

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

Papers in Plant Pathology

Plant Pathology Department

9-2-2003

The complete genome sequence of the *Arabidopsis* and tomato pathogen *Pseudomonas syringae* pv. *tomato* DC3000

C. Robin Buell

Institute for Genomic Research, Rockville, MD

Vinita Joardar

Institute for Genomic Research, Rockville, MD

Magdalen Lindeberg

Cornell University

Jeremy Selengut


Institute for Genomic Research, Rockville, MD

Ian T. Paulsen

Institute for Genomic Research, Rockville, MD

Follow this and additional works at: <https://digitalcommons.unl.edu/plantpathpapers>

See next page for additional authors

 Part of the [Plant Pathology Commons](#)

Buell, C. Robin; Joardar, Vinita; Lindeberg, Magdalen; Selengut, Jeremy; Paulsen, Ian T.; Gwinn, Michelle L.; Dodson, Robert J.; Deboy, Robert T.; Durkin, A. Scott; Kolonay, James F.; Radupu, Ramana; Daugherty, Sean; Brinkac, Lauren; Beanan, Maureen J.; Haft, Daniel H.; Nelson, William C.; Davidsen, Tanja; Zafar, Nikhat; Zhou, Liwei; Liu, Jia; Yuan, Qiaoping; Khouri, Hoda; Fedorova, Nadia; Tran, Bao; Russell, Daniel; Berry, Kristi; Utterback, Teresa; Van Aken, Susan E.; Feldblyum, Tamara V.; D'Ascenzo, Mark; Deng, Wen-Ling; Ramos, Adela R.; Alfano, James R.; Cartinhour, Samuel; Chatterjee, Arn K.; Delaney, Terrence P.; Lazarowitz, Sondra G.; Martin, Gregory B.; Schneider, David J.; Tang, Xiaoyan; Bender, Carol L.; White, Owen; Fraser, Claire M.; and Collmer, Alan, "The complete genome sequence of the *Arabidopsis* and tomato pathogen *Pseudomonas syringae* pv. *tomato* DC3000" (2003). *Papers in Plant Pathology*. 199. <https://digitalcommons.unl.edu/plantpathpapers/199>

This Article is brought to you for free and open access by the Plant Pathology Department at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Papers in Plant Pathology by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

Authors

C. Robin Buell, Vinita Joardar, Magdalen Lindeberg, Jeremy Selengut, Ian T. Paulsen, Michelle L. Gwinn, Robert J. Dodson, Robert T. Deboy, A. Scott Durkin, James F. Kolonay, Ramana Radupu, Sean Daugherty, Lauren Brinkac, Maureen J. Beanan, Daniel H. Haft, William C. Nelson, Tanja Davidsen, Nikhat Zafar, Liwei Zhou, Jia Liu, Qiaoping Yuan, Hoda Khouri, Nadia Fedorova, Bao Tran, Daniel Russell, Kristi Berry, Teresa Utterback, Susan E. Van Aken, Tamara V. Feldblyum, Mark D'Ascenzo, Wen-Ling Deng, Adela R. Ramos, James R. Alfano, Samuel Cartinhour, Arn K. Chatterjee, Terrence P. Delaney, Sondra G. Lazarowitz, Gregory B. Martin, David J. Schneider, Xiaoyan Tang, Carol L. Bender, Owen White, Claire M. Fraser, and Alan Collmer

The complete genome sequence of the *Arabidopsis* and tomato pathogen *Pseudomonas syringae* pv. *tomato* DC3000

C. Robin Buell*[†], Vinita Joardar*, Magdalen Lindeberg[‡], Jeremy Selengut*, Ian T. Paulsen*, Michelle L. Gwinn*, Robert J. Dodson*, Robert T. Deboy*, A. Scott Durkin*, James F. Kolonay*, Ramana Madupu*, Sean Daugherty*, Lauren Brinkac*, Maureen J. Beanan*, Daniel H. Haft*, William C. Nelson*, Tanja Davidsen*, Nikhat Zafar*, Liwei Zhou*, Jia Liu*, Qiaoping Yuan*, Hoda Khouri*, Nadia Fedorova*, Bao Tran*, Daniel Russell*, Kristi Berry*, Teresa Utterback*, Susan E. Van Aken*, Tamara V. Feldblyum*, Mark D'Ascenzo[§], Wen-Ling Deng[‡], Adela R. Ramos[‡], James R. Alfano[¶], Samuel Cartinhour^{||}, Arun K. Chatterjee^{**}, Terrence P. Delaney[‡], Sondra G. Lazarowitz[‡], Gregory B. Martin[§], David J. Schneider^{||}, Xiaoyan Tang^{††}, Carol L. Bender^{‡‡}, Owen White*, Claire M. Fraser*, and Alan Collmer[‡]

*The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850; [‡]Department of Plant Pathology, Cornell University, Ithaca, NY 14853; [§]Boyce Thompson Institute for Plant Research, Ithaca, NY 14853-1801; [¶]Plant Science Initiative and Department of Plant Pathology, University of Nebraska, Lincoln, NE 68588-0660; ^{||}United States Department of Agriculture Agricultural Research Service, Cornell Theory Center, Ithaca, NY 14853-2901; ^{**}Department of Plant Microbiology and Pathology, University of Missouri, Columbia, MO 65211; ^{††}Department of Plant Pathology, Kansas State University, Manhattan, KS 66502-5502; and ^{‡‡}Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK 74078

Edited by Robert Haselkorn, University of Chicago, Chicago, IL, and approved June 23, 2003 (received for review April 4, 2003)

We report the complete genome sequence of the model bacterial pathogen *Pseudomonas syringae* pathovar *tomato* DC3000 (DC3000), which is pathogenic on tomato and *Arabidopsis thaliana*. The DC3000 genome (6.5 megabases) contains a circular chromosome and two plasmids, which collectively encode 5,763 ORFs. We identified 298 established and putative virulence genes, including several clusters of genes encoding 31 confirmed and 19 predicted type III secretion system effector proteins. Many of the virulence genes were members of paralogous families and also were proximal to mobile elements, which collectively comprise 7% of the DC3000 genome. The bacterium possesses a large repertoire of transporters for the acquisition of nutrients, particularly sugars, as well as genes implicated in attachment to plant surfaces. Over 12% of the genes are dedicated to regulation, which may reflect the need for rapid adaptation to the diverse environments encountered during epiphytic growth and pathogenesis. Comparative analyses confirmed a high degree of similarity with two sequenced pseudomonads, *Pseudomonas putida* and *Pseudomonas aeruginosa*, yet revealed 1,159 genes unique to DC3000, of which 811 lack a known function.

The gamma subgroup of the Proteobacteria contains a number of important pathogens, including animal pathogenic *Escherichia*, *Salmonella*, *Shigella*, and *Yersinia* spp. and plant pathogenic *Erwinia*, *Pantoea*, *Xanthomonas*, *Xylella*, and *Pseudomonas* spp. (1). The genus *Pseudomonas* is notable because it contains the clinically important human pathogen *Pseudomonas aeruginosa*, the agriculturally important plant pathogen *Pseudomonas syringae*, and the nonpathogenic bioremediation agent *Pseudomonas putida*. Strains of *P. syringae* are noted for their diverse and host-specific interactions with plants and may be assigned to one of at least 50 pathovars based on host specificity (2). As a pathogen, *P. syringae* typically enters plant leaves through stomata, multiplies in the intercellular space (apoplast), and eventually produces necrotic lesions that are often surrounded by chlorotic halos (2).

P. syringae pv. *tomato* DC3000 (DC3000) causes bacterial speck of tomato (3), a worldwide, economically significant disease that is representative of numerous bacterial plant diseases for which effective controls are still needed (4). DC3000 is also a pathogen of the model plant *Arabidopsis thaliana* (5). Importantly, the pathogenicity of DC3000 resembles that of most animal and plant pathogens in the gamma Proteobacteria, which rely on a type III secretion system (TTSS) to inject virulence effector proteins into host cells (6). Highlighting the role of DC3000 as a model for

plant–pathogen interactions, >35 genes encoding TTSS substrates have been experimentally identified in this strain (7–12), which exceeds the number demonstrated for any other bacterial pathogen to date. Furthermore, the pathogenicity of DC3000 resembles that of many important bacterial and fungal pathogens of plants where host specificity is controlled by “gene-for-gene” interactions in which a dominant allele in the host and a dominant allele in the pathogen condition the outcome of the plant–pathogen interaction (13). In this study, we report the complete genome sequence of DC3000, highlight genes with a likely role in virulence, and compare the virulence gene arsenal of DC3000 with that of other plant and animal pathogens.

Materials and Methods

Sequencing and Annotation Methods. Strain DC3000 was originally isolated in 1960 from tomato in the Channel Islands in Guernsey, United Kingdom (ref. 3; D. Cuppels, personal communication). The culture was confirmed as pathogenic on susceptible host plants before high-throughput sequencing. The complete genome was sequenced as described previously (14) and detailed information is available as *Supporting Sequencing Methods*, which is published as supporting information on the PNAS web site, www.pnas.org. ORFs were identified by using the GLIMMER algorithm (15). Predicted proteins were searched against a nonredundant amino acid database and searched for domains by using HMMER with the Pfam (16) and TIGRFam databases (17). The ORFs were manually curated and assigned to role categories adapted from Riley (18). Paralogous families were constructed as described previously (19). Insertion-sequence (IS) elements were classified according to transposase gene similarity by using BLAST analysis with the ISFinder database (www-is.biotoul.fr/).

Comparative Genomics. The presence of putative orthologs of DC3000 virulence factors in nine completely sequenced genomes of pathogenic proteobacteria was determined by BLASTP analysis by

This paper was submitted directly (Track II) to the PNAS office.

Abbreviations: CMA, coronamic acid; COR, coronatine; DC3000, *Pseudomonas syringae* pv. *tomato* DC3000; GABA, γ -aminobutyric acid; IS, insertion sequence; Tfp, type IV pili; TTSS, type III secretion system.

Data deposition: The sequence and annotation of *P. syringae* pv. *tomato* DC3000 have been deposited in the GenBank database (accession nos. AE016853–AE016855).

[†]To whom correspondence should be addressed. E-mail: rbuell@tigr.org.

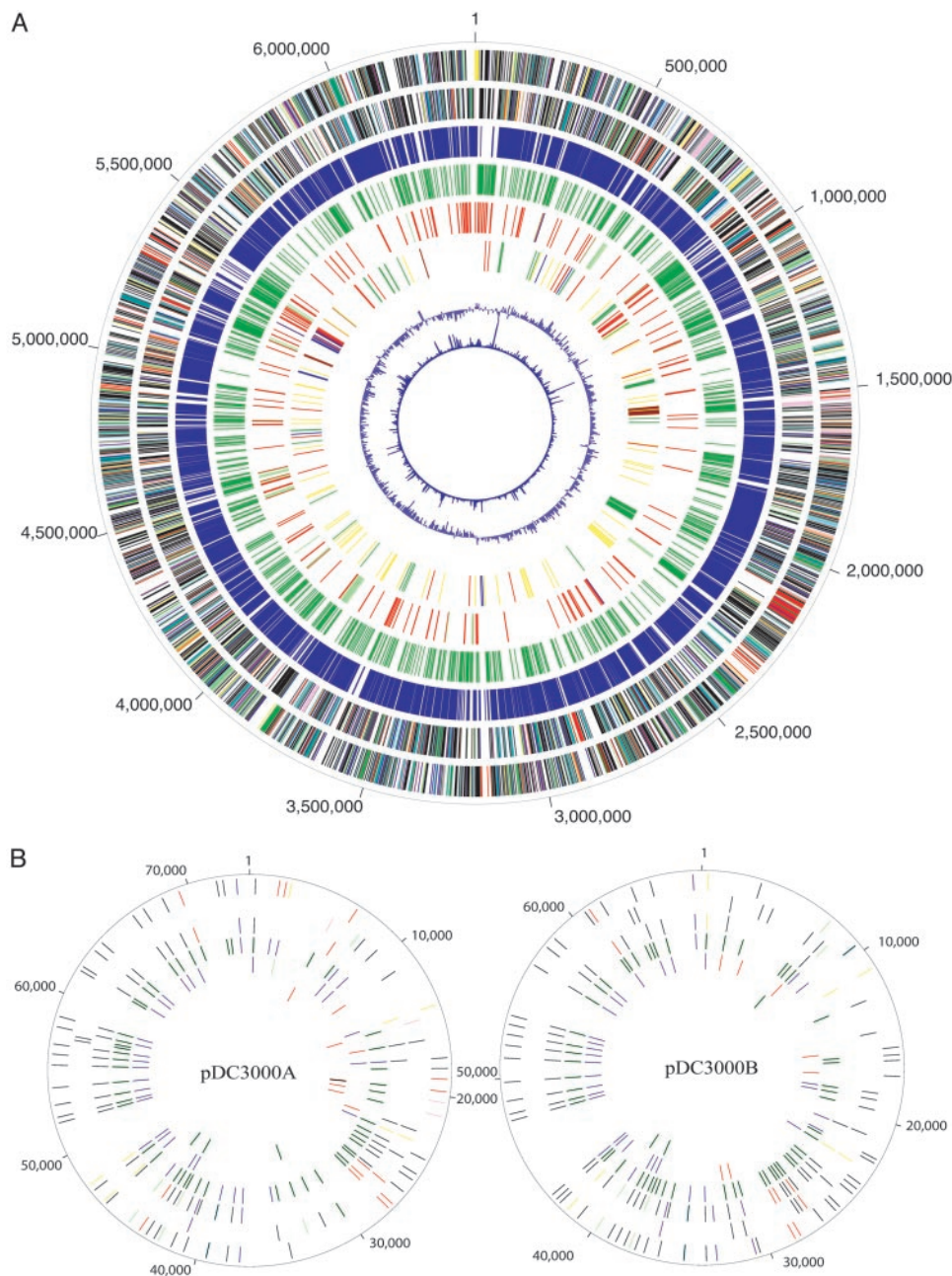


Fig. 1. Features of the DC3000 genome. (A) The chromosome, with the outermost circle depicting ORFs on the positive strand and the second circle depicting ORFs on the negative strand. The ORFs are color-coded based on the major grouping of role categories as follows: amino acid biosynthesis (salmon); biosynthesis of cofactors, prosthetic groups, and carriers (light blue); cell envelope (light green); cellular processes (red); central intermediary metabolism (brown); DNA metabolism (yellow); energy metabolism (green); fatty acid and phospholipid metabolism (purple); protein fate/synthesis (pink); purines, pyrimidines, nucleosides, and nucleotides (orange); regulatory functions (navy blue); transcription (gray); transport and binding proteins (teal); and unknown function, conserved hypothetical, and hypothetical (black). The third circle represents the ORFs with homologs present in all three *Pseudomonas* spp. ($E < 10^{-5}$). The fourth circle depicts the ORFs that are unique to DC3000 compared with *P. aeruginosa* and *P. putida* ($E \geq 10^{-5}$). The fifth circle represents mobile genetic elements, including IS elements (red), phage-related genes (light green), and plasmid-related functions (blue). The sixth circle depicts ORFs associated with virulence, which are color coded as follows: adhesins and other cell surface-associated factors (dark green), miscellaneous virulence factors (yellow), TTSS effectors, candidates, and helpers (red), TTSS regulatory and secretory proteins (brown), and low molecular weight diffusible factors (blue). The seventh circle is the GC skew, and the eighth circle represents atypical nucleotides. (B) The plasmids with the outermost circle representing ORFs on the positive strand and the second circle depicting ORFs on the negative strand, with the same color coding as A. The third circle represents ORFs shared by the two plasmids ($E < 10^{-5}$). The fourth circle depicts the ORFs with homologs present in all three *Pseudomonas* spp. ($E < 10^{-5}$) in navy blue and the ORFs that are unique to DC3000 compared with *P. aeruginosa* and *P. putida* ($E \geq 10^{-5}$) in green. The fifth circle represents mobile genetic elements (color-coded as in A). The sixth circle depicts ORFs associated with virulence (color-coded as in A).

using a cutoff criterion of $E < 10^{-5}$ (20). The reference genomes included the plant pathogens *Ralstonia solanacearum* (21), *Xylella fastidiosa* (22), *Agrobacterium tumefaciens* (23, 24), *Xanthomonas campestris* pv. *campestris* (25), and *Xanthomonas axonopodis* pv. *citri* (25) and the animal pathogens *P. aeruginosa* PAO1 (26), *Salmonella typhimurium* LT2 (27), *Yersinia pestis* CO92 (28), and *Escherichia coli* O157:H7 EDL933 (29).

Results and Discussion

Genome Features. The DC3000 genome is composed of one circular chromosome of 6,397,126 bp and two plasmids of 73,661 bp (pDC3000A) and 67,473 bp (pDC3000B) (Fig. 1 and Table 1). A total of 5,763 ORFs were identified within the DC3000 genome. Among the predicted genes, 3,510 (61%) have been assigned a putative function, with the remaining designated as encoding a protein with unknown function, a conserved hypothetical protein, or a hypothetical protein. Classification of the known proteins into

biological role categories (18) revealed that the largest category was transport and binding, followed by cellular processes (see Fig. 4, which is published as supporting information on the PNAS web site). DC3000 is representative of pathogenic bacteria that have diverse relationships with plants as epiphytes and pathogens and thus likely requires an array of regulatory genes to cope with diverse niches, host responses, and environmental conditions. Indeed, 12% (711) of the DC3000 genes could be assigned to role categories associated with gene regulation, signal transduction, and transcription. A high degree of gene duplication exists in DC3000, and 2,735 genes (48%) were assigned to 687 paralogous families. Although the majority of paralogous families contained two members (see Fig. 5, which is published as supporting information on the PNAS web site), 12 families have >25 members, and many of these large families encode either transporters or regulatory proteins. However, this group also includes families encoding methyl-accepting chemotaxis proteins, oxidoreductases of largely unknown specific-

Table 1. Features of the DC3000 genome

| Feature | Chromosome | pDC3000A | pDC3000B |
|--------------------------------|-------------|----------|----------|
| Size, bp | 6,397,126 | 73,661 | 67,473 |
| G+C, % | 58.4 | 55.1 | 56.1 |
| Number of ORFs | 5,615 | 71 | 77 |
| Percent coding | 86.8 | 81.9 | 84.7 |
| Average ORF length, nt | 988 | 849 | 742 |
| No. of ORFs encoding | | | |
| Protein with a known function | 3,402 (61%) | 52 (73%) | 46 (60%) |
| Hypothetical protein | 610 (11%) | 10 (14%) | 16 (21%) |
| Conserved hypothetical protein | 961 (17%) | 8 (11%) | 12 (16%) |
| Protein of unknown function | 642 (11%) | 1 (1%) | 3 (4%) |

ities, and transposases of the IS4 family. A total of 5 rRNA operons, 5 structural RNAs, and 63 tRNA genes were present, all on the chromosome.

Comparative Genomics with Fluorescent Pseudomonads. The complete genome sequences for two other pseudomonads, *P. aeruginosa* PAO1 (26), an opportunistic animal pathogen, and *P. putida* KT2440, a saprophytic soil bacterium (30), are available. Of the 5,608 ORFs in DC3000 that predict a functional protein, 4,449 (79%) have homologs (BLAST $E < 10^{-5}$) in either *P. aeruginosa* or *P. putida* and 3,797 (68%) are present in all three genomes (Fig. 1). The 1,159 (21% of the total) genes that are unique to DC3000 are heavily enriched in hypothetical proteins (551), conserved hypothetical proteins (203), mobile genetic elements (116), and proteins of unknown function (57). Other genes unique to DC3000 include 96 that are implicated in virulence (see below for more details).

Metabolism. The key metabolic pathways in DC3000 (glycolysis, gluconeogenesis, tricarboxylic acid, and pentose phosphate cycles) are shared with *P. putida* and *P. aeruginosa*. However, the absence of lactate dehydrogenase in DC3000 results in an inability to convert pyruvate to lactate. Taxonomic classification based on the arginine dihydrolase and oxidase tests also distinguishes DC3000 from *P. putida* and *P. aeruginosa*, which are positive in both tests (31). DC3000 lacks arginine dihydrolase and subunits of the *aa3*-type cytochrome *c* oxidase.

The utilization of γ -aminobutyric acid (GABA) occurs by means of the GABA transaminase-catalyzed deamination of GABA to succinic semialdehyde, which is then oxidized to succinate by succinate semialdehyde dehydrogenase (SSADH) before entering the tricarboxylic acid cycle. In DC3000, there are three copies each of GABA transaminase and SSADH, as well as a GABA permease. Although the composition of the apoplast during a compatible interaction with DC3000 is unknown, GABA is present at millimolar concentration in the apoplast during infection of tomato with the biotrophic fungal pathogen *Cladosporium fulvum* (32). Thus, if GABA is available in the apoplast during infection of tomato, DC3000 appears amply equipped to use this as a carbon and nitrogen source.

General Transport Systems. Like the other sequenced pseudomonads, DC3000 possesses very extensive transport capabilities. However, it differs significantly from *P. putida* and *P. aeruginosa* in having a greater capacity for sugar transport and a correspondingly decreased number of amino acid transporters. Importantly, DC3000 has 15 ABC transporter systems with predicted specificities for arabinose, xylose, ribose, and other plant-derived sugars, whereas *P. putida* and *P. aeruginosa* each encode only 4 ABC sugar transporters. In contrast, DC3000 encodes only 4 APC-family transporters for amino acids and other compounds, compared with the 21 APC transporters present in both *P. putida* and *P. aeruginosa*. DC3000 also encodes 9 RND-type efflux systems for drugs or cations, including probable orthologs of the Mex systems of *P.*

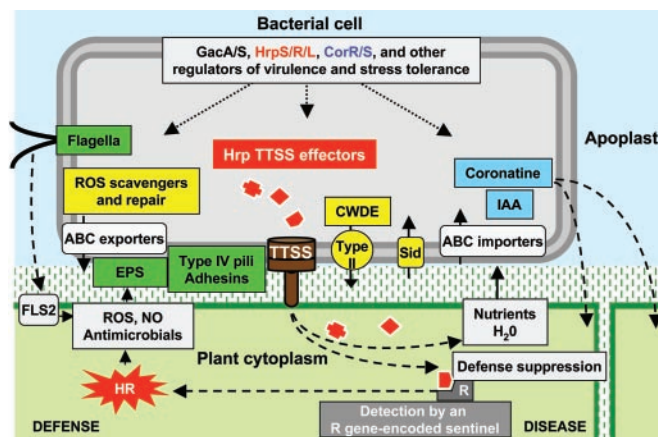


Fig. 2. Diagrammatic overview of *P. syringae*-plant interactions, with virulence factors color-coded as in Fig. 1. Host-pathogen factors associated with defense and disease are separately grouped on the left and right of the diagram, respectively. The central pathogenic process is the injection of multiple effector proteins into plant cells by the TTSS, which is depicted as the brown structure traversing the bacterial inner and outer membranes, plant cell wall, and plasma membrane. The effectors may suppress defenses and promote nutrient and water accumulation in the apoplast unless any one of them is detected by a resistance (R) gene-encoded sentinel, in which case strong defenses associated with the hypersensitive response (HR) are triggered. Motility favors bacterial epiphytic survival and entry into leaves, but flagellin is also recognized by means of the FLS2 receptor-like kinase as an elicitor of general defenses (62), which are not as strong as HR-associated defenses and may be suppressed by Hrp effectors. Exclusion or tolerance of reactive oxygen species (ROS) and other antimicrobials is likely promoted by extracellular polysaccharides (EPS), scavengers, and ABC exporters. Favoring virulence are type IV pili (Tfp) and possibly adhesins, coronatine synthesis and regulation, plant cell-wall-degrading enzymes (CWDE) and other variously secreted proteins, iron-scavenging siderophores (Sid), indoleacetic acid (IAA), and probably numerous ABC transporters and other nutrient uptake systems.

aeruginosa, as well as a broad range of other predicted efflux systems. Thus, broad export capabilities appear to be a common feature of the pseudomonads.

Type I secretion is one-step process exemplified by *E. coli* hemolysin secretion (33), and homologs of the essential components of the pathway are present in DC3000. The type II secretion pathway is an extension of the general secretory pathway (34), and 14 genes predicting components of this pathway were identified in DC3000. Genes similar to *gspC* and *gspO* were not found; however, *gspC* is not present in all systems, and the function of GspO can be replaced by the prepilin peptidase PilD, which is present in the genome. A functional type IV secretion system was not identified in DC3000.

Virulence Mechanisms. DC3000 encodes a wide range of proteins that are implicated in virulence (35). We are interpreting virulence here to include processes such as motility, adhesion, injection of effector proteins into host cells, degradation of host cell walls, production of phytotoxic compounds, iron acquisition, and interference with host defenses, which may promote epiphytic growth as well as actual disease expression (Fig. 2). We identified 298 genes (5% of the total) in the virulence category (Table 2, which is published as supporting information on the PNAS web site). The virulence genes are addressed below.

TTSS and Effectors. The TTSS is key to the plant parasitism of *P. syringae* pathovars (Fig. 2). Most of the *hrp* (hypersensitive response and pathogenicity) and *hrc* (*hrp* conserved) genes encoding the TTSS system are essential for pathogenicity, which indicates the collective importance of the effector proteins that are injected into plant cells by the system (6). Hrp effectors are primarily known as Hop (Hrp outer protein) or Avr (*av*irulence) proteins, based on the

phenotype by which they were discovered (11). Functional analysis of the DC3000 genome has yielded genes for 31 effectors and 7 additional proteins secreted by the Hrp system that likely have a role in translocating effectors across the plant cell wall and plasma membrane (8–12, 36). The associated *hop*, *avr*, and *hol* (Hop-like candidate) genes may provide markers to regions of the genome that are enriched in other virulence genes (Fig. 3). Over half of these TTSS effectors are encoded in one of several regions containing multiple effector genes (Fig. 1). One region with multiple effector genes is located on pDC3000A and contains *avrPpiB2_{Pto}*, *avrPphE_{Pto}*, *hopPtoS1*, and *hopPtoT1*. Interestingly, an identical copy of *avrPpiB2_{Pto}* is located on the chromosome, which could provide a site for integration of the plasmid in a manner similar to that observed with pFKN in *P. syringae* pv. *maculicola* M6 (37). Two other clusters of effector genes are found in the region encoding the phytotoxin coronatine (COR) (Fig. 3). Members of effector gene paralogous families are scattered around the genome and typically have an unusually low G+C content (Table 2), suggesting that such families may have grown by sequential horizontal acquisitions. Interestingly, at least four of the DC3000 effector genes are disrupted by mobile genetic elements (Tables 2 and 3, which are published as supporting information on the PNAS web site), as highlighted by comparison with orthologs in the draft genome of *P. syringae* pv. *syringae* B728a (12). Additional information on DC3000 TTSS effectors and an updated list can be found at <http://pseudomonas-syringae.org>.

Plasmid-Borne Virulence-Implicated Genes. Consistent with previous reports (38), DC3000 contains two plasmids (pDC3000A and pDC3000B) that are similar to the pPT23A family of *P. syringae* plasmids (39). There is substantial redundancy between the two plasmids, with 47 proteins sharing similarity ($E < 10^{-5}$). The majority of the conserved proteins are involved in plasmid replication, conjugation, or transposition-related functions. There also are many genes unique to each of the plasmids, with a clear enrichment of genes implicated in virulence on pDC3000A. However, we found no evidence for a major role of the plasmids in virulence. Using previously described methods (40), we inserted *sacB* in pDC3000A and *repA* in pDC3000B to construct DC3000 derivatives lacking pDC3000A, pDC3000B, or both plasmids. Assays involving dipping of tomato cv. MoneyMaker and *A. thaliana* Col-0 in inoculum (5×10^5 colony-forming units per ml) revealed no major difference in bacterial growth *in planta* or in symptom production (data not shown). This observation is consistent with the finding that most of the known plasmid-borne TTSS effector genes, which are all on pDC3000A, have paralogs on the chromosome.

Siderophores. Siderophores are low molecular weight, high-affinity iron(III) chelators that function as important virulence factors in many bacterial pathogens because of their role in sustaining growth in iron-limited host environments. Synthesis of the siderophore pyoverdinin is well documented among fluorescent pseudomonads (41), and the required genes are present in a single cluster in DC3000. Also, a cluster of genes homologous to those required for biosynthesis of the siderophore pyochelin by *P. aeruginosa* has been found. However, several observations suggest that the encoded proteins actually produce yersiniabactin, a siderophore that shares a common tricyclic core with pyochelin (42). First, DC3000 contains a gene encoding a large polyketide synthase (PKS) in the middle of the pyochelin gene cluster and this has no homolog in *P. aeruginosa* (or *P. putida*). This gene shows extremely high similarity with the PKS gene (*irp1*) found in the yersiniabactin gene cluster of *Y. pestis* (43). Second, there is no homolog of the pyochelin receptor gene of *P. aeruginosa* (*fptA*) in DC3000; however, a receptor gene is present that is highly similar to the pesticin/yersiniabactin receptor gene from *Y. pestis* (*fyuA*). Third, the structure of PSPTO2602, a nonribosomal peptide synthase in this cluster, differs from its *P. aeruginosa* counterpart in that a methylation domain and a terminal

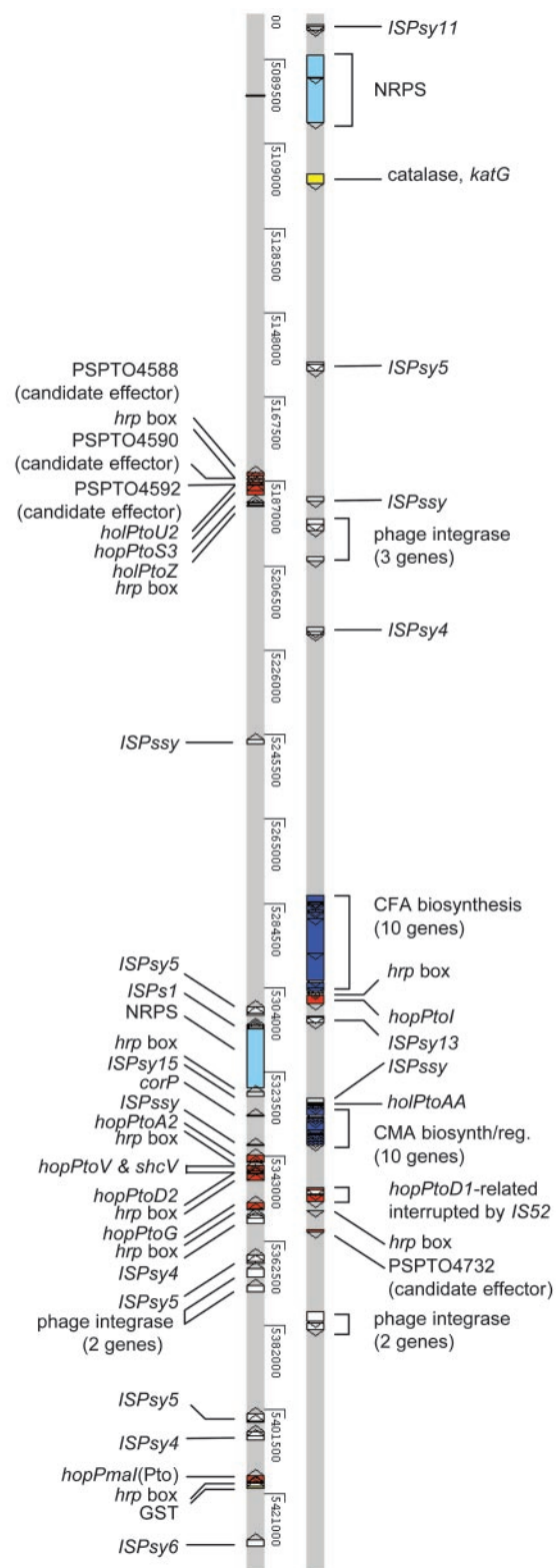


Fig. 3. Detailed view of one region of the DC3000 genome that is enriched in virulence factors and mobile genetic elements. Only virulence-related genes, “hrp box” promoters, and mobile genetic elements are shown. Features are color-coded as in Fig. 1 (circle 6), with the exception that a lighter blue is used for the nonribosomal peptide synthase genes, and the mobile genetic elements are white. The genome display was generated by using ARTEMIS (www.sanger.ac.uk/Software/Artemis/) to view the chromosome (AE016853) with the aid of input files for a variety of virulence-related features that are available at <http://pseudomonas-syringae.org> and <http://monod.cornell.edu>.

thioesterase domain are lacking, consistent with a yersiniabactin synthase.

Phytotoxins and Phytohormones. COR is a chlorosis-inducing phytotoxin produced by several *P. syringae* pathovars, including DC3000 (44). COR is hypothesized to function as a molecular mimic of methyl jasmonate and may promote colonization of host tissue by altering plant defense signaling pathways (45). COR is representative of biologically active small molecules that can diffuse in plant tissues (Fig. 2), and it is responsible for the chlorotic halos surrounding the necrotic lesions caused by DC3000 (44). The structure of COR consists of coronafacic acid and coronamic acid (CMA), joined by an amide linkage (46). Unlike many *P. syringae* pathovars where the COR genes are clustered and plasmid-encoded (46), the COR genes in DC3000 are chromosomally encoded, and the coronafacic acid and CMA structural genes are separated by 26 kb (Fig. 3). In DC3000, the CMA biosynthetic genes are linked with a modified two-component regulatory system, composed of *corS*, *corR*, and *corP* (46). Interestingly, analysis of the CMA region of DC3000 revealed four genes (PSPTO4707, 4708, 4711, and 4713) interspersed among those previously identified with roles in COR synthesis. Consistent with the annotation of the COR region, initial proteomic studies with DC3000 revealed that the HrpL-alternative σ factor, which regulates DC3000 *hrp* genes (8), induces production of a protein encoded by PSPTO4668 in the coronafacic acid region (D.J.S. and S.C., unpublished data; <http://monod.cornell.edu>). There is no evidence in the DC3000 genome for the biosynthesis of any of the known *P. syringae* lipodepsinone-peptide phytotoxins, including syringomycin, syringotoxin, syringostatin, and pseudomycin. Syringopeptin, a lipodepsipeptide produced by *P. syringae* pv. *syringae* (46), is also absent. However, DC3000 does contain five nonribosomal peptide synthetases in three separate gene clusters (PSPTO2829, -2830, -4518, -4519, and -4699) that may direct the biosynthesis of undescribed peptide or lipodepsipeptide products.

Production of the phytohormone indole-3-acetic acid (IAA) by certain *P. syringae* pathovars has been shown to influence bacterial growth in *planta* and the expression of other virulence factors (47, 48). The two genes required for IAA production, *iaaH* and *iaaM*, are present in DC3000. Interestingly, *iaaL* (IAA-lysine ligase), which can convert IAA to a less active derivative and is widespread in *P. syringae* pathovars (47), is present in the DC3000 genome but lacking in the genomes of all of the other fully sequenced plant pathogens (Table 2). The presence of a functional Hrp promoter upstream of *iaaL* additionally suggests a role in *P. syringae* virulence (8).

Adhesins. Pathogenic bacteria rely on a variety of cell surface-associated virulence factors to facilitate adhesion to the host and provide protection during colonization. Type IV pili (Tfp) represent one of the major adhesins found in pseudomonads (49). Tfp were previously identified in *P. syringae* and appear to play a role in epiphytic fitness (50). Analysis of the 23 Tfp-associated genes suggests that regulation of Tfp production differs significantly between DC3000 and *P. aeruginosa*. Filamentous hemagglutinin (FHA) has also been shown to be an adhesin and a virulence factor in animal pathogenic bacteria and the plant pathogen *Erwinia chrysanthemi* (51). Three genes predicting FHA-like proteins were identified in DC3000 (PSPTO3210, 3214, and 3229).

Extracellular Polysaccharides. Components of the polysaccharide capsule, such as the exopolysaccharide alginate, play a role in both adhesion and protection of the bacterial cells from external stress (52). Among plant pathogenic pseudomonads, alginate production has been linked to epiphytic fitness and the production of water-soaked lesions (53). All of the genes required for alginate biosynthesis in *P. aeruginosa* are present in DC3000, although some of the alginate regulatory genes are absent, indicating that the regulation

of alginate biosynthesis differs between *P. aeruginosa* and *P. syringae*, consistent with previous reports (54). Three genes encoding levansucrases, required for the biosynthesis of the polysaccharide levan, were also identified in DC3000.

Tolerance to Reactive Oxygen Species or Heavy Metals. *P. syringae* and other pathogens can trigger an oxidative burst in plants, which results in the production in the apoplast of reactive oxygen species such as superoxide anion and hydrogen peroxide (H₂O₂). Superoxide dismutases (SODs) convert superoxide to H₂O₂, which can be detoxified to water by catalase. In addition to its antimicrobial properties, H₂O₂ functions as a signaling molecule within plant cells in processes involving pathogen defense and programmed cell death (55). DC3000 has three catalases and three SODs. Other enzymes in DC3000 that may play a role in scavenging reactive oxygen species include six peroxidases, eight GSTs, and two glutathione reductases. In addition, DC3000 encodes a single peptide methionine sulfoxide reductase, which reduces methionine sulfoxide to methionine, thereby functioning as a repair enzyme for proteins inactivated by oxidation.

One strategy to control bacterial plant pathogens in the field is the use of copper-based bactericides, which are toxic to bacterial cells at high concentrations. For bacterial speck of tomato, this has led to the emergence of copper-resistant strains (56). In *P. syringae* pv. *tomato* strain PT23.2, resistance to copper is mediated by four structural genes, *copA–D*, as well as two regulatory genes, *copR* and *copS*, which encode a two-component regulatory system (57). DC3000 is not resistant to copper (C.L.B., unpublished data), and examination of the genome revealed that although *copA* and *copB* are present, DC3000 lacks the structural proteins CopC and CopD, as well as the regulatory proteins CopR and CopS. Interestingly, homologs of CopR and CopS (PSPTO3603, 1306) are present in DC3000 and may function in regulating responses to other heavy metals.

Other Proteins Relevant to Virulence. Pectic enzymes and cellulases were previously identified in other *Pseudomonas* spp., and pectate lyase has been shown to influence the final symptoms produced by *P. syringae* pv. *lachrymans* (58). Genes encoding cell-wall-degrading enzymes are present in DC3000 and include a pectin lyase, a polygalacturonase, and three enzymes predicted to have cellulolytic activity (PSPTO1029, PSPTO3534, and PSPTO0905). As previously noted, DC3000 has two insecticidal toxin gene clusters (9). Although *P. syringae* is not known to be an insect pathogen, insects may be casual vectors of epiphytic bacteria on wet leaves (2). It is also worth noting that DC3000 lacks a gene encoding the outer-membrane ice nucleation protein, which enables many strains of *P. syringae* to cause frost damage on plants (2).

Mobile Genetic Elements and Their Potential Impact on the Genome. A total of 382 genes (7%) in the DC3000 genome were classified as mobile genetic elements, including genes encoding 270 proteins that function in transposition, 54 proteins with plasmid functions, and 58 proteins with prophage functions. Compared with other published plant pathogen genomes (21–23, 25), this is the highest percentage seen to date, resulting in 24 ORFs interrupted by an IS element or phage protein (Table 3). The transposable element class, which includes the IS elements, accounts for 5% of the DC3000 ORFs (Table 4, which is published as supporting information on the PNAS web site). The IS elements vary widely in their copy number, presumably reflecting a combination of transposition frequency and residence time in the genome. Multiple prophage regions also are present in DC3000, which collectively encompass ~118 kbp of the genome (Table 5, which is published as supporting information on the PNAS web site). The impact of mobile genetic elements on the DC3000 genome is seen by their frequent association with regions that lack homologs in *P. aeruginosa* and/or *P. putida*, that are enriched in atypical nucleotides potentially indicative of hori-

zontal acquisition, and/or that encode either TTSS effectors or proteins of unknown function. One such region, shown in Fig. 3, contains a potpourri of known and candidate virulence factors, including catalase and GST genes, COR biosynthetic genes, a nonribosomal peptide synthase preceded by a Hrp promoter, and two clusters of effector genes, along with multiple mobile genetic elements, one of which has disrupted a *hopPtoD* paralog.

Comparative Genomics of Virulence. We performed a comparative analysis involving 298 putative virulence genes in DC3000 and the complete genome sequences of nine plant and animal pathogenic proteobacteria, which revealed that 86 genes are common to all of these pathogens (Table 2 and Fig. 6, which is published as supporting information on the PNAS web site). The pathogen with the most similar genes was *P. aeruginosa* PAO1 (191 genes; 64% of the virulence factors), which reflects the relatedness of DC3000 and PAO1 and the large number of similar genes involved in flagellum, alginate, and Tfp production. Not surprisingly, among the 65 virulence genes that are unique to DC3000, 33 encode TTSS effectors, helpers, and candidates, which is consistent with the specialized nature of TTSS-based host-pathogen interactions.

Another promising source of virulence candidates is the set of genes unique to DC3000 that were identified in comparative analyses with *P. putida* and *P. aeruginosa*. A search of the 811 genes of unknown function in this category revealed that 635 also were unique to DC3000 in comparisons with all eight of the reference pathogen genomes. However, four of these genes were present in all of the plant pathogenic bacteria, and another set of four were present exclusively in all animal pathogenic bacteria

(Table 6, which is published as supporting information on the PNAS web site).

In considering DC3000 virulence genomics, it is worth noting that pioneering genetic studies with *P. syringae* yielded a paradox that has long frustrated comprehensive exploration of the virulence of this pathogen (59, 60). That is, despite the many indications that *P. syringae* is a highly coevolved plant parasite, screens for mutants with reduced virulence have yielded primarily mutants disabled in a single system, the Hrp TTSS. The complete genome sequence of DC3000 clarifies the basis for this paradox in the redundancy of many of the candidate virulence factors. The sequence will now facilitate the construction of polymutants that can test the role of genes with overlapping function, and it will foster the identification of novel virulence factors through targeted investigation of genes that are unique or duplicated in comparison with *P. aeruginosa* and *P. putida* or in regions showing signatures of horizontal acquisition. In conclusion, *P. syringae* pathobiology has been described as a “highly dynamic, highly variable matrix of interactions of bacteria of widely variable genotypes with a broadly variable group of plants” (61), and the plethora of mobile genetic elements and associated virulence factors that we found provides a genomic basis for such a dynamic association with plants.

We thank the members of The Institute for Genome Research Sequencing Facility, Informatics Department, and Information Technology Support Group who contributed to the work. Funding for the work described in this study was provided by National Science Foundation Grants DBI-0077622 (to A.C., J.R.A., C.R.B., S.C., A.K.C., T.P.D., S.G.L., G.B.M., and X.T.) and IBN-0135286 (to C.L.B.) and National Institutes of Health Grant AI 43311 (to C.L.B.).

- Gupta, R. S. (2000) *FEMS Microbiol. Rev.* **24**, 367–402.
- Hirano, S. S. & Upper, C. D. (2000) *Microbiol. Mol. Biol. Rev.* **64**, 624–653.
- Cuppels, D. A. (1986) *Appl. Environ. Microbiol.* **51**, 323–327.
- Wilson, M., Campbell, H. L., Ji, P., Jones, J. B. & Cuppels, D. A. (2002) *Phytopathology* **92**, 1284–1292.
- Whalen, M. C., Innes, R. W., Bent, A. F. & Stankowicz, B. J. (1991) *Plant Cell* **3**, 49–59.
- Cornelis, G. R. & Van Gijsegem, F. (2000) *Annu. Rev. Microbiol.* **54**, 735–774.
- Boch, J., Joardar, V., Gao, L., Robertson, T. L., Lim, M. & Kunkel, B. N. (2002) *Mol. Microbiol.* **44**, 73–88.
- Fouts, D. E., Abramovitch, R. B., Alfano, J. R., Baldo, A. M., Buell, C. R., Cartinhour, S., Chatterjee, A. K., D’Ascenzo, M., Gwinn, M. L., Lazarowitz, S. G., et al. (2002) *Proc. Natl. Acad. Sci. USA* **99**, 2275–2280.
- Guttman, D. S., Vinatzer, B. A., Sarkar, S. F., Ranall, M. V., Kettler, G. & Greenberg, J. T. (2002) *Science* **295**, 1722–1726.
- Petnicki-Ocwieja, T., Schneider, D. J., Tam, V. C., Chancey, S. T., Shan, L., Jamir, Y., Schechter, L. M., Buell, C. R., Tang, X., Collmer, A., et al. (2002) *Proc. Natl. Acad. Sci. USA* **99**, 7652–7657.
- Collmer, A., Lindeberg, M., Petnicki-Ocwieja, T., Schneider, D. J. & Alfano, J. R. (2002) *Trends Microbiol.* **10**, 462–469.
- Greenberg, J. T. & Vinatzer, B. A. (2003) *Curr. Opin. Microbiol.* **6**, 20–28.
- Keen, N. T. (1990) *Annu. Rev. Genet.* **24**, 447–463.
- Tettelin, H., Nelson, K. E., Paulsen, I. T., Eisen, J. A., Read, T. D., Peterson, S., Heidelberg, J., DeBoy, R. T., Haft, D. H., Dodson, R. J., et al. (2001) *Science* **293**, 498–506.
- Delcher, A. L., Harmon, D., Kasif, S., White, O. & Salzberg, S. L. (1999) *Nucleic Acids Res.* **27**, 4636–4641.
- Bateman, A., Birney, E., Cerruti, L., Durbin, R., Ewinger, L., Eddy, S. R., Griffiths-Jones, S., Howe, K. L., Marshall, M. & Sonnhammer, E. L. (2002) *Nucleic Acids Res.* **30**, 276–280.
- Haft, D. H., Selengut, J. D. & White, O. (2003) *Nucleic Acids Res.* **31**, 371–373.
- Riley, M. (1993) *Microbiol. Rev.* **57**, 862–952.
- Nierman, W. C., Feldblyum, T. V., Laub, M. T., Paulsen, I. T., Nelson, K. E., Eisen, J. A., Heidelberg, J. F., Alley, M. R., Ohta, N., Maddock, J. R., et al. (2001) *Proc. Natl. Acad. Sci. USA* **98**, 4136–4141.
- Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D. J. (1997) *Nucleic Acids Res.* **25**, 3389–3402.
- Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Manganot, S., Arlat, M., Billault, A., Brottier, P., Camus, J. C., Cattolico, L., et al. (2002) *Nature* **415**, 497–502.
- Simpson, A. J. G., Reinach, F. C., Arruda, P., Abreu, F. A., Acencio, M., Avarenga, R., Alves, L. M., Araya, J. E., Baia, G. S., Baptista, C. S., et al. (2000) *Nature* **406**, 151–157.
- Wood, D. W., Setubal, J. C., Kaul, R., Monks, D. E., Kitajima, J. P., Okura, V. K., Zhou, Y., Chen, L., Wood, G. E., Almeida, N. F., Jr., et al. (2001) *Science* **294**, 2317–2323.
- Goodner, B., Hinkle, G., Gattung, S., Miller, N., Blanchard, M., Qurollo, B., Goldman, B. S., Cao, Y., Askenazi, M., Halling, C., et al. (2001) *Science* **294**, 2323–2328.
- Da Silva, A. C., Ferro, J. A., Reinach, F. C., Farah, C. S., Furlan, L. R., Quaggio, R. B., Monteiro-Vitorello, C. B., Sluys, M. A., Almeida, N. F., Alves, L. M., et al. (2002) *Nature* **417**, 459–463.
- Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, S. D., Warrenner, P., Hickey, M. J., Brinkman, F. S., Huffnagle, W. O., Kowalik, D. J., Lagrou, M., et al. (2000) *Nature* **406**, 959–964.
- McClelland, M., Sanderson, K. E., Spieth, J., Clifton, S. W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., et al. (2001) *Nature* **413**, 852–856.
- Parkhill, J., Wren, B. W., Thomson, N. R., Titball, R. W., Holden, M. T., Prentice, M. B., Sebahia, M., James, K. D., Churcher, C., Mungall, K. L., et al. (2001) *Nature* **413**, 523–527.
- Perna, N. T., Plunkett, G., III, Burland, V., Mau, B., Glasner, J. D., Rose, D. J., Mayhew, G. F., Evans, P. S., Gregor, J., Kirkpatrick, H. A., et al. (2001) *Nature* **409**, 529–533.
- Nelson, K. E. (2002) *Environ. Microbiol.* **4**, 777.
- Palleroni, N. J. (1984) in *Bergey’s Manual of Systematic Bacteriology*, eds. Krieg, N. R. & Holt, J. G. (Williams & Wilkins, Baltimore), pp. 141–199.
- Solomon, P. S. & Oliver, R. P. (2001) *Plantia* **213**, 241–249.
- Binet, R., Letoffe, S., Ghigo, J. M., Delepelaire, P. & Wandersman, C. (1997) *Gene* **192**, 7–11.
- Sandkvist, M. (2001) *Mol. Microbiol.* **40**, 271–283.
- Preston, G. M. (2000) *Mol. Plant Pathol.* **1**, 263–275.
- Zwiesler-Vollick, J., Plovanič-Jones, A. E., Nomura, K., Brandyopadhyay, S., Joardar, V., Kunkel, B. N. & He, S. Y. (2002) *Mol. Microbiol.* **45**, 1207–1218.
- Rohmer, L., Kjemtrup, S., Marchesini, P. & Dangel, J. L. (2003) *Mol. Microbiol.* **47**, 1545–1562.
- Cuppels, D. A. & Ainsworth, T. (1995) *Appl. Environ. Microbiol.* **61**, 3530–3536.
- Sesma, A., Sundin, G. W. & Murillo, J. (2000) *Microbiology* **146**, 2375–2384.
- Jackson, R. W., Athanassopoulos, E., Tsiamis, G., Mansfield, J. W., Sesma, A., Arnold, D. L., Gibbon, M. J., Murillo, J., Taylor, J. D. & Vivian, A. (1999) *Proc. Natl. Acad. Sci. USA* **96**, 10875–10880.
- Bultreys, A. & Gheysen, I. (2000) *Appl. Environ. Microbiol.* **66**, 325–331.
- Reimann, C., Patel, H. M., Serino, L., Barone, M., Walsh, C. T. & Haas, D. (2001) *J. Bacteriol.* **183**, 813–820.
- Pelludat, C., Rakin, A., Jacobi, C. A., Schubert, S. & Heesemann, J. (1998) *J. Bacteriol.* **180**, 538–546.
- Moore, R. A., Starratt, A. N., Ma, S. W., Morris, V. L. & Cuppels, D. A. (1989) *Can. J. Microbiol.* **35**, 910–917.
- Kloek, A. P., Verbsky, M. L., Sharma, S. B., Schoelz, J. E., Vogel, J., Klessig, D. F. & Kunkel, B. N. (2001) *Plant J.* **26**, 509–522.
- Bender, C. L., Alarcon-Chaidez, F. & Gross, D. C. (1999) *Microbiol. Mol. Biol. Rev.* **63**, 266–292.
- Glickmann, E., Gardan, L. & Dessaux, Y. (1998) *Mol. Plant-Microbe Interact.* **11**, 156–162.
- Mazzola, M. & White, F. F. (1994) *J. Bacteriol.* **176**, 1374–1382.
- Wall, D. & Kaiser, D. (1999) *Mol. Microbiol.* **32**, 1–10.
- Roine, E., Raineri, D. M., Romantschuk, M., Wilson, M. & Nunn, D. N. (1998) *Mol. Plant-Microbe Interact.* **11**, 1048–1056.
- Rojas, C. M., Ham, J. H., Deng, W.-L., Doyle, J. J. & Collmer, A. (2002) *Proc. Natl. Acad. Sci. USA* **99**, 13142–13147.
- Gacesa, P. (1998) *Microbiology* **144**, 1133–1143.
- Yu, J., Peñalosa-Vázquez, A., Chakrabarty, A. M. & Bender, C. L. (1999) *Mol. Microbiol.* **33**, 712–720.
- Peñalosa-Vázquez, A., Kidambi, S. P., Chakrabarty, A. M. & Bender, C. L. (1997) *J. Bacteriol.* **179**, 4464–4472.
- Mittler, R. (2002) *Trends Plant Sci.* **7**, 405–410.
- Bender, C. L. & Cooksey, D. A. (1987) *J. Bacteriol.* **169**, 470–474.
- Silver, S. & Phung, L. T. (1996) *Annu. Rev. Microbiol.* **50**, 753–789.
- Bauer, D. W. & Collmer, A. (1997) *Mol. Plant-Microbe Interact.* **10**, 369–379.
- Niepol, F., Anderson, D. & Mills, D. (1985) *Proc. Natl. Acad. Sci. USA* **82**, 406–410.
- Lindgren, P. B., Peet, R. C. & Panopoulos, N. J. (1986) *J. Bacteriol.* **168**, 512–522.
- Hirano, S. S. & Upper, C. D. (1990) *Annu. Rev. Phytopathol.* **28**, 155–177.
- Gomez-Gomez, L. & Boller, T. (2000) *Mol. Cell* **5**, 1003–1011.

Sequencing Methods

Figure 4. Functional classification of annotated ORFs in DC3000.

Figure 5. Distribution of ORFs in paralogous families in DC3000.

Figure 6. Classification of virulence determinants within DC3000 and distribution of these determinants in nine plant and animal bacterial pathogens.

Table 2. Factors implicated in virulence in *P. syringae* pv. *tomato* DC3000 and identification of putative homologs (BLASTPE $<10^{-5}$) in pathogenic bacteria

Table 3. The chromosomal and plasmid genes disrupted by IS elements or phage genes in *P. syringae* pv. *tomato* DC3000

Table 4. IS elements present in *P. syringae* pv. *tomato* DC3000

Table 5. Phage and bacteriocin regions of *P. syringae* pv. *tomato* DC3000

Table 6. Genes with unknown function unique to DC3000 identified from the comparative analysis with the *P. aeruginosa* PAO1 and *P. putida* KT2440 genomes and the identification of putative homologs (BLASTP $E < 10^{-5}$) in pathogenic bacteria

Sequencing Methods

Total *P. syringae* pv. *tomato* DC3000 (DC3000) genomic DNA was nebulized and size-fractionated on agarose gels, and after polishing of the ends with Bal 31 exonuclease and T4 DNA ligase, the DNA was ligated to modified pUC vector as described previously (1). Two libraries, a small insert library (2–3 kbp) and a large insert library (6–14 kbp), were constructed and end sequences were generated using ABI BigDye terminator chemistry using ABI 3700 sequencers (Applied Biosystems). The sequences (73,744 random sequences; average edited length of 697 nt) were assembled by using the TIGR assembler program (2). Sequencing and physical gaps were closed by using a combination of primer walking, transposon-mediated sequencing, PCR, and sequencing of PCR products.

1. Tettelin, H., Nelson, K. E., Paulsen, I. T., Eisen, J. A., Read, T. D., Peterson, S., Heidelberg, J., DeBoy, R. T., Haft, D. H., Dodson, R. J., *et al.* (2001) *Science* **293**, 498–506.
2. Sutton, G. G., White, O., Adams, M. D. & Kerlavage, A. R. (1995) *Genome* **1**, 9–19.

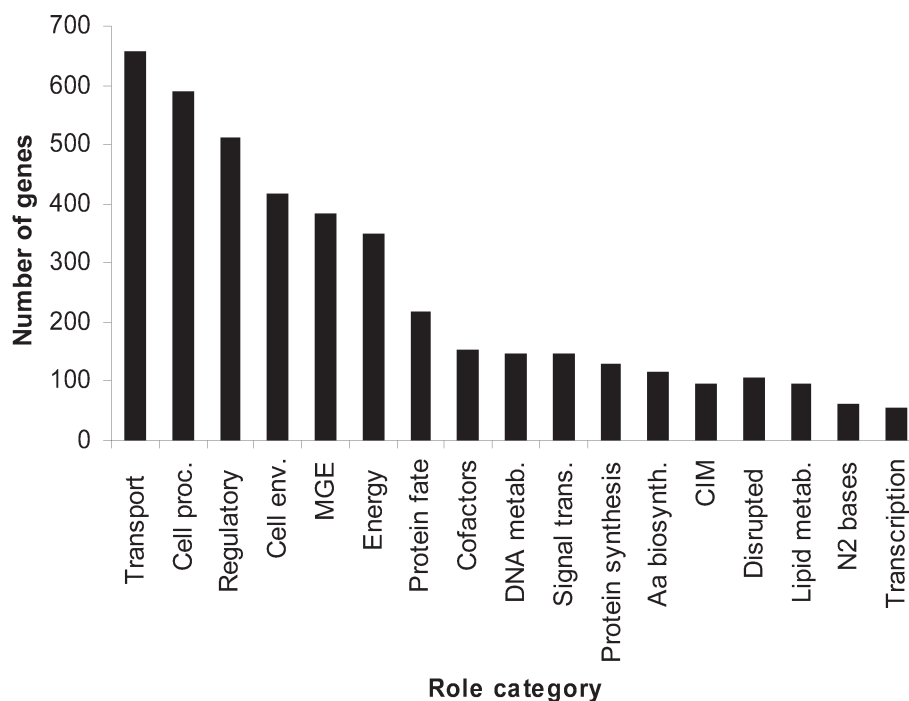


Figure 4. Functional classification of annotated ORFs in DC3000. The ORFs were assigned to role categories adapted from Riley (1) with only the broader categories represented here. Transport, transport and binding function; Cell proc., cellular processes; Regulatory, regulatory functions; Cell env., cellular envelope; MGE, mobile and extrachromosomal element functions; Energy, energy metabolism; Cofactors, biosynthesis of cofactors, prosthetic groups, and carriers; DNA metab., DNA metabolism; Signal trans., signal transduction; Aa biosynth., amino acid biosynthesis; CIM, central intermediary metabolism; Disrupted, disrupted reading frame; Lipid metab., fatty acid and phospholipid metabolism; N2 bases, purines, pyrimidines, nucleosides, and nucleotides.

1. Riley, M. (1993) *Microbiol. Rev.* **57**, 862–952.

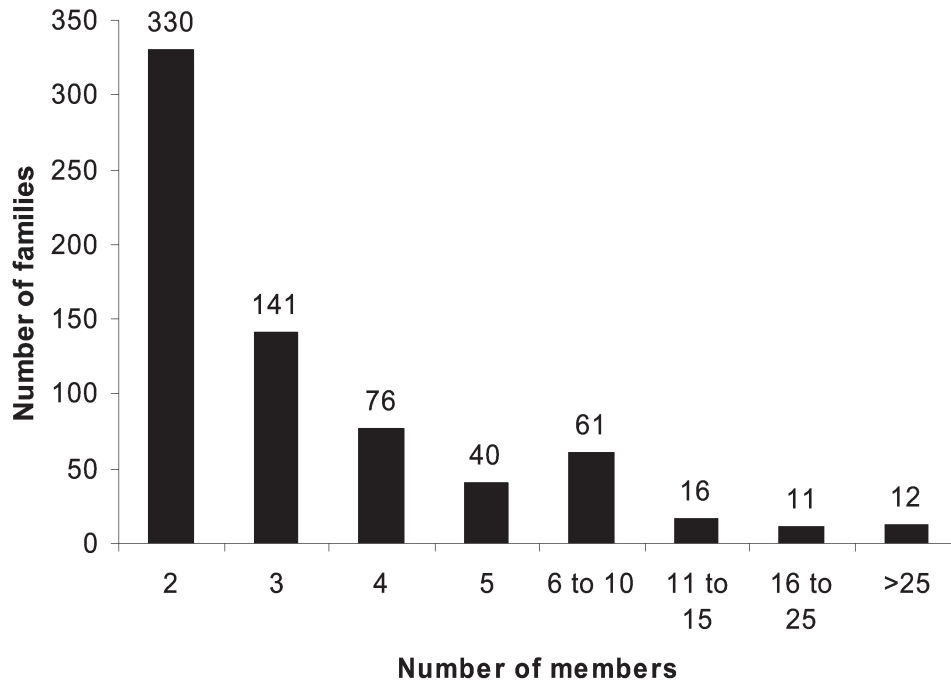


Figure 5. Distribution of ORFs in paralogous families in DC3000. The distribution of ORFs within the 687 paralogous families is shown.

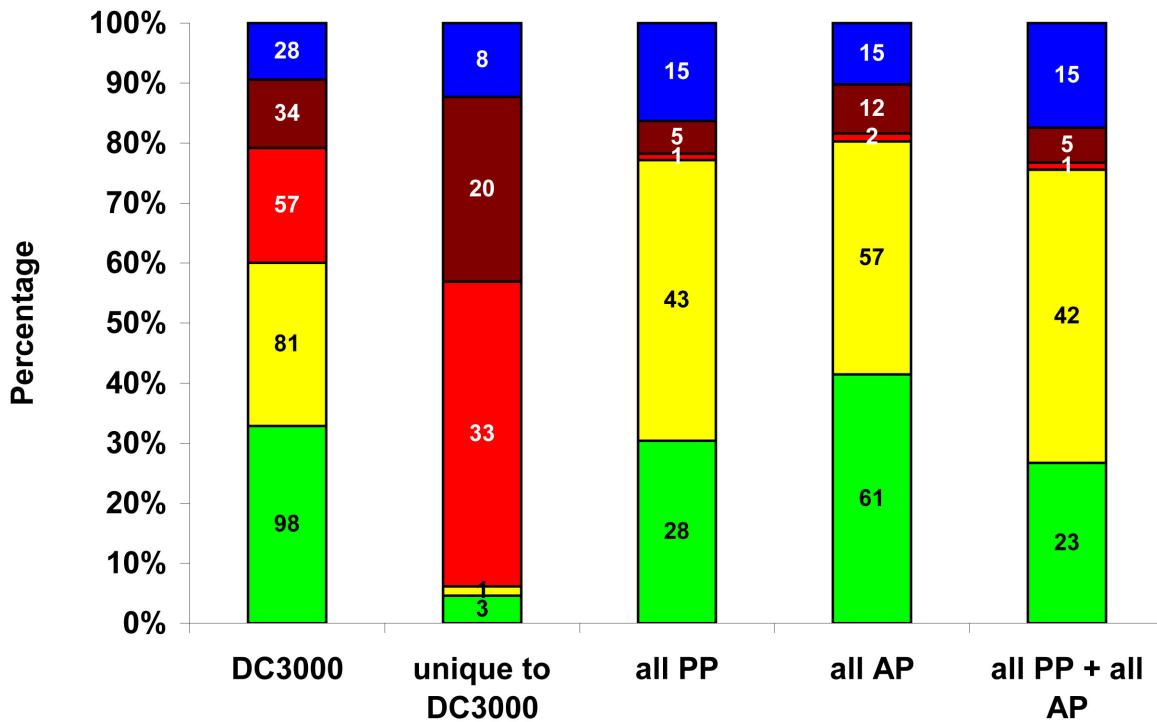


Figure 6. Classification of virulence determinants within DC3000 and distribution of these determinants in nine plant and animal bacterial pathogens. The bars represent all the virulence determinants in DC3000, virulence determinants unique to DC3000, virulence determinants in all plant pathogens (all PP), virulence determinants in all animal pathogens (all AP), and virulence determinants in all plant and animal pathogens (all PP + AP). The DC3000 virulence determinants were categorized into five classes: adhesins and other cell-surface-associated factors (green); miscellaneous virulence factors (yellow); TTSS effectors, candidates, and helpers (red); TTSS regulatory and secretory proteins (brown); and low molecular weight diffusible factors (blue).

Table 2. Factors implicated in virulence in *P. syringae* pv. *tomato* DC3000 and identification of putative homologs (BLASTPE <math><10^{-5}</math>) in pathogenic bacteria

| Locus | Location ^a | Predicted product | Category | GC% | Rs | Xcc | Xac | At | Xf | Pa | Yp | Ec | St |
|-----------|-----------------------|---|----------|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO4713 | C | alanyl tRNA synthetase-related protein (associated with coronatine) | 5 | 55.3 | CAD14690 | — | — | AAL42227 | — | — | — | AAG57801 | — |
| PSPTO1235 | C | alginate biosynthesis protein AlgI | 1 | 60 | — | — | — | — | — | AAG06936 | — | — | — |
| PSPTO1241 | C | alginate biosynthesis protein Alg44 | 1 | 60.5 | — | — | — | — | — | AAG06930 | — | — | — |
| PSPTO1242 | C | alginate biosynthesis protein Alg8 | 1 | 58.8 | — | — | — | — | — | AAG06929 | — | — | — |
| PSPTO1232 | C | alginate biosynthesis protein AlgA | 1 | 59.8 | — | NP_636017 | AAM38423 | AAL44166 | AAF83072 | AAG06939 | NP_406586 | AAG57109 | AAL21009 |
| PSPTO1243 | C | alginate biosynthesis protein AlgD | 1 | 57.8 | CAD14615 | NP_636875 | AAM36420 | AAL44949 | AAF84415 | AAG06928 | NP_405718 | AAG57087 | AAL20984 |
| PSPTO1239 | C | alginate biosynthesis protein AlgE | 1 | 62.1 | — | — | — | — | — | AAG06932 | — | — | — |
| PSPTO1233 | C | alginate biosynthesis protein AlgF | 1 | 60.4 | — | — | — | — | — | AAG06938 | — | — | — |
| PSPTO1238 | C | alginate biosynthesis protein AlgG | 1 | 58.1 | — | — | — | — | — | AAG06933 | — | — | — |
| PSPTO1234 | C | alginate biosynthesis protein AlgJ | 1 | 61.3 | — | — | — | — | — | AAG06937 | — | — | — |
| PSPTO1240 | C | alginate biosynthesis protein AlgK | 1 | 61.6 | — | — | — | — | — | AAG06931 | — | — | — |
| PSPTO1237 | C | alginate biosynthesis protein AlgX | 1 | 59.2 | — | — | — | — | — | AAG06934 | — | — | — |
| PSPTO1236 | C | alginate lyase AlgL | 1 | 57.8 | — | — | — | — | — | AAG06935 | — | — | — |
| PSPTO0134 | C | alginate regulator AlgQ | 1 | 56.7 | — | — | — | — | — | AAG08640 | NP_407187 | AAG59192 | AAL22993 |
| PSPTO0126 | C | alginate regulator FimS | 1 | 57.9 | CAD15053 | NP_638859 | AAM35509 | — | AAF84434 | AAG08647 | NP_407384 | AAG57194 | AAL21063 |
| PSPTO0334 | C | alginate regulatory protein AlgB | 1 | 61.8 | CAD13860 | NP_635584 | AAM35118 | AAL44574 | AAF85342 | AAG08868 | NP_406415 | AAG59201 | AAL23002 |
| PSPTO0127 | C | alginate regulatory protein AlgR | 1 | 58.9 | CAD15054 | NP_638858 | AAM35510 | AAL44596 | AAF84435 | AAG08646 | NP_406755 | AAG57193 | AAL21062 |
| PSPTO0136 | C | alginate regulatory protein AlgR3 | 1 | 61.2 | CAD16500 | NP_638223 | AAM38815 | AAL42873 | — | AAG08638 | NP_406242 | AAG56007 | AAL21483 |
| PSPTO4223 | C | alginate regulatory protein MucA | 1 | 59.2 | — | NP_636642 | — | — | — | AAG04152 | NP_406229 | AAG57688 | AAL21533 |
| PSPTO4222 | C | alginate regulatory protein MucB | 1 | 55.3 | CAD14759 | — | — | — | — | AAG04153 | NP_406230 | AAG57687 | AAL21532 |
| PSPTO2816 | C | alkylhydroperoxidase AhpD domain protein | 2 | 61.4 | CAD15590 | — | — | AAL46114 | — | AAG03658 | NP_405897 | — | — |
| PSPTO4204 | C | amidase family (indoleacetamide hydrolase IaaH) | 5 | 66.1 | CAD14119 | NP_636310 | AAM35198 | AAL44059 | — | AAG04093 | NP_406731 | — | — |
| PSPTO3864 | C | autoinducer synthesis protein PsyI | 2 | 55.5 | CAD17930 | — | — | AAL46278 | — | AAG04821 | NP_404601 | — | — |
| PSPTO3863 | C | autoinducer transcriptional regulator PsyR | 2 | 51.8 | CAD17075 | NP_638166 | AAM37021 | AAL43274 | — | AAG05287 | NP_405991 | AAG56931 | AAL20862 |
| PSPTO3582 | C | catalase KatB | 2 | 58.3 | CAD18732 | NP_639288 | AAM38864 | AAL46177 | — | AAG08001 | NP_404811 | AAG56718 | AAL20243 |
| PSPTO5263 | C | catalase KatE | 2 | 59 | CAD18732 | NP_636484 | AAM36083 | AAL46177 | — | AAG05535 | NP_404811 | AAG56718 | AAL20243 |
| PSPTO4530 | C | catalase/peroxidase KatG | 2 | 61.1 | CAD14477 | NP_636579 | AAM36172 | AAL45436 | AAF85031 | — | NP_406785 | AAG59143 | AAL22946 |
| PSPTO4683 | C | coronafacic acid beta-ketoacyl synthetase component Cfa3 | 5 | 67.1 | CAD14756 | NP_636396 | AAM36002 | AAL45010 | AAF83483 | AAG04762 | NP_405182 | AAG55841 | AAL20126 |
| PSPTO4686 | C | coronafacic acid polyketide synthase I Cfa6 | 5 | 67.6 | CAD17792 | NP_636396 | AAM36002 | AAL44484 | AAF83483 | AAG06356 | NP_405471 | AAG55841 | AAL20126 |

| | | | | | | | | | | | | | |
|------------------------|---|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO4687 | C | coronafacic acid polyketide synthetase II Cfa7 | 5 | 68.1 | CAD15508 | NP_636393 | AAM36002 | AAL44484 | AAF83483 | AAG04762 | NP_405471 | AAG55664 | AAL20126 |
| PSPTO4684 | C | coronafacic acid synthetase component Cfa4 | 5 | 65.3 | - | - | - | - | - | - | - | - | - |
| PSPTO4681 | C | coronafacic acid synthetase, acyl carrier protein component Cfa1 | 5 | 59 | - | - | - | - | - | - | - | - | - |
| PSPTO4707 | C | coronafacic acid synthetase, acyl carrier protein component, putative | 5 | 50.9 | - | - | - | - | - | - | - | - | - |
| PSPTO4682 | C | coronafacic acid synthetase, dehydratase component Cfa2 | 5 | 62.2 | CAD15117 | NP_636736 | AAM36281 | AAL42389 | AAF83854 | AAG07033 | NP_404668 | AAG54482 | AAL19191 |
| PSPTO4685 | C | coronafacic acid synthetase, ligase component Cfa5 | 5 | 65 | CAD13970 | NP_637223 | AAM36742 | AAL42672 | AAF83100 | AAG05812 | NP_404418 | AAG56794 | AAL20733 |
| PSPTO4680 | C | coronafacic acid synthetase, ligase component Cfl | 5 | 62.5 | CAD18416 | NP_636198 | AAM35769 | AAL45616 | AAF83100 | AAG05943 | NP_405626 | AAG56688 | AAL20275 |
| PSPTO4690 | C | coronafacic acid synthetase, thioesterase component Cfa9 | 5 | 59.5 | CAD15506 | - | - | AAL44497 | - | AAG05799 | NP_405469 | - | - |
| PSPTO4709 | C | coronamic acid synthetase, alloisoleucine ligase component CmaA | 5 | 56.9 | CAD17793 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05790 | NP_404403 | AAG54921 | AAL19539 |
| PSPTO4710 | C | coronamic acid synthetase, chlorinating enzyme component, putative | 5 | 55.4 | - | - | - | - | - | - | - | - | - |
| PSPTO4711 | C | coronamic acid synthetase, cyclase component, putative | 5 | 57.9 | - | - | - | - | - | - | - | - | - |
| PSPTO4712 | C | coronamic acid synthetase, thioesterase component CmaT | 5 | 58.2 | CAD15506 | - | - | AAL44497 | - | AAG07617 | NP_404399 | - | - |
| PSPTO4708 | C | coronatine biosynthesis protein, putative | 5 | 56.3 | - | - | - | - | - | - | - | - | - |
| PSPTO4706 | C | coronatine response regulator CorP | 5 | 57.9 | - | - | - | - | - | - | - | - | - |
| PSPTO4704 | C | coronatine response regulator CorR | 5 | 61.3 | CAD13820 | NP_638695 | AAM38323 | AAL41503 | AAF83782 | AAG06992 | NP_406531 | AAG56081 | AAL20682 |
| PSPTO4705 ^b | C | coronatine sensor histidine kinase CorS (authentic frameshift) | 5 | 59.9 | CAD16163 | NP_638694 | AAM38316 | AAL41545 | AAF83783 | AAG05380 | NP_403906 | AAG57899 | AAL20316 |
| PSPTO4689 | C | crotonyl-CoA reductase Cfa8 (associated with coronatine) | 5 | 62.3 | CAD16839 | NP_635424 | AAM34923 | AAL41642 | AAF84543 | AAG08812 | NP_403969 | AAG56765 | AAL20485 |
| PSPTO3598 | C | dyp-type peroxidase family protein | 2 | 63.5 | - | - | - | - | - | - | NP_405420 | AAG55637 | - |
| PSPTO1029 | C | endo-1,4-beta-D-glucanase | 2 | 65.1 | - | - | AAM38359 | AAL44120 | - | - | - | AAG58673 | AAL22477 |
| PSPTO3960 | C | endo-polygalacturonase | 2 | 59.4 | CAD18031 | NP_637621 | AAM37226 | AAL43945 | - | - | - | - | - |
| PSPTO3210 | C | filamentous hemagglutinin family protein | 1 | 55.4 | CAD15477 | NP_637159 | AAM36677 | AAL44779 | AAF83699 | AAG03431 | NP_406024 | - | - |
| PSPTO3229 | C | filamentous hemagglutinin, intein-containing, putative | 1 | 60.1 | CAD17691 | NP_637159 | AAM36677 | AAL44776 | AAF83699 | AAG05850 | NP_404241 | AAG55657 | AAL21407 |

| | | | | | | | | | | | | | |
|------------------------|---|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO3214 ^b | C | filamentous hemagglutinin family protein, putative (authentic point mutation) | 1 | 59.1 | CAD15477 | NP_637159 | AAM36677 | - | AAF84995 | AAG03431 | NP_406024 | AAG54838 | AAL21407 |
| PSPTO1925 | C | flagellar anti-transcription factor FlgM | 1 | 54.2 | - | NP_637320 | AAM36851 | - | - | AAG06739 | - | - | - |
| PSPTO1960 | C | flagellar assembly protein FliH, putative | 1 | 58.7 | CAD17543 | NP_637289 | AAM36814 | - | - | AAG04492 | NP_404348 | AAG56955 | AAL20883 |
| PSPTO1935 | C | flagellar basal-body rod modification protein FlgD | 1 | 57.8 | CAD17495 | NP_637315 | AAM36846 | AAL41596 | - | AAG04468 | NP_405366 | AAG55821 | AAL20106 |
| PSPTO1933 | C | flagellar basal-body rod protein FlgB | 1 | 57.3 | CAD17493 | NP_637317 | AAM36848 | - | - | AAG04466 | NP_405364 | AAG55819 | AAL20104 |
| PSPTO1934 | C | flagellar basal-body rod protein FlgC | 1 | 56.2 | CAD17494 | NP_637316 | AAM36847 | AAL41571 | - | AAG04467 | NP_404355 | AAG55820 | AAL20105 |
| PSPTO1939 | C | flagellar basal-body rod protein FlgF | 1 | 61.5 | CAD17497 | NP_637313 | AAM36844 | AAL41575 | - | AAG04470 | NP_405368 | AAG55823 | AAL20108 |
| PSPTO1940 | C | flagellar basal-body rod protein FlgG | 1 | 61.2 | CAD17498 | NP_637312 | AAM36843 | AAL41569 | - | AAG04471 | NP_405369 | AAG55824 | AAL20109 |
| PSPTO1976 | C | flagellar biosynthesis protein FlhA | 1 | 58.6 | CAD18544 | NP_637274 | AAM36798 | AAL41598 | - | AAG04841 | NP_405358 | AAG56869 | AAL20829 |
| PSPTO1975 | C | flagellar biosynthetic protein FlhB | 1 | 59.2 | CAD18545 | NP_637275 | AAM36799 | AAL41581 | - | AAG04838 | NP_405357 | AAG56870 | AAL20830 |
| PSPTO1972 | C | flagellar biosynthetic protein FliP | 1 | 57.1 | CAD17526 | NP_637281 | AAM36806 | AAL41563 | - | AAG04835 | NP_405386 | AAG56963 | AAL20891 |
| PSPTO1973 | C | flagellar biosynthetic protein FliQ | 1 | 58.8 | CAD17525 | NP_637280 | AAM36804 | AAL41597 | - | AAG04836 | NP_405385 | AAG56964 | AAL20892 |
| PSPTO1974 | C | flagellar biosynthetic protein FliR | 1 | 59.6 | CAD17524 | NP_637279 | AAM36803 | AAL41599 | - | AAG04837 | NP_405384 | AAG56965 | AAL20893 |
| PSPTO1936 | C | flagellar hook protein FlgE | 1 | 57.5 | CAD17496 | NP_637314 | AAM36845 | AAL41591 | AAF84783 | AAG04469 | NP_405367 | AAG55822 | AAL20107 |
| PSPTO1937 | C | flagellar hook protein FlgE | 1 | 60.8 | CAD17496 | NP_637314 | AAM36845 | AAL41591 | - | AAG04469 | NP_405367 | AAG55822 | AAL20107 |
| PSPTO1944 | C | flagellar hook-associated protein FlgK | 1 | 59.8 | CAD17502 | NP_637308 | AAM36839 | AAL41592 | AAF84783 | AAG04475 | NP_405373 | AAG55828 | AAL20113 |
| PSPTO1945 | C | flagellar hook-associated protein FlgL | 1 | 59.7 | CAD17503 | NP_637307 | AAM36838 | AAL41584 | - | AAG04476 | NP_405374 | AAG55829 | AAL20114 |
| PSPTO1951 | C | flagellar hook-associated protein FliD, FRAMESHIFT | 1 | 58.7 | CAD17534 | NP_637305 | AAM36836 | AAL44779 | AAF84783 | AAG04483 | NP_405405 | AAG56939 | AAL20872 |
| PSPTO1957 | C | flagellar hook-basal body complex protein FliE | 1 | 55.4 | CAD17540 | NP_637292 | AAM36817 | - | - | AAG04489 | NP_405397 | AAG56952 | AAL20880 |
| PSPTO1966 | C | flagellar hook-length control protein FliK | 1 | 61.7 | CAD17546 | NP_637286 | AAM36811 | - | - | AAG04830 | NP_405391 | AAG56958 | AAL20886 |
| PSPTO1941 | C | flagellar L-ring protein FlgH | 1 | 61.3 | CAD17499 | NP_637311 | AAM36842 | AAL41565 | - | AAG04472 | NP_404360 | AAG55825 | AAL20110 |
| PSPTO1959 | C | flagellar motor switch protein FliG | 1 | 58.5 | CAD17542 | NP_637290 | AAM36815 | AAL41580 | - | AAG04491 | NP_405395 | AAG56954 | AAL20882 |
| PSPTO1969 | C | flagellar motor switch protein FliM | 1 | 58.9 | CAD17529 | NP_637284 | AAM36809 | - | - | AAG04832 | NP_405389 | AAG56960 | AAL20888 |
| PSPTO1970 | C | flagellar motor switch protein FliN | 1 | 60.7 | CAD17528 | NP_637283 | AAM36808 | AAL41579 | - | AAG04833 | NP_405388 | AAG56961 | AAL20889 |
| PSPTO1958 | C | flagellar M-ring protein FliF | 1 | 60.3 | CAD17541 | NP_637291 | AAM36816 | AAL41541 | - | AAG04490 | NP_405396 | AAG56953 | AAL20881 |
| PSPTO1942 | C | flagellar P-ring protein FlgI | 1 | 61.7 | CAD17500 | NP_637310 | AAM36841 | AAL41567 | - | AAG04473 | NP_404361 | AAG55826 | AAL20111 |
| PSPTO1962 | C | flagellar protein FliJ, putative | 1 | 61.3 | CAD17545 | NP_637287 | AAM36812 | - | - | AAG04494 | NP_405392 | AAG56957 | AAL20885 |

| | | | | | | | | | | | | | |
|-----------|---|--|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO1968 | C | flagellar protein FliL, putative | 1 | 58.3 | CAD17530 | NP_637285 | AAM36810 | | | AAG04831 | NP_405390 | AAG56959 | AAL20887 |
| PSPTO5230 | C | flagellar protein FliL, putative | 1 | 56 | | NP_637285 | AAM36810 | | | AAG08618 | | | |
| PSPTO1971 | C | flagellar protein FliO | 1 | 63.2 | CAD17527 | NP_637282 | AAM36807 | | | AAG04834 | NP_405387 | AAG56962 | AAL20890 |
| PSPTO1952 | C | flagellar protein FliS | 1 | 58.7 | CAD17535 | NP_637304 | AAM36835 | | | AAG04484 | NP_405404 | AAG56940 | AAL20873 |
| PSPTO1926 | C | flagellar protein, putative | 1 | 58.6 | CAD17492 | NP_637319 | AAM36850 | AAL41568 | | AAG06738 | NP_404353 | | AAL20103 |
| PSPTO1954 | C | flagellar regulator FleQ | 1 | 59.3 | CAD17379 | NP_637298 | AAM36829 | AAL42452 | AAF85342 | AAG04486 | NP_403688 | AAG59201 | AAL23002 |
| PSPTO1956 | C | flagellar response regulator FleR | 1 | 61.6 | CAD13860 | NP_635584 | AAM38082 | AAL42452 | AAF84654 | AAG04488 | NP_404344 | AAG59201 | AAL23002 |
| PSPTO1955 | C | flagellar sensor histidine kinase FleS | 1 | 63 | CAD13859 | NP_638780 | AAM35574 | AAL45099 | AAF84264 | AAG04487 | NP_404513 | AAG59200 | AAL23001 |
| PSPTO1978 | C | flagellar synthesis regulator FleN | 1 | 60.6 | CAD16862 | NP_637272 | AAM36796 | AAL44064 | AAF84130 | AAG04843 | NP_405629 | AAG56026 | AAL20730 |
| PSPTO1950 | C | flagellin FlaG, putative | 1 | 51 | | | | | | AAG04482 | | | |
| PSPTO1949 | C | flagellin FliC | 1 | 55.9 | CAD17533 | NP_637306 | AAM36837 | AAL41559 | AAF84325 | AAG04481 | NP_405406 | AAG56938 | AAL20871 |
| PSPTO1961 | C | flagellum-specific ATP synthase FliI | 1 | 64.1 | CAD17544 | NP_637288 | AAM36813 | AAL41574 | AAF83953 | AAG04493 | NP_405393 | AAG56956 | AAL20884 |
| PSPTO3637 | C | FliH domain protein | 1 | 63.9 | CAD18545 | NP_637275 | AAM36799 | AAL41581 | | AAG04862 | NP_405357 | AAG56870 | AAL20830 |
| PSPTO3307 | C | general secretion pathway protein GspD | 2 | 60.9 | CAD16680 | NP_636062 | AAM38377 | AAL41244 | AAF84336 | AAG04074 | NP_404440 | AAG58491 | AAL22350 |
| PSPTO3317 | C | general secretion pathway protein GspE | 2 | 62.5 | CAD16824 | NP_636052 | AAM38387 | AAL46277 | AAF84326 | AAG06065 | NP_404439 | AAG54411 | AAL19107 |
| PSPTO3316 | C | general secretion pathway protein GspF | 2 | 62.8 | CAD16825 | NP_636053 | AAM38386 | | AAF84327 | AAG04076 | NP_406889 | AAG54410 | AAL19106 |
| PSPTO3315 | C | general secretion pathway protein GspG | 2 | 59.2 | CAD16017 | NP_636054 | AAM38385 | | AAF84328 | AAG06489 | NP_404438 | | |
| PSPTO3314 | C | general secretion pathway protein GspH | 2 | 62.5 | | NP_636055 | AAM38384 | | AAF84329 | | | | |
| PSPTO3313 | C | general secretion pathway protein GspI, putative | 2 | 62.7 | | NP_636056 | AAM38383 | | | AAG06061 | | | |
| PSPTO3312 | C | general secretion pathway protein GspJ, putative | 2 | 63.8 | | NP_636057 | AAM38382 | | AAF84331 | | | | |
| PSPTO3311 | C | general secretion pathway protein GspK, putative | 2 | 60.9 | | NP_636058 | AAM38381 | | AAF84332 | | | | |
| PSPTO3310 | C | general secretion pathway protein GspL, putative | 2 | 63.1 | | NP_636059 | AAM38380 | | AAF84333 | | | | |
| PSPTO3309 | C | general secretion pathway protein GspM, putative | 2 | 64.5 | | NP_636060 | AAM38379 | | AAF84334 | | | | |
| PSPTO3308 | C | general secretion pathway protein GspN, putative | 2 | 66.1 | | | | | AAF84335 | | | | |
| PSPTO1172 | C | glutathione peroxidase family protein | 2 | 57.4 | CAD16381 | NP_636786 | AAM36327 | | AAF84696 | AAG04227 | NP_405957 | AAG56697 | AAL20266 |
| PSPTO1719 | C | glutathione peroxidase family protein | 2 | 57.4 | CAD13835 | NP_636873 | AAM36418 | | AAF84413 | AAG04676 | NP_405957 | AAG56697 | AAL20266 |

| | | | | | | | | | | | | | |
|------------|----|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO1781 | C | glutathione peroxidase family protein | 2 | 56.1 | CAD16381 | NP_636786 | AAM36327 | - | AAF84696 | AAG06214 | NP_405957 | AAG56697 | AAL20266 |
| PSPTO3112 | C | glutathione reductase | 2 | 58.4 | CAD13542 | NP_637927 | AAM37595 | AAL42613 | AAF83678 | AAG05413 | NP_407417 | AAG58632 | AAL22457 |
| PSPTO4254 | C | glutathione reductase | 2 | 54.7 | CAD13542 | NP_637927 | AAM37595 | AAL42613 | AAF83678 | AAG05413 | NP_407417 | AAG58632 | AAL22457 |
| PSPTO3343 | C | glutathione S-transferase domain protein | 2 | 56.5 | - | NP_638907 | AAM35474 | AAL43250 | - | AAG05998 | - | AAG58235 | AAL22106 |
| PSPTO0929 | C | glutathione S-transferase family | 2 | 56.8 | CAD14519 | NP_636315 | AAM37083 | AAL45840 | AAF84020 | AAG04855 | NP_405903 | AAG56624 | AAL20373 |
| PSPTO2032 | C | glutathione S-transferase family | 2 | 56.7 | CAD15723 | NP_636804 | AAM36344 | AAL41850 | AAF84020 | AAG05044 | NP_407094 | AAG57431 | AAL22014 |
| PSPTO3856 | C | glutathione S-transferase family | 2 | 62 | CAD14686 | NP_639111 | AAM38661 | AAL44512 | AAF84020 | AAG06201 | NP_404909 | AAG55214 | AAL19798 |
| PSPTO4398 | C | glutathione S-transferase family | 2 | 62.1 | CAD13614 | NP_636213 | AAM35782 | AAL42400 | - | AAG07789 | NP_405903 | AAG57430 | AAL21249 |
| PSPTO0703 | C | glutathione S-transferase family protein | 2 | 58.9 | CAD15723 | NP_639301 | AAM38882 | AAL44397 | - | AAG04422 | NP_407094 | AAG58126 | AAL22014 |
| PSPTO1365 | C | glutathione S-transferase family protein | 2 | 58 | CAD14137 | NP_637641 | AAM37246 | AAL41850 | - | AAG06201 | NP_404909 | AAG55214 | AAL23091 |
| PSPTO4777 | C | glutathione S-transferase family protein | 2 | 58.5 | CAD14686 | NP_639111 | AAM39182 | AAL41850 | AAF84020 | AAG05279 | NP_404909 | AAG55214 | AAL19798 |
| PSPTO0448 | C | glutathione S-transferase, putative | 2 | 61.4 | CAD16428 | - | - | AAL42145 | - | AAG03856 | - | AAG58736 | AAL22543 |
| PSPTO3534 | C | glycosyl hydrolase, family 5 (cellulolytic activity) | 2 | 62.7 | - | - | - | - | - | AAG05625 | - | - | - |
| PSPTO3230 | C | hemolysin activator protein, HlyB family | 2 | 60.8 | CAD14590 | NP_637158 | AAM36676 | - | AAF85347 | AAG05851 | NP_407171 | AAG55658 | - |
| PSPTO1309 | C | HlyD family secretion protein | 2 | 61.4 | CAD18348 | NP_639132 | AAM38690 | AAL43469 | AAF85183 | AAG04824 | NP_406355 | AAG57137 | AAL21030 |
| PSPTO2753 | C | HlyD family secretion protein | 2 | 58.6 | CAD18348 | NP_639132 | AAM38690 | AAL43469 | AAF85183 | AAG05916 | NP_406355 | AAG57137 | AAL21030 |
| PSPTO3620 | C | HlyD family secretion protein | 2 | 63.9 | CAD16433 | NP_639503 | AAM39135 | AAL46225 | AAF84892 | AAG06692 | NP_407139 | AAG56633 | AAL22234 |
| PSPTO3703 | C | HlyD family secretion protein | 2 | 62.8 | CAD16433 | NP_638835 | AAM35530 | AAL42100 | - | AAG04626 | NP_406737 | AAG57794 | AAL21699 |
| PSPTO0371 | C | indoleacetate-lysine ligase IaaL | 5 | 53.3 | - | - | - | - | - | - | - | - | - |
| PSPTO1453 | C | levansucrase | 1 | 56.3 | - | - | - | - | - | - | - | - | - |
| PSPTO2305 | C | levansucrase | 1 | 57.3 | - | - | - | - | - | - | - | - | - |
| PSPTOA0032 | pA | levansucrase | 1 | 55.6 | - | - | - | - | - | - | - | - | - |
| PSPTO1378 | C | membrane-bound lytic murein transglycosylase D, putative (CEL ORF1) | 2 | 62.1 | CAD15218 | NP_636362 | AAM35961 | - | AAF84172 | AAG05201 | NP_404692 | AAG54507 | AAL19217 |
| PSPTO0405 | C | methionine sulfoxide reductase | 2 | 58.8 | CAD14294 | NP_636219 | AAM35788 | AAL41149 | AAF84742 | AAG08403 | NP_406984 | AAG59417 | AAL23228 |
| PSPTO2829 | C | non-ribosomal peptide synthase | 5 | 63.5 | CAD17793 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05787 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO2830 | C | non-ribosomal peptide synthase | 5 | 64.4 | CAD17793 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05787 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO4518 | C | non-ribosomal peptide synthase | 5 | 58 | CAD17792 | NP_639207 | AAM36951 | AAL44495 | AAF83100 | AAG05812 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO4519 | C | non-ribosomal peptide synthase | 5 | 59 | CAD17792 | NP_639207 | AAM36951 | AAL44495 | AAF83100 | AAG05787 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO4699 | C | non-ribosomal peptide synthase | 5 | 59.3 | CAD17793 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05790 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO4283 | C | pectin lyase | 2 | 59.5 | - | - | - | - | - | - | - | - | - |
| PSPTO1943 | C | peptidoglycan hydrolase FlgJ | 1 | 61.6 | CAD17501 | NP_637309 | AAM36840 | - | - | AAG04474 | NP_405372 | AAG55827 | AAL20112 |

| | | | | | | | | | | | | | |
|-----------|---|--|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO5162 | C | periplasmic glucan biosynthesis protein MdoG | 1 | 58.2 | CAD16615 | NP_639484 | AAM39119 | - | AAF85479 | AAG08463 | - | AAG55794 | AAL20080 |
| PSPTO5161 | C | periplasmic glucan biosynthesis protein MdoH | 1 | 60.3 | CAD16616 | NP_638861 | AAM35507 | AAL44122 | AAF84432 | AAG08462 | - | AAG55795 | AAL20081 |
| PSPTO3440 | C | polysaccharide biosynthesis protein, putative | 1 | 61 | - | NP_637799 | - | AAL44858 | - | - | - | - | - |
| PSPTO2153 | C | pyoverdine ABC transporter, ATP-binding/permease protein PvdE | 2 | 62 | CAD17789 | NP_636854 | AAM36399 | AAL44554 | AAF85379 | AAG05785 | NP_405474 | AAG57346 | AAL21165 |
| PSPTO2146 | C | pyoverdine biosynthesis regulatory gene, putative | 2 | 60.7 | - | - | - | - | - | AAG05691 | - | - | - |
| PSPTO2135 | C | pyoverdine chromophore precursor synthetase PvsA | 2 | 63.4 | CAD17792 | NP_639207 | AAM36951 | AAL44495 | AAF83100 | AAG05812 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO2147 | C | pyoverdine sidechain peptide synthetase I, epsilon-Lys module | 2 | 64.5 | CAD17792 | NP_639207 | AAM36951 | AAL44494 | AAF85054 | AAG05788 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO2148 | C | pyoverdine sidechain peptide synthetase II, D-Asp-L-Thr component | 2 | 61.4 | CAD17792 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05790 | NP_404403 | AAG54921 | AAL19539 |
| PSPTO2149 | C | pyoverdine sidechain peptide synthetase III, L-Thr-L-Ser component | 2 | 61.9 | CAD17792 | NP_639207 | AAM36951 | AAL44495 | AAF83100 | AAG05787 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO2150 | C | pyoverdine sidechain peptide synthetase IV, D-Asp-L-Ser component | 2 | 62.2 | CAD17792 | NP_639207 | AAM36952 | AAL44495 | AAF83100 | AAG05790 | NP_404403 | AAG54921 | AAL19539 |
| PSPTO2134 | C | pyoverdine synthetase, thioesterase component | 2 | 63.3 | CAD15506 | - | - | AAL44497 | - | AAG05813 | NP_404399 | - | - |
| PSPTO3024 | C | response regulator GacA | 2 | 56.2 | CAD13820 | NP_637450 | AAM36963 | AAL45956 | AAF85405 | AAG05974 | NP_405429 | AAG56929 | AAL20859 |
| PSPTO4224 | C | RNA polymerase sigma-24 factor AlgT | 1 | 54.1 | CAD14757 | NP_636641 | AAM36190 | AAL43900 | AAF85038 | AAG04151 | NP_406228 | AAG57689 | AAL21534 |
| PSPTO1565 | C | RNA polymerase sigma-38 factor RpoS | 2 | 56.4 | CAD14909 | NP_639081 | AAM38630 | AAL43156 | AAF84159 | AAG07010 | NP_406818 | AAG57848 | AAL21804 |
| PSPTO4453 | C | RNA polymerase sigma-54 factor RpoN | 2 | 58.2 | CAD13936 | NP_638150 | AAM37817 | AAL41354 | AAF84217 | AAG07850 | NP_407039 | AAG58336 | AAL22189 |
| PSPTO1691 | C | sensor histidine kinase/response regulator GacS | 2 | 62.6 | CAD16788 | NP_635875 | AAM35383 | AAL41365 | AAF83924 | AAG04317 | NP_407012 | AAG57899 | AAL21838 |
| PSPTO1675 | C | siderophore biosynthesis protein, putative | 2 | 63.7 | - | - | - | AAL45210 | - | AAG04554 | NP_405163 | AAG54917 | AAL19535 |
| PSPTO4156 | C | sodium-type flagellar protein MotY, putative | 1 | 62.2 | CAD17912 | NP_636809 | AAM36349 | AAL43703 | AAF83173 | AAG06914 | NP_404090 | AAG57716 | AAL19693 |
| PSPTO1338 | C | superoxide dismutase, Cu-Zn | 2 | 59.9 | CAD16075 | NP_635586 | AAM35102 | - | - | - | NP_406837 | AAG57201 | AAL19860 |
| PSPTO4363 | C | superoxide dismutase, Fe | 2 | 59.2 | CAD16233 | NP_637851 | AAM37524 | AAL41890 | AAF85411 | AAG07754 | NP_405922 | AAG56645 | AAL20353 |
| PSPTO4459 | C | superoxide dismutase, Mn | 2 | 56.3 | CAD16233 | NP_637633 | AAM37238 | AAL41890 | AAF85411 | AAG07856 | NP_407488 | AAG59102 | AAL22895 |
| PSPTO2752 | C | thiol peroxidase | 2 | 58.4 | CAD16497 | - | - | AAL42826 | - | AAG05920 | NP_405879 | AAG56478 | AAL20599 |

| | | | | | | | | | | | | | |
|------------|----|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO0341 | C | thiol:disulfide interchange protein DsbA | 2 | 59.3 | CAD13813 | NP_638746 | AAM35611 | - | AAF84246 | AAG08874 | NP_403682 | AAG59049 | AAL22836 |
| PSPTO0784 | C | TonB dependent siderophore receptor, putative | 2 | 60.3 | CAD17962 | NP_638414 | AAM38463 | AAL44724 | AAF84933 | AAG05310 | NP_404908 | AAG57293 | AAL21103 |
| PSPTO2151 | C | TonB dependent siderophore receptor, putative | 2 | 61 | CAD16627 | NP_638941 | AAM35068 | AAL45999 | AAF83409 | AAG05786 | NP_405123 | AAG55848 | AAL20133 |
| PSPTO2152 | C | TonB dependent siderophore receptor, putative | 2 | 61.3 | CAD18213 | NP_638941 | AAM35068 | AAL44823 | AAF83409 | AAG07609 | NP_405123 | AAG55848 | AAL20133 |
| PSPTO3462 | C | TonB-dependent siderophore receptor | 2 | 61.6 | CAD17565 | NP_636066 | AAM38373 | AAL44823 | AAF83409 | AAG05298 | NP_405322 | AAG58168 | AAL19318 |
| PSPTO4128 | C | TonB-dependent siderophore receptor | 2 | 59.1 | CAD17565 | NP_636066 | AAM38373 | AAL45999 | AAF83409 | AAG05298 | NP_405322 | AAG58168 | AAL20133 |
| PSPTO1206 | C | TonB-dependent siderophore receptor, putative | 2 | 60.8 | CAD16627 | NP_638941 | AAM37038 | AAL45999 | AAF83409 | AAG03859 | NP_404572 | AAG54454 | AAL19155 |
| PSPTO1610 | C | TonB-dependent siderophore receptor, putative | 2 | 61.9 | CAD17565 | NP_636066 | AAM38372 | AAL45999 | AAF83409 | AAG05298 | NP_405322 | AAG54454 | AAL20133 |
| PSPTO2463 | C | TonB-dependent siderophore receptor, putative | 2 | 60.5 | CAD17251 | NP_639060 | AAM38599 | AAL45999 | AAF83409 | AAG08222 | NP_404572 | AAG58168 | AAL19155 |
| PSPTO2484 | C | TonB-dependent siderophore receptor, putative | 2 | 60 | CAD16107 | NP_638390 | AAM38010 | AAL44724 | AAF84936 | AAG05978 | NP_407355 | AAG54918 | AAL19536 |
| PSPTO2605 | C | TonB-dependent siderophore receptor, putative | 2 | 60.6 | CAD15509 | NP_635493 | AAM38045 | AAL44499 | AAF83409 | AAG07543 | NP_405467 | AAG55323 | AAL20505 |
| PSPTO2607 | C | TonB-dependent siderophore receptor, putative | 2 | 63.3 | CAD17962 | NP_638426 | AAM38052 | AAL44724 | AAF84933 | AAG05477 | NP_404908 | AAG54918 | AAL21663 |
| PSPTO2846 | C | TonB-dependent siderophore receptor, putative | 2 | 56.5 | CAD18213 | NP_639060 | AAM38599 | AAL45999 | AAF83409 | AAG08222 | NP_405123 | AAG58168 | AAL19155 |
| PSPTO3574 | C | TonB-dependent siderophore receptor, putative | 2 | 59.8 | CAD16436 | NP_639060 | AAM38599 | AAL45999 | AAF83409 | AAG03541 | NP_404572 | AAG58168 | AAL19318 |
| PSPTO3692 | C | TonB-dependent siderophore receptor, putative | 2 | 59.9 | CAD18213 | NP_638864 | AAM38341 | AAL44823 | AAF83409 | AAG07609 | NP_405123 | AAG55848 | AAL20133 |
| PSPTO0518 | C | tryptophan 2-monooxygenase IaaM, putative | 5 | 60.9 | - | NP_638624 | AAM38269 | AAL46247 | - | - | - | - | - |
| PSPTO4589 | C | TTSS chaperone candidate protein | 4 | 59.2 | - | - | - | - | - | - | - | - | - |
| PSPTO4599 | C | TTSS chaperone candidate protein | 4 | 58 | - | - | - | - | - | - | - | - | - |
| PSPTOA0017 | pA | TTSS chaperone candidate protein | 4 | 54.9 | - | - | - | - | - | - | - | - | - |
| PSPTO1376 | C | TTSS chaperone candidate protein AvrF | 4 | 56.7 | - | - | - | - | - | - | - | - | - |
| PSPTO5353 | C | TTSS chaperone protein ShcA(Pto) | 4 | 54.9 | - | - | - | - | - | - | NP_395207 | - | - |
| PSPTO0503 | C | TTSS chaperone protein ShcF | 4 | 43.3 | - | - | - | - | - | - | - | - | - |
| PSPTO1374 | C | TTSS chaperone protein ShcM | 4 | 57.3 | - | - | - | - | - | - | - | - | - |
| PSPTO1369 | C | TTSS chaperone protein ShcN | 4 | 55.1 | - | - | - | - | - | - | - | - | - |
| PSPTO4721 | C | TTSS chaperone protein ShcV | 4 | 50 | - | - | - | - | - | - | - | - | - |

| | | | | | | | | | | | | | |
|------------------------|----|--|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO1384 | C | TTSS component protein HrcJ | 4 | 59.3 | CAD18018 | NP_636607 | AAM35300 | AAL41541 | | AAG05112 | NP_395193 | AAG57972 | AAL20333 |
| PSPTO1400 | C | TTSS component protein HrcN | 4 | 65.5 | CAD18021 | NP_636610 | AAM35303 | AAL41574 | AAF83953 | AAG05086 | NP_395174 | AAG58832 | AAL20339 |
| PSPTO1397 ^c | C | TTSS component protein HrcQa | 4 | 64.1 | | | | | | | | | |
| PSPTO1396 ^c | C | TTSS component protein HrcQb | 4 | 60.8 | | | | | | | NP_405388 | | |
| PSPTO1395 | C | TTSS component protein HrcR | 4 | 58.2 | CAD18011 | NP_636600 | AAM35293 | AAL41563 | | AAG05082 | NP_395178 | AAG58847 | AAL20343 |
| PSPTO1394 | C | TTSS component protein HrcS | 4 | 58.3 | CAD18010 | NP_636599 | AAM35292 | AAL41597 | | AAG05081 | NP_395179 | AAG58846 | AAL20344 |
| PSPTO1393 | C | TTSS component protein HrcT | 4 | 61 | CAD18023 | NP_636612 | AAM35305 | AAL41599 | | AAG05080 | NP_403924 | AAG57979 | AAL21768 |
| PSPTO1392 | C | TTSS component protein HrcU | 4 | 57.2 | CAD18015 | NP_636604 | AAM35297 | AAL41581 | | AAG05079 | NP_403925 | AAG58844 | AAL20346 |
| PSPTO1402 | C | TTSS component protein HrcV | 4 | 59.8 | CAD18014 | NP_637274 | AAM36798 | AAL41598 | | AAG05092 | NP_403917 | AAG58833 | AAL21776 |
| PSPTO1383 | C | TTSS component protein HrpB | 4 | 58.3 | | | | | | | | | |
| PSPTO1385 | C | TTSS component protein HrpD | 4 | 63.6 | | | | | | | | | |
| PSPTO1386 | C | TTSS component protein HrpE | 4 | 63.6 | | | | | | | | | |
| PSPTO1387 | C | TTSS component protein HrpF | 4 | 54.5 | | | | | | | | | |
| PSPTO1388 | C | TTSS component protein HrpG | 4 | 63.9 | | | | | | | | | |
| PSPTO1403 | C | TTSS component protein HrpJ | 4 | 59.4 | | | | | | | | | |
| PSPTO1399 | C | TTSS component protein HrpO | 4 | 58.1 | | | | | | | | | |
| PSPTO1398 | C | TTSS component protein HrpP | 4 | 62.3 | | | | | | | | | |
| PSPTO1401 | C | TTSS component protein HrpQ | 4 | 62.5 | | | | | | | | | |
| PSPTO1390 | C | TTSS component protein HrpT | 4 | 58.7 | | | | | | | | | |
| PSPTO1377 | C | TTSS effector avirulence protein AvrE(Pto) | 3 | 57.6 | CAD18432 | | | | | | | | |
| PSPTOA0012 | pA | TTSS effector avirulence protein AvrPphE(Pto) | 3 | 53.8 | CAD16866 | NP_636999 | AAM38068 | | | | | | |
| PSPTO1022 | C | TTSS effector avirulence protein AvrPpiB1(Pto) | 3 | 39.9 | | | | | | | | | |
| PSPTOA0005 | pA | TTSS effector avirulence protein AvrPpiB2(Pto) | 3 | 39.9 | | | | | | | | | |
| PSPTO4001 | C | TTSS effector avirulence protein AvrPto(DC3000) | 3 | 49.6 | | | | | | | | | |
| PSPTO3087 | C | TTSS effector avirulence protein AvrPtoB | 3 | 59.2 | | | | | | | | | |
| PSPTO0901 ^d | C | TTSS effector candidate HolPsyAG(Pto) | 3 | 53.1 | | | | | | | | | |
| PSPTO0905 | C | TTSS effector candidate HolPsyAH(Pto) (glycosyl hydrolase, family 5 (cellulolytic activity)) | 3 | 58.5 | | | | | | | | | |
| PSPTO0906 | C | TTSS effector candidate HolPsyAI(Pto) | 3 | 54 | | | | | | | | | |
| PSPTO4703 | C | TTSS effector candidate HolPtoAA | 3 | 50.6 | | | | | | | | | |

| | | | | | | | | | | | | | |
|---|---|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|---|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO4993 ^d , 4996 ^d | C | TTSS effector candidate HolPtoAC | 3 | 61.1 | - | - | - | - | - | - | - | - | - |
| PSPTO4732 | C | TTSS effector candidate HolPtoQ2 | 3 | 48.8 | CAD13773 | NP_636447 | AAM39163 | - | - | - | - | - | - |
| PSPTO0883 | C | TTSS effector candidate HolPtoR | 3 | 59.4 | CAD18432 | NP_636464 | - | - | - | - | - | - | - |
| PSPTO4593 | C | TTSS effector candidate HolPtoU2 | 3 | 55.4 | - | - | - | - | - | - | - | - | - |
| PSPTO4590 | C | TTSS effector candidate HolPtoU-related | 3 | 54.6 | - | - | - | - | - | - | - | - | - |
| PSPTO0061 | C | TTSS effector candidate HolPtoY | 3 | 58.5 | - | - | - | - | - | - | - | - | - |
| PSPTO4597 ^d , 4595 ^d | C | TTSS effector candidate HolPtoZ | 3 | 54.2 | - | - | - | - | - | - | - | - | - |
| PSPTO4588 | C | TTSS effector candidate HolPtoZ2 | 3 | 59.2 | - | - | - | - | - | - | - | - | - |
| PSPTO4724 ^{bd} , 4726 ^{bd} | C | TTSS effector candidate HopPtoD1-related protein (interruption) | 3 | 54.3 | - | - | - | - | - | - | - | - | - |
| PSPTO4592 | C | TTSS effector candidate HopPtoO-related | 3 | 54.2 | - | - | - | - | - | - | - | - | - |
| PSPTO0875 | C | TTSS effector candidate Ipx47 | 3 | 48.3 | - | - | - | - | - | - | - | - | - |
| PSPTO5061 | C | TTSS effector candidate Ipx53 | 3 | 64.3 | - | - | - | - | - | - | NP_404834 | - | AAL21797 |
| PSPTO0474 | C | TTSS effector candidate ORF01152 | 3 | 59.5 | - | - | - | - | - | - | - | - | - |
| PSPTO0869 | C | TTSS effector candidate ORF20 | 3 | 61.7 | - | - | AAM37122 | - | - | - | - | - | - |
| PSPTO4188 | C | TTSS effector candidate ORF36 | 3 | 49.1 | - | - | - | - | - | - | - | - | - |
| PSPTO4776 | C | TTSS effector HopPmaI(Pto) | 3 | 63.2 | CAD18035 | NP_635901 | AAM36964 | AAL42873 | - | AAG08638 | NP_406242 | AAG54315 | AAL19895 |
| PSPTO1179 | C | TTSS effector HopPmaJ(Pto) | 3 | 58.7 | - | - | - | - | - | - | - | - | - |
| PSPTO5354 | C | TTSS effector HopPsyA(Pto) | 3 | 53.3 | - | - | - | - | - | - | - | - | - |
| PSPTO1372 | C | TTSS effector HopPtoA1 | 3 | 61.1 | CAD18428 | - | - | - | - | - | - | - | - |
| PSPTO4718 | C | TTSS effector HopPtoA2 | 3 | 57.1 | CAD18428 | - | - | - | - | - | - | - | - |
| PSPTO1406 | C | TTSS effector HopPtoB1 | 3 | 55.5 | - | - | - | - | - | - | - | - | - |
| PSPTO0589 | C | TTSS effector HopPtoC | 3 | 47 | CAD17000 | - | - | - | - | - | - | - | - |
| PSPTO0876 | C | TTSS effector HopPtoD1 | 3 | 55.2 | CAD17455 | - | - | - | - | - | - | - | - |
| PSPTO4722 | C | TTSS effector HopPtoD2 | 3 | 51.7 | - | NP_637463 | - | - | - | - | - | - | - |
| PSPTO4331 | C | TTSS effector HopPtoE | 3 | 50.7 | - | - | - | - | - | - | - | - | - |
| PSPTO0502 | C | TTSS effector HopPtoF | 3 | 48 | CAD17973 | - | - | - | - | - | - | - | - |
| PSPTO4727 | C | TTSS effector HopPtoG | 3 | 43.7 | CAD17474 | NP_638946 | - | - | - | - | - | - | - |
| PSPTO0588 | C | TTSS effector HopPtoH | 3 | 47.4 | CAD17723 | NP_638604 | - | - | - | - | - | - | - |
| PSPTO4691 | C | TTSS effector HopPtoI | 3 | 48.9 | - | - | - | - | - | - | - | - | - |
| PSPTO1568 | C | TTSS effector HopPtoJ | 3 | 49.4 | - | - | - | - | - | - | - | - | - |
| PSPTO0044 | C | TTSS effector HopPtoK | 3 | 54.6 | - | - | AAM38509 | - | - | - | - | - | - |
| PSPTO2872 | C | TTSS effector HopPtoL | 3 | 61 | - | - | - | - | - | - | NP_405828 | - | AAL20513 |

| | | | | | | | | | | | | | |
|------------|----|--|---|------|--------------------------|---------------------------|--------------------------|--------------------------|---------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO1375 | C | TTSS effector HopPtoM | 3 | 58.5 | - | - | - | - | - | - | - | - | - |
| PSPTO1370 | C | TTSS effector HopPtoN | 3 | 53.6 | - | - | - | - | - | - | - | - | - |
| PSPTO0877 | C | TTSS effector HopPtoQ | 3 | 51.1 | CAD13773 | NP_636447 | AAM39163 | - | - | - | - | - | - |
| PSPTOA0018 | pA | TTSS effector HopPtoS1 | 3 | 46.5 | - | - | - | - | - | - | - | - | - |
| PSPTO0501 | C | TTSS effector HopPtoS2 | 3 | 46.5 | - | - | - | - | - | - | - | - | - |
| PSPTO4594 | C | TTSS effector HopPtoS3 | 3 | 49.8 | - | - | - | - | - | - | - | - | - |
| PSPTOA0019 | pA | TTSS effector HopPtoT1 | 3 | 51.9 | - | - | - | - | - | - | - | - | - |
| PSPTO4720 | C | TTSS effector HopPtoV | 3 | 51.5 | - | - | - | - | - | - | - | - | - |
| PSPTO0852 | C | TTSS helper protein HopPmaG(Pto) | 3 | 55.8 | CAD18391 | NP_639491 | AAM38069 | AAL44589 | AAF84983 | AAG07379 | NP_405633 | AAG57806 | AAL21711 |
| PSPTO4101 | C | TTSS helper protein HopPmaH(Pto) (harpin-like protein) | 3 | 56.8 | - | NP_636036 | AAM38405 | - | - | AAG08445 | - | - | - |
| PSPTO2678 | C | TTSS helper protein HopPtoP (harpin-like protein) | 3 | 59.7 | CAD16603 | NP_636615 | AAM35308 | - | - | - | - | AAG58843 | - |
| PSPTO1381 | C | TTSS helper protein HrpA(Pto) (pilin subunit) | 3 | 54.9 | - | - | - | - | - | - | - | - | - |
| PSPTO1405 | C | TTSS helper protein HrpK(Pto) | 3 | 58.4 | - | - | - | - | - | - | - | - | - |
| PSPTO1373 | C | TTSS helper protein HrpW(Pto) (harpin-like protein) | 3 | 58 | CAD16482 | NP_636593 | AAM37767 | - | AAF83628 | AAG04113 | - | - | - |
| PSPTO1382 | C | TTSS helper protein HrpZ(Pto) (harpin) | 3 | 60.2 | CAD18028 | - | AAM35307 | - | - | - | - | - | - |
| PSPTO1391 | C | TTSS negative regulator of hrp expression HrpV | 4 | 56.6 | - | - | - | - | - | - | - | - | - |
| PSPTO1389 | C | TTSS outer-membrane protein HrcC | 4 | 57.9 | CAD18025 | NP_636613 | AAM35306 | - | AAF83183 | AAG05105 | NP_395186 | AAG58839 | AAL20318 |
| PSPTO1404 | C | TTSS RNA polymerase sigma factor HrpL | 4 | 55.4 | CAD14757 | NP_636641 | AAM36190 | AAL43022 | AAF85038 | AAG06284 | NP_406228 | AAG57689 | AAL21534 |
| PSPTO1379 | C | TTSS transcriptional regulator HrpR | 4 | 59.4 | CAD13860 | NP_636405 | AAM35118 | AAL44112 | AAF84654 | AAG04724 | NP_405881 | AAG57601 | AAL21739 |
| PSPTO1380 | C | TTSS transcriptional regulator HrpS | 4 | 59.1 | CAD17160 | NP_636405 | AAM36008 | AAL44112 | AAF84654 | AAG08551 | NP_405881 | AAG57601 | AAL21739 |
| PSPTO4851 | C | type II/III secretion system protein homolog of GspD/HrcC | 4 | 62.5 | CAD18238 | NP_638574 | AAM38224 | AAL41244 | AAF83183 | AAG07692 | NP_403806 | AAG58491 | AAL22350 |
| PSPTO4853 | C | type II/IV secretion system protein, putative (GspE/VirB-11) | 2 | 62 | CAD18236 | NP_637830 | AAM37467 | AAL41241 | NP_061671 | AAG07690 | NP_404326 | AAG54411 | AAL19107 |
| PSPTO0811 | C | type IV pillin PilA, putative | 1 | 57.3 | CAD18443 | NP_637845 | AAM37516 | - | AAF82841 | AAG07938 | NP_404438 | - | - |
| PSPTO0319 | C | type IV pilus biogenesis protein | 1 | 61.2 | CAD16824 | NP_639427 | AAM39047 | AAL46277 | AAF85341 | AAG08595 | NP_404439 | AAG54411 | AAL19107 |
| PSPTO0810 | C | type IV pilus biogenesis protein | 1 | 57.4 | CAD14252 | NP_637837 | AAM37474 | - | AAF83283 | AAG07938 | - | - | - |
| PSPTO0816 | C | type IV pilus biogenesis protein | 1 | 56.6 | CAD16387 | NP_637838 | AAM37511 | - | AAF82846 | AAG07944 | NP_404438 | AAG54412 | AAL19108 |
| PSPTO0927 | C | type IV pilus biogenesis protein | 1 | 47.4 | CAD14088 | NP_638446 | AAM38085 | - | AAF85339 | AAG07913 | NP_406887 | AAG54412 | AAL19108 |

| | | | | | | | | | | | | | |
|------------|----|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|---------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTOA0045 | pA | type IV pilus biogenesis protein | 1 | 58.7 | CAD16388 | NP_635985 | AAM38450 | AAL46277 | AAF84441 | AAG03785 | NP_404557 | AAG58081 | AAL21974 |
| PSPTOB0052 | pB | type IV pilus biogenesis protein | 1 | 58.8 | CAD16388 | NP_635985 | AAM38450 | AAL46277 | AAF84441 | AAG03785 | NP_404557 | AAG58081 | AAL21974 |
| PSPTO0926 | C | type IV pilus biogenesis protein PilB | 1 | 54.4 | CAD16532 | NP_638444 | AAM38083 | AAL46277 | AAF85341 | AAG07914 | NP_406888 | AAG54411 | AAL19107 |
| PSPTO0925 | C | type IV pilus biogenesis protein PilC | 1 | 47.9 | CAD16533 | NP_638447 | AAM38086 | - | AAF85335 | AAG07915 | NP_406889 | AAG54410 | AAL19106 |
| PSPTO1432 | C | type IV pilus biogenesis protein PilF | 1 | 56.2 | CAD14915 | NP_637348 | AAM36879 | - | AAF83270 | AAG07192 | NP_406386 | - | - |
| PSPTO5031 | C | type IV pilus biogenesis protein PilJ | 1 | 61 | CAD14201 | NP_638270 | AAM37944 | AAL42908 | AAF84755 | AAG03800 | NP_405252 | AAG59538 | AAL22437 |
| PSPTO5132 | C | type IV pilus biogenesis protein PilM | 1 | 58.9 | CAD16684 | NP_638578 | AAM38228 | - | AAF83179 | AAG08429 | - | - | - |
| PSPTOB0007 | pB | type IV pilus biogenesis protein PilM, putative | 1 | 54.1 | - | - | - | - | - | - | - | - | - |
| PSPTO5131 | C | type IV pilus biogenesis protein PilN | 1 | 59.8 | CAD16683 | NP_638577 | AAM38227 | - | AAF83180 | AAG08428 | - | - | - |
| PSPTO5130 | C | type IV pilus biogenesis protein PilO | 1 | 56.5 | CAD16682 | NP_638576 | AAM38226 | - | AAF83181 | AAG08427 | - | - | - |
| PSPTO5129 | C | type IV pilus biogenesis protein PilP | 1 | 60.2 | CAD16681 | NP_638575 | AAM38225 | - | AAF83182 | AAG08426 | - | - | - |
| PSPTO5128 | C | type IV pilus biogenesis protein PilQ | 1 | 59 | CAD16680 | NP_638574 | AAM38224 | AAL41244 | AAF83183 | AAG08425 | NP_403806 | AAG58491 | AAL22350 |
| PSPTOA0042 | pA | type IV pilus biogenesis protein PilT | 1 | 59.3 | CAD16603 | NP_636615 | AAM35308 | - | - | - | - | AAG57967 | AAL21757 |
| PSPTOB0049 | pB | type IV pilus biogenesis protein PilT, putative | 1 | 59.3 | CAD16603 | NP_636615 | AAM35308 | - | - | - | - | AAG57967 | AAL21757 |
| PSPTO3825 | C | type IV pilus biogenesis protein PilZ | 1 | 59.6 | CAD15488 | NP_636400 | AAM36006 | - | AAF83487 | AAG06348 | - | - | - |
| PSPTO0924 | C | type IV pilus prepilin peptidase PilD | 1 | 59.3 | CAD16534 | NP_638448 | AAM38087 | - | AAF85334 | AAG07916 | NP_404431 | AAG58443 | AAL22305 |
| PSPTO5032 | C | type IV pilus protein PilI | 1 | 61.6 | - | NP_638271 | AAM37945 | AAL43066 | AAF84756 | AAG03799 | - | - | - |
| PSPTO0823 | C | type IV pilus regulatory protein pilR | 1 | 60.3 | CAD16514 | NP_638443 | AAM38082 | AAL42452 | AAF85342 | AAG07935 | NP_406415 | AAG59201 | AAL23002 |
| PSPTO0824 | C | type IV pilus regulatory sensor protein PilS | 1 | 60.1 | CAD16515 | NP_638442 | AAM38081 | AAL45099 | AAF85343 | AAG07934 | NP_403906 | AAG59200 | AAL23001 |
| PSPTO5034 | C | type IV pilus response regulator PilG | 1 | 52.9 | CAD14198 | NP_638273 | AAM37947 | AAL41534 | AAF84757 | AAG03797 | NP_403738 | AAG56982 | AAL20028 |
| PSPTO5033 | C | type IV pilus response regulator PilH | 1 | 58.1 | CAD14199 | NP_636424 | AAM36026 | AAL42303 | AAF83260 | AAG03798 | NP_406679 | AAG54745 | AAL19351 |
| PSPTO0531 | C | type IV secretion system protein, putative | 1 | 52.4 | - | - | - | AAL45856 | NP_061664 | - | - | - | - |
| PSPTO0533 | C | type IV secretion system protein, truncation | 1 | 51.6 | - | - | - | AAL45857 | NP_061667 | - | - | - | - |

| | | | | | | | | | | | | | |
|-----------|---|---|---|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| PSPTO2602 | C | yersiniabactin non-ribosomal peptide synthetase | 2 | 63.4 | CAD15508 | NP_639207 | AAM38759 | AAL44494 | AAF83100 | AAG07614 | NP_405472 | AAG54921 | AAL19539 |
| PSPTO2600 | C | yersiniabactin polyketide/non-ribosomal peptide hybrid synthetase | 2 | 64.3 | CAD17792 | NP_636396 | AAM36002 | AAL44493 | AAF83483 | AAG07613 | NP_405471 | AAG55841 | AAL20126 |
| PSPTO2597 | C | yersiniabactin synthetase, salicylate ligase component | 2 | 65.8 | CAD17188 | NP_636198 | AAM35769 | AAL45616 | AAF83100 | AAG07616 | NP_405468 | AAG54929 | AAL19547 |
| PSPTO2599 | C | yersiniabactin synthetase, thiazolinyln reductase component | 2 | 65.7 | CAD15507 | – | – | – | – | AAG07612 | NP_405470 | – | – |
| PSPTO2598 | C | yersiniabactin synthetase, thioesterase component | 2 | 64.1 | CAD15506 | – | – | AAL44497 | – | AAG07617 | NP_405469 | – | – |

The inferred proteomes of nine pathogenic bacteria were searched with the 298 DC3000 proteins implicated in virulence by using a BLASTP cutoff criterion of

$E < 10^{-5}$, which will identify putative homologs as well as paralogous gene family members (note, for example, that Hrc proteins and HrpR show similarity to flagellar proteins and transcriptional regulators in *A. tumefaciens*, a pathogen that lacks a TTSS). Rs = *Ralstonia solanacearum*, Xac = *Xanthomonas axonopodis* pv *citri*, Xcc = *Xanthomonas campestris* pv *campestris*, Xf = *Xylella fastidiosa*, At = *Agrobacterium tumefaciens* (U. Wash seq.), Pa = *Pseudomonas aeruginosa* PAO1, St = *Salmonella typhimurium* LT2, Yp = *Yersinia pestis* CO92, and Ec = *Escherichia coli* O157:H7 EDL933. Categories are as follows: 1, Adhesins and other cell surface associated factors; 2, Miscellaneous virulence factors; 3, TTSS effectors, helpers, and candidates; 4, TTSS secretion and regulatory proteins; and 5, low molecular weight diffusible factors.

^a C, chromosome; pA, plasmid pDC3000A; pB, plasmid pDC3000B.

^b This gene does not have a protein record in GenBank.

^c HrcQa and HrcQb are present as one protein in other TTSS pathogens.

^d Indicates a gene disrupted by IS elements, with PSPTO numbers given for both the N-terminal and C-terminal regions. Only the N-terminal part is proposed as a candidate virulence factor (see Table 3).

Table 3. The chromosomal and plasmid genes disrupted by IS elements or phage genes in *P. syringae* pv. *tomato* DC3000

| | N-terminus | C-terminus | Gene assignment |
|----|------------|------------|--|
| 1 | PSPTO0198 | PSPTO0195 | ISPsy5, Orf1 |
| 2 | PSPTO0843 | PSPTO0845 | ISPsy5, transposase |
| 3 | PSPTO0846 | PSPTO0841 | membrane protein, putative |
| 4 | PSPTO1018 | PSPTO1021 | hypothetical protein |
| 5 | PSPTO1225 | PSPTO1228 | insecticidal toxin protein |
| 6 | PSPTO1314 | PSPTO1316 | fimbrial biogenesis usher protein |
| 7 | PSPTO0901 | - | TTSS effector candidate HolPsyAG(Pto) |
| 8 | PSPTO2329 | PSPTO2327 | response regulator |
| 9 | PSPTO2462 | PSPTO2459 | conserved hypothetical protein |
| 10 | PSPTO2540 | PSPTO2542 | conserved hypothetical protein |
| 11 | PSPTO3015 | PSPTO3012 | conserved hypothetical protein |
| 12 | PSPTO3431 | PSPTO3434 | ISPsy6, transposase |
| 13 | PSPTO3611 | PSPTO3614 | IS52, transposase |
| 14 | PSPTO4268 | PSPTO4271 | sulfate permease family protein |
| 15 | PSPTO4565 | PSPTO4568 | peptide ABC transporter, ATP-binding protein |
| 16 | PSPTO4597 | PSPTO4595 | TTSS effector candidate HolPtoZ |
| 17 | PSPTO4724 | PSPTO4726 | TTSS effector candidate HopPtoD1-related protein |
| 18 | PSPTO4728 | PSPTO4731 | ISPsy10, transposase |
| 19 | PSPTO4993 | PSPTO4996 | TTSS effector candidate HolPtoAC |
| 20 | PSPTO5366 | PSPTO5369 | ISPsy4, transposase |
| 21 | PSPTO5572 | PSPTO5570 | membrane protein |
| 22 | PSPTO5574 | PSPTO5577 | response regulator |
| 23 | PSPTOB0038 | PSPTOB0041 | transcriptional regulator, GntR family |

24 PSPTOA0003 PSPTOA0006 ultraviolet light resistance protein B

Table 4. IS elements present in *P. syringae* pv. *tomato* DC3000

| Element | Family | Copies ^a | Length / DR ^b | | Structure | Left and right ends of newly identified elements (5'-3') |
|---------|--------------|---------------------|--------------------------|------|-----------|---|
| IS52 | IS5 | 3(2) | ND ^c | ND | Orf A | previously identified: M14366 |
| ISPs1 | IS5 | 1(2) | ND | ND | Orf AB | previously identified: M11035 |
| ISPssy | IS5 | 36(8) | ND | ND | Orf A | previously identified: AB023075 |
| ISPsy3 | IS91 | 2(4) | ND | ND | Orf A | previously identified: AB063176 |
| ISPsy4 | IS21 | 23(1) | 1962 | 6 | Orf AB | TGTCACCGCCACTGTAAAAATGACCCCCTAACGCCAAC TGTC AACGCCAACTAAAAAGTGACCCCCTTCCGTGCTA |
| ISPsy5 | IS66 | 35(13) | 2059 | 8 | Orf AB | GTATCCGATCCACGAACCCACATTTCAAGCCACTGGC GTAAGCGATCCACCAACCACACCTACCATCAGATGCGG |
| ISPsy6 | unclassified | 14(1) | 1603 | 4(5) | Orf A | CAGACTGTGTGAAAACCTAGCAATCTGCGCAGCGCTCA CAGACTGTGTGAAAACACACTGATGAAGGCCCAAGCAA |
| ISPsy7 | IS110 | 10 | 1356 | 0 | Orf A | ATAATGAGATGGTCAGCCCGATCCGAGAAACCCGGAGT TAGGCAAATGTATGGTCAGCCCACCTCCTGCAATCGCA |
| ISPsy8 | IS3 | 5 | 1432 | 3 | Orf AB | TGGACTGCCCCCAAGAAGTTGGACACCAATCCGACCTA TGGACTGCCCCCGGAAGTTGGACAGTTTTAGCTTGCC |
| ISPsy9 | IS3 | 1 | 1452 | 3 | Orf AB | TGGTGTGACCCCCGAAGTTGGATGCAACCTTTGGAGG TGGTGTGACCCCCGAAGTTGGACAATTATCCACCTAC |
| ISPsy10 | IS5 | (3) | ND | ND | Orf A | ND ND |
| ISPsy11 | IS3 | 3 | 1313 | 3 | Orf AB | TGTCCCGTCCTGAATAAGGTTTACACCTTCTGACCTTT |

| | | | | | |
|--------------|-----|----|----|--------|--|
| ISPsy12 IS3 | 1 | ND | ND | Orf AB | TGTCTAGTCCTGAAATAGGTTTACACCTGTTTCACGCT ND ND |
| ISPsy13 IS3 | 1 | ND | ND | Orf AB | ND ND |
| ISPsy14 IS21 | 1 | ND | ND | Orf AB | ND ND |
| ISPsy15 IS5 | (2) | ND | ND | Orf A | ND ND |

^a The number of full-length copies and the number of incomplete copies in parentheses.

^b Size in base pairs of the element (length) and the direct repeat (DR) generated by insertion into the target site.

^c ND = not determined.

Table 4. IS elements present in *P. syringae* pv. *tomato* DC3000

| Element | Family | Copies ^a | Length / DR ^b | | Structure | Left and right ends of newly identified elements (5'-3') |
|---------|--------------|---------------------|--------------------------|------|-----------|---|
| IS52 | IS5 | 3(2) | ND ^c | ND | Orf A | previously identified: M14366 |
| ISPs1 | IS5 | 1(2) | ND | ND | Orf AB | previously identified: M11035 |
| ISPssy | IS5 | 36(8) | ND | ND | Orf A | previously identified: AB023075 |
| ISPsy3 | IS91 | 2(4) | ND | ND | Orf A | previously identified: AB063176 |
| ISPsy4 | IS21 | 23(1) | 1962 | 6 | Orf AB | TGTCACCGCCACTGTAAAAATGACCCCCTAACGCCAAC TGTC AACGCCAACTAAAAAGTGACCCCCTTCCGTGCTA |
| ISPsy5 | IS66 | 35(13) | 2059 | 8 | Orf AB | GTATCCGATCCACGAACCCACATTTCAAGCCACTGGC GTAAGCGATCCACCAACCACACCTACCATCAGATGCGG |
| ISPsy6 | unclassified | 14(1) | 1603 | 4(5) | Orf A | CAGACTGTGTGAAAACCTAGCAATCTGCGCAGCGCTCA CAGACTGTGTGAAAACACACTGATGAAGGCCCAAGCAA |
| ISPsy7 | IS110 | 10 | 1356 | 0 | Orf A | ATAATGAGATGGTCAGCCCGATCCGAGAAACCCGGAGT TAGGCAAATGTATGGTCAGCCCACCTCCTGCAATCGCA |
| ISPsy8 | IS3 | 5 | 1432 | 3 | Orf AB | TGGACTGCCCCCAAGAAGTTGGACACCAATCCGACCTA TGGACTGCCCCCGGAAGTTGGACAGTTTTAGCTTGCC |
| ISPsy9 | IS3 | 1 | 1452 | 3 | Orf AB | TGGTGTGACCCCCGAAGTTGGATGCAACCTTTGGAGG TGGTGTGACCCCCGAAGTTGGACAATTATCCACCTAC |
| ISPsy10 | IS5 | (3) | ND | ND | Orf A | ND ND |
| ISPsy11 | IS3 | 3 | 1313 | 3 | Orf AB | TGTCCCGTCCTGAATAAGGTTTACACCTTCTGACCTTT |

| | | | | | |
|--------------|-----|----|----|--------|--|
| ISPsy12 IS3 | 1 | ND | ND | Orf AB | TGTCTAGTCCTGAAATAGGTTTACACCTGTTTCACGCT ND ND |
| ISPsy13 IS3 | 1 | ND | ND | Orf AB | ND ND |
| ISPsy14 IS21 | 1 | ND | ND | Orf AB | ND ND |
| ISPsy15 IS5 | (2) | ND | ND | Orf A | ND ND |

^a The number of full-length copies and the number of incomplete copies in parentheses.

^b Size in base pairs of the element (length) and the direct repeat (DR) generated by insertion into the target site.

^c ND = not determined.

Table 5. Phage and bacteriocin regions of *P. syringae* pv. *tomato* DC3000

| Feature | 5' end | 3' end | Size (bp) | Type of Feature |
|-----------|-----------|-----------|-----------|--------------------------------------|
| PYOCIN001 | 625,118 | 647,483 | 22,365 | Putative F-type pyocin |
| PHAGE02 | 2,252,628 | 2,264,996 | 12,368 | Defective prophage region |
| PHAGE03 | 3,824,683 | 3,865,352 | 40,669 | Putative P2-like integrated prophage |
| PHAGE04 | 4,445,530 | 4,453,456 | 7,926 | Defective prophage region |
| PHAGE05 | 4,515,380 | 4,530,373 | 14,993 | Defective prophage region |
| PHAGE06 | 4,543,843 | 4,563,492 | 19,649 | Putative lysogenic prophage region |

Table 6. Genes with unknown function unique to DC3000 identified from the comparative analysis with the *P. aeruginosa* PAO1 and *P. putida* KT2440 genomes and the identification of putative homologs (BLASTP $E < 10^{-5}$) in pathogenic bacteria

| Locus | Location | Clustering | | Predicted product ^c | GC% | Length (aa) | Plant pathogens | | | | | Animal pathogens | | | |
|-----------|----------|--------------------|-------------------|--|------|----------------|-----------------|-----|-----|----|----|------------------|----|----|--|
| | | Genes ^a | TTSS ^b | | | | Rs | Xcc | Xac | At | Xf | Yp | Ec | St | |
| PSPTO0007 | C | + | + | hypothetical protein | 55.2 | 294 | | | | | | | | | |
| PSPTO0011 | C | + | + | conserved hypothetical protein | 55.9 | 236 | Rs | Xcc | Xac | At | Xf | | | | |
| PSPTO0012 | C | + | + | hypothetical protein | 54.9 | 167 | | | | | | | | | |
| PSPTO0013 | C | + | + | hypothetical protein | 58 | 189 | | | | | | | | | |
| PSPTO0014 | C | + | + | hypothetical protein | 66.3 | 96 | | | | | | | | | |
| PSPTO0015 | C | + | + | hypothetical protein | 55.7 | 203 | | | | | | | | | |
| PSPTO0016 | C | + | + | hypothetical protein | 53.5 | 155 | | | | | | | | | |
| PSPTO0020 | C | + | + | hypothetical protein | 54.9 | 116 | | | | | | | | | |
| PSPTO0021 | C | + | + | hypothetical protein | 51.2 | 746 | | | | | | | | | |
| PSPTO0022 | C | + | + | DNA-binding protein | 56.2 | 281 | | | | | | | | | |
| PSPTO0023 | C | + | + | hypothetical protein | 53.9 | 199 | | | | | | | | | |
| PSPTO0024 | C | + | + | hypothetical protein | 60 | 45 | | | | | | | | | |
| PSPTO0025 | C | + | + | hydrolase, haloacid dehalogenase-like family | 56.6 | 209 | | | | | | | | | |
| PSPTO0026 | C | + | + | hypothetical protein | 53 | 348 | | | | | | | | | |
| PSPTO0027 | C | + | + | hypothetical protein | 51.7 | 240 | | | | | | | | | |
| PSPTO0032 | C | + | + | conserved hypothetical protein | 48.9 | 322 | | | | At | | | | | |
| PSPTO0034 | C | + | + | recombinase, putative | 50.3 | 518 | Rs | | | At | | | | | |
| PSPTO0037 | C | + | + | helicase domain protein | 53.4 | 1636 | | | | | | Yp | | | |
| PSPTO0038 | C | + | + | conserved domain protein | 53.4 | 696 | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|---|------|-----|----|--|--|--|----|--|--|--|--|--|--|
| PSPTO0041 | C | + | + | hypothetical protein | 54.2 | 128 | | | | | | | | | | | |
| PSPTO0043 | C | + | + | cytidine/deoxycytidylate deaminase family protein | 51.4 | 520 | | | | | | | | | | | |
| PSPTO0045 | C | + | + | hypothetical protein | 53.2 | 52 | | | | | | | | | | | |
| PSPTO0048 | C | + | + | hypothetical protein | 50 | 388 | | | | | | | | | | | |
| PSPTO0049 | C | + | + | conserved hypothetical protein | 49.8 | 247 | | | | | | | | | | | |
| PSPTO0050 | C | + | + | conserved hypothetical protein | 47.8 | 443 | | | | | | | | | | | |
| PSPTO0051 | C | + | + | conserved hypothetical protein | 53.7 | 147 | Rs | | | | | | | | | | |
| PSPTO0052 | C | + | + | hypothetical protein | 53.1 | 589 | | | | | | | | | | | |
| PSPTO0053 | C | + | + | hypothetical protein | 55.6 | 481 | | | | | | | | | | | |
| PSPTO0054 | C | + | + | hypothetical protein | 57 | 203 | | | | | | | | | | | |
| PSPTO0059 | C | + | + | hypothetical protein | 54.2 | 206 | | | | | | | | | | | |
| PSPTO0088 | C | | | hypothetical protein | 58.3 | 44 | | | | | | | | | | | |
| PSPTO0093 | C | | | hypothetical protein | 51.8 | 83 | | | | | | | | | | | |
| PSPTO0104 | C | | | hypothetical protein | 53.9 | 34 | | | | | | | | | | | |
| PSPTO0122 | C | | | hypothetical protein | 59.9 | 54 | | | | | | | | | | | |
| PSPTO0133 | C | | | hypothetical protein | 54 | 50 | | | | | | | | | | | |
| PSPTO0142 | C | | | hypothetical protein | 49.1 | 76 | | | | | | | | | | | |
| PSPTO0149 | C | | | conserved hypothetical protein | 48.9 | 225 | | | | | | | | | | | |
| PSPTO0160 | C | | | hypothetical protein | 60.3 | 125 | | | | | | | | | | | |
| PSPTO0167 | C | | | hypothetical protein | 53.8 | 140 | | | | | | | | | | | |
| PSPTO0172 | C | | | hypothetical protein | 54 | 97 | | | | | | | | | | | |
| PSPTO0192 | C | | | recombinase, putative | 50.1 | 518 | Rs | | | | At | | | | | | |
| PSPTO0205 | C | + | | hypothetical protein | 48.4 | 331 | | | | | | | | | | | |
| PSPTO0206 | C | + | | conserved hypothetical protein | 55.3 | 158 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|-----------------------------------|------|-----|----|-----|-----|--|----|--|--|--|----|--|--|--|
| PSPTO0208 | C | + | | hypothetical protein | 58 | 207 | | | | | | | | | | | | |
| PSPTO0216 | C | + | | hypothetical protein | 50.7 | 46 | | | | | | | | | | | | |
| PSPTO0240 | C | + | | prevent-host-death family protein | 51.8 | 83 | | | Xac | | | | | | Yp | | | |
| PSPTO0242 | C | + | | hypothetical protein | 57.7 | 190 | | | | | | | | | | | | |
| PSPTO0243 | C | + | | conserved hypothetical protein | 49 | 273 | | | | | | | | | | | | |
| PSPTO0244 | C | + | | hypothetical protein | 62.3 | 237 | | | | | At | | | | | | | |
| PSPTO0245 | C | + | | acetyltransferase, GNAT family | 62.5 | 285 | | | | | At | | | | | | | |
| PSPTO0246 | C | + | | hypothetical protein | 54.7 | 137 | | | | | | | | | | | | |
| PSPTO0260 | C | | | conserved hypothetical protein | 62.8 | 218 | | | | | | | | | | | | |
| PSPTO0274 | C | + | | hypothetical protein | 61.9 | 84 | | | | | | | | | | | | |
| PSPTO0275 | C | + | | DNA-binding protein | 56.1 | 377 | Rs | Xcc | | | | | | | Xf | | | |
| PSPTO0277 | C | + | | hypothetical protein | 51.6 | 162 | | | | | | | | | | | | |
| PSPTO0279 | C | + | | conserved hypothetical protein | 54 | 118 | | | | | | | | | | | | |
| PSPTO0283 | C | + | | hypothetical protein | 54.4 | 147 | | | | | | | | | | | | |
| PSPTO0285 | C | + | | conserved domain protein | 53.3 | 360 | | | | | | | | | | | | |
| PSPTO0289 | C | + | | hypothetical protein | 56.2 | 51 | | | | | | | | | | | | |
| PSPTO0290 | C | + | | conserved hypothetical protein | 59.8 | 78 | | | | | | | | | | | | |
| PSPTO0293 | C | + | | hypothetical protein | 54.2 | 102 | | | | | | | | | | | | |
| PSPTO0294 | C | + | | hypothetical protein | 62.6 | 66 | | | | | | | | | | | | |
| PSPTO0295 | C | + | | hypothetical protein | 55.3 | 73 | | | | | | | | | | | | |
| PSPTO0296 | C | + | | hypothetical protein | 58.3 | 107 | | | | | | | | | | | | |
| PSPTO0297 | C | + | | hypothetical protein | 56.9 | 96 | | | | | | | | | | | | |
| PSPTO0302 | C | + | | hypothetical protein | 49.4 | 58 | | | | | | | | | | | | |
| PSPTO0331 | C | | | hypothetical protein | 50.5 | 74 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|------|----|-----|-----|----|--|--|--|----|--|--|--|--|--|
| PSPTO0332 | C | | | hypothetical protein | 54.4 | 95 | | | | | | | | | | | | | |
| PSPTO0342 | C | | | hypothetical protein | 52.2 | 46 | | | | | | | | | | | | | |
| PSPTO0354 | C | | | hypothetical protein | 52.6 | 52 | | | | | | | | | | | | | |
| PSPTO0368 | C | | | hypothetical protein | 56.5 | 111 | | | | | | | | | | | | | |
| PSPTO0374 | C | | | hypothetical protein | 61.2 | 195 | | | | | | | | | | | | | |
| PSPTO0391 | C | | | hypothetical protein | 53.8 | 83 | | | | | | | | | | | | | |
| PSPTO0392 | C | | | hypothetical protein | 50.8 | 63 | | | | | | | | | | | | | |
| PSPTO0442 | C | | | hypothetical protein | 58.6 | 33 | | | | | | | | | | | | | |
| PSPTO0447 | C | | | hypothetical protein | 68.3 | 60 | | | | | | | | | | | | | |
| PSPTO0467 | C | + | + | hypothetical protein | 51.6 | 51 | | | | | | | | | | | | | |
| PSPTO0473 | C | + | + | hypothetical protein | 59.8 | 1073 | | Xcc | Xac | | | | | | | | | | |
| PSPTO0475 | C | + | + | hypothetical protein | 55.2 | 143 | | | | | | | | | | | | | |
| PSPTO0476 | C | + | + | hypothetical protein | 53.2 | 148 | | | | | | | | | | | | | |
| PSPTO0477 | C | + | + | hypothetical protein | 49.2 | 147 | | | | | | | | | | | | | |
| PSPTO0478 | C | + | + | hypothetical protein | 50.6 | 308 | | | | | | | | | | | | | |
| PSPTO0482 | C | + | + | hypothetical protein | 56.3 | 116 | | | | | | | | | | | | | |
| PSPTO0521 | C | + | + | DNA-binding protein | 63.8 | 94 | | | | | | | | | | | | | |
| PSPTO0522 | C | + | + | conserved domain protein | 58.5 | 408 | Rs | Xcc | | At | | | | | | | | | |
| PSPTO0526 | C | + | + | hypothetical protein | 54.3 | 70 | | | | | | | | | | | | | |
| PSPTO0527 | C | + | + | hypothetical protein | 52.4 | 650 | | | | | | | | | | | | | |
| PSPTO0528 | C | + | + | hypothetical protein | 50.7 | 295 | | | | | | | | | | | | | |
| PSPTO0529 | C | + | + | hypothetical protein | 51 | 266 | | | | | | | | | | | | | |
| PSPTO0530 | C | + | + | conserved hypothetical protein | 53.9 | 173 | | | | | | | | Xf | | | | | |
| PSPTO0561 | C | | | hypothetical protein | 61.4 | 57 | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|----|--|--|----|----|----|--|--|
| PSPTO0582 | C | + | + | hypothetical protein | 51.2 | 213 | | | | | | | | | | | |
| PSPTO0583 | C | + | + | hypothetical protein | 47.2 | 229 | | | | | | | | | | | |
| PSPTO0585 | C | + | + | hypothetical protein | 50.5 | 155 | | | | | | | | | | | |
| PSPTO0590 | C | + | + | hypothetical protein | 45.4 | 47 | | | | | | | | | | | |
| PSPTO0608 | C | | | hypothetical protein | 30.3 | 33 | | | | | | | | | | | |
| PSPTO0657 | C | + | | hypothetical protein | 55.1 | 196 | | | | | | | | | | | |
| PSPTO0658 | C | + | | hypothetical protein | 49.7 | 181 | | | | | | | | | | | |
| PSPTO0665 | C | + | | ROK family protein | 60.1 | 376 | | Xcc | Xac | At | | | Yp | Ec | St | | |
| PSPTO0666 | C | + | | hypothetical protein | 53 | 173 | | | | | | | | | | | |
| PSPTO0684 | C | | | hypothetical protein | 56.3 | 183 | | | | | | | | | | | |
| PSPTO0702 | C | + | | conserved hypothetical protein | 56.8 | 339 | Rs | | Xac | | | | | Ec | St | | |
| PSPTO0707 | C | + | | hypothetical protein | 56 | 204 | | | | | | | | | | | |
| PSPTO0709 | C | + | | hypothetical protein | 54.9 | 240 | | | | | | | | | | | |
| PSPTO0710 | C | + | | conserved domain protein | 56.1 | 98 | | | | | | | | | | | |
| PSPTO0711 | C | + | | hypothetical protein | 54.5 | 591 | | | | | | | | | | | |
| PSPTO0712 | C | + | | hypothetical protein | 52.4 | 201 | | | | | | | | | | | |
| PSPTO0713 | C | + | | conserved hypothetical protein | 55.3 | 347 | | | | | | | | | | | |
| PSPTO0715 | C | + | | conserved hypothetical protein | 58.5 | 265 | Rs | | | | | | | | | | |
| PSPTO0717 | C | + | | DNA-binding protein | 54.2 | 80 | | | Xac | | | | | | | | |
| PSPTO0718 | C | + | | hypothetical protein | 55.8 | 132 | | | | | | | | | | | |
| PSPTO0719 | C | + | | hypothetical protein | 48.9 | 58 | | | | | | | | | | | |
| PSPTO0745 | C | | | hypothetical protein | 54.8 | 76 | | | | | | | | | | | |
| PSPTO0746 | C | | | hypothetical protein | 62.4 | 465 | | | | | | | | | | | |
| PSPTO0792 | C | | | hypothetical protein | 65.2 | 44 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----------|---|---|---|--|------|-----|----|-----|-----|----|----|----|----|--|--|
| PSPTO0803 | C | | | hypothetical protein | 53.1 | 32 | | | | | | | | | |
| PSPTO0819 | C | | | conserved hypothetical protein | 58.3 | 248 | Rs | Xcc | | At | Xf | | | | |
| PSPTO0831 | C | + | + | conserved hypothetical protein | 56 | 642 | | Xcc | Xac | | Xf | | | | |
| PSPTO0837 | C | + | + | conserved hypothetical protein | 44.2 | 200 | | | Xac | | | | | | |
| PSPTO0840 | C | + | + | hypothetical protein | 50.2 | 138 | | | | | | | | | |
| PSPTO0847 | C | + | + | hypothetical protein | 50 | 122 | | | | | | | | | |
| PSPTO0848 | C | + | + | conserved hypothetical protein | 57.8 | 457 | | Xcc | Xac | | | | | | |
| PSPTO0849 | C | + | + | conserved hypothetical protein | 59.5 | 312 | | Xcc | Xac | | | | | | |
| PSPTO0850 | C | + | + | conserved hypothetical protein | 58.5 | 138 | | | Xac | | | | | | |
| PSPTO0851 | C | + | + | conserved hypothetical protein | 51.6 | 162 | | | | | | Yp | Ec | | |
| PSPTO0854 | C | + | + | hypothetical protein | 51.1 | 73 | | | | | | | | | |
| PSPTO0856 | C | + | + | conserved hypothetical protein | 52 | 272 | | | | | | | | | |
| PSPTO0858 | C | + | + | hypothetical protein | 53.2 | 99 | | | | | | | | | |
| PSPTO0859 | C | + | + | conserved hypothetical protein | 56.1 | 889 | | | Xac | | | | | | |
| PSPTO0860 | C | + | + | conserved hypothetical protein | 58.1 | 151 | | | | | | | | | |
| PSPTO0861 | C | + | + | conserved hypothetical protein | 58.2 | 498 | | | Xac | | | | | | |
| PSPTO0862 | C | + | + | conserved hypothetical protein | 58.5 | 307 | | | Xac | | | | | | |
| PSPTO0863 | C | + | + | conserved hypothetical protein | 59.6 | 222 | | | | | | | | | |
| PSPTO0866 | C | + | + | hypothetical protein | 59.8 | 121 | | | Xac | | | | | | |
| PSPTO0867 | C | + | + | conserved hypothetical protein | 59 | 122 | | | Xac | | | | | | |
| PSPTO0868 | C | + | + | hypothetical protein | 61.2 | 49 | | | | | | | | | |
| PSPTO0870 | C | + | + | hypothetical protein | 49 | 66 | | | | | | | | | |
| PSPTO0874 | C | + | + | nikkomycin biosynthesis domain protein | 49.2 | 417 | | | | | | | | | |
| PSPTO0878 | C | + | + | conserved domain protein | 59.4 | 105 | | | | | | | | | |

| | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|----|--|----|----|----|
| PSPTO0880 | C | + | + | conserved hypothetical protein | 56.9 | 249 | | | Xac | | | | | |
| PSPTO0881 | C | + | + | conserved domain protein | 57.9 | 293 | | | Xac | | | | | |
| PSPTO0882 | C | + | + | hypothetical protein | 50.8 | 177 | | | | | | | | |
| PSPTO0891 | C | | + | hypothetical protein | 57 | 76 | | | | | | | | |
| PSPTO0895 | C | + | + | hypothetical protein | 50.4 | 168 | | | | | | | | |
| PSPTO0899 | C | + | + | conserved domain protein | 55.3 | 155 | Rs | | | | | | | |
| PSPTO0900 | C | + | + | hypothetical protein | 63.4 | 93 | | | | | | | | |
| PSPTO0904 | C | + | + | mutT/nudix family protein | 51.9 | 504 | | | | | | | | |
| PSPTO0907 | C | + | + | hypothetical protein | 53.1 | 403 | | | | | | | | |
| PSPTO0914 | C | + | + | STAS domain protein | 63.9 | 96 | | Xcc | Xac | | | | | |
| PSPTO0918 | C | + | + | conserved hypothetical protein | 60 | 35 | | | | | | | | |
| PSPTO0921 | C | + | + | hypothetical protein | 44.2 | 43 | | | | | | | | |
| PSPTO0930 | C | + | | conserved hypothetical protein | 55.8 | 230 | | | | | | | | |
| PSPTO0931 | C | + | | hypothetical protein | 51.9 | 135 | | | | | | | | |
| PSPTO0932 | C | + | | conserved hypothetical protein | 56.2 | 181 | | | | | | | | |
| PSPTO0933 | C | + | | conserved hypothetical protein | 60.1 | 332 | | | | | | Yp | Ec | |
| PSPTO0935 | C | + | | conserved hypothetical protein | 62.7 | 377 | | | | | | Yp | Ec | |
| PSPTO0936 | C | + | | conserved hypothetical protein | 59.5 | 252 | | | | | | Yp | Ec | |
| PSPTO0937 | C | + | | conserved hypothetical protein | 62.5 | 364 | | | | | | Yp | Ec | |
| PSPTO0938 | C | + | | conserved hypothetical protein | 60.1 | 316 | | | | | | Yp | Ec | |
| PSPTO0966 | C | | | hypothetical protein | 53.4 | 58 | | | | | | | | |
| PSPTO0974 | C | | | hypothetical protein | 54.3 | 35 | | | | | | | | |
| PSPTO0987 | C | | | conserved domain protein | 50.4 | 76 | | | | | | | | |
| PSPTO1003 | C | | | acetyltransferase, GNAT family | 58.2 | 145 | | | | At | | | | St |

| | | | | | | | | | | | | | | |
|-----------|---|---|---|------|-----|----|-----|-----|----|----|--|----|----|----|
| PSPTO1006 | C | | hypothetical protein | 57.6 | 33 | | | | | | | | | |
| PSPTO1016 | C | | hypothetical protein | 53.2 | 534 | | | | | | | | | |
| PSPTO1036 | C | + | hypothetical protein | 47.7 | 153 | | | | | | | | | |
| PSPTO1038 | C | + | conserved hypothetical protein | 63.5 | 149 | | | | | | | Yp | | |
| PSPTO1044 | C | + | hypothetical protein | 55.9 | 59 | | | | | | | | | |
| PSPTO1045 | C | + | PIN domain protein | 54.2 | 134 | | | | At | Xf | | | | St |
| PSPTO1046 | C | + | conserved hypothetical protein | 52.2 | 76 | | | | | | | | | St |
| PSPTO1055 | C | + | hypothetical protein | 53.7 | 72 | | | | | | | | | |
| PSPTO1057 | C | + | conserved hypothetical protein TIGR00305 | 56.4 | 136 | | | | | | | Xf | | |
| PSPTO1058 | C | + | conserved hypothetical protein | 53.2 | 79 | | | | | | | Xf | | |
| PSPTO1060 | C | + | hypothetical protein | 52.5 | 47 | | | | | | | | | |
| PSPTO1062 | C | + | hypothetical protein | 54 | 87 | | | | | | | | | |
| PSPTO1082 | C | | hypothetical protein | 54.2 | 72 | | | | | | | | | |
| PSPTO1088 | C | + | conserved hypothetical protein | 58.6 | 350 | Rs | | Xac | | | | | Ec | St |
| PSPTO1090 | C | + | hypothetical protein | 38.1 | 325 | | | | | | | | | |
| PSPTO1091 | C | + | conserved hypothetical protein | 39.1 | 138 | | | | | | | | | |
| PSPTO1093 | C | + | relaxase/mobilization nuclease domain protein | 52.8 | 805 | | | | | | | | | |
| PSPTO1094 | C | + | conserved hypothetical protein | 53.1 | 125 | | | | | | | | | |
| PSPTO1113 | C | | hypothetical protein | 54.1 | 194 | | | | | | | | | |
| PSPTO1114 | C | | hypothetical protein | 55.9 | 74 | | Xcc | Xac | | | | | | |
| PSPTO1124 | C | | hypothetical protein | 56.7 | 40 | | | | | | | | | |
| PSPTO1125 | C | | hypothetical protein | 58.7 | 71 | | | | | | | | | |
| PSPTO1137 | C | | hypothetical protein | 62 | 36 | | | | | | | | | |
| PSPTO1142 | C | | hypothetical protein | 60.5 | 86 | | Xcc | Xac | | | | | | |

| | | | | | | | | | | | | | | | |
|-----------|---|---|---|-------------------------------------|------|-----|----|-----|-----|--|--|--|----|--|----|
| PSPTO1161 | C | | | hypothetical protein | 60.4 | 64 | | | | | | | | | |
| PSPTO1176 | C | | + | conserved domain protein | 51.8 | 114 | | | | | | | | | |
| PSPTO1185 | C | + | + | hypothetical protein | 56.2 | 201 | | | | | | | | | |
| PSPTO1193 | C | + | + | conserved hypothetical protein | 62.8 | 654 | Rs | | | | | | | | |
| PSPTO1195 | C | + | + | hypothetical protein | 63.7 | 713 | | | | | | | | | |
| PSPTO1198 | C | + | + | hypothetical protein | 57.5 | 40 | | | | | | | | | |
| PSPTO1199 | C | | | hypothetical protein | 46.7 | 45 | | | | | | | | | |
| PSPTO1259 | C | | | hypothetical protein | 50.6 | 58 | | | | | | | | | |
| PSPTO1297 | C | | | hypothetical protein | 55.3 | 44 | | | | | | | | | |
| PSPTO1311 | C | + | | hypothetical protein | 55.7 | 125 | | | | | | | | | |
| PSPTO1319 | C | + | | hypothetical protein | 59.6 | 95 | | | | | | | | | |
| PSPTO1321 | C | + | | hypothetical protein | 61.4 | 51 | | | | | | | | | |
| PSPTO1322 | C | + | | acetyltransferase, GNAT family | 62.8 | 157 | | | | | | | | | |
| PSPTO1341 | C | + | | hypothetical protein | 58 | 322 | | | | | | | | | |
| PSPTO1342 | C | + | | conserved domain protein | 53.6 | 352 | | | | | | | | | St |
| PSPTO1344 | C | + | | hypothetical protein | 59.1 | 190 | | Xcc | Xac | | | | | | |
| PSPTO1350 | C | + | + | hypothetical protein | 61.4 | 400 | | | | | | | | | |
| PSPTO1351 | C | + | + | hypothetical protein | 55.8 | 98 | | | | | | | | | |
| PSPTO1353 | C | + | + | conserved hypothetical protein | 61.1 | 131 | | Xcc | Xac | | | | Yp | | |
| PSPTO1367 | C | + | + | acetyltransferase, GNAT family | 53.4 | 148 | | | | | | | | | |
| PSPTO1408 | C | + | + | hypothetical protein | 64.5 | 61 | | | | | | | | | |
| PSPTO1409 | C | + | + | conserved hypothetical protein | 49.3 | 281 | | | | | | | Yp | | St |
| PSPTO1410 | C | + | + | exchangeable effector locus protein | 53.6 | 138 | | | | | | | | | |
| PSPTO1411 | C | + | + | hypothetical protein | 49.6 | 191 | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|--|----|----|----|----|--|--|--|--|
| PSPTO1442 | C | | | hypothetical protein | 58.2 | 178 | | | | | | | | | | | | |
| PSPTO1451 | C | | | conserved hypothetical protein | 51.3 | 393 | Rs | Xcc | | | | | Yp | Ec | | | | |
| PSPTO1452 | C | | | hypothetical protein | 57.9 | 38 | | | | | | | | | | | | |
| PSPTO1463 | C | | | hypothetical protein | 57.6 | 48 | | | | | | | | | | | | |
| PSPTO1530 | C | | | hypothetical protein | 54.6 | 282 | | | | | | | | | | | | |
| PSPTO1566 | C | + | + | hypothetical protein | 62.5 | 32 | | | | | | | | | | | | |
| PSPTO1569 | C | + | + | conserved domain protein | 50 | 88 | | | | | | | | | | | | |
| PSPTO1570 | C | + | + | hypothetical protein | 56.2 | 51 | | | | | | | | | | | | |
| PSPTO1571 | C | + | + | hypothetical protein | 52.6 | 523 | | | | | | | | | | | | |
| PSPTO1572 | C | + | + | hypothetical protein | 47.4 | 104 | | | | | | | | | | | | |
| PSPTO1573 | C | + | + | conserved hypothetical protein | 52.8 | 60 | | | | | | Xf | | Ec | | | | |
| PSPTO1575 | C | + | + | hypothetical protein | 56.6 | 103 | | | | | | | | | | | | |
| PSPTO1577 | C | + | + | hypothetical protein | 56.9 | 370 | | | Xac | | | | | | | | | |
| PSPTO1581 | C | + | + | conserved domain protein | 55.2 | 212 | Rs | | | | | Xf | | | | | | |
| PSPTO1586 | C | + | + | hypothetical protein | 56.1 | 123 | | | | | | | | | | | | |
| PSPTO1591 | C | + | + | hypothetical protein | 51.7 | 40 | | | | | | | | | | | | |
| PSPTO1594 | C | + | + | conserved hypothetical protein | 63.9 | 134 | Rs | | | | At | | | | | | | |
| PSPTO1595 | C | + | + | hypothetical protein | 57.8 | 225 | | | | | | | | | | | | |
| PSPTO1601 | C | + | | hypothetical protein | 59.6 | 166 | | | | | | | | | | | | |
| PSPTO1603 | C | + | | hypothetical protein | 58.1 | 39 | | | | | | | | | | | | |
| PSPTO1611 | C | + | | hypothetical protein | 65.8 | 37 | | | | | | | | | | | | |
| PSPTO1614 | C | + | | hypothetical protein | 56.6 | 179 | | | | | | | | | | | | |
| PSPTO1615 | C | + | | hypothetical protein | 48.7 | 290 | | | | | | | | | | | | |
| PSPTO1619 | C | + | | hypothetical protein | 54.9 | 226 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|--|--|-----|--|--|--|--|--|--|--|--|----|----|----|----|
| PSPTO1634 | C | | | conserved hypothetical protein | 50.6 | 60 | | | | | | | | | | | | Yp | | | |
| PSPTO1635 | C | | | conserved hypothetical protein | 53.5 | 134 | | | | | | | | | | | | | Yp | | |
| PSPTO1641 | C | | | hypothetical protein | 57.7 | 93 | | | | | | | | | | | | | | | |
| PSPTO1651 | C | + | | conserved hypothetical protein | 58.7 | 96 | | | | | | | | | | | | | | Ec | |
| PSPTO1653 | C | + | | conserved domain protein | 53.4 | 517 | | | Xcc | | | | | | | | | | | Yp | |
| PSPTO1654 | C | + | | conserved hypothetical protein | 54.9 | 424 | | | Xcc | | | | | | | | | | | Yp | |
| PSPTO1655 | C | + | | hypothetical protein | 51.7 | 158 | | | | | | | | | | | | | | | |
| PSPTO1656 | C | + | | conserved hypothetical protein | 53.5 | 629 | | | | | | | | | | | | | | | Ec |
| PSPTO1657 | C | + | | hypothetical protein | 51.4 | 556 | | | | | | | | | | | | | | | |
| PSPTO1662 | C | | | hypothetical protein | 55.9 | 65 | | | | | | | | | | | | | | | |
| PSPTO1668 | C | | | hypothetical protein | 57.3 | 82 | | | | | | | | | | | | | | | |
| PSPTO1676 | C | | | conserved hypothetical protein | 53.1 | 157 | | | | | | | | | | | | | | | |
| PSPTO1678 | C | | | hypothetical protein | 58.9 | 116 | | | | | | | | | | | | | | | |
| PSPTO1681 | C | | | hypothetical protein | 54.3 | 94 | | | | | | | | | | | | | | | |
| PSPTO1722 | C | + | | hypothetical protein | 63.7 | 101 | | | | | | | | | | | | | | | |
| PSPTO1723 | C | + | | hypothetical protein | 48.2 | 47 | | | | | | | | | | | | | | | |
| PSPTO1726 | C | + | | hypothetical protein | 50 | 104 | | | | | | | | | | | | | | | |
| PSPTO1727 | C | + | | hypothetical protein | 59.3 | 50 | | | | | | | | | | | | | | | |
| PSPTO1761 | C | | | hypothetical protein | 54.9 | 68 | | | | | | | | | | | | | | | |
| PSPTO1774 | C | | | hypothetical protein | 57.6 | 59 | | | | | | | | | | | | | | | |
| PSPTO1804 | C | | | hypothetical protein | 57.8 | 30 | | | | | | | | | | | | | | | |
| PSPTO1816 | C | | | hypothetical protein | 51 | 70 | | | | | | | | | | | | | | | |
| PSPTO1820 | C | | | hypothetical protein | 57.6 | 59 | | | | | | | | | | | | | | | |
| PSPTO1837 | C | | | hypothetical protein | 58.8 | 119 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|-----------------------------------|------|-----|----|-----|-----|----|----|--|--|--|--|--|----|
| PSPTO1840 | C | | | hypothetical protein | 50 | 52 | | | | | | | | | | | |
| PSPTO1848 | C | + | | hypothetical protein | 53.2 | 77 | | | | | | | | | | | |
| PSPTO1849 | C | + | | hypothetical protein | 49.5 | 171 | | | | | | | | | | | |
| PSPTO1850 | C | + | | hypothetical protein | 54.8 | 532 | | Xcc | | | | | | | | | |
| PSPTO1851 | C | + | | hypothetical protein | 54.9 | 720 | | Xcc | | | | | | | | | |
| PSPTO1853 | C | + | | hypothetical protein | 50.5 | 35 | | | | | | | | | | | |
| PSPTO1858 | C | + | | conserved hypothetical protein | 53.4 | 293 | | | | | | | | | | | Ec |
| PSPTO1869 | C | + | | conserved hypothetical protein | 60.8 | 96 | | | Xac | | | | | | | | |
| PSPTO1872 | C | + | | hypothetical protein | 57 | 31 | | | | | | | | | | | |
| PSPTO1876 | C | + | | hypothetical protein | 60.2 | 67 | | | | | | | | | | | |
| PSPTO1895 | C | + | | conserved hypothetical protein | 55.6 | 87 | Rs | | | | | | | | | | |
| PSPTO1897 | C | + | | BNR/Asp-box repeat protein | 61 | 432 | | Xcc | Xac | At | | | | | | | St |
| PSPTO1900 | C | + | | hypothetical protein | 52.7 | 31 | | | | | | | | | | | |
| PSPTO1903 | C | + | | hypothetical protein | 49.3 | 228 | | | | | | | | | | | |
| PSPTO1905 | C | + | | hypothetical protein | 58.6 | 79 | | | | | | | | | | | |
| PSPTO1913 | C | | | conserved hypothetical protein | 53.7 | 98 | | | | | | | | | | | |
| PSPTO1932 | C | | | hypothetical protein | 56.4 | 52 | | | | | | | | | | | |
| PSPTO1938 | C | | | hypothetical protein | 61.7 | 47 | | | | | | | | | | | |
| PSPTO1967 | C | | | hypothetical protein | 53.1 | 59 | | | | | | | | | | | |
| PSPTO1999 | C | + | | PIN domain protein | 58.4 | 150 | Rs | | Xac | At | Xf | | | | | | |
| PSPTO2000 | C | + | | prevent-host-death family protein | 57.8 | 83 | | | | | | | | | | | |
| PSPTO2006 | C | + | | hypothetical protein | 55.4 | 157 | | | | | | | | | | | |
| PSPTO2012 | C | + | | hypothetical protein | 52.8 | 178 | | | | | | | | | | | |
| PSPTO2013 | C | + | | hypothetical protein | 53.5 | 220 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|---|------|-----|--|-----|-----|--|--|--|--|--|--|----|--|--|
| PSPTO2027 | C | | | hypothetical protein | 61.4 | 38 | | | | | | | | | | | | |
| PSPTO2058 | C | + | | hypothetical protein | 52.7 | 62 | | | | | | | | | | | | |
| PSPTO2062 | C | + | | conserved hypothetical protein | 56.9 | 123 | | | | | | | | | | | | |
| PSPTO2067 | C | + | | hypothetical protein | 58.1 | 39 | | | | | | | | | | | | |
| PSPTO2068 | C | + | | conserved hypothetical protein | 54.4 | 109 | | Xcc | Xac | | | | | | | | | |
| PSPTO2069 | C | + | | hypothetical protein | 57.9 | 61 | | | | | | | | | | | | |
| PSPTO2073 | C | + | | hypothetical protein | 54 | 182 | | | | | | | | | | | | |
| PSPTO2074 | C | + | | hypothetical protein | 54.3 | 97 | | | | | | | | | | | | |
| PSPTO2076 | C | + | | hypothetical protein | 46.6 | 153 | | | | | | | | | | | | |
| PSPTO2077 | C | + | | conserved domain protein | 59.5 | 121 | | | | | | | | | | | | |
| PSPTO2078 | C | + | | hypothetical protein | 57.3 | 125 | | | | | | | | | | | | |
| PSPTO2079 | C | + | | hypothetical protein | 57.8 | 120 | | | | | | | | | | | | |
| PSPTO2080 | C | + | | conserved hypothetical protein, internal deletion | 56.3 | 126 | | | | | | | | | | Yp | | |
| PSPTO2081 | C | + | | hypothetical protein | 61.6 | 150 | | | | | | | | | | | | |
| PSPTO2083 | C | + | | hypothetical protein | 47.4 | 175 | | | | | | | | | | | | |
| PSPTO2084 | C | + | | conserved hypothetical protein | 58.6 | 83 | | | | | | | | | | | | |
| PSPTO2085 | C | + | | conserved hypothetical protein | 59.5 | 131 | | | | | | | | | | | | |
| PSPTO2086 | C | + | | hypothetical protein | 61.1 | 60 | | | | | | | | | | | | |
| PSPTO2087 | C | + | | hypothetical protein | 62.4 | 102 | | | | | | | | | | | | |
| PSPTO2088 | C | + | | conserved hypothetical protein | 60.9 | 132 | | | | | | | | | | | | |
| PSPTO2090 | C | + | | hypothetical protein | 49.5 | 122 | | | | | | | | | | | | |
| PSPTO2095 | C | + | | conserved domain protein | 56.7 | 70 | | | | | | | | | | | | |
| PSPTO2096 | C | + | | hypothetical protein | 60.5 | 414 | | | | | | | | | | | | |
| PSPTO2122 | C | | | hypothetical protein | 57.4 | 97 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|--|--|--|-----|--|--|--|--|--|----|--|--|
| PSPTO2124 | C | | | hypothetical protein | 54.5 | 85 | | | | | | | | | | | | |
| PSPTO2157 | C | | | hypothetical protein | 64.4 | 568 | | | | | | | | | | | | |
| PSPTO2162 | C | | | hypothetical protein | 55.5 | 164 | | | | | | | | | | | | |
| PSPTO2219 | C | | | hypothetical protein | 56.8 | 54 | | | | | | | | | | | | |
| PSPTO2260 | C | + | | conserved hypothetical protein | 59.8 | 409 | | | | | | | | | | | | |
| PSPTO2262 | C | + | | hypothetical protein | 52.9 | 347 | | | | | | | | | | | | |
| PSPTO2263 | C | + | | hypothetical protein | 53.8 | 145 | | | | | | | | | | | | |
| PSPTO2264 | C | + | | hypothetical protein | 59 | 109 | | | | | | | | | | | | |
| PSPTO2271 | C | + | | hypothetical protein | 58.6 | 37 | | | | | | | | | | | | |
| PSPTO2273 | C | + | | hypothetical protein | 51.5 | 57 | | | | | | | | | | | | |
| PSPTO2308 | C | | | hypothetical protein | 55.4 | 65 | | | | | | | | | | | | |
| PSPTO2318 | C | | | hypothetical protein | 46.5 | 104 | | | | | | | | | | | | |
| PSPTO2323 | C | | | hypothetical protein | 51.3 | 596 | | | | | | | | | | | | |
| PSPTO2325 | C | | | hypothetical protein | 46.9 | 86 | | | | | | | | | | | | |
| PSPTO2332 | C | | | hypothetical protein | 61.1 | 155 | | | | | | | | | | | | |
| PSPTO2356 | C | + | | hypothetical protein | 55.6 | 127 | | | | | | | | | | | | |
| PSPTO2357 | C | + | | hypothetical protein | 58.6 | 141 | | | | | | | | | | | | |
| PSPTO2360 | C | + | | hypothetical protein | 56.2 | 89 | | | | | | | | | | | | |
| PSPTO2361 | C | + | | conserved domain protein | 61.8 | 76 | | | | Xac | | | | | | Yp | | |
| PSPTO2363 | C | + | | hypothetical protein | 54.4 | 79 | | | | | | | | | | | | |
| PSPTO2377 | C | | | hypothetical protein | 59.7 | 101 | | | | | | | | | | | | |
| PSPTO2389 | C | + | | hypothetical protein | 57.1 | 260 | | | | | | | | | | | | |
| PSPTO2390 | C | + | | hypothetical protein | 46.1 | 256 | | | | | | | | | | | | |
| PSPTO2391 | C | + | | hypothetical protein | 55.7 | 106 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|----|-----|--|----|----|--|--|--|----|--|--|
| PSPTO2394 | C | + | | radical SAM domain protein | 46.3 | 306 | | | | | | | | | | | |
| PSPTO2407 | C | | | conserved hypothetical protein | 58.3 | 214 | Rs | Xcc | | At | Xf | | | | | | |
| PSPTO2431 | C | | | conserved hypothetical protein | 43.5 | 305 | | | | | | | | | | | |
| PSPTO2433 | C | | | hypothetical protein | 45.7 | 43 | | | | | | | | | | | |
| PSPTO2442 | C | | | CheW domain protein | 63.3 | 487 | | | | | | | | | Yp | | |
| PSPTO2443 | C | | | hypothetical protein | 54.5 | 41 | | | | | | | | | | | |
| PSPTO2455 | C | | | hypothetical protein | 57.3 | 78 | | | | | | | | | | | |
| PSPTO2456 | C | | | hypothetical protein | 56.1 | 38 | | | | | | | | | | | |
| PSPTO2497 | C | + | | hypothetical protein | 50.4 | 41 | | | | | | | | | | | |
| PSPTO2498 | C | + | | hypothetical protein | 65.8 | 40 | | | | | | | | | | | |
| PSPTO2501 | C | + | | hypothetical protein | 58.1 | 89 | | | | | | | | | | | |
| PSPTO2502 | C | + | | hypothetical protein | 60.2 | 67 | | | | | | | | | | | |
| PSPTO2503 | C | + | | hypothetical protein | 58.7 | 189 | | | | | | | | | | | |
| PSPTO2512 | C | | | hypothetical protein | 53.2 | 173 | | | | | | | | | | | |
| PSPTO2513 | C | | | hypothetical protein | 54.3 | 35 | | | | | | | | | | | |
| PSPTO2530 | C | + | | hypothetical protein | 54.8 | 42 | | | | | | | | | | | |
| PSPTO2531 | C | + | | hypothetical protein | 57.1 | 94 | | | | | | | | | | | |
| PSPTO2534 | C | + | | hypothetical protein | 49.6 | 226 | | | | | | | | | | | |
| PSPTO2536 | C | + | | hypothetical protein | 56 | 147 | | | | | | | | | | | |
| PSPTO2537 | C | + | | conserved domain protein | 52.5 | 155 | | | | | | | | | | | |
| PSPTO2584 | C | + | | conserved hypothetical protein | 61.1 | 227 | | | | At | | | | | | | |
| PSPTO2587 | C | + | | hypothetical protein | 52.5 | 40 | | | | | | | | | | | |
| PSPTO2589 | C | + | | hypothetical protein | 58.9 | 111 | | | | | | | | | | | |
| PSPTO2613 | C | + | | hypothetical protein | 54.8 | 191 | | | | | | | | | | | |

| | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|----|--|----|----|----|
| PSPTO2615 | C | + | | GAF domain protein | 54.3 | 165 | | Xcc | Xac | At | | | | |
| PSPTO2619 | C | + | | hypothetical protein | 60.6 | 218 | | | | | | | | |
| PSPTO2631 | C | | | hypothetical protein | 59.6 | 197 | | | | | | | | |
| PSPTO2647 | C | | | hypothetical protein | 57 | 246 | | | | | | | | |
| PSPTO2648 | C | | | hypothetical protein | 57 | 155 | | | | | | | | |
| PSPTO2669 | C | + | + | conserved hypothetical protein | 58.3 | 96 | Rs | | | At | | | | |
| PSPTO2675 | C | + | + | conserved hypothetical protein | 58.2 | 196 | | | | | | | | |
| PSPTO2679 | C | + | + | hypothetical protein | 60.8 | 40 | | | | | | | | |
| PSPTO2682 | C | + | + | hypothetical protein | 59.5 | 199 | | | Xac | At | | | | |
| PSPTO2695 | C | + | + | conserved hypothetical protein | 60.9 | 353 | | Xcc | Xac | | | | | |
| PSPTO2698 | C | + | + | hypothetical protein | 59.6 | 104 | | | | | | | | |
| PSPTO2700 | C | + | + | hypothetical protein | 56.9 | 184 | | | | | | | | |
| PSPTO2727 | C | | | hypothetical protein | 49.5 | 31 | | | | | | | | |
| PSPTO2768 | C | + | | hypothetical protein | 50.6 | 58 | | | | | | | | |
| PSPTO2770 | C | + | | hypothetical protein | 60 | 35 | | | | | | | | |
| PSPTO2772 | C | + | | hypothetical protein | 55.1 | 141 | | | | | | | | |
| PSPTO2774 | C | + | | conserved hypothetical protein | 57.5 | 131 | | | | | | Yp | | |
| PSPTO2781 | C | + | | conserved hypothetical protein | 62.8 | 411 | Rs | | | At | | | | |
| PSPTO2789 | C | | | hypothetical protein | 43.1 | 48 | | | | | | | | |
| PSPTO2796 | C | | | conserved hypothetical protein | 60.2 | 283 | | | | At | | | | |
| PSPTO2797 | C | | | hypothetical protein | 63.1 | 56 | | | | | | | | |
| PSPTO2809 | C | + | | conserved hypothetical protein | 64.6 | 486 | Rs | Xcc | Xac | At | | | Ec | St |
| PSPTO2815 | C | + | | conserved hypothetical protein | 61.3 | 173 | Rs | | | At | | Yp | | |
| PSPTO2817 | C | + | | conserved domain protein | 62.8 | 61 | | Xcc | Xac | At | | Yp | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------------|------|------|----|-----|-----|----|--|----|----|----|----|--|--|
| PSPTO2819 | C | + | | conserved hypothetical protein | 58.9 | 262 | | | | | | | | | | | |
| PSPTO2820 | C | + | | hypothetical protein | 63.8 | 371 | | | | | | | | | | | |
| PSPTO2821 | C | + | | hypothetical protein | 65.6 | 302 | | | | | | | | | | | |
| PSPTO2823 | C | + | | hypothetical protein | 59.3 | 249 | | | | | | | | | | | |
| PSPTO2824 | C | + | | auxin-responsive GH3-related protein | 61.8 | 487 | | | | | | | | | | | |
| PSPTO2826 | C | + | | conserved domain protein | 58.9 | 99 | | | | At | | | Yp | Ec | | | |
| PSPTO2827 | C | + | | conserved domain protein | 60.8 | 80 | | | | At | | | Yp | | St | | |
| PSPTO2835 | C | | | conserved domain protein | 58.7 | 50 | | | | At | | | | | | | |
| PSPTO2858 | C | + | + | hypothetical protein | 51.7 | 118 | | | | | | | | | | | |
| PSPTO2859 | C | + | + | conserved hypothetical protein | 56.2 | 866 | | | | | | | Yp | | | | |
| PSPTO2860 | C | + | + | helicase domain protein | 57.5 | 459 | | | | | | | | Ec | | | |
| PSPTO2866 | C | + | + | cupin family protein | 57.1 | 133 | | Xcc | Xac | At | | | Yp | | | | |
| PSPTO2867 | C | + | + | TspO/MBR family protein | 56.8 | 146 | | Xcc | Xac | At | | | | | | | |
| PSPTO2868 | C | + | + | conserved hypothetical protein | 59.4 | 392 | Rs | | | | | Xf | | | | | |
| PSPTO2869 | C | + | + | hypothetical protein | 43.3 | 40 | | | | | | | | | | | |
| PSPTO2871 | C | + | + | conserved hypothetical protein | 59.7 | 1044 | | | | | | | Yp | | St | | |
| PSPTO2873 | C | + | + | conserved hypothetical protein | 61.2 | 345 | | | | | | | | | | | |
| PSPTO2880 | C | + | + | conserved hypothetical protein | 61.6 | 423 | | | | | | | | | | | |
| PSPTO2881 | C | + | + | hypothetical protein | 61.5 | 32 | | | | | | | | | | | |
| PSPTO2888 | C | + | + | conserved domain protein | 45.1 | 48 | | | | | | | | | | | |
| PSPTO2889 | C | + | + | hypothetical protein | 55 | 37 | | | | | | | | | | | |
| PSPTO2892 | C | + | + | hypothetical protein | 52.1 | 32 | | | | | | | | | | | |
| PSPTO2894 | C | + | + | lectin repeat domain protein | 50 | 801 | | | | | | | | | | | |
| PSPTO2895 | C | + | + | hypothetical protein | 57.1 | 339 | | | | At | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|----|----|--|----|----|----|--|--|
| PSPTO2897 | C | + | + | conserved hypothetical protein | 58.9 | 380 | | Xcc | Xac | | | | | | | | |
| PSPTO2899 | C | + | + | conserved hypothetical protein | 59.1 | 394 | | Xcc | Xac | | | | | | | | |
| PSPTO2908 | C | + | | hypothetical protein | 56.8 | 230 | | | | | | | | | | | |
| PSPTO2918 | C | + | | conserved hypothetical protein | 61.2 | 135 | Rs | Xcc | Xac | At | | | | | | | |
| PSPTO2924 | C | + | | hypothetical protein | 54.7 | 53 | | | | | | | | | | | |
| PSPTO2929 | C | + | | hypothetical protein | 53.5 | 320 | | | | | | | | | | | |
| PSPTO2931 | C | + | | conserved hypothetical protein | 59.3 | 394 | | | | | | | | | | | |
| PSPTO2939 | C | + | | hypothetical protein | 54.5 | 170 | | | | | | | | | | | |
| PSPTO2942 | C | + | | hypothetical protein | 57.8 | 34 | | | | | | | | | | | |
| PSPTO2959 | C | + | | conserved hypothetical protein | 64.2 | 551 | | | | | | | | | | | |
| PSPTO2963 | C | + | | oxidoreductase, FAD-binding | 65 | 379 | Rs | Xcc | Xac | At | | | | | | | |
| PSPTO2965 | C | + | | conserved hypothetical protein | 57.9 | 130 | Rs | | | | | | | | | | |
| PSPTO2977 | C | + | | conserved hypothetical protein | 51.7 | 211 | | | | | | | | | | | |
| PSPTO2979 | C | + | | conserved hypothetical protein | 52.3 | 128 | | | | | | | | | | | |
| PSPTO2982 | C | + | | conserved hypothetical protein | 62.3 | 576 | | Xcc | | At | | | | | | | |
| PSPTO2998 | C | | | conserved hypothetical protein | 58.7 | 142 | Rs | Xcc | Xac | At | Xf | | | | | | |
| PSPTO2999 | C | | | hypothetical protein | 54.4 | 250 | | | | | | | | | | | |
| PSPTO3016 | C | | | conserved hypothetical protein | 48.4 | 117 | Rs | | | | | | Yp | Ec | St | | |
| PSPTO3018 | C | | | conserved hypothetical protein | 58.6 | 307 | Rs | | | At | | | Yp | | St | | |
| PSPTO3026 | C | | | conserved hypothetical protein | 55.1 | 81 | | Xcc | | | | | | | | | |
| PSPTO3055 | C | | | hypothetical protein | 54.4 | 49 | | | | | | | | | | | |
| PSPTO3067 | C | | + | hypothetical protein | 59.1 | 230 | | | | | | | | | | | |
| PSPTO3078 | C | | + | conserved hypothetical protein | 52.9 | 128 | | | | | | | | | | | |
| PSPTO3092 | C | | + | conserved hypothetical protein | 60.1 | 278 | | Xcc | Xac | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|-----------------------------------|------|-----|--|--|----|--|--|--|----|----|----|--|--|
| PSPTO3104 | C | | | hypothetical protein | 59 | 48 | | | | | | | | | | | |
| PSPTO3117 | C | | | hypothetical protein | 57.2 | 60 | | | | | | | | | | | |
| PSPTO3120 | C | | | Cof-like hydrolase family protein | 60.4 | 272 | | | | | | | Yp | Ec | St | | |
| PSPTO3151 | C | | | conserved hypothetical protein | 64.5 | 61 | | | At | | | | | | | | |
| PSPTO3166 | C | + | | conserved domain protein | 58.5 | 320 | | | | | | | | | | | |
| PSPTO3167 | C | + | | hypothetical protein | 60.7 | 101 | | | | | | | | | | | |
| PSPTO3168 | C | + | | hypothetical protein | 39.1 | 46 | | | | | | | | | | | |
| PSPTO3169 | C | + | | hypothetical protein | 62.1 | 87 | | | | | | | | | | | |
| PSPTO3177 | C | | | conserved hypothetical protein | 57.6 | 99 | | | | | | | | | | | |
| PSPTO3187 | C | | | hypothetical protein | 53.9 | 86 | | | | | | | | | | | |
| PSPTO3189 | C | | | conserved hypothetical protein | 62.1 | 317 | | | | | | | | | | | |
| PSPTO3200 | C | + | | hypothetical protein | 60.5 | 290 | | | | | | | | | | | |
| PSPTO3201 | C | + | | hypothetical protein | 60.6 | 259 | | | | | | | | | | | |
| PSPTO3203 | C | + | | conserved hypothetical protein | 51.7 | 154 | | | | | | | | | | | |
| PSPTO3211 | C | | | conserved hypothetical protein | 40.5 | 171 | | | | | | | Yp | | | | |
| PSPTO3217 | C | + | | hypothetical protein | 50.3 | 55 | | | | | | | | | | | |
| PSPTO3218 | C | + | | hypothetical protein | 52.6 | 398 | | | | | | | | | | | |
| PSPTO3219 | C | + | | hypothetical protein | 57.7 | 41 | | | | | | | | | | | |
| PSPTO3222 | C | + | | hypothetical protein | 53.1 | 71 | | | | | | | | | | | |
| PSPTO3228 | C | + | | hypothetical protein | 53 | 56 | | | | | | | | | | | |
| PSPTO3236 | C | | | hypothetical protein | 51.9 | 131 | | | | | | | | | | | |
| PSPTO3241 | C | | | phytase domain protein | 62.9 | 640 | | | | | | | | | | | |
| PSPTO3246 | C | | | hypothetical protein | 59.3 | 232 | | | | | | | | Ec | St | | |
| PSPTO3253 | C | | | conserved hypothetical protein | 55 | 240 | | | | | | | Yp | Ec | St | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|----|-----|-----|----|----|----|----|--|--|--|--|----|
| PSPTO3261 | C | | | hypothetical protein | 58.3 | 84 | | | | | | | | | | | | |
| PSPTO3270 | C | + | | conserved hypothetical protein | 55.7 | 94 | | | | | | | | | | | | |
| PSPTO3271 | C | + | | hypothetical protein | 60.3 | 110 | | | | | | | | | | | | |
| PSPTO3276 | C | + | | hypothetical protein | 44.4 | 39 | | | | | | | | | | | | |
| PSPTO3289 | C | + | | hypothetical protein | 54.6 | 72 | | | | | | | | | | | | |
| PSPTO3292 | C | + | | hypothetical protein | 53.1 | 404 | Rs | | | | | | | | | | | |
| PSPTO3293 | C | + | | hypothetical protein | 57.2 | 416 | | | | | | | | | | | | |
| PSPTO3303 | C | | | hypothetical protein | 55.4 | 62 | | | | | | | | | | | | |
| PSPTO3305 | C | | | hypothetical protein | 54.2 | 280 | | | | | | | | | | | | |
| PSPTO3324 | C | | | hypothetical protein | 50.5 | 35 | | | | | | | | | | | | |
| PSPTO3337 | C | | | hypothetical protein | 53.2 | 195 | | | | | | | | | | | | |
| PSPTO3384 | C | + | | hypothetical protein | 52.9 | 68 | | | | | | | | | | | | |
| PSPTO3386 | C | + | | hypothetical protein | 50.4 | 784 | | | | At | | | | | | | | |
| PSPTO3387 | C | + | | conserved hypothetical protein | 41.6 | 109 | | | | | | | | | | | | Ec |
| PSPTO3402 | C | | | hypothetical protein | 62.7 | 92 | | | | | | | | | | | | |
| PSPTO3414 | C | + | | hypothetical protein | 61.1 | 48 | | | | | | | | | | | | |
| PSPTO3415 | C | + | | conserved domain protein | 57.6 | 128 | | | | | | | | | | | | |
| PSPTO3420 | C | + | | hypothetical protein | 56.8 | 199 | Rs | | | | | | | | | | | |
| PSPTO3422 | C | + | | hypothetical protein | 55 | 191 | | | | | | | | | | | | |
| PSPTO3424 | C | + | | hypothetical protein | 54.6 | 124 | | | | | | | | | | | | |
| PSPTO3426 | C | + | | hypothetical protein | 53.3 | 140 | | | | | | | | | | | | |
| PSPTO3428 | C | + | | conserved domain protein | 55.7 | 152 | Rs | | | | | | | | | | | |
| PSPTO3429 | C | + | | DNA-binding protein, putative | 53.8 | 80 | Rs | | Xac | | Xf | Yp | Ec | | | | | |
| PSPTO3468 | C | | | conserved hypothetical protein | 65.2 | 467 | | Xcc | Xac | At | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|--|-----|-----|----|----|--|--|----|----|--|--|
| PSPTO3478 | C | + | | hypothetical protein | 53.2 | 79 | | Xcc | Xac | | | | | | | | |
| PSPTO3481 | C | + | | hypothetical protein | 55.7 | 76 | | | | | | | | | | | |
| PSPTO3483 | C | + | | hypothetical protein | 52.7 | 282 | | | | | | | | | | | |
| PSPTO3486 | C | + | | hypothetical protein | 50.9 | 38 | | | | | | | | | | | |
| PSPTO3491 | C | + | | hypothetical protein | 58.2 | 122 | | | | | | | | | | | |
| PSPTO3509 | C | | | hypothetical protein | 47.5 | 40 | | | | | | | | | | | |
| PSPTO3518 | C | | | hypothetical protein | 60.2 | 41 | | | | | | | | | | | |
| PSPTO3525 | C | | | hypothetical protein | 52.9 | 143 | | | | | | | | | | | |
| PSPTO3542 | C | + | | conserved hypothetical protein | 60.7 | 305 | | | | | | | | | | | |
| PSPTO3544 | C | + | | conserved hypothetical protein | 60.1 | 381 | | | | At | | | | | | | |
| PSPTO3546 | C | + | | hypothetical protein | 51.8 | 47 | | | | | | | | | | | |
| PSPTO3560 | C | + | | GDA1/CD39 family protein | 50.7 | 402 | | | | | | | | | | | |
| PSPTO3562 | C | + | | hypothetical protein | 60.6 | 33 | | | | | | | | | | | |
| PSPTO3567 | C | + | | hypothetical protein | 60.4 | 466 | | | | | | | | | | | |
| PSPTO3568 | C | + | | hypothetical protein | 53.7 | 41 | | | | | | | | | | | |
| PSPTO3571 | C | + | | hypothetical protein | 57.9 | 38 | | | | | | | | | | | |
| PSPTO3575 | C | + | | hypothetical protein | 53.6 | 173 | | | | | | | | | | | |
| PSPTO3578 | C | + | | hypothetical protein | 53.3 | 162 | | | | | | | | | | | |
| PSPTO3597 | C | + | | conserved hypothetical protein | 63.2 | 402 | | | | | | | | Yp | Ec | | |
| PSPTO3599 | C | + | | conserved domain protein | 58.5 | 274 | | | | | | | | Yp | Ec | | |
| PSPTO3606 | C | + | | hypothetical protein | 47.4 | 52 | | | | | | | | | | | |
| PSPTO3610 | C | + | | hypothetical protein | 47.4 | 559 | | | | | | | | | | | |
| PSPTO3616 | C | + | | hypothetical protein | 45.1 | 328 | | Xcc | Xac | | Xf | | | | | | |
| PSPTO3622 | C | | | hypothetical protein | 60.7 | 112 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--|------|-----|----|-----|-----|----|--|----|----|----|--|--|--|
| PSPTO3623 | C | | | hypothetical protein | 60.3 | 121 | | | | | | | | | | | |
| PSPTO3640 | C | | | conserved hypothetical protein | 63.1 | 378 | Rs | | | At | | | | | | | |
| PSPTO3650 | C | + | | hypothetical protein | 42.3 | 426 | | | | | | | | | | | |
| PSPTO3654 | C | + | | acetyltransferase, GNAT family | 59.3 | 162 | | | | | | | | | | | |
| PSPTO3655 | C | + | | conserved hypothetical protein | 60.7 | 388 | Rs | | | At | | | | | | | |
| PSPTO3673 | C | | | hypothetical protein | 53.3 | 40 | | | | | | | | | | | |
| PSPTO3682 | C | + | | conserved hypothetical protein | 63.4 | 375 | Rs | Xcc | Xac | | | | | | | | |
| PSPTO3683 | C | + | | hypothetical protein | 54.6 | 61 | | | | | | | | | | | |
| PSPTO3684 | C | + | | hypothetical protein | 54.6 | 133 | | | | | | | | | | | |
| PSPTO3690 | C | | | conserved hypothetical protein | 48.7 | 286 | | | Xac | | | | | | | | |
| PSPTO3693 | C | | | hypothetical protein | 60.4 | 95 | | | | | | | | | | | |
| PSPTO3697 | C | | | hypothetical protein | 61.4 | 38 | | | | | | | | | | | |
| PSPTO3710 | C | | | acetyltransferase, GNAT family | 57.4 | 184 | | | | | | | | | | | |
| PSPTO3728 | C | | | hypothetical protein | 56.1 | 38 | | | | | | | | | | | |
| PSPTO3732 | C | | | hypothetical protein | 52.3 | 79 | | | | | | | | | | | |
| PSPTO3736 | C | | | conserved hypothetical protein | 57 | 90 | Rs | | | At | | | | | | | |
| PSPTO3754 | C | | | hypothetical protein | 50.7 | 297 | | | | | | | | | | | |
| PSPTO3767 | C | | | hypothetical protein | 52.7 | 86 | | | | | | | | | | | |
| PSPTO3775 | C | + | | hypothetical protein | 59.9 | 94 | | | | | | | | | | | |
| PSPTO3776 | C | + | | hypothetical protein | 47.5 | 148 | | | | | | | | | | | |
| PSPTO3780 | C | + | | glutathionylspermidine synthase family protein | 58.2 | 385 | | Xcc | Xac | At | | Yp | Ec | St | | | |
| PSPTO3781 | C | + | | conserved hypothetical protein | 61.4 | 240 | | Xcc | Xac | | | | Ec | | | | |
| PSPTO3782 | C | + | | conserved hypothetical protein | 59.3 | 135 | Rs | Xcc | Xac | At | | | Ec | St | | | |
| PSPTO3783 | C | + | | conserved hypothetical protein | 59.5 | 218 | | Xcc | Xac | | | | Ec | St | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|------------------------------------|------|------|----|-----|-----|--|--|--|----|----|----|--|--|
| PSPTO3785 | C | + | | rhomboid family protein | 58.4 | 185 | | Xcc | Xac | | | | | | | | |
| PSPTO3794 | C | + | | hypothetical protein | 53.8 | 137 | | | | | | | | | | | |
| PSPTO3795 | C | + | | hypothetical protein | 50.2 | 97 | | | | | | | | | | | |
| PSPTO3851 | C | + | | hypothetical protein | 58.9 | 1104 | | | | | | | | | | | |
| PSPTO3852 | C | + | | hypothetical protein | 55.2 | 306 | | | | | | | | | | | |
| PSPTO3853 | C | + | | hypothetical protein | 55 | 299 | | | | | | | | | | | |
| PSPTO3865 | C | + | | conserved hypothetical protein | 56.2 | 398 | | | | | | | | | | | |
| PSPTO3866 | C | + | | hypothetical protein | 57.6 | 177 | | | | | | | | | | | |
| PSPTO3868 | C | + | | hypothetical protein | 58 | 285 | | | | | | | | | | | |
| PSPTO3891 | C | + | | hypothetical protein | 59.4 | 471 | | | | | | | | | | | |
| PSPTO3892 | C | + | | hypothetical protein | 60 | 205 | | | | | | | | | | | |
| PSPTO3895 | C | + | | hypothetical protein | 51.9 | 131 | | | | | | | | | | | |
| PSPTO3896 | C | + | | hypothetical protein | 51.2 | 41 | | | | | | | | | | | |
| PSPTO3904 | C | | | hypothetical protein | 52 | 50 | | | | | | | | | | | |
| PSPTO3907 | C | | | conserved hypothetical protein | 54 | 250 | | | | | | | | | | | |
| PSPTO3927 | C | + | | hypothetical protein | 54.1 | 221 | | | | | | | | | | | |
| PSPTO3931 | C | + | | hypothetical protein | 60.3 | 47 | | | | | | | | | | | |
| PSPTO3934 | C | + | | tail fiber assembly domain protein | 54.7 | 92 | Rs | | | | | | Yp | Ec | St | | |
| PSPTO3938 | C | + | | hypothetical protein | 49.5 | 122 | | | | | | | | | | | |
| PSPTO3942 | C | + | | hypothetical protein | 59.5 | 200 | | | | | | | | | | | |
| PSPTO3944 | C | + | | hypothetical protein | 58.8 | 225 | | | | | | | | | | | |
| PSPTO3945 | C | + | | hypothetical protein | 61.1 | 66 | | | | | | | | | | | |
| PSPTO3946 | C | + | | hypothetical protein | 56.8 | 155 | | | | | | | | | | | |
| PSPTO3947 | C | + | | hypothetical protein | 56.1 | 85 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|--|--|--|--|--|--|--|--|--|--|--|--|
| PSPTO3948 | C | + | | hypothetical protein | 61.9 | 127 | | | | | | | | | | | | |
| PSPTO3961 | C | + | | hypothetical protein | 41.4 | 66 | | | | | | | | | | | | |
| PSPTO3962 | C | + | | hypothetical protein | 43.1 | 34 | | | | | | | | | | | | |
| PSPTO3965 | C | + | | hypothetical protein | 51.3 | 517 | | | | | | | | | | | | |
| PSPTO4003 | C | + | + | conserved hypothetical protein | 62.9 | 178 | | | | | | | | | | | | |
| PSPTO4004 | C | + | + | conserved hypothetical protein | 63.1 | 310 | | | | | | | | | | | | |
| PSPTO4005 | C | + | + | hypothetical protein | 58.5 | 142 | | | | | | | | | | | | |
| PSPTO4007 | C | + | + | conserved hypothetical protein | 61.9 | 174 | | | | | | | | | | | | |
| PSPTO4008 | C | + | + | hypothetical protein | 59.8 | 135 | | | | | | | | | | | | |
| PSPTO4011 | C | + | + | hypothetical protein | 57.1 | 94 | | | | | | | | | | | | |
| PSPTO4012 | C | + | + | hypothetical protein | 58.6 | 253 | | | | | | | | | | | | |
| PSPTO4015 | C | + | + | hypothetical protein | 55.3 | 82 | | | | | | | | | | | | |
| PSPTO4016 | C | + | + | hypothetical protein | 56.4 | 68 | | | | | | | | | | | | |
| PSPTO4017 | C | + | + | hypothetical protein | 53.8 | 179 | | | | | | | | | | | | |
| PSPTO4028 | C | | | hypothetical protein | 59.3 | 41 | | | | | | | | | | | | |
| PSPTO4035 | C | + | | hypothetical protein | 57.7 | 208 | | | | | | | | | | | | |
| PSPTO4040 | C | + | | conserved domain protein | 49.7 | 122 | | | | | | | | | | | | |
| PSPTO4042 | C | + | | conserved hypothetical protein | 60.1 | 132 | | | | | | | | | | | | |
| PSPTO4043 | C | + | | hypothetical protein | 61.3 | 200 | | | | | | | | | | | | |
| PSPTO4044 | C | + | | hypothetical protein | 61.2 | 194 | | | | | | | | | | | | |
| PSPTO4045 | C | + | | hypothetical protein | 51.2 | 99 | | | | | | | | | | | | |
| PSPTO4047 | C | + | | hypothetical protein | 50.8 | 120 | | | | | | | | | | | | |
| PSPTO4048 | C | + | | conserved hypothetical protein | 58.2 | 83 | | | | | | | | | | | | |
| PSPTO4049 | C | + | | conserved hypothetical protein | 60.1 | 132 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--|------|-----|----|-----|-----|----|----|--|--|--|--|----|--|----|
| PSPTO4050 | C | + | | hypothetical protein | 62.1 | 250 | | | | | | | | | | | | |
| PSPTO4051 | C | + | | hypothetical protein | 59.9 | 191 | | | | | | | | | | | | |
| PSPTO4052 | C | + | | hypothetical protein | 56.8 | 288 | | | | | | | | | | | | |
| PSPTO4053 | C | + | | hypothetical protein | 54.2 | 32 | | | | | | | | | | | | |
| PSPTO4054 | C | + | | hypothetical protein | 59.5 | 270 | | | | | | | | | | | | |
| PSPTO4055 | C | + | | hypothetical protein | 58.3 | 64 | | | | | | | | | | | | |
| PSPTO4056 | C | + | | hypothetical protein | 53.2 | 195 | | | | | | | | | | | | |
| PSPTO4066 | C | + | | conserved domain protein | 52.6 | 97 | | | | | | | | | | | | |
| PSPTO4069 | C | + | | hypothetical protein | 46.9 | 54 | | | | | | | | | | | | |
| PSPTO4070 | C | + | | conserved hypothetical protein | 50.3 | 145 | | | | | | | | | | Yp | | |
| PSPTO4071 | C | + | | conserved hypothetical protein | 57.4 | 191 | | | Xac | | | | | | | | | |
| PSPTO4085 | C | | | hypothetical protein | 61.7 | 54 | | | | | | | | | | | | |
| PSPTO4086 | C | | | hypothetical protein | 61.1 | 54 | | | | | | | | | | | | |
| PSPTO4096 | C | + | + | conserved domain protein | 56.5 | 46 | | | | | | | | | | | | St |
| PSPTO4099 | C | + | + | hypothetical protein | 57.8 | 49 | | | | | | | | | | | | |
| PSPTO4102 | C | + | + | hypothetical protein | 54.9 | 65 | | | | | | | | | | | | |
| PSPTO4118 | C | | | hypothetical protein | 44.7 | 38 | | | | | | | | | | | | |
| PSPTO4150 | C | | | hypothetical protein | 56.7 | 120 | | | | | | | | | | | | |
| PSPTO4153 | C | | | hypothetical protein | 57.3 | 132 | | | | | | | | | | | | |
| PSPTO4177 | C | + | | 2-hydroxychromene-2-carboxylate isomerase family protein | 58.8 | 215 | Rs | Xcc | Xac | At | Xf | | | | | | | |
| PSPTO4184 | C | + | | hypothetical protein | 61.1 | 66 | | | | | | | | | | | | |
| PSPTO4186 | C | + | | hypothetical protein | 43.5 | 226 | | | | | | | | | | | | |
| PSPTO4187 | C | + | | hypothetical protein | 47.8 | 217 | | | | | | | | | | | | |
| PSPTO4189 | C | + | | hypothetical protein | 43.4 | 229 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|----|----|--|--|--|--|--|--|--|
| PSPTO4190 | C | + | | hypothetical protein | 49.5 | 289 | | | | | | | | | | | | |
| PSPTO4197 | C | + | | conserved hypothetical protein | 62.6 | 398 | | | | At | | | | | | | | |
| PSPTO4199 | C | + | | conserved hypothetical protein | 63.6 | 99 | | | | | | | | | | | | |
| PSPTO4207 | C | + | | hypothetical protein | 61.5 | 291 | | Xcc | Xac | | | | | | | | | |
| PSPTO4209 | C | + | | hypothetical protein | 58.9 | 223 | | Xcc | Xac | | | | | | | | | |
| PSPTO4241 | C | | | conserved hypothetical protein | 61.5 | 241 | | | | At | | | | | | | | |
| PSPTO4242 | C | | | conserved hypothetical protein | 59.3 | 205 | | | | At | | | | | | | | |
| PSPTO4250 | C | | | DNA-binding protein | 53.2 | 378 | | | | | | | | | | | | |
| PSPTO4261 | C | + | | isomerase, putative | 50.4 | 232 | Rs | Xcc | Xac | At | Xf | | | | | | | |
| PSPTO4264 | C | + | | conserved hypothetical protein | 55.4 | 184 | | | | | | | | | | | | |
| PSPTO4272 | C | + | | hypothetical protein | 47.8 | 494 | | | | | | | | | | | | |
| PSPTO4282 | C | + | | hypothetical protein | 55.1 | 46 | | | | | | | | | | | | |
| PSPTO4284 | C | + | | acetyltransferase, GNAT family | 60.1 | 148 | | | | | | | | | | | | |
| PSPTO4286 | C | + | | conserved hypothetical protein | 57.1 | 406 | Rs | | | | | | | | | | | |
| PSPTO4287 | C | + | | hypothetical protein | 52 | 336 | | | | | | | | | | | | |
| PSPTO4311 | C | | | hypothetical protein | 53.6 | 74 | | | | | | | | | | | | |
| PSPTO4313 | C | | | hypothetical protein | 61.4 | 69 | | | | | | | | | | | | |
| PSPTO4321 | C | + | + | hypothetical protein | 55.1 | 330 | | | | | | | | | | | | |
| PSPTO4322 | C | + | + | hypothetical protein | 52.6 | 606 | | | | | | | | | | | | |
| PSPTO4323 | C | + | + | conserved hypothetical protein | 53.2 | 159 | | | | | | | | | | | | |
| PSPTO4324 | C | + | + | hypothetical protein | 54.4 | 98 | | | | | | | | | | | | |
| PSPTO4325 | C | + | + | hypothetical protein | 54.5 | 502 | | | | | | | | | | | | |
| PSPTO4326 | C | + | + | conserved hypothetical protein | 52.4 | 313 | | | Xac | | | | | | | | | |
| PSPTO4327 | C | + | + | hypothetical protein | 51.4 | 109 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | |
|-----------|---|---|---|----------------------------------|------|-----|--|-----|-----|--|--|--|----|----|
| PSPTO4346 | C | | | hypothetical protein | 48.5 | 114 | | | | | | | Yp | St |
| PSPTO4348 | C | | | hypothetical protein | 49.3 | 161 | | | | | | | | |
| PSPTO4364 | C | | | hypothetical protein | 57.3 | 32 | | | | | | | | |
| PSPTO4378 | C | + | | hypothetical protein | 52.8 | 36 | | | | | | | | |
| PSPTO4384 | C | + | | hypothetical protein | 56.4 | 107 | | | | | | | | |
| PSPTO4386 | C | + | | hypothetical protein | 52 | 523 | | | | | | | | |
| PSPTO4387 | C | + | | hypothetical protein | 52.1 | 455 | | | | | | | | |
| PSPTO4388 | C | + | | hypothetical protein | 60.3 | 52 | | | | | | | | |
| PSPTO4440 | C | | | hypothetical protein | 60.3 | 42 | | | | | | | | |
| PSPTO4520 | C | + | | methyltransferase domain protein | 57.8 | 783 | | | | | | | | |
| PSPTO4525 | C | + | | hypothetical protein | 55.2 | 55 | | | | | | | | |
| PSPTO4529 | C | + | | hypothetical protein | 50.2 | 162 | | | | | | | | |
| PSPTO4532 | C | + | | hypothetical protein | 55.2 | 102 | | | | | | | | |
| PSPTO4542 | C | | | GAF domain protein | 55.8 | 166 | | Xcc | Xac | | | | | |
| PSPTO4552 | C | | | hypothetical protein | 47.2 | 36 | | | | | | | | |
| PSPTO4556 | C | | | conserved domain protein | 59.3 | 559 | | | | | | | | |
| PSPTO4570 | C | + | + | hypothetical protein | 53.5 | 337 | | | | | | | | |
| PSPTO4571 | C | + | + | hypothetical protein | 52.5 | 399 | | | | | | | | |
| PSPTO4573 | C | + | + | hypothetical protein | 48.1 | 36 | | | | | | | | |
| PSPTO4574 | C | + | + | hypothetical protein | 48 | 370 | | | | | | | | |
| PSPTO4591 | C | + | + | hypothetical protein | 50.3 | 96 | | | | | | | | |
| PSPTO4599 | C | + | + | hypothetical protein | 58 | 157 | | | | | | | | |
| PSPTO4605 | C | + | + | conserved hypothetical protein | 54.9 | 745 | | | Xac | | | | | Ec |
| PSPTO4606 | C | + | + | conserved hypothetical protein | 49 | 132 | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|-----|----|-----|-----|--|----|--|--|--|--|--|--|--|
| PSPTO4607 | C | + | + | hypothetical protein | 49 | 819 | | | | | | | | | | | | |
| PSPTO4609 | C | + | + | hypothetical protein | 56 | 81 | | | | | | | | | | | | |
| PSPTO4614 | C | + | + | conserved hypothetical protein | 51.7 | 200 | | | | | | | | | | | | |
| PSPTO4617 | C | + | + | hypothetical protein | 51.3 | 80 | | | | | | | | | | | | |
| PSPTO4618 | C | + | + | hypothetical protein | 54.5 | 107 | | | | | | | | | | | | |
| PSPTO4620 | C | + | + | conserved hypothetical protein | 49.2 | 107 | | | | | | | | | | | | |
| PSPTO4627 | C | + | + | hypothetical protein | 48.3 | 817 | | | | | | | | | | | | |
| PSPTO4628 | C | + | + | hypothetical protein | 55.4 | 68 | | | | | | | | | | | | |
| PSPTO4629 | C | + | | hypothetical protein | 54.3 | 35 | | | | | | | | | | | | |
| PSPTO4649 | C | | | hypothetical protein | 49.7 | 57 | | | | | | | | | | | | |
| PSPTO4655 | C | | | hypothetical protein | 62.1 | 289 | | | | | | | | | | | | |
| PSPTO4658 | C | | | conserved domain protein | 58.4 | 329 | Rs | | | | | | | | | | | |
| PSPTO4670 | C | + | | hypothetical protein | 54.7 | 265 | | Xcc | Xac | | | | | | | | | |
| PSPTO4672 | C | + | | hypothetical protein | 57.9 | 57 | | | | | | | | | | | | |
| PSPTO4674 | C | + | | hypothetical protein | 51.7 | 58 | | | | | | | | | | | | |
| PSPTO4676 | C | + | | hypothetical protein | 56 | 69 | | | | | | | | | | | | |
| PSPTO4677 | C | + | | hypothetical protein | 57 | 213 | | | | | | | | | | | | |
| PSPTO4688 | C | | + | hypothetical protein | 65.1 | 147 | | | | | | | | | | | | |
| PSPTO4716 | C | + | + | hypothetical protein | 54.7 | 165 | | | | | | | | | | | | |
| PSPTO4717 | C | + | + | hypothetical protein | 59.6 | 89 | | | | | | | | | | | | |
| PSPTO4719 | C | + | + | hypothetical protein | 60 | 55 | | | | | | | | | | | | |
| PSPTO4723 | C | + | + | conserved hypothetical protein | 48.4 | 102 | Rs | | | | At | | | | | | | |
| PSPTO4733 | C | + | + | hypothetical protein | 44.9 | 179 | | | | | | | | | | | | |
| PSPTO4734 | C | + | + | conserved domain protein | 58.7 | 75 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|---|------|-----|--|--|--|--|--|--|--|----|--|--|----|
| PSPTO4741 | C | + | + | hypothetical protein | 45 | 140 | | | | | | | | | | | |
| PSPTO4743 | C | + | + | hypothetical protein | 44 | 633 | | | | | | | | | | | |
| PSPTO4747 | C | + | + | hypothetical protein | 53 | 212 | | | | | | | | | | | |
| PSPTO4750 | C | + | + | hypothetical protein | 54.7 | 159 | | | | | | | | | | | |
| PSPTO4752 | C | + | + | hypothetical protein | 56.1 | 321 | | | | | | | | | | | |
| PSPTO4753 | C | + | + | hypothetical protein | 56.2 | 363 | | | | | | | | | | | |
| PSPTO4754 | C | + | + | hypothetical protein | 51.4 | 281 | | | | | | | | | | | |
| PSPTO4756 | C | + | + | hypothetical protein | 53.8 | 44 | | | | | | | | | | | |
| PSPTO4757 | C | + | + | hypothetical protein | 55.3 | 73 | | | | | | | | | | | |
| PSPTO4758 | C | + | + | hypothetical protein | 51.5 | 44 | | | | | | | | | | | |
| PSPTO4761 | C | + | + | hypothetical protein | 51.4 | 673 | | | | | | | | | | | Ec |
| PSPTO4762 | C | + | + | von Willebrand factor type A domain protein | 52.8 | 224 | | | | | | | | Yp | | | Ec |
| PSPTO4763 | C | + | + | hypothetical protein | 55 | 260 | | | | | | | | | | | Ec |
| PSPTO4766 | C | + | + | hypothetical protein | 54.6 | 102 | | | | | | | | | | | |
| PSPTO4767 | C | + | + | pentapeptide repeat protein | 45.4 | 327 | | | | | | | | | | | |
| PSPTO4772 | C | + | + | hypothetical protein | 50.8 | 346 | | | | | | | | | | | |
| PSPTO4780 | C | + | + | hypothetical protein | 59.2 | 179 | | | | | | | | | | | |
| PSPTO4783 | C | + | + | hypothetical protein | 55.8 | 49 | | | | | | | | | | | |
| PSPTO4785 | C | + | + | hypothetical protein | 51.9 | 36 | | | | | | | | | | | |
| PSPTO4797 | C | | | hypothetical protein | 50 | 72 | | | | | | | | | | | |
| PSPTO4801 | C | | | hypothetical protein | 45.8 | 51 | | | | | | | | | | | |
| PSPTO4811 | C | | | hypothetical protein | 59 | 39 | | | | | | | | | | | |
| PSPTO4815 | C | | | hypothetical protein | 51.5 | 68 | | | | | | | | | | | |
| PSPTO4838 | C | | | hypothetical protein | 55.1 | 49 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|--|--------------------------------|------|-----|----|-----|-----|--|--|----|--|--|--|--|--|----|
| PSPTO4870 | C | + | | hypothetical protein | 55 | 211 | | | | | | | | | | | | |
| PSPTO4871 | C | + | | hypothetical protein | 55 | 211 | | | | | | | | | | | | |
| PSPTO4872 | C | + | | hypothetical protein | 57.3 | 232 | | | | | | | | | | | | |
| PSPTO4884 | C | | | hypothetical protein | 57 | 768 | | | | | | | | | | | | |
| PSPTO4902 | C | | | hypothetical protein | 55.8 | 77 | | | | | | | | | | | | |
| PSPTO4927 | C | | | hypothetical protein | 54.3 | 914 | | | | | | | | | | | | |
| PSPTO4966 | C | + | | hypothetical protein | 52.9 | 128 | | | | | | | | | | | | |
| PSPTO4967 | C | + | | hypothetical protein | 44.4 | 220 | | | | | | | | | | | | |
| PSPTO4968 | C | + | | hypothetical protein | 54.6 | 213 | | | | | | | | | | | | |
| PSPTO5025 | C | | | hypothetical protein | 43.6 | 123 | | | | | | | | | | | | |
| PSPTO5026 | C | | | hypothetical protein | 55.6 | 36 | | | | | | | | | | | | |
| PSPTO5042 | C | | | hypothetical protein | 65.2 | 46 | | | | | | | | | | | | |
| PSPTO5059 | C | | | hypothetical protein | 56.6 | 189 | | | | | | | | | | | | |
| PSPTO5073 | C | | | hypothetical protein | 49.4 | 79 | | | | | | | | | | | | |
| PSPTO5088 | C | | | hypothetical protein | 52.5 | 33 | | | | | | | | | | | | |
| PSPTO5091 | C | + | | conserved hypothetical protein | 60.1 | 239 | Rs | Xcc | Xac | | | | | | | | | Ec |
| PSPTO5098 | C | + | | conserved hypothetical protein | 63.9 | 315 | Rs | Xcc | Xac | | | Xf | | | | | | Ec |
| PSPTO5101 | C | + | | conserved hypothetical protein | 59.8 | 204 | Rs | Xcc | Xac | | | | | | | | | Ec |
| PSPTO5108 | C | + | | conserved hypothetical protein | 62.9 | 151 | Rs | Xcc | Xac | | | | | | | | | Ec |
| PSPTO5113 | C | + | | conserved hypothetical protein | 52.6 | 422 | | | | | | | | | | | | St |
| PSPTO5114 | C | + | | conserved domain protein | 53 | 214 | | | | | | | | | | | | |
| PSPTO5122 | C | | | hypothetical protein | 52.1 | 32 | | | | | | | | | | | | |
| PSPTO5124 | C | | | hypothetical protein | 56.3 | 32 | | | | | | | | | | | | |
| PSPTO5183 | C | | | hypothetical protein | 59.7 | 239 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----------|---|---|---|-----------------------------------|------|-----|--|--|--|--|--|--|--|--|--|--|----|--|
| PSPTO5199 | C | + | | hypothetical protein | 56.8 | 54 | | | | | | | | | | | | |
| PSPTO5202 | C | + | | hypothetical protein | 53.1 | 332 | | | | | | | | | | | | |
| PSPTO5203 | C | + | | hypothetical protein | 52.6 | 359 | | | | | | | | | | | Yp | |
| PSPTO5205 | C | + | | hypothetical protein | 51.9 | 77 | | | | | | | | | | | | |
| PSPTO5206 | C | + | | EF hand domain protein | 45.4 | 310 | | | | | | | | | | | | |
| PSPTO5209 | C | + | | hypothetical protein | 45.2 | 392 | | | | | | | | | | | | |
| PSPTO5210 | C | + | | EF hand domain protein | 44.3 | 310 | | | | | | | | | | | | |
| PSPTO5234 | C | + | | hypothetical protein | 51.8 | 191 | | | | | | | | | | | | |
| PSPTO5235 | C | + | | hypothetical protein | 56.5 | 118 | | | | | | | | | | | | |
| PSPTO5236 | C | + | | hypothetical protein | 58.6 | 37 | | | | | | | | | | | | |
| PSPTO5257 | C | | | hypothetical protein | 59 | 216 | | | | | | | | | | | | |
| PSPTO5281 | C | | | hypothetical protein | 54.3 | 78 | | | | | | | | | | | | |
| PSPTO5298 | C | | | hypothetical protein | 58.7 | 63 | | | | | | | | | | | | |
| PSPTO5331 | C | | | hypothetical protein | 53.8 | 630 | | | | | | | | | | | | |
| PSPTO5332 | C | | | trypsin domain protein | 58.2 | 510 | | | | | | | | | | | | |
| PSPTO5345 | C | + | + | hypothetical protein | 53.8 | 318 | | | | | | | | | | | | |
| PSPTO5346 | C | + | + | hypothetical protein | 60.8 | 397 | | | | | | | | | | | | |
| PSPTO5347 | C | + | + | hypothetical protein | 59.4 | 83 | | | | | | | | | | | | |
| PSPTO5348 | C | + | + | hypothetical protein | 53.3 | 366 | | | | | | | | | | | | |
| PSPTO5349 | C | + | + | prevent-host-death family protein | 54.7 | 75 | | | | | | | | | | | | |
| PSPTO5355 | C | + | + | hypothetical protein | 56.7 | 161 | | | | | | | | | | | | |
| PSPTO5364 | C | + | + | hypothetical protein | 55 | 100 | | | | | | | | | | | | |
| PSPTO5365 | C | + | + | conserved domain protein | 41.5 | 345 | | | | | | | | | | | | |
| PSPTO5373 | C | + | + | hypothetical protein | 39.9 | 360 | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----------|---|---|---|--------------------------------|------|------|----|-----|-----|--|--|----|----|--|----|
| PSPTO5374 | C | + | + | conserved hypothetical protein | 51.7 | 107 | Rs | | | | | Xf | Yp | | |
| PSPTO5384 | C | + | | conserved hypothetical protein | 52.8 | 113 | | | | | | | | | |
| PSPTO5385 | C | + | | hypothetical protein | 57.3 | 245 | | | | | | | | | |
| PSPTO5386 | C | + | | hypothetical protein | 56.2 | 35 | | | | | | | | | |
| PSPTO5392 | C | + | | hypothetical protein | 54.2 | 75 | | | | | | | | | |
| PSPTO5410 | C | | | hypothetical protein | 63.3 | 270 | Rs | | | | | | | | |
| PSPTO5413 | C | | | EF hand domain protein | 49.1 | 792 | | | | | | | | | |
| PSPTO5429 | C | | | hypothetical protein | 43.9 | 38 | | | | | | | | | |
| PSPTO5437 | C | | | hypothetical protein | 55.7 | 227 | | | | | | | | | |
| PSPTO5442 | C | + | | hypothetical protein | 61.1 | 119 | | | | | | | | | |
| PSPTO5446 | C | + | | hypothetical protein | 55.8 | 40 | | | | | | | | | |
| PSPTO5447 | C | + | | conserved hypothetical protein | 51.6 | 142 | | Xcc | Xac | | | | | | St |
| PSPTO5449 | C | + | | hypothetical protein | 61.4 | 166 | | | | | | | | | |
| PSPTO5450 | C | + | | conserved hypothetical protein | 59.7 | 101 | | Xcc | | | | | | | |
| PSPTO5455 | C | + | | conserved hypothetical protein | 60.9 | 258 | | | | | | | | | |
| PSPTO5456 | C | + | | hypothetical protein | 58.6 | 309 | | | | | | | | | |
| PSPTO5458 | C | + | | conserved hypothetical protein | 53.4 | 158 | | | | | | | | | |
| PSPTO5459 | C | | | hypothetical protein | 50.5 | 31 | | | | | | | | | |
| PSPTO5471 | C | | | hypothetical protein | 59.6 | 142 | | | | | | | | | |
| PSPTO5481 | C | | | hypothetical protein | 57.4 | 1550 | | | | | | | | | |
| PSPTO5495 | C | + | | hypothetical protein | 53.7 | 210 | | | | | | | | | |
| PSPTO5496 | C | + | | hypothetical protein | 52.3 | 51 | | | | | | | | | |
| PSPTO5497 | C | + | | hypothetical protein | 52.2 | 210 | | | | | | | | | |
| PSPTO5513 | C | | | hypothetical protein | 58.4 | 73 | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|------------|----|---|---|--------------------------------|------|-----|----|-----|-----|----|----|--|--|----|----|----|----|
| PSPTO5514 | C | | | conserved domain protein | 52.1 | 103 | | | | | | | | | | | |
| PSPTO5531 | C | | | hypothetical protein | 61.7 | 346 | | | | | | | | | | | |
| PSPTO5552 | C | | | hypothetical protein | 61.8 | 41 | | | | | | | | | | | |
| PSPTO5555 | C | | | hypothetical protein | 54.1 | 77 | | | | | | | | | | | |
| PSPTO5565 | C | | | hypothetical protein | 51.6 | 213 | | | | | | | | | | | |
| PSPTO5568 | C | | | hypothetical protein | 52.4 | 49 | | | | | | | | | | | |
| PSPTO5583 | C | | | Ais protein, putative | 52.6 | 228 | | | | | | | | | | Ec | St |
| PSPTO5592 | C | | | hypothetical protein | 53.5 | 293 | | | | | | | | | | | |
| PSPTOA0015 | pA | + | + | conserved hypothetical protein | 50.5 | 72 | | | | | | | | | | | |
| PSPTOA0022 | pA | + | + | hypothetical protein | 54.2 | 193 | | | | | | | | | | | |
| PSPTOA0023 | pA | + | + | hypothetical protein | 65.5 | 116 | | | | | | | | | | | |
| PSPTOA0024 | pA | + | + | hypothetical protein | 56 | 125 | | | | | | | | | | | |
| PSPTOA0025 | pA | + | + | conserved hypothetical protein | 56.4 | 278 | Rs | | | | | | | | | Ec | |
| PSPTOA0026 | pA | + | + | conserved hypothetical protein | 52.7 | 62 | | | | | | | | | | | |
| PSPTOA0031 | pA | + | + | conserved hypothetical protein | 50.6 | 393 | Rs | Xcc | | | | | | Yp | Ec | | |
| PSPTOA0033 | pA | + | + | hypothetical protein | 56.1 | 132 | | | | | | | | | | | |
| PSPTOA0038 | pA | + | + | hypothetical protein | 40.4 | 61 | | | | | | | | | | | |
| PSPTOA0040 | pA | + | | conserved hypothetical protein | 55 | 177 | | | | | | | | Yp | Ec | St | |
| PSPTOA0046 | pA | + | | hypothetical protein | 57.5 | 69 | | | | | | | | | | | |
| PSPTOA0057 | pA | + | | conserved hypothetical protein | 57.1 | 91 | | Xcc | Xac | At | Xf | | | | | | |
| PSPTOA0058 | pA | + | | conserved hypothetical protein | 57.1 | 66 | | | | | Xf | | | | Ec | | |
| PSPTOA0061 | pA | + | | hypothetical protein | 56.8 | 78 | | | | | | | | | | | |
| PSPTOA0069 | pA | | | hypothetical protein | 51.7 | 140 | | | | | | | | | | | |
| PSPTOA0070 | pA | | | hypothetical protein | 59.3 | 207 | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|------------|----|---|--|--------------------------------|------|-----|----|-----|-----|--|--|--|----|----|----|
| PSPTOB0003 | pB | + | | conserved hypothetical protein | 44.8 | 157 | | Xcc | | | | | Yp | | |
| PSPTOB0006 | pB | + | | hypothetical protein | 61.9 | 42 | | | | | | | | | |
| PSPTOB0012 | pB | + | | hypothetical protein | 56.8 | 352 | | | Xac | | | | | | |
| PSPTOB0015 | pB | + | | hypothetical protein | 50 | 98 | | | | | | | | | |
| PSPTOB0016 | pB | + | | conserved domain protein | 57.3 | 117 | | | | | | | | | |
| PSPTOB0020 | pB | + | | hypothetical protein | 53.9 | 315 | | | | | | | | | |
| PSPTOB0023 | pB | + | | hypothetical protein | 52.5 | 73 | | | | | | | | | |
| PSPTOB0027 | pB | + | | hypothetical protein | 57.7 | 138 | | | | | | | | | |
| PSPTOB0028 | pB | + | | hypothetical protein | 68.1 | 91 | | | | | | | | | |
| PSPTOB0029 | pB | + | | hypothetical protein | 58.7 | 84 | | | | | | | | | |
| PSPTOB0030 | pB | + | | conserved hypothetical protein | 57.1 | 278 | Rs | | | | | | | Ec | |
| PSPTOB0031 | pB | + | | conserved hypothetical protein | 49.5 | 66 | | | | | | | | | |
| PSPTOB0033 | pB | + | | hypothetical protein | 48.4 | 93 | | | | | | | | | |
| PSPTOB0034 | pB | + | | hypothetical protein | 52.3 | 114 | | | | | | | | | |
| PSPTOB0037 | pB | + | | hypothetical protein | 50.7 | 69 | | | | | | | | | |
| PSPTOB0044 | pB | + | | hypothetical protein | 37.2 | 61 | | | | | | | | | |
| PSPTOB0046 | pB | + | | conserved hypothetical protein | 55.6 | 177 | | | | | | | Yp | Ec | St |
| PSPTOB0047 | pB | + | | hypothetical protein | 51.3 | 102 | | | | | | | | | |
| PSPTOB0053 | pB | + | | hypothetical protein | 55.7 | 231 | | | | | | | | | |
| PSPTOB0055 | pB | + | | hypothetical protein | 56.8 | 81 | | | | | | | | | |
| PSPTOB0070 | pB | + | | hypothetical protein | 54.1 | 90 | | | | | | | | | |
| PSPTOB0072 | pB | + | | conserved hypothetical protein | 59 | 400 | | | | | | | | | |
| PSPTOB0073 | pB | + | | PIN domain protein | 57.3 | 125 | | | | | | | | | |
| PSPTOB0074 | pB | + | | conserved hypothetical protein | 56.6 | 66 | | | | | | | | | |

The inferred proteomes of eight pathogenic bacteria were searched with the 811 genes unique to DC3000 by using a BLASTP cutoff criterion of $E < 10^{-5}$ which will identify putative homologs as well as paralogous gene family members. Rs = *Ralstonia solanacearum*, Xac = *Xanthomonas axonopodis* pv. *citri*, Xcc = *Xanthomonas campestris* pv. *campestris*, At = *Agrobacterium tumefaciens* (U. Wash seq.), Xf = *Xylella fastidiosa*, Yp = *Yersinia pestis* CO92, St = *Salmonella typhimurium* LT2, and Ec = *Escherichia coli* O157:H7 EDL933.

^a Individual unique genes that cluster with one another at a density of at least three genes within a 10-kb region.

^b Genes or clusters (as defined in ^a) that are present within 20 kb of TTSS components and effectors.

^c The annotation of some of the genes in the table is based on multiple alignments to a nonredundant amino acid database as well as Hidden Markov Models (HMMs), which identify domains in protein families (Pfam and TIGRFAMs). Additional information on the individual loci and protein families is available in The Institute for Genomic Research Comprehensive Microbial Resource (<http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.spl>).