$56125         \$8.8         219         httpothetical protein PSM_gp63 [Pseudomonas         1e-43         YP_002364373.1           FH9087c         \$56125         \$8.9         231         httpothetical protein PSM_gp63 [Pseudomonas         1e-43         YP_002364373.1           FH9087c         \$56355         \$8.9         231         httpothetical protein PSM_gp63 [Pseudomonas         0         YP_002364373.1           FH9087c         \$5752         \$5	FHP077c	54311 - 55228	58.0	918	putative thymidylate synthase [ <i>Pseudomonas</i> hage KPP12]	0	YP_007238213.1
FHP078c         55.228 - 55434         51.7         207         Inpotentical protein (Pseudomonas phage RP12) hypothetical protein (PSu godomonas phage PA5)         74-40         VP_00738212.11 APD20762.1           FHP078c         55.47         231         Inpotentical protein (PSu godomonas phage PA5)         5e-49         VP_00218859.1           FHP078c         55.705 - 55223         53.9         219         Inpotentical protein PSN gp63 (Pseudomonas phage 14.1)         1e-48         VP_002364370.1           FHP080c         55705 - 55223         53.9         219         Inpotentical protein (PSu gp63 (Pseudomonas phage 14.1)         1e-43         AKJ71595.1           FHP081c         55807 - 56125         58.0         219         Inpotentical protein (PA G65 (Pseudomonas phage 14.1)         1e-43         AKJ71595.1           FHP082c         56125 - 56335         58.9         231         Inpotentical protein (P1A1 gp65 (Pseudomonas phage 14.1)         1e-43         VP_00702611.1           FHP082c         56443 - 57444         55.3         1002         Inpotentical protein P1A1 gp65 (Pseudomonas phage 14.1)         1e-43         VP_002364373.1           FHP084c         57552 - 58370         56.1         1002         Inpotentical protein P1A1 gp65 (Pseudomonas phage 14.1)         1e-49         VP_00236437.1           FHP084c         57532 - 58370 <td< td=""><td></td><td>00110</td><td></td><td></td><td>putative thymidylate synthase [<i>Pseudomonas</i> phage JG024]</td><td>0</td><td>YP_006200825.1</td></td<>		00110			putative thymidylate synthase [ <i>Pseudomonas</i> phage JG024]	0	YP_006200825.1
55434         Functional protein (Pseudomonas phage PAS)         1e-39         APD20762.1           FHP079c         55672         \$6.7         231         hypothetical protein (PSNLgp63 (Pseudomonas phage PAS)         5e-49         YP_002364370.1           FHP080c         55705 - 5539         53.9         219         hypothetical protein (PSLgp63 (Pseudomonas phage PAS)         2e-46         YP_002154296.1           FHP080c         55075 - 5539         58.0         219         hypothetical protein (Pscudomonas phage PAS)         2e-46         AK771594.1           FHP081c         5507 - 5635         58.0         219         hypothetical protein (PScudomonas phage PAS)         2e-46         AK771594.1           FHP082c         56125 - 5635         58.0         219         hypothetical protein PP141_gp65 (Pseudomonas phage PAS)         4e-43         AK771595.1           FHP082c         56125 - 5635         58.9         231         hypothetical protein PP141_gp65 (Pseudomonas phage PAS)         4e-177         AMQ76185.1           FHP082c         5537         55.3         1002         hypothetical protein PP141_gp66 (Pseudomonas phage PAS)         4e-177         AMQ76185.1           FHP084c         5752 - 5872         55.1         1188         putative ATP-dependent exonuclease V [Pseudomonas phage PAS]         4e-177         AMQ76185.1 <td>FHP078c</td> <td>55228 -</td> <td>51.7</td> <td>207</td> <td>hypothetical protein [<i>Pseudomonas</i> phage KPP12]</td> <td>7e-40</td> <td>YP_007238214.1</td>	FHP078c	55228 -	51.7	207	hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	7e-40	YP_007238214.1
FHP079C         5542 - 5572         56.7         231         hypothetical protein PPAL1gp62 (Pseudomonas phage SN) hypothetical protein PLA1_gp62 (Pseudomonas phage 14) hypothetical protein PLA1_gp65 (Pseudomonas phage 14) hypothetical protein PLA1_gp66 (Pseudomonas phage 14) hypothetical protein PLA1_gp67 (Pseudomonas phage 14) hypothetical protein PLA1_gp77 (Pseudomonas phage 14) hypothetical protein PLA1_gp77 (Pseudomonas phage 14) hypothetical protein PLA1_gp77 (Pseu		55434			hypothetical protein [Pseudomonas phage PA5]	1e-39	APD20762.1
Image         Image <th< td=""><td>FHP079c</td><td>55442 - 55672</td><td>56.7</td><td>231</td><td>hypothetical protein PPSN_gp63 [<i>Pseudomonas</i> phage SN]</td><td>5e-49</td><td>YP_002418869.1</td></th<>	FHP079c	55442 - 55672	56.7	231	hypothetical protein PPSN_gp63 [ <i>Pseudomonas</i> phage SN]	5e-49	YP_002418869.1
FHP080c         5570 - 55923         53.9         219         hypothetical protein LMA2_gp62 [ <i>Pseudomonas</i> phage LMA2]         2e-46         YP_002154296.1           FHP081c         55907 - 55125         58.0         219         hypothetical protein [ <i>Pseudomonas</i> phage phage phi/TN6]         9e-46         AKJ71595.1           FHP081c         55907 - 55125         58.0         219         hypothetical protein IPA_065c [ <i>Pseudomonas</i> phage phi/TN6]         1e-43         AKJ71595.1           FHP081c         55125         58.0         231         hypothetical protein PP141_gp65 [ <i>Pseudomonas</i> phage NH-4]         1e-43         VP_002364373.1           FHP082c         56125 - 56335         58.9         231         hypothetical protein PP141_gp65 [ <i>Pseudomonas</i> phage 14-1]         1e-49         VP_002364374.1           FHP084c         5752 - 5744         55.3         1002         hypothetical protein PP141_gp67 [ <i>Pseudomonas</i> phage 14-1]         0         VP_002364375.1           FHP084c         57552 - 59719         55.1         1188         putative ATP-dependent exonuclease V [ <i>Pseudomonas</i> phage SN]         2e-102         VP_002364375.1           FHP084c         59706 - 60128         56.7         423         hypothetical protein PP141_gp67 [ <i>Pseudomonas</i> phage PB3]         0         VP_002364375.1           FHP084c         59706 - 60128 <td< td=""><td></td><td></td><td></td><td></td><td>hypothetical protein PP141_gp62 [<i>Pseudomonas</i> phage 14-1]</td><td>1e-48</td><td>YP_002364370.1</td></td<>					hypothetical protein PP141_gp62 [ <i>Pseudomonas</i> phage 14-1]	1e-48	YP_002364370.1
Interface         Interface         Interface         Interface         Interface         Product	FHP080c	55705 - 55923	53.9	219	hypothetical protein LMA2_gp62 [ <i>Pseudomonas</i> phage LMA2]	2e-46	YP_002154296.1
FHP081c55907 - 5612558.0219Mypothetical protein pikTN6_063 [Pseudomonas phage NH-4]1e-43AKJ71595.1FHP082c56125 - 5635558.9231Mypothetical protein PP141_gp65 [Pseudomonas phage 14.1] hypothetical protein PP141_gp65 [Pseudomonas phage 14.1] hypothetical protein DP141_gp66 [Pseudomonas phage 14.1]6e-50YP_002364373.1FHP083c5643 - 574455.31002Mypothetical protein PP141_gp66 [Pseudomonas phage 14.1] hypothetical protein ORF065 [Pseudomonas phage phage 14.1]0YP_002364374.1FHP084c5755 - 5837062.0819Mypothetical protein ORF065 [Pseudomonas phage phage 14.1]0YP_002364375.1FHP084c5755 - 5837055.11188putative ATP-dependent exonuclease V Protein PP141_gp67 [Pseudomonas phage phage 14.1]0YP_0024802.1FHP085c59705 - 5971955.11188putative ATP-dependent exonuclease V Protein PP141_gp67 [Pseudomonas phage phage 14.1]0YP_002364377.1FHP085c59705 - 6012855.11188putative ATP-dependent exonuclease V phage 14.1]0YP_002364377.1FHP085c59705 - 6012855.51305Mypothetical protein PP141_gp67 [Pseudomonas phage 14.1]4e-98YP_002364377.1FHP085c59705 - 6012858.682.2Mypothetical protein PP141_gp67 [Pseudomonas phage 14.1]4e-98YP_002364377.1FHP085c59705 - 6012858.682.682.2Mypothetical protein PP141_gp70 [Pseudomonas phage 14.1]4e-98 </td <td></td> <td>00020</td> <td></td> <td></td> <td>tail assembly protein [<i>Pseudomonas</i> phage phiKTN6]</td> <td>9e-46</td> <td>AKJ71594.1</td>		00020			tail assembly protein [ <i>Pseudomonas</i> phage phiKTN6]	9e-46	AKJ71594.1
Image         Image <th< td=""><td>FHP081c</td><td>55907 - 56125</td><td>58.0</td><td>219</td><td>hypothetical protein phiKTN6_063 [<i>Pseudomonas</i> phage phiKTN6]</td><td>1e-43</td><td>AKJ71595.1</td></th<>	FHP081c	55907 - 56125	58.0	219	hypothetical protein phiKTN6_063 [ <i>Pseudomonas</i> phage phiKTN6]	1e-43	AKJ71595.1
FHP082c         56125 - 56355         58.9         231         hypothetical protein PP141_gp65 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp62 [Pseudomonas phage 14-1]         6e-50         YP_002364373.1           FHP083c         56443 - 57444         55.3         1002         hypothetical protein PP141_gp66 [Pseudomonas phage 14-1]         0         YP_002364374.1           FHP084c         5752 - 58370         62.0         819         hypothetical protein ORF065 [Pseudomonas phage NP3]         4e-177         AMQ76185.1           FHP084c         57552 - 58370         55.1         1188         putative ATP-dependent exonuclease V [Pseudomonas phage SN]         0         YP_002364375.1           FHP086c         59705 - 60128         55.7         25.1         1188         putative ATP-dependent exonuclease V [Pseudomonas phage SN]         0         YP_002364377.1           FHP086c         59706 - 60128         56.7         423         hypothetical protein ORF068 [Pseudomonas phage 14-1]         4e-98         YP_002364377.1           FHP087         60297 - 61128         58.6         822         hypothetical protein ORF068 [Pseudomonas phage 16024]         4e-98         YP_002364378.1           FHP088         61129 - 62433         58.7         1305         hypothetical protein P141_gp70 [Pseudomonas phage 16024]         0         YP_002364379.1					hypothetical protein I7A_065c [ <i>Pseudomonas</i> phage NH-4]	1e-43	YP_007002611.1
BODDProblemP	FHP082c	56125 - 56355	58.9	231	hypothetical protein PP141_gp65 [ <i>Pseudomonas</i> phage 14-1]	6e-50	YP_002364373.1
FHP083c56.43 5744455.31002hypothetical protein PP141_gp66 [Pseudomonas phage 14-1] hypothetical protein ORF065 [Pseudomonas phage PS] hypothetical protein ORF065 [Pseudomonas phage NP3] hege 14-1]0YP_001294482.1FHP084c57552 \$837062.0819hypothetical protein PP141_gp67 [Pseudomonas phage 14-1]4e-177 2e-102AMQ76185.1 YP_002364375.1FHP085c58532 - \$971955.11188putative ATP-dependent exonuclease V PB10YP_002418875.1FHP086c59706 - 6012856.7423hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1] hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein PP341_gp73 [Pseudomonas phage 14-1] hypothetical protein P934_gp73 [Pseudomonas phage 14-1] hypothetical protein P944_gp73 [Pseudomonas phag		50555			hypothetical protein LBL3_gp62 [ <i>Pseudomonas</i> phage LBL3]	1e-49	YP_002154207.1
Image: Probability of the second se	FHP083c	56443 - 57444	55.3	1002	hypothetical protein PP141_gp66 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364374.1
FHP084c57552 - 5837062.0819hypothetical protein [Pseudomonas phage NP3] hypothetical protein PP141_gp67 [Pseudomonas phage 14-1]4e-177 2e-102AMQ76185.1 YP_002364375.1FHP085c58532 - 5971955.11188putative ATP-dependent exonuclease V [Pseudomonas phage SN] ATP-dependent exonuclease [Pseudomonas phage PB1]0YP_002456000.1FHP086c59706 - 6012856.7423hypothetical protein PP141_gp69 [Pseudomonas phage PB1]4e-98YP_002456000.1FHP08760297 - 6111858.6822hypothetical protein ORF068 [Pseudomonas phage 14-1] hypothetical protein PP141_gp70 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]0YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp70 [Pseudomonas phage 14-1] hypothetical protein PB141_gp70 [Pseudomonas phage 14-1] hypothetical protein PB141_gp70 [Pseudomonas phage 14-1] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1] hypothetical protein PB141_gp70 [Pseudomonas phage 14-1] hypothetical protein PB141_gp70 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypo					hypothetical protein ORF065 [ <i>Pseudomonas</i> phage F8]	0	YP_001294482.1
58370Image 1hypothetical protein PP141_gp67 [Pseudomonas phage 14-1]2e-102YP_002364375.1FHP085c58532 - 5971955.11188putative ATP-dependent exonuclease V [Pseudomonas phage SN] ATP-dependent exonuclease [Pseudomonas phage PB1]0YP_002418875.1FHP086c59706 - 6012856.7423hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein ORF068 [Pseudomonas phage 14-1] hypothetical protein PI624_071 [Pseudomonas phage 16024] hypothetical protein PI624_071 [Pseudomonas phage 14-1]4e-98YP_002364377.1 P002364377.1FHP08760297 - 6111858.6822hypothetical protein PI624_071 [Pseudomonas phage 16024] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1] hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein IBL3_gp68 [Pseudomonas phage 14-1] hypothetical protein IBL3_gp68 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein	FHP084c	57552 -	62.0	819	hypothetical protein [Pseudomonas phage NP3]	4e-177	AMQ76185.1
FHP085c58532 - 5971955.11188putative ATP-dependent exonuclease V [Pseudomonas phage SN] ATP-dependent exonuclease [Pseudomonas phage PB1]0YP_002418875.1 YP_002456000.1FHP086c59706 - 6012856.7423hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein ORF068 [Pseudomonas phage 14-1] hypothetical protein PP141_gp70 [Pseudomonas phage I4-1] hypothetical protein PP141_gp70 [Pseudomonas phage I4-1] hypothetical protein PP141_gp70 [Pseudomonas phage I4-1] hypothetical protein PP141_gp70 [Pseudomonas phage I4-1] hypothetical protein PP141_gp71 [Pseudomonas phage I4-1] hypothetical protein PP141_gp72 [Pseudomonas phage I8130YP_002364379.1FHP08962457 - 6290658.0450hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage I4-1] hypothetical protein PP141_gp73 [Pseudomonas phage I4-1] hypothetical protein PP141_gp73 [Pseudomonas phage VB_PaeM_LS1] bypothetical protein VBPaeMLS1_59 [Pseudomonas phage VB_PaeM_LS1]0VP_002364381.1 AVJ48828.1		58370			hypothetical protein PP141_gp67 [ <i>Pseudomonas</i> phage 14-1]	2e-102	YP_002364375.1
ATP-dependent exonuclease [Pseudomonas phage PB1]0YP_002456000.1FHP086c59706 - 6012856.742.3hypothetical protein PP141_gp69 [Pseudomonas phage 14-1] hypothetical protein ORF068 [Pseudomonas phage F8]4e-98YP_002364377.1FHP08760297 - 6111858.682.2hypothetical protein PJ624_071 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage JG024]0YP_002364378.1FHP08760297 - 6111858.682.2hypothetical protein PP141_gp70 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]0YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp68 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas fe39060YP_002364380.1FHP09062903 - 6397957.51077hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein VBPaeMLS1_59 [Pseu	FHP085c	58532 - 59719	55.1	1188	putative ATP-dependent exonuclease V [Pseudomonas phage SN]	0	YP_002418875.1
FHP086c59706 - 6012856.7423hypothetical protein PP141_gp69 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein ORF068 [ <i>Pseudomonas</i> phage [F8]4e-98YP_002364377.1 YP_001294485.1FHP08760297 - 6111858.6822hypothetical protein PJG24_071 [ <i>Pseudomonas</i> phage 1024] hypothetical protein PP141_gp70 [ <i>Pseudomonas</i> phage 14-1]0YP_006200835.1 YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp68 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein PP141_gp72 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein IBL3_gp68 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein IP141_gp72 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein IP141_gp72 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein PP141_gp73 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein VBPaeMLS1_59 [ <i>Pseudomonas</i> phage VB_PaeM_LS1]0YP_002364381.1 AVJ48828.1					ATP-dependent exonuclease [ <i>Pseudomonas</i> phage PB1]	0	YP_002456000.1
FHP08760297 - 6111858.6822hypothetical protein ORF068 [Pseudomonas phage F8]2e-97YP_001294485.1FHP08760297 - 6111858.6822hypothetical protein PJG24_071 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]0YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp68 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp72 [Pseudomonas phage 14-1] hypothetical protein PP141_gp73 [Pseudomonas phage 14-1] hypothetical protein vBPaeMLS1_59 [Pseudomon	FHP086c	59706 - 60128	56.7	423	hypothetical protein PP141_gp69 [ <i>Pseudomonas</i> phage 14-1]	4e-98	YP_002364377.1
FHP08760297 - 6111858.6822hypothetical protein PJG24_071 [Pseudomonas phage JG024] hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]0YP_006200835.1 YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [Pseudomonas 		00120			hypothetical protein ORF068 [ <i>Pseudomonas</i> phage F8]	2e-97	YP_001294485.1
FHP08861129 - 6243358.51305hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]0YP_002364378.1FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp68 [Pseudomonas phage 18L3]0YP_002364379.1FHP08962457 - 	FHP087	60297 - 61118	58.6	822	hypothetical protein PJG24_071 [ <i>Pseudomonas</i> phage [G024]	0	YP_006200835.1
FHP08861129 - 6243358.51305hypothetical protein PP141_gp71 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp68 [Pseudomonas phage LBL3]0YP_002364379.1 YP_002154213.1FHP08962457 - 6290658.0450hypothetical protein PP141_gp72 [Pseudomonas 		01110			hypothetical protein PP141_gp70 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364378.1
HP08962457 - 6290658.0450hypothetical protein LBL3_gp68 [Pseudomonas phage LBL3]0YP_002154213.1FHP08962457 - 6290658.0450hypothetical protein PP141_gp72 [Pseudomonas 	FHP088	61129 - 62433	58.5	1305	hypothetical protein PP141_gp71 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364379.1
FHP089       62457 - 62906       58.0       450       hypothetical protein PP141_gp72 [ <i>Pseudomonas</i> phage 14-1]       4e-106       YP_002364380.1         FHP090       62903 - 63979       57.5       1077       hypothetical protein [ <i>Pseudomonas</i> phage NP3]       6e-106       AMQ76190.1         FHP090       62903 - 63979       57.5       1077       hypothetical protein PP141_gp73 [ <i>Pseudomonas</i> phage 14-1]       0       YP_002364381.1         hypothetical protein vBPaeMLS1_59 [ <i>Pseudomonas</i> phage vB_PaeM_LS1]       0       AVJ48828.1					hypothetical protein LBL3_gp68 [Pseudomonas phage LBL3]	0	YP_002154213.1
FHP090         62903 - 63979         57.5         1077         hypothetical protein [Pseudomonas phage NP3] phage 14-1] hypothetical protein vBPaeMLS1_59 [Pseudomonas phage vB_PaeM_LS1]         6e-106         AMQ76190.1	FHP089	62457 - 62906	58.0	450	hypothetical protein PP141_gp72 [ <i>Pseudomonas</i> phage 14-1]	4e-106	YP_002364380.1
FHP090       62903 - 63979       57.5       1077       hypothetical protein PP141_gp73 [ <i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeMLS1_59 [ <i>Pseudomonas</i> phage vB_PaeM_LS1]       0       YP_002364381.1					hypothetical protein [Pseudomonas phage NP3]	6e-106	AMQ76190.1
hypothetical protein vBPaeMLS1_59 [ <i>Pseudomonas</i> 0 AVJ48828.1 phage vB_PaeM_LS1]	FHP090	62903 - 63979	57.5	1077	hypothetical protein PP141_gp73 [ <i>Pseudomonas</i>	0	YP_002364381.1
		03979			hypothetical protein vBPaeMLS1_59 [ <i>Pseudomonas</i> phage vB_PaeM_LS1]	0	AVJ48828.1

## Supplementary material

FHP091	63985 -	50	150	hypothetical protein ORF073 [Pseudomonas phage	3e-10	YP_001294490.1
	64134			F8]		
				hypothetical protein phiKTN6_073 [Pseudomonas	3e-10	AKJ71605.1
				phage phiKTN6]		
FHP092	64317 -	54.0	1740	putative DNA primase [Pseudomonas phage	0	AKP24459.1
	66056			vB_PaeM_CEB_DP1]		
				DNA primase [Pseudomonas phage vB_Pae436M-8]	0	ANT44262.1

#### Table S4: Predicted genes of P. aeruginosa phage PA1P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein lenght (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no.
PA1P1_001	604 - 1185	58.2	193	hypothetical protein [ <i>Pseudomonas</i> phage vB. PaeM. PAO1. Ab27]	4E-137	YP_009124304.1
				hypothetical protein LMA2_gp76 [ <i>Pseudomonas</i> phage LMA2]	3E-136	YP_002154309.1
PA1P1_002c	1953 - 1342	55.1	203	hypothetical protein PP141_gp77 [ <i>Pseudomonas</i> phage 14-1]	5E-144	YP_002364385.1
				hypothetical protein SL1_26 [ <i>Pseudomonas</i> phage SL1]	3E-143	AUS03301.1
PA1P1_003c	2829 - 2143	60.0	228	hypothetical protein PP141_gp78 [ <i>Pseudomonas</i> phage 14-1]	3E-157	YP_002364386.1
				hypothetical protein vBPaeME215_00057 [Pseudomonas phage vB PaeM E215]	1E-156	ASZ72535.1
PA1P1_004c	3151 - 2840	55.8	103	hypothetical protein vBPaeMDP1_0076 [Pseudomonas phage vB PaeM CEB DP1]	1E-71	AKP24463.1
				hypothetical protein BrSP1_5 [ <i>Pseudomonas</i> phage BrSP1]	4E-71	ATI16257.1
PA1P1_005c	3425 - 3204	52.7	73	hypothetical protein PP141_gp80 [ <i>Pseudomonas</i> phage 14-1]	3E-44	YP_002364388.1
				hypothetical protein I7A_082c [ <i>Pseudomonas</i> phage NH-4]	5E-44	YP_007002628.1
PA1P1_006c	3689 - 3435	56.9	84	hypothetical protein PP141_gp81 [ <i>Pseudomonas</i> phage 14-1]	2E-53	YP_002364389.1
				hypothetical protein [Pseudomonas phage KPP22]	5E-49	BAU20633.1
PA1P1_007c	3967 - 3743	55.6	74	hypothetical protein LBL3_gp79 [ <i>Pseudomonas</i> phage LBL3]	3E-47	YP_002154224.1
				hypothetical protein PPSN_gp83 [ <i>Pseudomonas</i> phage SN]	2E-46	YP_002418889.1
PA1P1_008c	4359 - 4033	55.4	108	hypothetical protein [Pbunalikevirus phiVader] hypothetical protein [ <i>Pseudomonas</i> phage E79]	2E-73 2E-73	ALJ99257.1 AXF41825.1
PA1P1_009c	5003 - 4356	59.7	215	hypothetical protein LBL3_gp81 [ <i>Pseudomonas</i> phage LBL3]	1E-154	YP_002154226.1
				hypothetical protein vB_Pae_PS44_00086 [ <i>Pseudomonas</i> phage vB_Pae_PS44]	2E-152	YP_009211410.1
PA1P1_010c	5247 - 5035	56.3	70	hypothetical protein phiKTN6_084 [ <i>Pseudomonas</i> phage phiKTN6]	2E-45	AKJ71616.1
				hypothetical protein [Pseudomonas phage KPP12]	4E-44	YP_007238238.1
PA1P1_011c	5432 - 5244	49.2	62	hypothetical protein LBL3_gp83 [ <i>Pseudomonas</i> phage LBL3]	4E-38	YP_002154228.1
				hypothetical protein LMA2_gp86 [ <i>Pseudomonas</i> phage LMA2]	4E-35	YP_002154319.1
PA1P1_012c	5644 - 5429	53.7	71	hypothetical protein LBL3_gp84 [ <i>Pseudomonas</i> phage LBL3]	1E-43	YP_002154229.1
				hypothetical protein PB1_gp89 [ <i>Pseudomonas</i> phage PB1]	2E-43	YP_002456018.1
PA1P1_013c	5841 - 5641	54.2	66	hypothetical protein PPSN_gp89 [ <i>Pseudomonas</i> phage SN]	4E-41	YP_002418895.1
				hypothetical protein [Pseudomonas phage NP3]	3E-40	AMQ76208.1
PA1P1_014c	6089 -	52.0	83	hypothetical protein PJG24_092 [ <i>Pseudomonas</i> phage	2E-53	YP_006200856.1
	5838			JG024] hypothetical protein PII10A_13 [ <i>Pseudomonas</i>	1E-52	SB196695.1
PA1P1_015c	6364 -	49.7	62	hypothetical protein PP141_gp89 [ <i>Pseudomonas</i>	3E-39	YP_002364397.1
	01/0			hypothetical protein PII10A_14 [ <i>Pseudomonas</i>	5E-37	SBT96696.1
PA1P1_016c	7284 -	54.6	305	tail length tape-measure protein [ <i>Pseudomonas</i> phage	0	AMQ76211.1
	0507			tail length tape-measure protein [ <i>Pseudomonas</i> phage F79]	0	AXF41778.1
PA1P1_017c	7633 - 7331	53.1	100	hypothetical protein PPSN_gp01 [ <i>Pseudomonas</i> phage SN]	1E-63	YP_002418807.1
				,	8E-61	AVJ48808.1

				hypothetical protein vBPaeMLS1_39 [Pseudomonas		
PA1P1 018c	7862 -	54.0	57	phage vB_PaeM_LS1] hypothetical protein PPSN_gp03 [ <i>Pseudomongs</i> phage	QF_25	VP_002/18808_1
PAIPI_0180	7689	54.0	57	SN]	96-55	19_002418808.1
	1005			hypothetical protein PII10A_17 [ <i>Pseudomonas</i> aeruginosa]	2E-34	SBT96699.1
PA1P1_019c	8059 - 7913	53.1	48	hypothetical protein PPSN_gp03 [ <i>Pseudomonas</i> phage SN]	5E-23	YP_002418809.1
				hypothetical protein SAMN05216409_118116 [Pseudomonas lutea]	6E-13	SER37912.1
PA1P1_020	8236 - 9618	52.4	460	putative terminase, large subunit [ <i>Pseudomonas</i> aeruginosa]	0	SBT96701.1
				terminase large subunit [Pseudomonas phage E79]	0	AXF41768.1
PA1P1_021c	10038 -	59.1	127	hypothetical protein PP141_gp04 [ <i>Pseudomonas</i>	3E-86	YP_002364312.1
	9655			pnage 14-1] hypothetical protein [ <i>Pseudomonas</i> phage NP3]	7E-86	AMQ76120.1
PA1P1_022c	10253 -	54.8	72	hypothetical protein [Pseudomonas aeruginosa]	4E-46	WP_015994883.1
PA1P1 023c	10033 -	61.3	116	hypothetical protein LBL3 gp05 [Pseudomonas phage	4E-78	YP 002154150.1
	10253		-	LBL3]		
				hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1]	8E-76	AUS03281.1
PA1P1_024c	11050 - 10649	59.5	133	hypothetical protein PP141_gp07 [ <i>Pseudomonas</i> phage 14-1]	2E-89	YP_002364315.1
	10045			hypothetical protein PJG24_008 [ <i>Pseudomonas</i> phage	1E-88	YP_006200773.1
PA1P1_025c	11832 -	56.9	259	hypothetical protein PP141_gp08 [ <i>Pseudomonas</i>	0	YP_002364316.1
	11053			phage 14-1]		ND 000045400.4
PA1P1 026c	12356 -	61.4	145	hypothetical protein [ <i>Pseudomonds</i> phage DL68]	0 4F-98	YP_009215128.1 YP_006200775_1
17111_0200	11919	01.4	145	JG024]	42 50	
DA1D1 027c	12060	EQ 2	105	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	7E-98	YP_009215127.1
FAIF1_0270	12300 -	56.5	195	hypothetical protein [P32ddomonds phage W 3] hypothetical protein PP141_gp10 [Pseudomonas	2E-143	YP_002364318.1
				phage 14-1]		_
PA1P1_028c	13065 -	49.0	31	hypothetical protein [ <i>Pseudomonas</i> phage NP3]	9E-138	AMQ76126.1
	12570			phage 14-1]	52 157	11_002304310.1
PA1P1_029c	13994 -	57.2	310	hypothetical protein vB_Pae_PS44_00013	0	YP_009211337.1
	13062			[Pseudomonas phage vB_Pae_P544] hypothetical protein PPSN_gp13 [Pseudomonas phage	0	YP_002418819.1
PA1P1_030c	14597 -	55.7	166	SN] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i>	4E-120	YP_002364321.1
	14097			phage 14-1]	25 110	
				JG024]	2E-119	YP_006200778.1
PA1P1_031c	14964 -	53.4	115	hypothetical protein PP141_gp14 [ <i>Pseudomonas</i>	5E-77	YP_002364322.1
	14017			hypothetical protein [ <i>Pseudomonas</i> phage DL68]	7E-77	YP 009215123.1
PA1P1_032c	15524 -	51.3	103	hypothetical protein [Pseudomonas phage DL68]	2E-68	YP_009215122.1
	15213			hypothetical protein PJG24_015 [ <i>Pseudomonas</i> phage IG024]	2E-67	YP_006200780.1
PA1P1_033c	15733 -	58.3	67	hypothetical protein [Pseudomonas phage DL68]	3E-41	YP_009215121.1
	15530			hypothetical protein phiKT28_017 [ <i>Pseudomonas</i> phage phiKT28]	1E-40	AKJ71455.1
PA1P1_034c	16053 -	55.6	107	hypothetical protein PP141_gp16 [ <i>Pseudomonas</i>	1E-74	YP_002364324.1
	15730			phage 14-1] hypothetical protein RIG24, 016 [Recudements phage	65 72	VP 006200781 1
				JG024]	02-73	17_000200781.1
PA1P1_035c	16485 - 16084	53.7	133	hypothetical protein PP141_gp17 [ <i>Pseudomonas</i> phage 14-1]	2E-92	YP_002364325.1
				hypothetical protein phiKT28_019 [ <i>Pseudomonas</i>	9E-92	AKJ71457.1
PA1P1 036	16665 -	56.9	729	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	0	YP_009215210.1
_	18962			minor head-like protein [Pseudomonas phage 14-1]	0	YP_002364326.1
PA1P1_037	18962 - 19798	53.4	278	putative minor head protein [ <i>Pseudomonas</i> phage SN] putative minor head protein [ <i>Pseudomonas</i> phage	0	YP_002418826.1
	10,00			SL1]	0	AUS03359.1
PA1P1_038	19817 -	55.6	68	hypothetical protein PPSN_gp21 [Pseudomonas phage	2E-41	YP_002418827.1
	20023			SNJ hypothetical protein LBL3_gp17 [Pseudomonas phage	6E-40	YP_002154162.1
				LBL3]		_
PA1P1_039	20020 - 20160	53.2	46	hypothetical protein PPSN_gp22 [ <i>Pseudomonas</i> phage SN]	4E-23	YP_002418828.1
					3E-22	YP_006200786.1

				hypothetical protein PJG24_021 [ <i>Pseudomonas</i> phage		
DA1D1 040	20714	EQ 2	161	JG024]	0	VD 000215206 1
PAIP1_040	20714 - 22108	58.3	404	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PP141_gp22 [Pseudomonas	0	YP_009215206.1 YP_002364330.1
DA1D1 0/1	22112 -	62.6	211	phage 14-1] hypothetical protein PP141, gp23 [ <i>Pseudomongs</i>	5E-1/8	VP 002364331 1
FAIF1_041	22747	02.0	211	phage 14-1]	JL-140	11_002304331.1
				structural protein [Pseudomonas phage SN]	1E-147	YP_002418830.1
PA1P1_042	22757 -	61.0	382	putative major structural protein [ <i>Pseudomonas</i>	0	AKP24411.1
	23905			phage vB_PaeM_CEB_DP1] hypothetical protein PP141_gp24 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364332.1
PA1P1_043	24007-	55.0	145	hypothetical protein vBPaeMDP1_0025	6E-104	AKP24412.1
	24444			[Pseudomonas phage vB_PaeM_CEB_DP1]		
DA1D1 044	24450	50.2	155	hypothetical protein [Pseudomonas phage KPP12]	2E-103	YP_007238179.1
FAIF1_044	24439 -	39.2	155	KPP12]	46-110	1F_007238180.1
				structural protein [Pseudomonas phage phiKTN6]	1E-109	AKJ71557.1
PA1P1_045	24923 -	52.1	132	putative structural protein [Pseudomonas phage	2E-91	YP_007238181.1
	25321			KPP12]	CF 01	
PA1P1 046	25320 -	18.4	193	structural protein [ <i>Pseudomonas</i> phage phik i N6]	6E-91 3E-133	AKJ/1558.1 VP_007238182.1
FAIF1_040	25880	40.4	105	hypothetical protein vB Pae PS44 00031	5E-133	YP 009211355.1
				[ <i>Pseudomonas</i> phage vB_Pae_PS44]		-
PA1P1_047	25877 -	54.8	193	hypothetical protein ORF028 [Pseudomonas phage F8]	3E-137	YP_001294445.1
	26458			hypothetical protein [Pseudomonas phage KPP12]	1E-136	YP_007238183.1
PA1P1_048	26474 - 27988	59.1	504	hypothetical protein I7A_031 [ <i>Pseudomonas</i> phage NH-4]	0	YP_007002577.1
	27500			hypothetical protein vBPaeMDP1_0030	0	AKP24417.1
				[Pseudomonas phage vB_PaeM_CEB_DP1]		
PA1P1_049	28047 -	59.6	150	putative structural protein [Pseudomonas phage	2E-103	YP_002154264.1
	28499			LMA2]	25 102	AK171 471 1
PA1P1 050	28/00 -	54.6	107	putative structural protein [Pseudomonas phage phik128]	2E-102 2E-75	AKJ/14/1.1 VP_00215/265_1
FAIF1_050	28822	54.0	107	LMA2]	22-75	17_002134203.1
				putative structural protein [ <i>Pseudomonas</i> phage	5E-75	YP_006200797.1
PA1P1 051	28819 -	53.0	116	putative structural protein [ <i>Pseudomonas</i> phage	3E-78	YP 002154266.1
	29169			LMA2]		
DA4D4 052	20171	64.4	142	structural protein [ <i>Pseudomonas</i> phage SL1]	1E-77	AUS03345.1
PAIPI_052	29171 -	64.1	143	Nypotnetical protein PPSN_gp35 [Pseudomonds phage SN]	8E-93	YP_002418841.1
	25002			hypothetical protein PII10A_51 [ <i>Pseudomonas</i>	2E-92	SBT96733.1
				aeruginosa]		
PA1P1_053	29612 -	52.2	167	structural protein [Pseudomonas phage SN]	3E-115	YP_002418842.1
	30115			putative structural protein [ <i>Pseudomonas</i> phage	1E-114	YP_002154268.1
	20115	F1 1	170	LMA2]	FF 100	VD 002154260 1
PAIP1_054	30115 -	51.1	179	IMA21	5E-128	1P_002154269.1
				putative structural protein [ <i>Pseudomongs</i> phage	2E-127	YP 002154178.1
				LBL3]		
PA1P1_055	30663 -	46.8	197	putative structural protein [Pseudomonas phage	3E-140	YP_007238190.1
	31256			KPP12]		
				hypothetical protein vBPaeME217_00038	2E-139	ASZ72422.1
	21266	57.1	140	[Pseudomonds phage VB_PaeM_E217]	4E 101	VD_0021E4190_1
PAIPI_050	31694	57.1	142	nhage [B] 3]	46-101	1P_002154160.1
				hypothetical protein phiKTN6 037 [ <i>Pseudomonas</i>	2E-100	AKJ71569.1
				phage phiKTN6]		
PA1P1_057	31698 -	58.2	858	putative lytic tail protein [Pseudomonas phage	0	YP_002154272.1
	34274			LMA2]		
DA454	24274	52.1	207	internal (core) protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76156.1
PA1P1_058	342/4 - 35137	52.1	287	putative structural protein [ <i>Pseudomonas</i> phage	U	YP_002154273.1
	55157			LIVIAZJ putative structural protein [ <i>Pseudomonas</i> phage	0	ΔΚΡ24427 1
				vB PaeM CEB DP1]		/31X1 27727.1
PA1P1_059	35137 -	48.3	177	hypothetical protein PP141_gp41 [ <i>Pseudomonas</i>	2E-127	YP_002364349.1
_	35670			phage 14-1]		
				hypothetical protein [Pseudomonas phage DL68]	5E-127	YP_009215187.1
PA1P1_060	35726 -	53.0	221	hypothetical protein LMA2_gp41 [ <i>Pseudomonas</i>	2E-160	YP_002154275.1
	36391			phage LMA2]	45 160	VD 007220405 1
1	1	1	I	putative baseplate [Pseudomonds phage KPP12]	4E-100	18_00/238195.1

PA1P1_061A	36402 -	42.6	17	hypothetical protein PB1_gp43 [Pseudomonas	3E-09	YP_002455973.1
	36455			phage PB1] putative baseplate protein [ <i>Pseudomonas</i> phage	2E-04	YP_002418850.1
PA1P1_061B	36448 - 37701	57.9	417	hypothetical protein BrSP1_62 [ <i>Pseudomonas</i> phage BrSP1]	0	ATI16244.1
				putative baseplate protein [ <i>Pseudomonas</i> phage NH-4]	0	YP_007002590.1
PA1P1_062	37698 - 39212	55.7	504	hypothetical protein I7A_045 [ <i>Pseudomonas</i>	0	YP_007002591.1
	00111			putative structural protein [ <i>Pseudomonas</i> phage JG024]	0	YP_006200809.1
PA1P1_063	39217 - 42105	57.8	962	tail fibers protein [ <i>Pseudomonas</i> phage NP3] putative tail fiber component [ <i>Pseudomonas</i> phage NH-4]	0 0	AMQ76163.1 YP_007002592.1
PA1P1_064	42107 - 42535	58.3	142	hypothetical protein [ <i>Pseudomonas</i> phage NP3] putative tail fiber component [ <i>Pseudomonas</i> phage JG024]	4E-98 7E-97	AMQ76164.1 YP_006200811.1
PA1P1_065	42535 - 43197	60.5	220	lytic enzyme [ <i>Pseudomonas</i> phage NP3] putative endolysin [ <i>Pseudomonas</i> phage JG024]	2E-161 7E-161	AMQ76165.1 YP 006200812.1
PA1P1_066c	43472 -	51.2	83	hypothetical protein PP141_gp48 [Pseudomonas	2E-50	YP_002364356.1
	43221			phage 14-1] hypothetical protein LMA2_gp47 [ <i>Pseudomonas</i> phage LMA2]	3E-50	YP_002154281.1
PA1P1_067c	44663 -	56.6	303	DNA ligase [ <i>Pseudomonas</i> phage phiKT28]	0	AKJ71489.1
DA1D1 069c	45752	E1 9	19/	putative DNA ligase [Pseudomonas phage JG024]	U 1E 121	YP_006200814.1
FAIFI_0080	44718	54.8	104	hypothetical protein PJG24_051 [ <i>Pseudomonas</i>	9E-131	YP_006200815.1
PA1P1_069c	45874 - 45269	59.6	201	hypothetical protein ORF050 [ <i>Pseudomonas</i> phage	3E-137	YP_001294467.1
	43203			Poj hypothetical protein PP141_gp51 [Pseudomonas phage 14-1]	6E-137	YP_002364359.1
PA1P1_070c	46827 - 45928	59.3	299	hypothetical protein PP141_gp52 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364360.1
				hypothetical protein [ <i>Pseudomonas</i> phage DL68]	0	YP_009215176.1
PA1P1_071c	47536 -	53.6	206	hypothetical protein vBPaeMLS1_79	3E-145	AVJ48847.1
	40910			hypothetical protein SL1_50 [ <i>Pseudomonas</i> phage SL1]	1E-144	AUS03325.1
PA1P1_072c	49190 -	55.2	519	putative helicase [ <i>Pseudomonas</i> phage KPP12]	0	YP_007238207.1
	47631			putative DNA helicase [ <i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0	AKP24441.1
PA1P1_073c	49597 -	55.2	136	hypothetical protein [Pseudomonas phage KPP12]	2E-94	YP_007238208.1
PA1P1 074c	49187 52697 -	55.0	1035	putative DNA helicase [ <i>Pseudomonas</i> phage NH-4] putative DNA polymerase [ <i>Pseudomonas</i> phage	2E-94 0	YP_007002602.1 YP_007238209.1
_	49590			KPP12]		-
				phage vB_PaeM_LS1]	0	AVJ48844.1
PA1P1_075c	53251 - 52697	53.3	184	putative DNA polymerase III epsilon subunit [Pseudomongs phage NH-4]	2E-135	YP_007002604.1
				putative DNA polymerase III, epsilon subunit [ <i>Pseudomonas</i> phage LMA2]	3E-135	YP_002154290.1
PA1P1_076c	54358 - 53327	58.4	343	putative 3'-phosphatase, 5'-polynucleotide kinase	0	SBT96767.1
				putative polynucleotide kinase [ <i>Pseudomonas</i> phage KPP12]	0	YP_007238211.1
PA1P1_077c	54552 - 54361	48.4	63	hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024]	3E-35	YP_006200824.1
				hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	1E-34	YP_007238212.1
PA1P1_078c	55471 - 54554	58.6	305	putative thymidylate synthase [Pseudomonas phage JG024]	0	YP_006200825.1
				phage 14-1]	U	18_002364368.1
PA1P1_079c	55677 -	52.2	68	hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	1E-40	YP_007238214.1
	55471			hypothetical protein SL1_42 [ <i>Pseudomonas</i> phage SL1]	2E-40	AUS03317.1
PA1P1_080c	55951 -	56.9	88	hypothetical protein [Pseudomonas phage PA5]	2E-56	APD20761.1
	55685			hypothetical protein phiKT28_064 [ <i>Pseudomonas</i> phage phiKT28]	5E-56	AKJ71502.1

PA1P1_081c	56169 - 55951	55.7	72	hypothetical protein PPSN_gp64 [ <i>Pseudomonas</i> phage SN]	2E-46	YP_002418870.1
				hypothetical protein LMA2_gp62 [ <i>Pseudomonas</i> phage LMA2]	3E-46	YP_002154296.1
PA1P1_082c	56371 - 56153	59.8	72	hypothetical protein LBL3_gp61 [ <i>Pseudomonas</i> phage LBL3]	5E-43	YP_002154206.1
				hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	2E-42	YP_007238217.1
PA1P1_083c	56601 - 56371	58.9	76	hypothetical protein PP141_gp65 [ <i>Pseudomonas</i> phage 14-1]	6E-50	YP_002364373.1
				hypothetical protein LBL3_gp62 [ <i>Pseudomonas</i> phage LBL3]	1E-49	YP_002154207.1
PA1P1_084c	57691 -	56.2	333	hypothetical protein [Pseudomonas phage DL68]	0	YP_009215162.1
	56690			hypothetical protein vB_Pae_PS44_00069 [ <i>Pseudomonas</i> phage vB_Pae_PS44]	0	YP_009211393.1
PA1P1_085c	58680 - 57796	62.1	294	hypothetical protein PP141_gp67 [ <i>Pseudomonas</i> phage 14-1]	0	YP_002364375.1
				hypothetical protein [Pseudomonas phage DL68]	0	YP_009215161.1
PA1P1_086c	60029 - 58842	55.4	395	putative ATP-dependent exonuclease V [ <i>Pseudomonas</i> phage SN]	0	YP_002418875.1
				hypothetical protein ORF067 [ <i>Pseudomonas</i> phage F8]	0	YP_001294484.1
PA1P1_087c	60438 - 60016	57.0	140	hypothetical protein ORF068 [ <i>Pseudomonas</i> phage F8]	3E-98	YP_001294485.1
				hypothetical protein [Pseudomonas phage NP3]	1E-97	AMQ76187.1
PA1P1_088	60607 - 61392	59.2	261	hypothetical protein PP141_gp70 [Pseudomonas phage 14-1]	0	YP_002364378.1
				hypothetical protein ORF069 [ <i>Pseudomonas</i> phage F8]	0	YP_001294486.1
PA1P1_089	61403 -	59.1	407	hypothetical protein vBPaeME215_00050	0	ASZ72528.1
	62626			[Pseudomonas phage vB_PaeM_E215]	0	VD 002154212 1
				phage LBL3]	0	19_002154213.1
PA1P1_090	62650 - 63099	58.2	149	hypothetical protein PP141_gp72 [ <i>Pseudomonas</i> phage 14-1]	3E-105	YP_002364380.1
				hypothetical protein [Pseudomonas phage NP3]	5E-105	AMQ76190.1
PA1P1_091	63096 -	57.7	358	hypothetical protein [ <i>Pseudomonas</i> phage DL52]	0	AKF13701.1
	64172			hypothetical protein PP141_gp73 [Pseudomonas phage 14-1]	0	YP_002364381.1
PA1P1_092	64178 -	47.8	61	hypothetical protein ORF073 [ <i>Pseudomonas</i> phage	4E-33	YP_001294490.1
	04303			hypothetical protein phiKT28_076 [Pseudomongs	3E-32	AKJ71514.1
				phage phiKT28]		
PA1P1_093	64511 -	53.3	579	putative Ploop ATPase [Pseudomonas aeruginosa]	0	SBT96795.1
	66250			virulence-associated protein E [Pseudomonas	0	YP_009211402.1
		1		phage vB_Pae_PS44]		

#### Table S5: Predicted genes of P. aeruginosa phage PA8P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC	Protein lenght	Amino acid sequence identity/similarity to best homologs	E-value (BLAST)	Accession no
LUCUS tag	FOSICION		(ac)	(% amine acid identity)		Accession no.
		(%)	(aa)	(% amino acid identity)		
PA8P1_001	601 - 1170	59.1	189	hypothetical protein PP141_gp76 [Pseudomonas phage 14-	4E-138	YP_002364384.1
				1]		
				hypothetical protein [Pseudomonas phage S12-1]	1E-137	BAU16489.1
PA8P1_002c	1949 - 1338	54.7	203	hypothetical protein vBPaeME215_00056 [Pseudomonas	3E-142	ASZ72534.1
				phage vB_PaeM_E215]		
				hypothetical protein PP141_gp77 [Pseudomonas phage 14-	6E-142	YP_002364385.1
				1]		_
PA8P1_003c	2834 - 2139	60.5	231	hypothetical protein PP141_gp78 [Pseudomonas phage 14-	2E-166	YP_002364386.1
				1]		
				hypothetical protein vBPaeME215_00057 [Pseudomonas		
				phage vB_PaeM_E215]	5E-166	ASZ72535.1
PA8P1_004c	3156 - 2845	56.1	103	hypothetical protein PP141_gp79 [Pseudomonas phage 14-	1E-72	YP_002364387.1
_				1]		_
				hypothetical protein vBPaeME217 00082 [Pseudomonas	6E-72	ASZ72466.1
				phage vB PaeM E217]		
PA8P1 005c	3427 - 3206	53.2	73	hypothetical protein I7A 082c [ <i>Pseudomonas</i> phage NH-4]	2E-44	YP 007002628.1
				hypothetical protein PP141 gp80 [Pseudomonas phage 14-	5E-44	YP_002364388.1
				1]		

PA8P1_006c	3707 - 3483	54.7	74	hypothetical protein PPSN_gp83 [ <i>Pseudomonas</i> phage SN] hypothetical protein LBL3_gp79 [ <i>Pseudomonas</i> phage LBL3]	4E-47 2F-46	YP_002418889.1 YP_002154224.1
PA8P1_007c	4099 - 3773	56.3	108	hypothetical protein PII10A_07 [Pseudomonas phage Laba]	7E-74	SBT96689.1
DA8D1 008-	4744 4100	50.7	214	hypothetical protein LBL3_gp80 [Pseudomonus phage LBL3]	2E-73	YP_002154225.1
PA8P1_008C	4744 - 4100	59.7	214	hypothetical protein [Pseudomonas phage DLos] hypothetical protein PJG24_088 [Pseudomonas phage JG024]	4E-154	YP_006200852.1
PA8P1_009c	4985 - 4776	58.6	69	hypothetical protein [Pseudomonas aeruginosa]	7E-45	WP_015994944.1
				hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27]	7E-40	YP_009124313.1
PA8P1_010c	5197 - 4982	52.3	71	hypothetical protein [Pseudomonas phage DL68]	7E-44	YP_009215142.1
				hypothetical protein PJG24_090 [ <i>Pseudomonas</i> phage JG024]	3E-43	YP_006200854.1
PA8P1_011c	5394 - 5194	56.7	66	hypothetical protein [Pseudomonas phage KPP22]	2E-39	BAU20627.1
				hypothetical protein vBPaeMDP1_0085 [Pseudomonas phage vB_PaeM_CEB_DP1]	2E-39	AKP24472.1
PA8P1_012c	5642 - 5391	51.6	83	hypothetical protein vBPaeME217_00092 [Pseudomonas	1E-53	ASZ72476.1
				phage vB_PaeM_E217] hypothetical protein I7A_091c [ <i>Pseudomonas</i> phage NH-4]	2E-53	YP_007002637.1
PA8P1 013c	5917 - 5729	54.5	62	hypothetical protein PJG24_093 [ <i>Pseudomonas</i> phage	8E-36	YP 006200857.1
	001/ 0/20	55	02	JG024]	75.25	VD 000245420 4
DA9D1 014c	6642 5020	EE C	240	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	7E-35	YP_009215139.1
PA6P1_014C	0042 - 5920	55.0	240	JG024]	SE-100	1P_006200858.1
				hypothetical protein BrSP1_16 [Pseudomonas phage BrSP1]	5E-165	ATI16268.1
PA8P1_015c	6963 - 6661	54.1	100	hypothetical protein vBPaeMDP1_0001 [Pseudomonas	1E-63	AKP24388.1
				phage vB_PaeM_CEB_DP1]	25 62	VP 006200766 1
				JG024]	3L-03	1F_000200700.1
PA8P1_016c	7192 - 7019	53.4	57	hypothetical protein PPSN_gp02 [Pseudomonas phage SN]	5E-34	YP_002418808.1
DA9D1 017c	7200 7242	52.1	10	hypothetical protein PILIDA_17 [Pseudomonas deruginosa]	1E-33	SB196699.1
PAGPI_017C	/369 - /243	33.1	40	hypothetical protein SAMN05216409 118116	6E-13	SER37912.1
				[Pseudomonas lutea]		
PA8P1_018	7437 - 7559	49.6	40	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	2E-19	YP_009215134.1
PA8P1 019	7564 - 8946	52.4	460	terminase large subunit [ <i>Pseudomonus</i> phage DL68]	8E-13 0	VP_002154146.1
	7504 0540	52.4	400	large terminase protein [ <i>Pseudomonas</i> phage	0	ASZ72553.1
DA8D1 020a	0266 0002	FO 1	107	VB_PaeM_E215]	25.96	VD 002264212.1
PA6P1_0200	9200 - 9992	59.1	127	1]	3E-00	TP_002364312.1
				hypothetical protein [Pseudomonas phage NP3]	7E-86	AMQ76120.1
PA8P1_021c	9581 - 9363	54.8	72	hypothetical protein [ <i>Pseudomonas aeruginosa</i> ]	4E-46	WP_015994883.1
DA9D1 022c	0021 0591	60.7	116	hypothetical protein [Pseudomonas phage NP3]	3E-45	AMQ76121.1
FAOF 1_0220	3331 - 3381	00.7	110	hypothetical protein LBL5_gp05 [F3eudomonus phage LBL5]	11-10	11 _002134130.1
PA8P1 023c				hypothetical protein SL1 06 [ <i>Pseudomonas</i> phage SL1]	2E-76	AUS03281.1
	10373 -	59.4	132	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68]	2E-76 1E-87	AUS03281.1 YP_009215129.1
	10373 - 9975	59.4	132	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3]	2E-76 1E-87 2E-86	AUS03281.1 YP_009215129.1 YP_002154151.1
PA8P1_024c	10373 - 9975 11155 - 10276	59.4 57.2	132 259	hypothetical protein SL1_06 [Pseudomonas phage SL1] hypothetical protein [Pseudomonas phage DL68] hypothetical protein LBL3_gp06 [Pseudomonas phage LBL3] hypothetical protein PP141_gp08 [Pseudomonas phage 14- 11	2E-76 1E-87 2E-86 0	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1
PA8P1_024c	10373 - 9975 11155 - 10376	59.4 57.2	132 259	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68]	2E-76 1E-87 2E-86 0	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1
PA8P1_024c	10373 - 9975 11155 - 10376 11679 -	59.4 57.2 60.3	132 259 145	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i>	2E-76 1E-87 2E-86 0 0 2E-98	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1
PA8P1_024c	10373 - 9975 11155 - 10376 11679 - 11242	59.4 57.2 60.3	132 259 145	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1
PA8P1_024c	10373 - 9975 11155 - 10376 11679 - 11242	59.4 57.2 60.3	132 259 145	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 CF_44F	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1
PA8P1_024c PA8P1_025c PA8P1_026c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11606	59.4 57.2 60.3 56.8	132 259 145 195	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein [ <i>Pseudomonas</i> phage S12-1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 15 144	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_009154154.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 -	59.4 57.2 60.3 56.8	132 259 145 195	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp11 [ <i>Pseudomonas</i> phage 14-	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2F-11	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293	59.4 57.2 60.3 56.8 51.0	132 259 145 195 31	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp11 [ <i>Pseudomonas</i> phage 14- 1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293	59.4 57.2 60.3 56.8 51.0	132 259 145 195 31	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_004221739.1
PA8P1_024c PA8P1_025c PA8P1_025c PA8P1_026c PA8P1_028c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385	59.4 57.2 60.3 56.8 51.0 56.6	132 259 145 195 31 310	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp12 [ <i>Pseudomonas</i> phage 14- 1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_004221739.1 YP_002364320.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385	59.4 57.2 60.3 56.8 51.0 56.6	132 259 145 195 31 310	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage VB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein VBPaeME215_00085 [ <i>Pseudomonas</i>	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_004221739.1 YP_002364320.1 ASZ72563.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385	59.4 57.2 60.3 56.8 51.0 56.6	132 259 145 195 31 310	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein VP141_gp11 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein VBPaeME215_00085 [ <i>Pseudomonas</i> phage vB_PaeM_E215]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0 0	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002364319.1 YP_002364319.1 YP_002364320.1 ASZ72563.1
PA8P1_024c PA8P1_025c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420	59.4 57.2 60.3 56.8 51.0 56.6 56.3	132 259 145 195 31 310 166	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein vBPaeME215_00085 [ <i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein vBPaeME215_00085 [ <i>Pseudomonas</i> phage vB_PaeM_E215]	2E-76         1E-87         2E-86         0         0         2E-98         2E-97         6E-145         1E-144         2E-11         3E-11         0         0         0         4E-120	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c PA8P1_029c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420	59.4 57.2 60.3 56.8 51.0 56.6 56.3	132 259 145 195 31 310 166	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein VBPaeME215_00085 [ <i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0 4E-120 2E-119	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_006200778.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c PA8P1_028c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420	59.4 57.2 60.3 56.8 51.0 56.6 56.3	132 259 145 195 31 310 166	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp11 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein VBPaeME215_00085 [ <i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJ624_013 [ <i>Pseudomonas</i> phage 14- 1]	2E-76         1E-87         2E-86         0         0         2E-98         2E-97         6E-145         1E-144         2E-11         3E-11         0         0         4E-120         2E-119	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_006200778.1
PA8P1_024c PA8P1_025c PA8P1_025c PA8P1_027c PA8P1_028c PA8P1_029c PA8P1_029c PA8P1_030c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420 13420	59.4 57.2 60.3 56.8 51.0 56.6 56.3 54.0	132         259         145         195         31         310         166         115	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp12 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJ624_013 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJ624_013 [ <i>Pseudomonas</i> phage 14- 1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0 4E-120 2E-119 9E-76	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_002364322.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c PA8P1_029c PA8P1_030c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420 13420 14287 - 13940	59.4 57.2 60.3 56.8 51.0 56.6 56.3 56.3	132         259         145         195         31         310         166         115	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp11 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp12 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJG24_013 [ <i>Pseudomonas</i> phage 14- 1]	2E-76         1E-87         2E-86         0         0         2E-98         2E-97         6E-145         1E-144         2E-11         3E-11         0         4E-120         2E-119         9E-76         1E-75	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002154154.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_002364322.1 YP_002364322.1 YP_009215123.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c PA8P1_029c PA8P1_030c PA8P1_031c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420 14287 - 13940 14847 -	59.4 57.2 60.3 56.8 51.0 56.6 56.3 56.3 54.0	132         259         145         195         31         310         166         115         103	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae436M-8_10 [ <i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp11 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp12 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJG24_013 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage DL68]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0 4E-120 2E-119 9E-76 1E-75 4E-67	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_002364322.1 YP_002364322.1 YP_009215123.1 YP_009215122.1
PA8P1_024c PA8P1_025c PA8P1_026c PA8P1_027c PA8P1_028c PA8P1_029c PA8P1_030c PA8P1_031c	10373 - 9975 11155 - 10376 11679 - 11242 12283 - 11696 12388 - 12293 13317 - 12385 13920 - 13420 14287 - 13940 14847 - 14536	59.4 57.2 60.3 56.8 51.0 56.6 56.3 56.3 54.0	132         259         145         195         31         310         166         115         103	hypothetical protein SL1_06 [ <i>Pseudomonas</i> phage SL1] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein PP141_gp08 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein ( <i>Pseudomonas</i> phage DL68] hypothetical protein ( <i>Pseudomonas</i> phage NP3] Phage vB_Pae436M-8] hypothetical protein [ <i>Pseudomonas</i> phage NP3] Phage protein [ <i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp09 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein LBL3_gp88 [ <i>Pseudomonas</i> phage LBL3] hypothetical protein PP141_gp12 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PP141_gp13 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJG24_013 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJG24_015 [ <i>Pseudomonas</i> phage 14- 1] hypothetical protein PJG24_015 [ <i>Pseudomonas</i> phage 14- 1]	2E-76 1E-87 2E-86 0 0 2E-98 2E-97 6E-145 1E-144 2E-11 3E-11 0 0 4E-120 2E-119 9E-76 1E-75 4E-67 3E-66	AUS03281.1 YP_009215129.1 YP_002154151.1 YP_002364316.1 YP_009215128.1 ANT44196.1 AMQ76125.1 BAU16423.1 YP_002364319.1 YP_002364320.1 ASZ72563.1 YP_002364321.1 YP_002364322.1 YP_002364322.1 YP_009215123.1 YP_009215123.1 YP_009215122.1 YP_006200780.1

## Supplementary material

PA8P1_032c	15056 - 14853	56.4	67	hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein PPGF8SP_0081 [ <i>Pseudomonas</i> phage SPM-1]	2E-39 4E-37	YP_009215121.1 AHH02940.1
PA8P1_033c	15376 - 15053	56.2	107	hypothetical protein vBPaeME215_00090 [ <i>Pseudomonas</i> phage vB_PaeM_E215]	9E-75	ASZ72568.1
				hypothetical protein vB_Pae_PS44_00019 [ <i>Pseudomonas</i> phage vB_Pae_PS44]	5E-74	YP_009211343.1
PA8P1_034c	15808 - 15407	53.0	133	hypothetical protein vBPaeME215_00091 [ <i>Pseudomonas</i> phage vB PaeM E215]	1E-92	ASZ72569.1
				hypothetical protein PP141_gp17 [ <i>Pseudomonas</i> phage 14- 1]	1E-91	YP_002364325.1
PA8P1_035	15988 - 18285	56.7	765	hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein vBPaeME215_00092 [ <i>Pseudomonas</i>	0 0	YP_009215210.1 ASZ72570.1
DA0D1 036	40205	52.4	270	phage vB_PaeM_E215]		VD 0000040074
PA8P1_036	19121	53.4	278	1]	0	YP_002364327.1
PA8P1 037	19140 -	55.1	68	hypothetical protein phiKT28 022 [Pseudomonas phage phage	0 1E-41	AKJ71460.1
	19346			phiKT28]		
				hypothetical protein vBPaeMDP1_0020 [Pseudomonas phage vB_PaeM_CEB_DP1]	5E-41	AKP24407.1
PA8P1_038	19343 - 19483	53.2	46	hypothetical protein LMA2_gp20 [ <i>Pseudomonas</i> phage LMA2]	2E-23	YP_002154254.1
				hypothetical protein BrSP1_38 [ <i>Pseudomonas</i> phage BrSP1]	9E-23	ATI16221.1
PA8P1_039	20035 -	58.2	464	hypothetical protein [ <i>Pseudomonas</i> phage DL68] hypothetical protein PP141, gp22 [ <i>Pseudomonas</i> phage 14-	0	YP_009215206.1
	21425			1]	0	11_002304330.1
PA8P1_040	21433 - 22068	62.7	211	hypothetical protein PP141_gp23 [ <i>Pseudomonas</i> phage 14- 1]	5E-148	YP_002364331.1
				structural protein [Pseudomonas phage SN]	1E-147	YP_002418830.1
PA8P1_041	22078 -	61.3	382	capsid and scaffold protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76141.1
	23220			vB_PaeM_CEB_DP1]	0	ART 24411.1
PA8P1_042	23328 -	54.1	145	hypothetical protein PPSN_gp26 [ <i>Pseudomonas</i> phage SN] hypothetical protein LBL3_gp22 [ <i>Pseudomonas</i> phage LBL3]	1E-103 3E-103	YP_002418832.1 YP_002154167.1
PA8P1_043	23780 -	58.3	155	structural protein [ <i>Pseudomonas</i> phage SN]	2E-109	YP_002418833.1
	24247			hypothetical protein [Pseudomonas phage DL68]	3E-109	YP_009215202.1
PA8P1_044	24244 - 24642	51.4	132	hypothetical protein [ <i>Pseudomonas</i> phage NP3] structural protein [ <i>Pseudomonas</i> phage SN]	3E-92 8E-92	AMQ76144.1 YP_002418834.1
PA8P1_045	24650 -	48.0	183	hypothetical protein LBL3_gp25 [Pseudomonas phage LBL3]	9E-133	YP_002154170.1
	25201			hypothetical protein LMA2_gp27 [ <i>Pseudomonas</i> phage LMA2]	1E-132	YP_002154261.1
PA8P1_046	25198 -	54.8	193	hypothetical protein ORF028 [Pseudomonas phage F8]	3E-137	YP_001294445.1
DA0D1 047	25779	50.5	504	hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	1E-136	YP_007238183.1
PA8P1_047	25795 - 27309	59.5	504	hypothetical protein I/A_031 [ <i>Pseudomonas</i> phage NH-4] hypothetical protein vBPaeMDP1_0030 [ <i>Pseudomonas</i>	0	AKP24417.1
DA9D1 049	27260	50.9	150	phage vB_PaeM_CEB_DP1	25 102	VP 002154264 1
FAOF1_040	27820	55.8	150	structural protein [ <i>Pseudomonas</i> phage phiKT28]	2E-103	AKJ71471.1
PA8P1_049	27820 -	54.6	107	putative structural protein [ <i>Pseudomonas</i> phage LMA2]	2E-75	YP_002154265.1
PA8P1 050	28143	53.6	116	putative structural protein [ <i>Pseudomonas</i> phage JG024]	3E-78	YP 002154266.1
	28490			structural protein [Pseudomonas phage SL1]	1E-77	AUS03345.1
PA8P1_051	28492 -	65.0	143	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	3E-92	YP_009215194.1
PA8P1_052	28933 -	52.2	167	structural protein [ <i>Pseudomonas</i> phage SN]	3E-115	YP_002418842.1
-	29436	FF 7	170	putative structural protein [ <i>Pseudomonas</i> phage LMA2]	1E-114	YP_002154268.1
PA8P1_053	29436 - 29975	55.7	1/9	putative structural protein [ <i>Pseudomonas</i> phage LMA2] putative structural protein [ <i>Pseudomonas</i> phage LBL3]	3E-127 9E-127	YP_002154269.1 YP_002154178.1
PA8P1_054	29984 -	46.6	197	hypothetical protein vBPaeME217_00038 [Pseudomonas	5E-140	ASZ72422.1
	30577			phage vB_PaeM_E217]	2F-139	VP 007228100 1
PA8P1 055	30587 -	57.1	142	hypothetical protein LBL3 gp35 [Pseudomonas phage LBL3]	4E-101	YP_002154180.1
_	31015			hypothetical protein phiKTN6_037 [ <i>Pseudomonas</i> phage	25-100	- AK171560 1
PA8P1_056	31019 -	57.9	858	putative lytic tail protein [ <i>Pseudomonas</i> phage LMA2]	0	YP_002154272.1
	33595			internal (core) protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76156.1
PA8P1_057	33595 - 34458	51.7	287	putative structural protein [ <i>Pseudomonas</i> phage LMA2]	0	YP_002154273.1 AKP24427 1
	550	L		vB_PaeM_CEB_DP1]	-	
PA8P1_058	34458 - 34991	47.8	177	hypothetical protein PP141_gp41 [Pseudomonas phage 14- 1]	2E-127	YP_002364349.1
	-			hypothetical protein [Pseudomonas phage DL68]	5E-127	YP_009215187.1

PA8P1_059	35047 - 35712	53.0	221	hypothetical protein LMA2_gp41 [ <i>Pseudomonas</i> phage 2E-160		YP_002154275.1
	55712			putative baseplate [ <i>Pseudomonas</i> phage KPP12]	4E-160	YP_007238195.1
PA8P1_060A	35723 -	42.6	17	hypothetical protein PB1_gp43 [ <i>Pseudomonas</i> phage	3E-09	 YP_002455973.1
	35776			PB1] putative baseplate protein [ <i>Pseudomonas</i> phage SN]	2E-04	YP_002418850.1
PA8P1_060B	35769 -	57.7	417	putative structural protein [ <i>Pseudomonas</i> phage LMA2]	0	YP_002154276.1
_	37022			putative baseplate protein [Pseudomonas phage SN]	0	YP_002418850.1
PA8P1_061	37019 - 38533	56.0	504	hypothetical protein PP141_gp44 [ <i>Pseudomonas</i> phage 14- 1] ctructural protein [ <i>Pseudomonas</i> phage vB_Pae/36M-8]	0	YP_002364352.1
PA8P1 062	38538 -	57.1	962	putative tail fiber component [ <i>Pseudomonas</i> phage NH-4]	0	YP 007002592.1
_	41426			tail fibers protein [Pseudomonas phage NP3]	0	 AMQ76163.1
PA8P1_063	41428 -	58.3	142	hypothetical protein [Pseudomonas phage NP3]	9E-99	AMQ76164.1
<b>D</b> 40D4 0C4	41856	60 F	220	putative tail fiber component [ <i>Pseudomonas</i> phage JG024]	2E-97	YP_006200811.1
PA8P1_064	41856 - 42518	60.5	220	lytic enzyme [ <i>Pseudomonas</i> phage NP3] putative endolysin [ <i>Pseudomonas</i> phage JG024]	2E-161 7E-161	AMQ76165.1 YP 006200812.1
PA8P1 065c	42793 -	51.2	83	hypothetical protein PP141 gp48 [ <i>Pseudomonas</i> phage 14-	2E-50	YP 002364356.1
_	42542			1]		-
				hypothetical protein LMA2_gp47 [Pseudomonas phage LMA2]	3E-50	YP_002154281.1
PA8P1_066c	43984 -	55.7	303	DNA ligase [ <i>Pseudomonas</i> phage phiKT28]	0	AKJ71489.1
PA8P1 067c	45075	54.4	184	DNA hinding protein [ <i>Pseudomongs</i> phage DI 68]	0 2F-132	YP_000200814.1
FAOF 1_007C	44039	J4.4	104	hypothetical protein PJG24 051 [ <i>Pseudomonas</i> phage	2E-132 2E-131	YP_006200815.1
				JG024]		
PA8P1_068c	45195 -	60.2	201	hypothetical protein ORF050 [Pseudomonas phage F8]	4E-139	YP_001294467.1
	44590			hypothetical protein PP141_gp51 [Pseudomonas phage 14-	9E-139	YP_002364359.1
DA9D1 060c	46149	50.0	200	1] hypothetical protain DD141, gp52 [Occurdemongs phage 14	0	VD 002264260 1
PA6P1_009C	40148 - 45249	59.9	299	1]	0	1P_002304300.1
	13213			hypothetical protein [ <i>Pseudomonas</i> phage DL68]	0	YP 009215176.1
PA8P1_070c	46857 -	53.3	206	hypothetical protein vBPaeMLS1_79 [Pseudomonas phage	3E-145	AVJ48847.1
	46237			vB_PaeM_LS1]		
				hypothetical protein SL1_50 [ <i>Pseudomonas</i> phage SL1]	1E-144	AUS03325.1
PA8P1_0/1c	48511 -	55.1	519	nypothetical protein PPSN_gp55 [ <i>Pseudomonas</i> phage SN]	0	YP_002418861.1 ANT44241 1
PA8P1 072c	48918 -	55.2	136	hypothetical protein LBL3 gp52 [Pseudomongs phage LBL3]	6E-95	YP 002154197.1
	48508			hypothetical protein [ <i>Pseudomonas</i> phage NP3]	6E-95	AMQ76173.1
PA8P1_073c	52018 -	54.9	1035	hypothetical protein PP141_gp56 [Pseudomonas phage 14-	0	YP_002364364.1
	48911			1]		
				UNA polymerase III subunit alpha [ <i>Pseudomonds</i> phage VB_Pae_PS44]	0	YP_009211383.1
PA8P1 074c	52572 -	52.8	184	putative DNA polymerase III. epsilon subunit [ <i>Pseudomonas</i>	3E-135	YP 002154290.1
	52018		-	phage LMA2]		
				putative DNA polymerase III epsilon subunit [Pseudomonas	3E-135	YP_007002604.1
				phage NH-4]		
PA8P1_075c	53679 - 52648	58.4	343	putative 3'-phosphatase, 5'-polynucleotide kinase	0	SB196767.1
	52040			putative polynucleotide kinase [ <i>Pseudomonas</i> phage	0	YP 007238211.1
					-	
PA8P1_076c				KPP12]		
	53873 -	49.0	63	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage	3E-35	YP_006200824.1
	53873 - 53682	49.0	63	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage (19012)]	3E-35	YP_006200824.1
PA8P1 077c	53873 - 53682 54792 -	49.0	63	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein PP141_gp60 [ <i>Pseudomonas</i> phage 14-	3E-35 1E-34 0	YP_006200824.1 YP_007238212.1 YP_002364368_1
PA8P1_077c	53873 - 53682 54792 - 53875	49.0 58.1	63 305	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein PP141_gp60 [ <i>Pseudomonas</i> phage 14- 1]	3E-35 1E-34 0	YP_006200824.1 YP_007238212.1 YP_002364368.1
PA8P1_077c	53873 - 53682 54792 - 53875	49.0 58.1	63 305	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein PP141_gp60 [ <i>Pseudomonas</i> phage 14- 1] putative thymidylate synthase [ <i>Pseudomonas</i> phage JG024]	3E-35 1E-34 0	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1
PA8P1_077c PA8P1_078c	53873 - 53682 54792 - 53875 54998 -	49.0 58.1 50.1	63 305 68	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein PP141_gp60 [ <i>Pseudomonas</i> phage 14- 1] putative thymidylate synthase [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	3E-35 1E-34 0 0 4E-41	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1
PA8P1_077c PA8P1_078c	53873 - 53682 54792 - 53875 54998 - 54792	49.0 58.1 50.1	63 305 68	KPP12] hypothetical protein PJG24_060 [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein PP141_gp60 [ <i>Pseudomonas</i> phage 14- 1] putative thymidylate synthase [ <i>Pseudomonas</i> phage JG024] hypothetical protein [ <i>Pseudomonas</i> phage KPP12] hypothetical protein SL1_42 [ <i>Pseudomonas</i> phage SL1]	3E-35 1E-34 0 0 4E-41 8E-41	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1
PA8P1_077c PA8P1_078c PA8P1_079c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006	49.0 58.1 50.1 57.1	63 305 68 76	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SN]         hypothetical protein PPSN_sp63 [Assuration phage SN]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002464270.1
PA8P1_077c PA8P1_078c PA8P1_079c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006	49.0 58.1 50.1 57.1	63 305 68 76	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SN]         hypothetical protein PP141_gp62 [Pseudomonas phage 14-1]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002364370.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 -	49.0 58.1 50.1 57.1 54.8	63 305 68 76 72	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SN]         hypothetical protein PP141_gp62 [Pseudomonas phage SN]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 2E-46	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002364370.1 YP_002418870.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269	49.0 58.1 50.1 57.1 54.8	63 305 68 76 72	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PP141_gp62 [Pseudomonas phage SN]         hypothetical protein PP141_gp62 [Pseudomonas phage SN]         hypothetical protein PP141_gp62 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage SN]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 2E-46 3E-46	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002364370.1 YP_002418870.1 YP_002154296.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269	49.0 58.1 50.1 57.1 54.8	63 305 68 76 72	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SN]         hypothetical protein PP141_gp62 [Pseudomonas phage 14-1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage LMA2]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002418869.1 YP_002364370.1 YP_002418870.1 YP_002154296.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55487 -	49.0 58.1 50.1 57.1 54.8 59.4	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14- 1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 2E-42 65 42	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_006200825.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002418869.1 YP_002364370.1 YP_002154296.1 YP_002154206.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55471 55919 -	49.0 58.1 50.1 57.1 54.8 59.4	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> <li>76</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]         hypothetical protein BP3_gp64 [Pseudomonas phage LBL3]         hypothetical protein BP3_gp64 [Pseudomonas phage LBL3]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 2E-42 6E-50	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_002364368.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002418869.1 YP_002418870.1 YP_002154296.1 YP_002154296.1 YP_007238217.1 YP_002364373.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c PA8P1_082c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55471 55919 - 55689	<ul> <li>49.0</li> <li>58.1</li> <li>50.1</li> <li>57.1</li> <li>54.8</li> <li>59.4</li> <li>58.9</li> </ul>	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> <li>76</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]         hypothetical protein RPSN_gp64 [Pseudomonas phage LBL3]         hypothetical protein PP141_gp65 [Pseudomonas phage LBL3]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 2E-42 6E-42 6E-50	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_002364368.1 YP_007238214.1 AUS03317.1 YP_002418869.1 YP_002418870.1 YP_002418870.1 YP_002154296.1 YP_002154296.1 YP_002364373.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c PA8P1_082c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55471 55919 - 55689	<ul> <li>49.0</li> <li>58.1</li> <li>50.1</li> <li>57.1</li> <li>54.8</li> <li>59.4</li> <li>58.9</li> </ul>	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> <li>76</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SN]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LMA2_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]         hypothetical protein RPSN_gp64 [Pseudomonas phage LBL3]         hypothetical protein LBL3_gp65 [Pseudomonas phage 14-1]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 3E-46 2E-42 6E-50 1E-49	YP_006200824.1 YP_007238212.1 YP_002364368.1 YP_002364368.1 YP_007238214.1 AUS03317.1 YP_002364370.1 YP_002364370.1 YP_002154296.1 YP_002154206.1 YP_002364373.1 YP_002364373.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c PA8P1_082c PA8P1_083c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55471 55919 - 55689 55689 -	49.0 58.1 50.1 57.1 54.8 59.4 58.9 55.6	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> <li>76</li> <li>333</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LBL3_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]         hypothetical protein PP141_gp65 [Pseudomonas phage 14-1]         hypothetical protein PP141_gp66 [Pseudomonas phage 14-1]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 3E-46 2E-42 6E-50 1E-49 0	YP_006200824.1           YP_007238212.1           YP_002364368.1           YP_002364368.1           YP_00238214.1           AUS03317.1           YP_002418869.1           YP_002418870.1           YP_002154296.1           YP_002364373.1           YP_002364373.1           YP_002364373.1           YP_002364374.1
PA8P1_077c PA8P1_078c PA8P1_079c PA8P1_080c PA8P1_081c PA8P1_082c PA8P1_083c	53873 - 53682 54792 - 53875 54998 - 54792 55236 - 55006 55487 - 55269 55689 - 55471 55919 - 55689 55689 557008 - 56007	49.0 58.1 50.1 57.1 54.8 59.4 58.9 55.6	<ul> <li>63</li> <li>305</li> <li>68</li> <li>76</li> <li>72</li> <li>72</li> <li>76</li> <li>333</li> </ul>	KPP12]         hypothetical protein PJG24_060 [Pseudomonas phage         JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein PP141_gp60 [Pseudomonas phage 14-1]         putative thymidylate synthase [Pseudomonas phage JG024]         hypothetical protein [Pseudomonas phage KPP12]         hypothetical protein SL1_42 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp63 [Pseudomonas phage SL1]         hypothetical protein PPSN_gp64 [Pseudomonas phage SN]         hypothetical protein LBL3_gp62 [Pseudomonas phage SN]         hypothetical protein LBL3_gp61 [Pseudomonas phage LBL3]         hypothetical protein LBL3_gp62 [Pseudomonas phage LBL3]         hypothetical protein LBL3_gp62 [Pseudomonas phage 14-1]         hypothetical protein LBL3_gp62 [Pseudomonas phage LBL3]         hypothetical protein LBL3_gp63 [Pseudomonas phage 14-1]         hypothetical protein PP141_gp65 [Pseudomonas phage 14-1]         hypothetical protein PP141_gp66 [Pseudomonas phage 14-1]         hypothetical protein LBL3_gp62 [Pseudomonas phage 14-1]	3E-35 1E-34 0 0 4E-41 8E-41 1E-47 1E-47 1E-47 2E-46 3E-46 3E-46 2E-42 6E-50 1E-49 0	YP_006200824.1           YP_007238212.1           YP_002364368.1           YP_002364368.1           YP_00238214.1           AUS03317.1           YP_002418869.1           YP_002418870.1           YP_002154296.1           YP_002364373.1           YP_002364373.1           YP_002364374.1           YP_002364374.1

## Supplementary material

PA8P1_084c	58003 -	63.2	296	hypothetical protein [Pseudomonas phage PA5]	1E-169	APD20755.1
	57113			putative structural protein [Pseudomonas phage KPP12]	2E-169	YP_007238220.1
PA8P1_085c	59351 -	55.0	395	putative ATP-dependent exonuclease V [Pseudomonas	0	YP_002418875.1
	58164			phage SN]		
				hypothetical protein ORF067 [Pseudomonas phage F8]	0	YP_001294484.1
PA8P1_086c	59760 -	56.7	140	hypothetical protein ORF068 [Pseudomonas phage F8]	1E-97	YP_001294485.1
	59338			hypothetical protein I7A_070c [Pseudomonas phage NH-4]	3E-97	YP_007002616.1
PA8P1_087	59929 -	59.0	261	hypothetical protein LMA2_gp69 [Pseudomonas phage	0	YP_002154303.1
	60714			LMA2]		
				hypothetical protein vBPaeMLS1_62 [Pseudomonas phage	0	AVJ48831.1
				vB_PaeM_LS1]		
PA8P1_088	60725 -	57.6	333	hypothetical protein [Pseudomonas aeruginosa]	2E-92	WP_051488611.1
	61726			hypothetical protein vB_Pae436M-8_72 [Pseudomonas	5E-77	ANT44258.1
				phage vB_Pae436M-8]		
PA8P1_089	61726 -	58.2	149	hypothetical protein [Pseudomonas phage DL60]	7E-104	YP_009193759.1
	62175			hypothetical protein [Pseudomonas phage NP3]	9E-103	AMQ76190.1
PA8P1_090	62172 -	57.5	358	hypothetical protein PP141_gp73 [Pseudomonas phage 14-	0	YP_002364381.1
	63248			1]		
				hypothetical protein vBPaeMLS1_59 [Pseudomonas phage	0	AVJ48828.1
				vB_PaeM_LS1]		
PA8P1_091	63254 -	50.5	61	hypothetical protein LMA2_gp73 [Pseudomonas phage	9E-34	YP_002154307.1
	63439			LMA2]		
				hypothetical protein PPSN_gp75 [Pseudomonas phage SN]	2E-33	YP_002418881.1
PA8P1_092	63587 -	53.3	579	putative Ploop ATPase [Pseudomonas aeruginosa]	0	SBT96795.1
	65326			virulence-associated protein E [Pseudomonas phage	0	YP_009211402.1
				vB Pae PS44]		

#### Table S6: Predicted genes of P. aeruginosa phage PA11P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein lenght (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no.
PA11P1_001	604 - 1173	58.9	189	hypothetical protein [ <i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	5E-138	YP_009124304.1
				hypothetical protein LMA2_gp76 [ <i>Pseudomonas</i> phage LMA2]	5E-137	YP_002154309.1
PA11P1_002c	1952 -	55.1	203	hypothetical protein vBPaeME215_00056	2E-143	ASZ72534.1
	1341			[Pseudomonas phage vB_PaeM_E215] hypothetical protein PP141_gp77 [Pseudomonas	5F-143	VP 002364385 1
				phage 14-1]	52 145	11_002304303.1
PA11P1_003c	2828 -	60.0	228	hypothetical protein PP141_gp78 [Pseudomonas	3E-157	YP_002364386.1
	2142			phage 14-1]	45.450	10770505.4
				[Pseudomongs phage vB_PaeM_E215]	1E-156	ASZ/2535.1
PA11P1_004c	3150 -	55.8	103	hypothetical protein vBPaeMDP1_0076	1E-71	AKP24463.1
	2839			[Pseudomonas phage vB_PaeM_CEB_DP1]		
				hypothetical protein BrSP1_5 [ <i>Pseudomonas</i> phage	4E-71	ATI16257.1
PA11P1 005c	3424 -	52.7	73	BISP1 hypothetical protein PP141_gn80 [Pseudomongs	3F-44	YP 002364388 1
	3203	52.7	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	phage 14-1]	02	
				hypothetical protein I7A_082c [ <i>Pseudomonas</i> phage NH-4]	5E-44	YP_007002628.1
PA11P1_006c	3688 -	56.9	84	hypothetical protein PP141_gp81 [Pseudomonas	1E-53	YP_002364389.1
	3434			phage 14-1]	55.40	BAU20622 4
PA11P1 007c	3966 -	55.6	74	hypothetical protein [Pseudomonds phage KPP22]	5E-49 3F-47	BAU20633.1 VP_002154224_1
1,411,1_00/6	3742	55.0	/ -	phage LBL3]	52 47	11_002134224.1
				hypothetical protein PPSN_gp83 [Pseudomonas	2E-46	YP_002418889.1
				phage SN]		
PA11P1_008c	4358 -	56.3	108	hypothetical protein PII10A_07 [Pseudomonas	/E-/4	SB196689.1
	4032			hypothetical protein LBL3 gp80 [ <i>Pseudomonas</i>		
				phage LBL3]	2E-73	YP_002154225.1
PA11P1_009c	5003 -	59.7	214	hypothetical protein [Pseudomonas phage DL68]	2E-154	YP_009215144.1
	4359			hypothetical protein PJG24_088 [ <i>Pseudomonas</i> phage IG024]	4E-154	YP_006200852.1
PA11P1_010c	5244 -	58.6	69	hypothetical protein [Pseudomonas aeruginosa]	7E-45	WP_015994944.1
	5035			hypothetical protein [Pseudomonas phage	7E-40	YP_009124313.1
	5450	53.0		vB_PaeM_PAO1_Ab27]	75.44	
PA11P1_011c	5456 - 5241	52.3	/1	hypothetical protein [ <i>Pseudomonas</i> phage DL68]	/E-44 3E-43	YP_009215142.1
	5241			phage JG024]	51-45	11_000200834.1

PA11P1_012c	5653 -	56.7	66	hypothetical protein [Pseudomonas phage KPP22]	2E-39	BAU20627.1
	5453			hypothetical protein vBPaeMDP1_0085	2E-39	BAU16501.1
DA11D1 012c	5001	F1 6	02	[Pseudomonus priage VB_Paelvi_CEB_DP1]	15 52	AS772476 1
PAILPI_015C	5901 -	51.0	05	[Recudamonas phage vB_ReeM_E217]	16-22	A32/24/0.1
	5050			hypothetical protein I7A_091c [Pseudomongs phage	2F-53	YP_007002637.1
				NH-4]	22 33	11_007002037.1
PA11P1 014c	6176 -	54.5	62	hypothetical protein PIG24_093 [Pseudomonas	8E-36	YP 006200857.1
	5988			phage JG024]		
				hypothetical protein [ <i>Pseudomonas</i> phage DL68]	7E-35	YP_009215139.1
PA11P1_015c	6865 -	55.7	228	hypothetical protein PJG24_094 [Pseudomonas	3E-166	YP_006200858.1
_	6179			phage JG024]		
				hypothetical protein BrSP1_16 [Pseudomonas phage	5E-165	ATI16268.1
				BrSP1]		
PA11P1_016c	7222 -	54.1	100	hypothetical protein vBPaeMDP1_0001	1E-63	AKP24388.1
	6920			[Pseudomonas phage vB_PaeM_CEB_DP1]		
				hypothetical protein PJG24_001 [ <i>Pseudomonas</i>	3E-63	YP_006200766.1
DA11D1 017-	7454	52.4	F.7	phage JGU24]	55.24	VD 002440000 4
PA11P1_01/c	7451 -	53.4	57	hypothetical protein PPSN_gp02 [Pseudomonas	5E-34	YP_002418808.1
	1218			priage SNJ	15 22	SPT06600 1
				aeruginosal	11-33	36190099.1
DA11D1 018c	7648 -	52.1	18	hypothetical protein PPSN_gp03 [Pseudomongs	6F-23	VP 002/18800 1
171111_0100	7502	55.1	40	nhage SN]	02 25	11_002410005.1
	1002			hypothetical protein SAMN05216409 118116	6E-13	SER37912.1
				[Pseudomonas lutea]		
PA11P1 019	7823 -	52.4	460	terminase large subunit [ <i>Pseudomonas</i> phage DL68]	0	YP 009215133.1
-	9205			large terminase protein [Pseudomonas phage	0	
				vB_PaeM_E215]		
PA11P1_020c	9625 -	59.1	127	hypothetical protein PP141_gp04 [Pseudomonas	3E-86	YP_002364312.1
	9242			phage 14-1]		
				hypothetical protein [Pseudomonas phage NP3]	7E-86	AMQ76120.1
PA11P1_021c	9840 -	54.8	72	hypothetical protein [Pseudomonas aeruginosa]	4E-46	WP_015994883.1
	9622			hypothetical protein [Pseudomonas phage NP3]	3E-45	AMQ76121.1
PA11P1_022c	10190 -	60.7	116	hypothetical protein LBL3_gp05 [Pseudomonas	1E-78	YP_002154150.1
	9840			phage LBL3]	25.70	411500004 4
				hypothetical protein SL1_06 [ <i>Pseudomonds</i> phage	2E-76	AUS03281.1
DA11D1 022c	10622	EQ 4	122	SLIJ	15.07	VD 00031E130 1
PATIPI_023C	10032 -	59.4	132	hypothetical protein [Pseudomonus phage DL68]	1E-87	YP_009215129.1
	10234			nhage [B] 3]	22-00	1F_002134131.1
PA11P1 024c	11414 -	57.2	259	hypothetical protein PP141 gp08 [Pseudomongs	0	YP 002364316.1
	10635	57.12	200	phage 14-1]	Ũ	
				hypothetical protein [ <i>Pseudomonas</i> phage DL68]	0	YP 009215128.1
PA11P1_025c	11938 -	60.3	145	hypothetical protein vB_Pae436M-8_10	2E-98	ANT44196.1
	11501			[Pseudomonas phage vB_Pae436M-8]		
				hypothetical protein [Pseudomonas phage NP3]	2E-97	AMQ76125.1
PA11P1_026c	12542 -	56.8	195	Phage protein [Pseudomonas phage S12-1]	6E-145	BAU16423.1
	11955			hypothetical protein LBL3_gp09 [Pseudomonas	1E-144	YP_002154154.1
				phage LBL3]		
PA11P1_027c	12647 -	51.0	31	hypothetical protein PP141_gp11 [ <i>Pseudomonas</i>	2E-11	YP_002364319.1
	12552			phage 14-1]	25 11	VD 004221720 1
				nypothetical protein LBL3_gp88 [Pseudomonas	3E-11	1P_004221739.1
PA11P1 028c	13576 -	56.6	310	hypothetical protein PP141 gn12 [Pseudomongs	0	VP_002364320_1
	12644	55.0	510	phage 14-1]	Ĩ	002004020.1
				hypothetical protein vBPaeME215 00085	0	ASZ72563.1
		1		[Pseudomonas phage vB_PaeM_E215]		
PA11P1_029c	14179 -	56.3	166	hypothetical protein PP141_gp13 [Pseudomonas	4E-120	YP_002364321.1
	13679	1		phage 14-1]		
				hypothetical protein PJG24_013 [Pseudomonas	1E-119	YP_006200778.1
	ļ	1		phage JG024]		
PA11P1_030c	14546 -	54.0	115	hypothetical protein PP141_gp14 [Pseudomonas	9E-76	YP_002364322.1
	14199	1		pnage 14-1]	15 75	VD 000045400 4
DA11D1 021-	15100	50.2	102	hypothetical protein [Pseudomonas phage DL68]	1E-/5	TP_009215123.1
PATIPI_0310	1/1205	50.3	102	hypothetical protein PIG24_015 [Providements]	4E-07 3E-66	1P_009215122.1
	14/33			nhage IG024]	3L-00	1F_000200780.1
PA11P1 032c	15315 -	56.4	67	hypothetical protein [ <i>Pseudomongs</i> phage DI 68]	2F-39	YP 009215121 1
	15112	50.4	, , , , , , , , , , , , , , , , , , ,	hypothetical protein PPGF8SP_0081 [Pseudomonas	4E-37	AHH02940.1
		1		phage SPM-1]		
PA11P1 033c	15635 -	56.2	107	hypothetical protein vBPaeME215 00090	9E-75	ASZ72568.1
	15312	1		[Pseudomonas phage vB_PaeM E215]		
		1		hypothetical protein vB_Pae_PS44_00019	5E-74	YP_009211343.1
		4	1	[Decudence where the Dec. DC 11]	1	1

PA11P1_034c	16067 -	53.0	133	hypothetical protein vBPaeME215_00091	1E-92	ASZ72569.1
	15666			[Pseudomonas phage vB_PaeM_E215]	15.01	ND 0000004005 4
				hypothetical protein PP141_gp17 [Pseudomonds phage 14-1]	1E-91	YP_002364325.1
PA11P1 035	16247 -	56.8	729	hypothetical protein [ <i>Pseudomongs</i> phage DI 68]	0	YP 009215210.1
	18544	5010	. 25	hypothetical protein vBPaeME215_00092	0	ASZ72570.1
				[Pseudomonas phage vB_PaeM_E215]		
PA11P1_036	18544 -	53.4	278	putative minor head protein [Pseudomonas phage	0	YP_002418826.1
	19380			SN]	0	411002050 1
				si 1	U	AUSU3359.1
PA11P1 037	19399 -	55.6	68	hypothetical protein PPSN gp21 [Pseudomonas	2E-41	YP 002418827.1
_	19605			phage SN]		_
				hypothetical protein LBL3_gp17 [Pseudomonas	6E-40	YP_002154162.1
DA11D1 028	10000	52.2	40	phage LBL3]	45.22	VD 002410828 1
PAILP1_038	19602 -	53.2	40	nypothetical protein PPSN_gp22 [Pseudomonus nhage SN]	4E-23	1P_002418828.1
	13742			hypothetical protein PJG24 021 [ <i>Pseudomonas</i>	3E-22	YP 006200786.1
				phage JG024]		-
PA11P1_039	20296 -	58.3	464	hypothetical protein [Pseudomonas phage DL68]	0	YP_009215206.1
	21690			hypothetical protein PP141_gp22 [ <i>Pseudomonas</i>	0	YP_002364330.1
PA11P1 040	21604 -	62.6	211	pnage 14-1] hypothetical protein PP141, gp23 [ <i>Pseudomongs</i>	5F-1/8	VP 00236/331 1
FAIIF1_040	22329	02.0	211	phage 14-1]	JL-140	17_002304331.1
				structural protein [Pseudomonas phage SN]	1E-147	YP_002418830.1
PA11P1_041	22339 -	61.0	382	putative major structural protein [Pseudomonas	0	AKP24411.1
	23487			phage vB_PaeM_CEB_DP1]		
				hypothetical protein PP141_gp24 [ <i>Pseudomonas</i>	0	YP_002364332.1
PA11P1 042	23589 -	55.0	145	hypothetical protein vBPaeMDP1_0025	6F-104	AKP24412.1
	24026	5510	1.0	[ <i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	02 20 .	
				hypothetical protein [Pseudomonas phage KPP12]	2E-103	YP_007238179.1
PA11P1_043	24041 -	59.2	155	putative structural protein [Pseudomonas phage	4E-110	YP_007238180.1
	24508			KPP12] structural protein [ <i>Beaudomonae</i> phago phiKTN6]	15 100	AV171557 1
PA11P1 044	24505 -	52.1	132	putative structural protein [Pseudomonas phage	2F-91	YP 007238181.1
171111_044	24903	52.1	132	KPP12]	20 91	11_00/250101.1
				structural protein [Pseudomonas phage phiKTN6]	6E-91	AKJ71558.1
PA11P1_045	24911 -	48.6	183	hypothetical protein [Pseudomonas phage KPP12]	3E-133	YP_007238182.1
	25462			hypothetical protein vB_Pae_PS44_00031	5E-133	YP_009211355.1
PA11P1 046	25459 -	54.8	193	hypothetical protein ORE028 [Pseudomongs phage	3F-137	YP 001294445.1
	26040	5	200	F8]	01 107	
				hypothetical protein [Pseudomonas phage KPP12]	1E-136	YP_007238183.1
PA11P1_047	26056 -	59.1	504	hypothetical protein I7A_031 [ <i>Pseudomonas</i> phage	0	YP_007002577.1
	27570			NH-4] hypothetical protoin yPPacMDP1_0020	0	AVD24417 1
				[Pseudomongs phage vB PaeM CEB DP1]	0	AKF 24417.1
PA11P1_048	27629 -	59.6	150	putative structural protein [ <i>Pseudomonas</i> phage	2E-103	YP_002154264.1
_	28081			LMA2]		
				structural protein [ <i>Pseudomonas</i> phage phiKT28]	2E-102	AKJ71471.1
PA11P1_049	28081 -	54.6	107	putative structural protein [ <i>Pseudomonas</i> phage	2E-75	YP_002154265.1
	20404			putative structural protein [ <i>Pseudomonas</i> phage	5E-75	YP 006200797.1
				JG024]		
PA11P1_050	28401 -	53.0	116	putative structural protein [Pseudomonas phage	3E-78	YP_002154266.1
	28751			LMA2]	15 77	
PA11P1 051	28753 -	64 1	143	hypothetical protein PPSN gn35 [Preudomonas	8F-93	YP 002418841 1
1,41111_031	29184	04.1	145	phage SN1	02 55	11_002410041.1
				hypothetical protein PII10A_51 [Pseudomonas	2E-92	SBT96733.1
				aeruginosa]		
PA11P1_052	29194 -	52.2	167	structural protein [ <i>Pseudomonas</i> phage SN]	3E-115	YP_002418842.1
	29097			I MA21	1F-114	YP 002154268.1
PA11P1_053	29697 -	51.1	179	putative structural protein [ <i>Pseudomonas</i> phage	5E-128	YP_002154269.1
_	30236			LMA2]		
				putative structural protein [Pseudomonas phage	2E-127	YP_002154178.1
DA11D1 054	20245	46.0	107	LBL3]	25.140	VD 0072220400.4
PAILPI_054	30245 -	46.8	191	Putative structural protein [ <i>Pseudomonas</i> phage KPP12]	3E-14U	1P_00/238190.1
				hypothetical protein vBPaeME217 00038	2E-139	ASZ72422.1
				[Pseudomonas phage vB_PaeM_E217]		
PA11P1_055	30848 -	57.1	142	hypothetical protein LBL3_gp35 [Pseudomonas	4E-101	YP_002154180.1
	31276			phage LBL3]		

				hypothetical protein phiKTN6_037 [Pseudomonas	2E-100	AKJ71569.1
	21280	50.2	050	phage phiKTN6]	0	VD 002154272.1
PAILP1_056	31280 -	58.2	858		0	TP_002154272.1
	55656			internal (core) protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76156.1
PA11P1_057	33856 -	52.1	287	putative structural protein [Pseudomonas phage	0	YP_002154273.1
	34719			LMA2]		
				putative structural protein [ <i>Pseudomonas</i> phage	0	AKP24427.1
DA11D1 058	3/1710 -	/8.3	177	VB_PaeM_CEB_DPI	2E-127	VP 00236/3/0 1
FAIIF1_058	35252	40.5	1//	phage 14-1]	22-127	11_002304349.1
				hypothetical protein [Pseudomonas phage DL68]	5E-127	YP_009215187.1
PA11P1_059	35308 -	53	221	putative baseplate protein [Pseudomonas phage	5E-71	YP_006200807.1
	35973			JG024]	CE 71	AK171572 1
PA11P1 060A	35984 -	42.6	17	hypothetical protein PB1 gp43 [Pseudomongs	3E-09	YP 002455973 1
	36037			phage PB1]	52 05	11_00210007011
				putative baseplate protein [ <i>Pseudomonas</i> phage	2E-04	YP_002418850.1
				SN]		
PA11P1_060B	36030 -	57.8	417	putative baseplate protein [ <i>Pseudomonas</i> phage NH-	0	YP_007002590.1
	37283			4] hypothetical protein BrSP1_62 [ <i>Pseudomongs</i> phage	0	ATI16244 1
				BrSP1]	0	A1110244.1
PA11P1_061	37280 -	55.7	504	hypothetical protein I7A_045 [Pseudomonas phage	0	YP_007002591.1
	38794			NH-4]		ND 00000000 4
				IG024	0	YP_006200809.1
PA11P1 062	38799 -	57.8	962	tail fibers protein [ <i>Pseudomonas</i> phage NP3]	0	AMQ76163.1
_	41687			putative tail fiber component [Pseudomonas phage	0	YP_007002592.1
<b>D</b> 4 4 <b>D</b> 4 0 C 2	44.600	50.0	1.12	NH-4]	45.00	
PA11P1_063	41689 -	58.3	142	hypothetical protein [ <i>Pseudomonas</i> phage NP3] nutative tail fiber component [ <i>Pseudomonas</i> phage	4E-98 6E-97	AMQ/6164.1
	42117			JG024]	02-37	11_000200811.1
PA11P1_064	42117 -	60.5	220	lytic enzyme [Pseudomonas phage NP3]	2E-161	AMQ76165.1
	42779			putative endolysin [Pseudomonas phage JG024]	7E-161	YP_006200812.1
PA11P1_065c	43054 -	51.2	83	hypothetical protein PP141_gp48 [ <i>Pseudomonas</i>	2E-50	YP_002364356.1
	42805			hypothetical protein LMA2 gp47 [ <i>Pseudomongs</i>	3E-50	YP 002154281.1
				phage LMA2]		-
PA11P1_066c	44245 -	56.6	303	DNA ligase [ <i>Pseudomonas</i> phage phiKT28]	0	AKJ71489.1
DA11D1 067c	43334	54.4	19/	DNA hinding protoin [Regulamongs phage DL69]	0	YP_006200814.1
FAIIFI_007C	44834 -	54.4	104	hypothetical protein PJG24 051 [Pseudomonas	2E-132 2E-131	YP 006200815.1
				phage JG024]		
PA11P1_068c	45456 -	60.2	201	hypothetical protein ORF050 [Pseudomonas phage	4E-139	YP_001294467.1
	44851			F8] hypothetical protein PP141, gp51 [ <i>Pseudomongs</i>	0F-130	VP 00236/359 1
				phage 14-1]	52 135	11_0023043333.1
PA11P1_069c	46409 -	59.9	299	hypothetical protein PP141_gp52 [Pseudomonas	0	YP_002364360.1
	45510			phage 14-1]		ND 0000454764
PA11P1_070c	<i>1</i> 7118 -	52.2	206	hypothetical protein (Pseudomonds phage DL68)	U 3E-145	YP_009215176.1
FAILT1_0700	46498	55.5	200	phage vB PaeM LS1]	3L-143	AVJ40047.1
				hypothetical protein SL1_50 [Pseudomonas phage	1E-144	AUS03325.1
D.44.04 074	40770	55.4	540	SL1]		ND 000440054 4
PA11P1_071c	48//2 - 47213	55.1	519	nypothetical protein PPSN_gp55 [Pseudomonas	0	YP_002418861.1
	47213			DNA helicase [ <i>Pseudomonas</i> phage vB_Pae436M-8]	0	ANT44241.1
PA11P1_072c	49179 -	55.2	136	hypothetical protein LBL3_gp52 [Pseudomonas	6E-95	YP_002154197.1
	48769			phage LBL3]		ANAO76172 1
PA11P1 073c	52279 -	54.9	1035	hypothetical protein PP141 gp56 [Pseudomonas	0	YP 002364364.1
	49172			phage 14-1]		
				DNA polymerase III subunit alpha [ <i>Pseudomonas</i>	0	YP_009211383.1
PA11P1 074c	52833 -	52.6	184	pulage VB_Pae_P344j putative DNA polymerase III. ensilon subunit	3E-135	YP 002154290.1
	52279			[Pseudomonas phage LMA2]		
				putative DNA polymerase III epsilon subunit	3E-135	YP_007002604.1
DA11D1 075c	52040	E0 /	3/13	[Pseudomonas phage NH-4]	0	SBT06767 1
PATI-1_0/30	52909	50.4	545	[Pseudomonas aeruginosa]	0	50190701.1
				putative polynucleotide kinase [Pseudomonas phage	0	YP_007238211.1
				KPP12]		

PA11P1_076c	54134 -	48.4	63	hypothetical protein PJG24_060 [Pseudomonas	3E-35	YP_006200824.1
	53943			phage JG024]		
DA11D1 077c	55052	E 9 6	205	hypothetical protein [ <i>Pseudomonas</i> phage KPP12]	1E-34	YP_00/238212.1
PAILPI_077C	55053 -	58.0	305	IG024]	0	1P_006200825.1
	54150			hypothetical protein PP141 gp60 [ <i>Pseudomonas</i>	0	YP 002364368.1
				phage 14-1]		-
PA11P1_078c	55259 -	51.2	68	hypothetical protein [Pseudomonas phage KPP12]	4E-41	YP_007238214.1
	55053			hypothetical protein SL1_42 [ <i>Pseudomonas</i> phage	8E-41	AUS03317.1
PA11P1 079c	55522 -	56.9	88	SLI hypothetical protein [ <i>Rseudomonas</i> phage PA5]	2F-56	APD20761 1
FAIIFI_0790	55267	50.9	00	hypothetical protein phiKT28_064 [Pseudomonas	5E-56	AFD20701.1 AKJ71502.1
				phage phiKT28]		
PA11P1_080c	55751 -	55.7	72	hypothetical protein PPSN_gp64 [Pseudomonas	2E-46	YP_002418870.1
	55533			phage SN]		
				hypothetical protein LMA2_gp62 [ <i>Pseudomonas</i>	3E-46	YP_002154296.1
PA11P1 081c	55953 -	59.8	72	pridge LIVIA2] hypothetical protein LBL3_gp61 [ <i>Pseudomongs</i>	5F-43	VP_002154206.1
	55735	55.0	72	phage LBL3]	52 45	11_002134200.1
				hypothetical protein [Pseudomonas phage KPP12]	2E-42	YP_007238217.1
PA11P1_082c	56183 -	59.7	76	hypothetical protein PP141_gp65 [Pseudomonas	6E-50	YP_002364373.1
	55953			phage 14-1]	45.40	ND 0004540074
				nypotnetical protein LBL3_gp62 [ <i>Pseudomonas</i>	1E-49	YP_002154207.1
PA11P1 083c	57272 -	56.2	333	hypothetical protein [ <i>Pseudomonas</i> phage NP3]	0	AM076184.1
	56271	5012		hypothetical protein PPSN gp67 [ <i>Pseudomonas</i>	0	YP 002418873.1
				phage SN]		_
PA11P1_084c	58117 -	61.7	246	hypothetical protein [Pseudomonas phage NP3]	2E-161	AMQ76185.1
	57377			putative structural protein [ <i>Pseudomonas</i> phage	4E-94	YP_002154300.1
DA11D1 085c	59/66 -	55.3	205	LMA2	0	VP_00215/210_1
1,41111_00000	58279	55.5	333	phage LBL3]	Ū	11_002134210.1
				putative ATP-dependent exonuclease V	0	YP_002418875.1
			<u> </u>	[Pseudomonas phage SN]		
PA11P1_086c	59,875 -	56.7	140	hypothetical protein ORF068 [Pseudomonas	3E-98	YP_001294485.1
	59453			phage F8] hypothetical protein [Resudemence phage ND2]	15.07	AM076187 1
				hypothetical protein [Pseudomonus phage NPS]	15-37	AWIQ/0107.1
PA11P1 087	60044 -	58.8	261	hypothetical protein ORF069 [Pseudomongs phage	0	YP 001294486.1
-	60829			F8]		-
				hypothetical protein PPSN_gp71 [Pseudomonas	0	YP_002418877.1
D.4.4.D.4. 000	600.40	50.4	407	phage SN]		10770500.4
PAILPI_088	60840 - 62063	59.1	407	IPseudomongs phage vB PaeM E215	0	ASZ/2528.1
	02003			hypothetical protein LBL3 gp68 [ <i>Pseudomonas</i>	0	YP 002154213.1
				phage LBL3]	-	
PA11P1_089	62087 -	58.2	149	hypothetical protein PP141_gp72 [Pseudomonas	3E-105	YP_002364380.1
	62536			phage 14-1]	55 405	
PA11P1 000	62533 -	575	258	hypothetical protein [ <i>Pseudomonds</i> phage NP3]	5E-105	AMQ/6190.1
FAIIF1_050	63609	57.5	558	hypothetical protein [P32ddomonds phage bL32]	0	YP 002364381.1
				phage 14-1]		
PA11P1_091	63615 -	47.8	61	hypothetical protein ORF073 [Pseudomonas phage	3E-33	YP_001294490.1
	63800			F8]		
				hypothetical protein phiKT28_076 [ <i>Pseudomonas</i>	3E-32	AKJ71514.1
PA11P1 092	63948 -	53.3	579	pilage pilikizoj nutative Ploon ATPase [Pseudomonas geruginosa]	0	SBT96795 1
	65687	55.5	5,5	virulence-associated protein E [ <i>Pseudomonas</i> phage	0	YP_009211402.1
			1	vB_Pae_PS44]		_

Table S7: Summarized results of the host range screenings. See also Fig. S1 for details.

Pseudomonas aeruginosa strain access number	PA1P1	PA8P1	PA11P1	fHo-Pae01
5513	+	-	-	-
5514	+/-	-	+/-	-
5525	+	+	+	+
5537	+	+/-	+	-
5538	-	-	-	-
5539	+	+/-	+	+/-

5548	-	-	-	-
5550	+	+	+	+
5551	-	-	-	-
5553	-	-	-	-
5668	+	+/-	+/-	-
5669	+	+	+	+
5670	+/-	-	+/-	-
5671	+	+	+	+
5672	+	+	+	+/-
5740	-	-	-	-
5741	+	+	+	+
5742	+	-	+	-
5743	+	+	+	+
5745	+	+	+	+
5746	+	-	+	-
5747	+	+	+	-
5826	+	+	+	+
5827	+	+	+	+
5828	+	+	+	+/-
5829	+/-	-	+	-
5831	+	+	+	-
5832	-	-	-	-
5833	+	+	+	+
5834	+	+	+	+
5835	+	+	+	+
5836	+	+	+	-
5837	+	+	+	+/-
5838	+	+	+	-
5839	+	+	+	-
5840	-	-	-	-
5841	-	-	-	-
5842	-	-	-	-
5844	-	-	-	-
5845	-	-	-	-
5846	+	+	+	+
5847	+	-	+	-
5848	+	-	+/-	+/-
PA1 (6327)	+	+/-	+	-
PA8 (6329)	+	+	+	+
PA11 (6331)	+	+	+	-
6663	+	+	+	-

In each well, 190  $\mu$ l of 1:40 dilution of the host bacteria overnight culture was mixed with 10  $\mu$ l lysate (10<sup>9</sup> pfu/ml) of one of the phages.

+ : infection was observed, - : no infection, +/- : partial infection



*Fig. S1. A representative image of the evaluation of the host range screening results in Table S5. + : infection was observed, - : no infection, +/- : partial infection.* 



*Fig. S2. Linear gradient purification of phage fHo-Pae01. The peak predicted to contain the phage is indicated with an arrow. Buffer A (20 mM Tris-Cl, pH 8.5), buffer B (20 mM Tris-Cl, 1M NaCl, pH 8.5)* 



*Fig. S3. Step-gradient purification of phage fHo-Pae01. The peak predicted to contain the phage is indicated with an arrow. Fractions G7 and G8 were harvested. Buffer A: 20 mM Tris-Cl, pH 8.5; buffer B: 20 mM Tris-Cl, 1M NaCl, pH 8.5.* 

#### References

**Mattila S, Ruotsalainen P, Jalasvuori M**. On-demand isolation of bacteriophages against drugresistant bacteria for personalized phage therapy. *Frontiers in Microbiology* 2015 Nov 13;6.