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errata

The yeast genome directory

Nature 387 (suppl.) (1997)

In the list of authors given on page 5 of this supplement, the names of some authors were omitted or misspelled (asterisks). These were: R. Altmann; W. Arnold*; M. de Haan*; K. Hamberg; K. Hinni; L. Jones; W. Kramer; H. Küster*; K. C. T. Maurer*; D. Niblett; N. Paricio*; A. G. Parle-McDermott*; C. Rebischung; C. Richards; L. Rifkin*; J. Robben; C. Rodrigues-Pousada*; I. Schaaff-Gerstenschläger*; P. H. M. Smits*; Y. Su*; Q. J. M. van der Aart*; J. C. van Vliet-Reedijk*; A. Wach; M. Yamazaki*.

Measurements of elastic anisotropy due to solidification texturing and the implications for the Earth's inner core

Michael I. Bergman

Nature **389**, 60–63 (1997)

Owing to a typographical error, this Letter appeared under the title "Measurements of electric anisotropy due to solidification texturing and the implications for the Earth's inner core". The word 'elastic' in the first line was erroneously replaced with 'electric'.

cAMP-induced switching in turning direction of nerve growth cones

Hong-jun Song, Guo-li Ming & Mu-ming Poo

Nature 388, 275-279 (1997)

The order of panels in Fig. 3 of this Letter is incorrect as published. Figure 3a-e should be labelled as f-j, and Fig. 3f-j should be labelled a-e.

corrections

Synthesis and X-ray structure of dumb-bell-shaped C₁₂₀

Guan-Wu Wang, Koichi Komatsu, Yasujiro Murata & Motoo Shiro

Nature **387**, 583–586 (1997)

In this Letter, we overlooked a citation of G. Oszlanyi *et al.*, *Phys. Rev. B* **54**, 11849 (1996), who reported the observation of covalently bound $(C_{60})_2^{2-}$ dianions from the X-ray powder diffraction patterns of the metastable phases of KC_{60} and RbC_{60} .

The complete genome sequence of the gastric pathogen *Helicobacter pylori*

Jean-F. Tomb, Owen White, Anthony R. Kerlavage, Rebecca A. Clayton, Granger G. Sutton, Robert D. Fleischmann, Karen A. Ketchum, Hans Peter Klenk, Steven Gill, Brian A. Dougherty, Karen Nelson, John Quackenbush, Lixin Zhou, Ewen F. Kirkness, Scott Peterson, Brendan Loftus, **Delwood Richardson, Robert Dodson,** Hanif G. Khalak, Anna Glodek, Keith McKenney, Lisa M. Fitzegerald, Norman Lee, Mark D. Adams, Erin K. Hickey, Douglas E. Berg, Jeanine D. Gocayne, Teresa R. Utterback, Jeremy D. Peterson, Jenny M. Kelley, Matthew D. Cotton, Janice M. Weidman, Claire Fujii, Cheryl Bowman, Larry Watthey, Erik Wallin, William S. Hayes, Mark Borodovsky, Peter D. Karp, Hamilton O. Smith, Claire M. Fraser & J. Craig Venter

Nature 388, 539-547 (1997)

In this Article, we incorrectly stated that the amino acids lysine and arginine are twice as abundant in *H. pylori* proteins as they are in those of *Haemophilus influenzae* and *Escherichia coli*. This statement was derived from amino-acid analyses that compared absolute differences in abundance, but these do not reflect the frequencies with which amino acids are found in the organisms in question. The actual abundance of arginine in *H. pylori*, *H. influenzae* and *E. coli* is 3.5, 4.5 and 5.5%, respectively; the abundance of lysine in these organisms is 8.9, 6.3 and 4.4%, respectively. This oversight is particularly unfortunate because Russell H. Doolittle, who wrote an accompanying News and Views on our Article and brought this to our attention, was led to comment on the significance of our inaccurate observation. We regret this and any other misunderstanding that our error may have caused.

The complete genome sequence of the gastric pathogen *Helicobacter pylori*

Jean-F. Tomb*, Owen White*, Anthony R. Kerlavage*, Rebecca A. Clayton*, Granger G. Sutton*, Robert D. Fleischmann*, Karen A. Ketchum*, Hans Peter Klenk*, Steven Gill*, Brian A. Dougherty*, Karen Nelson*, John Quackenbush*, Lixin Zhou*, Ewen F. Kirkness*, Scott Peterson*, Brendan Loftus*, Delwood Richardson*, Robert Dodson*, Hanif G. Khalak*, Anna Glodek*, Keith McKenney*, Lisa M. Fitzegerald*, Norman Lee*, Mark D. Adams*, Erin K. Hickey*, Douglas E. Berg†, Jeanine D. Gocayne*, Teresa R. Utterback*, Jeremy D. Peterson*, Jenny M. Kelley*, Matthew D. Cotton*, Janice M. Weidman*, Claire Fujii*, Cheryl Bowman*, Larry Watthey*, Erik Wallin‡, William S. Hayes§, Mark Borodovsky§, Peter D. Karp||, Hamilton O. Smith§, Claire M. Fraser* & J. Craig Venter*

Helicobacter pylori, strain 26695, has a circular genome of 1,667,867 base pairs and 1,590 predicted coding sequences. Sequence analysis indicates that *H. pylori* has well-developed systems for motility, for scavenging iron, and for DNA restriction and modification. Many putative adhesins, lipoproteins and other outer membrane proteins were identified, underscoring the potential complexity of host-pathogen interaction. Based on the large number of sequence-related genes encoding outer membrane proteins and the presence of homopolymeric tracts and dinucleotide repeats in coding sequences, *H. pylori*, like several other mucosal pathogens, probably uses recombination and slipped-strand mispairing within repeats as mechanisms for antigenic variation and adaptive evolution. Consistent with its restricted niche, *H. pylori* has a few regulatory networks, and a limited metabolic repertoire and biosynthetic capacity. Its survival in acid conditions depends, in part, on its ability to establish a positive inside-membrane potential in low pH.

For most of this century the cause of peptic ulcer disease was thought to be stress-related and the disease to be prevalent in hyperacid producers. The discovery¹ that *Helicobacter pylori* was associated with gastric inflammation and peptic ulcer disease was initially met with scepticism. However, this discovery and subsequent studies on *H. pylori* have revolutionized our view of the gastric environment, the diseases associated with it, and the appropriate treatment regimens².

Helicobacter pylori is a micro-aerophilic, Gram-negative, slowgrowing, spiral-shaped and flagellated organism. Its most characteristic enzyme is a potent multisubunit urease³ that is crucial for its survival at acidic pH and for its successful colonization of the gastric environment, a site that few other microbes can colonize². H. pylori is probably the most common chronic bacterial infection of humans, present in almost half of the world population². The presence of the bacterium in the gastric mucosa is associated with chronic active gastritis and is implicated in more severe gastric diseases, including chronic atrophic gastritis (a precursor of gastric carcinomas), peptic ulceration and mucosa-associated lymphoid tissue lymphomas². Disease outcome depends on many factors, including bacterial genotype, and host physiology, genotype and dietary habits^{4,5}. H. pylori infection has also been associated with persistent diarrhoea and increased susceptibility to other infectious diseases⁶.

Because of its importance as a human pathogen, our interest in its biology and evolution, and the value of complete genome sequence information for drug discovery and vaccine development, we have

Table 1 Genome features

General

Coding regions (91.0%) Stable RNA (0.7%) Non-coding repeats (2.3%) Intergenic sequence (6.0%)

RNA

 Ribosomal RNA
 Coordinates

 235-5S
 445,306-448,642 bp

 23S-5S
 1,473,557-1,473,919 bp

 16S
 1,209,082-1,207,584 bp

 16S
 1,511,138-1,512,635 bp

 5S
 448,041-448,618 bp

Transfer RNA

36 species (7 clusters, 12 single genes)

Structural RNA

1 species (ssrD)

Insertion sequences

IS605 13 copies (5 full-length, 8 partial)

IS606 4 copies (2 full-length, 2 partial)

Distinct G + C regions

region 1 (33% G + C) 452-479 kb region 2 (35% G + C) 539-579 kb region 3 (33% G + C) 1,049-1,071 kb

 $\begin{array}{lll} \text{region 3 (33% G} + \text{C) 1,049-1,071 kb} & \text{IS605} \\ \text{region 4 (43% G} + \text{C) 1,264-1,276 kb} & \beta \text{ and} \\ \text{region 5 (33% G} + \text{C) 1,590-1,602 kb} & \text{two region 5 (33% G} + \text{C) 1,590-1,602 kb} \end{array}$

Coding sequences

1,590 coding sequences (average 945 bp)
1,091 identified database match

Associated genes IS605, 5SRNA and repeat 7; virB4 cag PAI (Fig. 4) IS605, 5SRNA and repeat 7 β and β' RNA polymerase, EF-G (fusA) two restriction/modification systems

539

629.845-630.124 bp

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sequenced the genome of a representative *H. pylori* strain by the whole-genome random sequencing method as described for *Haemophilus influenzae*⁷, *Mycoplasma genitalium*⁸ and *Methanococcus jannaschii*⁹.

General features of the genome

Genome analysis. The genome of H. pylori strain 26695 consists of a circular chromosome with a size of 1,667,867 base pairs (bp) and average G + C content of 39% (Figs 1 and 2). Five regions within the genome have a significantly different G + C composition (Table 1 and Fig. 1). Two of them contain one or more copies of the insertion sequence IS605 (see below) and are flanked by a 5S ribosomal RNA sequence at one end and a 521 bp repeat (repeat 7) near the other. These two regions are also notable because they contain genes involved in DNA processing and one contains 2 orthologues of the virB4/ptl gene, the product of which is required for the transfer of oncogenic T-DNA of Agrobacterium and the secretion of the pertussis toxin by Bordetella pertussis¹⁰. Another region is the cag pathogenicity island (PAI), which is flanked by 31-bp direct repeats, and appears to be the product of lateral transfer¹¹.

RNA and repeat elements. Thirty-six tRNA species were identified using tRNAscan-SE¹². These are organized into 7 clusters plus 12 single genes. Two separate sets of 23S–5S and 16S ribosomal RNA (rRNA) genes were identified, along with one orphan 5S gene and one structural RNA gene (Table 1). Associated with each of the two 23S–5S gene clusters is a 6-kilobase (kb) repeat containing a possible operon of 5 ORFs that have no database matches.

Eight repeat families (>97% identity) varying in length from 0.47 to 3.8 kb were found in the chromosome (Figs 1 and 2). Members of repeat 7 are found in intergenic regions, while the others are associated with coding sequences and may represent gene duplications. Repeats 1, 2, 3 and 6 are associated with genes that encode outer-membrane proteins (OMP) (Fig. 3).

Two distinct insertion sequence (IS) elements are present. There are five full-length copies of the previously described IS605^{11,13} and two of a newly discovered element designated IS606. In addition, there are eight partial copies of IS605 and two partial copies of IS606. Both elements encode two divergently transcribed transposases (TnpA and TnpB). IS606 has less than 50% nucleotide identity with IS605 and the IS606 transposases have 29% amino-acid identity with their IS605 counterpart. Both copies of the IS606 TnpB may be non-functional owing to frameshifts.

Origin of replication. As a typical eubacterial origin of replication was not identified¹⁴, we arbitrarily designated basepair one at the start of a 7-mer repeat, (AGTGATT)₂₆, that produces translational stops in all reading frames, as this repeated DNA is unlikely to contain any coding sequence.

Open reading frames. One thousand five hundred and ninety predicted coding sequences were identified. They were searched against a non-redundant protein database resulting in 1,091 putative identifications that were assigned biological roles using a classification system adapted from Riley¹⁵ (Table 2). The 1,590 predicted genes had an average size of 945 bp, similar to that observed in other prokaryotes^{7–9}, and no genome-wide strand bias was observed (Fig. 2). More than 70% of the predicted proteins in *H. pylori* have a calculated isoelectric point (pI) greater than 7.0, compared to \sim 40% in *H. influenzae* and *E. coli*. The basic amino acids, arginine and lysine, occur twice as frequently in *H. pylori* proteins as in those of *H. influenzae* and *E. coli*, perhaps reflecting an adaptation of *H. pylori* to gastric acidity.

Paralagous families. Ninety-five paralogous gene families comprising 266 gene products (16% of the total) were identified (www.tigr.org/tdb/mdb/hpdb/hpdb.html). Of these, 67 (173 proteins) have an assigned role. Sixty-four have only 2 members, while the porin/adhesin-like outer membrane protein family (Fig. 2) is the largest with 32 members. The largest number of paralogues with assigned roles fall into the functional categories of cell

envelope, transport and binding proteins, and proteins involved in replication. The large number of cell envelope proteins might reflect either a reduced biosynthetic capacity or a need to adapt to the challenging gastric environment.

Cell division and protein secretion

The gene content of *H. pylori* suggests that the basic mechanisms of replication, cell division and secretion are similar to those of *E. coli* and *H. influenzae*. However, important differences are noted. For example, apparently missing from the *H. pylori* genome are orthologues of DnaC, MinC, and the secretory chaperonin, SecB. In oriC-type primosome formation, the DnaB and DnaC proteins form a B–C complex that delivers the DnaB helicase to the developing primosome complex¹⁶. The apparent absence of DnaC in *H. pylori* suggests that either a novel mechanism for recruiting DnaB exists or a DnaC orthologue with no detectable sequence similarity is present. Similar arguments can be made for other seemingly missing important functions.

H. pylori has a classical set of bacterial chaperones (DnaK, DnaJ, CbpA, GrpE, GroEL, GroES, and HtpG). The transcriptional regulation of *H. pylori* chaperone genes is likely to be different from that in *E. coli*, as it seems not to have the sigma factors that upregulate chaperone synthesis in *E. coli* (heat-shock sigma 32 and stationary-phase sigma S).

In addition to the SecA-dependent secretory pathway, *H. pylori* has two specialized export systems. One is associated with the *cag* pathogenicity island¹¹ and the other is the flagellar export pathway which is assembled from orthologues of FliH, FliI, FliP, FlhA, FlhB, FliQ, FliR and FliP¹⁷. Apparently absent from *H. pylori* is a type IV signal peptidase and orthologues of the dsbABC system, which in other species are required for the maturation of pili and pilin-like structures¹⁸ and assembly of surface structures involved in virulence and DNA transformation¹⁹.

Recombination, repair and restriction systems

Systems for homologous recombination and post-replication, mismatch, excision and transcription-coupled repair appear to be present in *H. pylori*. Also present are genes with similarity to DNA glycosylases which have associated AP endonuclease activity. The RecBCD pathway, which mediates homologous recombination and double-strand break repair, and RecT and RecE orthologues, proteins involved in strand exchange during recombination²⁰, seem to be absent. The ability of *H. pylori* to perform mismatch repair is suggested by the presence of methyl transferases, mutS and uvrD. However, orthologues of MutH and MutL were not identified. Components of an SOS system also appear to be absent.

Bacteria commonly use restriction and modification systems to degrade foreign DNA. In *H. pylori*, this defence system is well developed with eleven restriction-modification systems identified on the basis of gene order and similarity to endonucleases, methyltransferases, and specificity subunits. Three type I, one type II, and three type IIS systems were identified, as well as four type III systems, including the recently identified epithelial responsive

Figure 1 Linear representation of the *H. pylori* 26695 chromosome illustrating the location of each predicted protein-coding region, RNA gene, and repeat elements in the genome. Symbols are as follows: ++, Co²⁺, Zn²⁺, Cd²⁺; ?, unknown; A/G/S, p-alanine/glycine/p-serine; B12, B12/ferric siderophores; E, glutamate; Mo, molybdenum; P, proline; P/G, proline/glycine betaine; Q, glutamine; S, serine; a-k, α-ketoglutarate; a/o, arginine/ornithine; aa, amino acids (specificity unknown); aa2, dipeptides; aaX, oligopeptides; fum, fumarate, succinate; glu, glucose/galactose; h, hemin; lac, L-lactate; mal, malate 2-oxoglutarate; nic, nicotinamide mononucleotides; pyr, pyrimidine nucleosides. Numbers associated with tRNA symbols represent the number of tRNAs at a locus. Numbers associated with GES represent the number of membrane-spanning domains according to the Goldman, Engelman and Steitz scale as calculated by TopPred⁴⁷.

endonuclease, *iceA1*, and its associated DNA adenine methyltransferase (M. HypI) genes^{21,22}. In addition to the complete systems, seven adenine-specific, and four cytosine-specific methyltransferases, and one of unknown specificity were found. Each of these has an adjacent gene with no database match, suggesting that they may function as part of restriction-modification systems.

Transcription and translation

Although analysis of gene content suggests that *H. pylori* has a basic transcriptional and translational machinery similar to that of *E. coli*, interesting differences are observed. For example, no genes for a catalytic activity in tRNA maturation (*rnd*, *rph*, or *rnpB*) were identified and of the three known ribonucleases involved in mRNA degradation, only polyribonucleotide phosphorylase was found. Twenty-one genes coding for 18 of the 20 tRNA synthetases normally required for protein biosynthesis were found.

As in most other completely sequenced bacterial genomes, the gene for glutaminyl-tRNA synthetase, glnS, is missing, and the existence of a transamidation process is assumed. It is also possible that the product of the second glutamyl-tRNA synthetase gene, *gltX*, present in H. pylori, may have acquired the glutaminyl-tRNA synthetase function. H. pylori provides the first example of a bacterial genome apparently lacking an asparaginyl-tRNA synthetase gene, asnS. A transamidation process to form Asn-tRNAAsn from Asp-tRNAAsn has been reported for the archaeon Haloferax volcanii²² and may also operate in H. pylori. Most intriguing, however, is the finding that in H. pylori the genes encoding the β and β' subunits of RNA polymerase are fused. In all studied prokaryotes the two genes are contiguous, but separate, and are part of the same transcriptional unit. Whether this gene fusion in H. pylori results in a fused protein, or whether the transcriptional or translational product of the fusion is subject to splicing, is currently not known. It is worth noting that an artificial fusion of the E. coli

rpoB and *rpoC* genes is viable and results in a transcriptional complex, which has the same stoichiometry as the native complex (K. Severinov, personal communication).

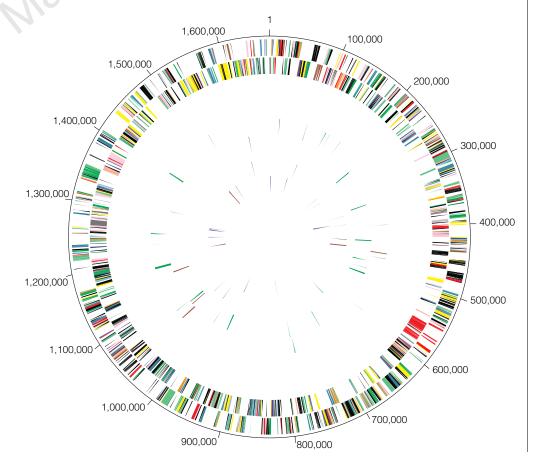
Adhesion and adaptive antigenic variation

Most pathogens show tropism to specific tissues or cell types and often use several adherence mechanisms for successful attachment. *H. pylori* may use at least five different adhesins to attach to gastric epithelial cells⁵. One of them, HpaA (HP0797), was previously identified as a lipoprotein in the flagellar sheath and outer membrane^{5,23}. In addition to the HpaA orthologue, we have identified 19 other lipoproteins. Few have an identifiable function, but some are likely to contribute to the adherence capacity of the organism.

Two adhesins^{24–26}, one of which mediates attachment to the Lewis^b histo-blood group antigens, belong to the large family of outer membrane proteins (OMP) (Fig. 3) (T. Boren and R. Haas, personal communication). It is conceivable that other members of these closely related proteins also act as adhesins. Given the large number of sequence-related genes encoding putative surface-exposed proteins, the potential exists for recombinational events leading to mosaic organization. This could be the basis for antigenic variation in *H. pylori* and an effective mechanism for host defence evasion, as seen in *M. genitalium*²⁷.

At least one other mechanism for antigenic variation could operate in *H. pylori*. The DNA sequence at the beginning of eight genes, including five members of the OMP family, contain stretches of CT or AG dinucleotide repeats (Table 3a). In addition, poly(C) or poly(G) tracts occur within the coding sequence of nine other genes (Table 3b). Slipped-strand mispairing within such repeats are documented features of one mechanism of genotypic variation^{28,29}. These mechanisms may have evolved in bacterial pathogens to increase the frequency of phenotypic variation in genes involved in

Figure 2 Circular representation of the H. pylori 26695 chromosome. Outer concentric circle: predicted coding regions on the plus strand classified as to role according to the colour code in Fig. 1 (except for unknowns and hypotheticals, which are in black). Second concentric circle: predicted coding regions on the minus strand. Third and fourth concentric circles: IS elements (red) and other repeats (green) on the plus and minus strand, respectively. Fifth and sixth concentric circles: tRNAs (blue), rRNAs (red), and sRNAs (green) on the plus and minus strand, respectively.



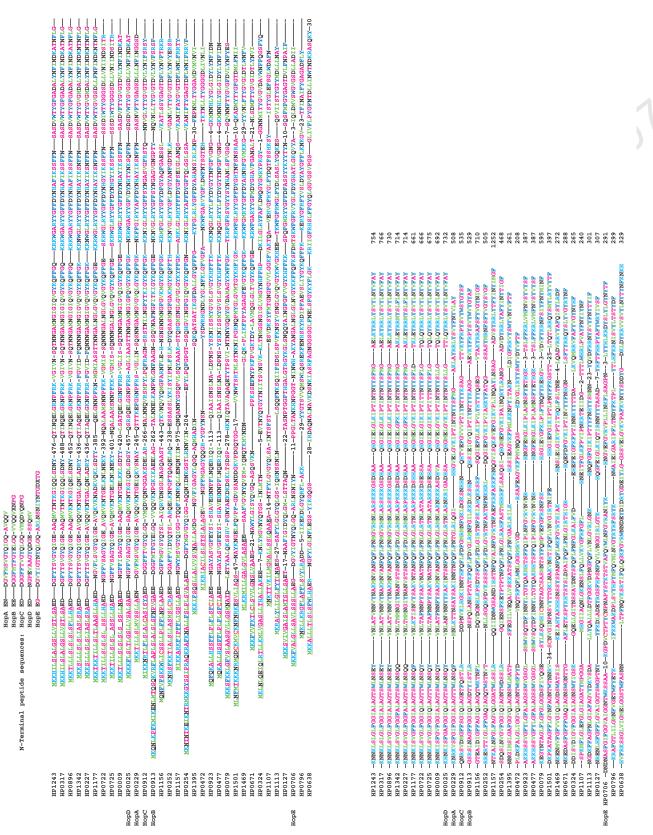


Figure 3 Multiple sequence alignment of members of the outer membrane protein family of *H. pylori*. These proteins were identified as OMPs based on the characteristic alternating hydrophobic residues at their carboxy termini. All members of this family have one domain of similarity at the amino-terminal end and seven domains of similarity at their carboxy-terminal end. Note that the first 11 of these OMPs share extensive similarity over their entire length. Four of the OMPs were identified as porins (Hops) based on identity to published aminoterminal sequences, represented at the top of the alignment⁵⁰. The most likely

candidate for HopD is HP0913, which has 15 matches to the first 20-residue N-terminal peptide sequence⁵⁰. These differences may be due to strain variability. The program Signal-P⁴⁸ was used to identify cleavage sites and signal peptides (underlined). Four of the OMPs have TTG start codons (HP1156, HP0252, HP1113, HP0796). Numbers embedded in the sequences represent amino acids omitted from the alignment. The star symbols indicate that HP722, HP725 and HP9 proteins contain a frameshift in their signal-peptide-coding region. These frameshifts are associated with the presence of dinucleotide repeats (Table 3).

critical interactions with their hosts²⁸. Such 'contingency' genes encode surface structures like pilins, lipoproteins or enzymes that produce lipopolysaccharide molecules²⁸. Our analysis suggests that the seventeen genes reported in Table 3a,b belong to this category and thus may provide an example of adaptive evolution in *H. pylori*.

Phenotypic variation at the transcriptional level may also operate in *H. pylori*. Examples of repetitive DNA mediating transcriptional control have been documented by the presence of oligonucleotide repeats in promoter regions²⁹. Homopolymeric tracts of A or T in potential promoter regions of eighteen genes were found, including eight members of the OMP family (Table 3c).

Virulence

The virulence of individual *H. pylori* isolates has been measured by their ability to produce a cytotoxin-associated protein (CagA) and

an active vacuolating cytotoxin (VacA)⁵. The *cagA* gene, though not a virulence determinant, is positioned at one end of a pathogenecity island containing genes that elicit the production of interleukin (IL)-8 by gastric epithelial cells^{11,30}. Consistent with its more virulent character, *H. pylori* strain 26695 contains a single contiguous PAI region¹¹ (Fig. 4).

VacA induces the formation of acidic vacuoles in host epithelial cells, and its presence is associated epidemiologically with tissue damage and disease³¹. VacA may not be the only ulcer-causing factor as 40% of *H. pylori* strains do not produce detectable amounts of the cytotoxin *in vitro*⁵. Sequence differences at the amino terminus and central sections are noted among VacA proteins derived from Tox⁺ and Tox⁻ strains³¹. This Tox⁺ *H. pylori* strain contains the more toxigenic S1a/m1 type cytotoxin and three additional large proteins with moderate similarities to the carboxy-terminal end of the active

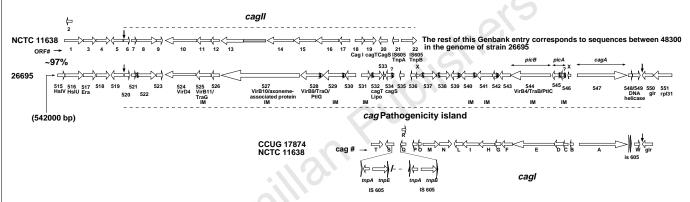


Figure 4 Comparison between the Cag pathogenicity islands of the sequenced strain, 26695 and the NCTC11638 strain. The twenty nine ORFs of the contiguous PAI in strain 26695 are represented together with the corresponding ORFs from the PAI present in NCTC11638 (AC000108 and U60176). The PAI in NCTC11638 is divided by the IS 605 elements into two regions, cagl and cagll. The PAI in NCTC11638 is flanked by a 31-bp (TTACAATTTGAGCCCATTCTTTAGCTTGTTTT) direct repeat (vertical arrows) as described11. Some of the genes encode proteins with similarity to proteins involved either in DNA transfer (Vir and Tra proteins) or in export of a toxin (Ptl protein)10. However, these genes do not have the conserved contiguous arrangement found in the VirB, Tra and Ptl operons, suggesting that this PAI is not derived from these systems. Most genes of the PAI have no database match, contrary to a previous suggestion¹¹. Thirteen of the proteins have a signal peptide (squiggle line), three of them with a weaker probability (squiggled line+?). The average length of the signal peptides is 25 amino acids, suggesting that this PAI is of Gram-negative origin. Eight proteins are predicted to have at least two membrane-spanning domains and to be integral membrane proteins

(IM)⁴⁷. Although the two PAI are ~97% identical at the nucleotide level, there are several notable and perhaps biologically relevant differences between the two sequences. Four of the genes differ in size. In the PAI of strain 26695, HP 520 and 521 are shorter, whereas HP523 is longer, and HP 527 actually spans both ORF13 and 14. In addition, the N-terminal part of HP527 is 129 amino acids longer than the corresponding region in ORF14. HP548/549 contains a frameshift and is therefore probably inactive in strain 26695. The stippled box preceding ORF13 represents an N-terminal extension not annotated in the Genbank entry for the PAI of NCTC11638. The 'x' indicates ORFs that are neither GeneMark-positive nor GeneSmith-positive, so were not included in our gene list. However, these ORFs may be biologically significant. We do not represent cagR as an ORF, because it is completely contained within ORFQ, and is GeneMark-negative.

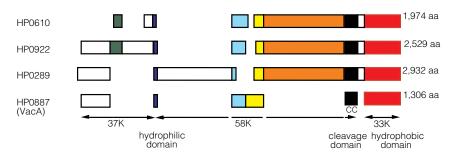


Figure 5 Conserved domains of VacA and related proteins. HP887 is the vacuolating cytotoxin (vacA) gene from *H. pylori* 26695 strain. HP610, HP922 and HP289 are related proteins. Blocks of aligned sequence and the length of each protein are shown. Arrows designate the extents of each VacA domain. The hydrophilic domain (blue boxes) contains the site in VacA at which the N-terminal domain is cleaved into 37K and 58K fragments. The putative cleavage site (ANNNQQNS) differs from that of three cytotoxic strains (CCUG 1784, 60190, G39;

AKNDKXES) and is not conserved in the other three VacA-related proteins. The cleavage domain (black boxes) of VacA contains a pair of Cys residues 60 residues upstream from the site at which the C terminus is cleaved. These residues are not conserved in the other three proteins. The 33K C-terminal hydrophobic domain (red boxes) in VacA is thought to form a pore through which the toxin is secreted. The other three proteins show 26-31% sequence similarity to VacA in this region. The other coloured boxes represent regions of similarity.

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cytotoxin (\sim 26–31%) (Fig. 5). However, they lack the paired-cysteine residues and the cleavage site required for release of the VacA toxin from the bacterial membrane³¹ (Fig. 5). We propose that these proteins may be retained on the outside surface of the cell membrane and contribute to the interaction between *H. pylori* and host cells.

The surface-exposed lipopolysaccharide (LPS) molecule plays an important role in *H. pylori* pathogenesis³². The LPS of *H. pylori* is several orders of magnitude less immunogenic than that of enteric bacteria³³ and the O antigen of many *H. pylori* isolates is known to mimic the human Lewis^x and Lewis^y blood group antigen³². Genes for synthesis of the lipid A molecule, the core region, and the O antigen were identified. Two genes with low similarity to fucosyltransferases (HP379, HP651) were found and may play a role in the LPS-Lewis antigen molecular mimicry. Our analysis also suggests that three genes, two glycosyltransferases (HP208 and HP619) and one fucosyltransferase (HP379), may be subject to phase variation (Table 3a, b).

As with other pathogens, H. pylori probably requires an ironscavenging system for survival in the host⁵. Genome analysis suggests that H. pylori has several systems for iron uptake. One is analogous to the siderophore-mediated iron-uptake fec system of E. coli³⁴, except that it lacks the two regulatory proteins (FecR and FecI) and is not organized in a single operon. Unlike other studied systems, H. pylori has three copies of each of fecA, exbB and exbD. A second system, consisting of a feoB-like gene without feoA, suggests that H. pylori can assimilate ferrous iron in a fashion similar to the anaerobic feo system of *E. coli*. Other systems for iron uptake present in H. pylori consist of the three frpB genes which encode proteins similar to either haem- or lactoferrin-binding proteins. Finally, H. pylori contains NapA, a bacterioferritin³⁴, and Pfr, a non-haem cytoplasmic iron-containing ferritin used for storage of iron³⁵. The global ferric uptake regulator (Fur) characterized in other bacteria is also present in H. pylori. Consensus sequences for Fur-binding boxes were found upstream of two *fecA* genes, the three *frnB* genes and *fur*.

H. pylori motility is essential for colonization³⁶. It enables the bacterium to spread into the viscous mucous layer covering the gastric epithelium. At least forty proteins in the *H. pylori* genome appear to be involved in the regulation, secretion and assembly of the flagellar architecture. As has bene reported for the *flaA* and *flaB* genes, we identified sigma 28 and sigma 54-like promoter elements upstream of many flagellar genes, underscoring the complexity of the transcriptional regulation of the flagellar regulon⁵.

Acidity, pH and acid tolerance

H. pylori is unusual among pathogenic bacteria in its ability to colonize host cells in an environment of high acidity. As it enters the gastric environment by oral ingestion, the organism is transiently subjected to the extreme pH of the lumen side of the gastric mucous layer (pH \sim 2). The survival of *H. pylori* in acidic environments is probably due to its ability to establish a positive inside-membrane potential³⁷ and subsequently to modify its microenvironment through the action of urease and the release of factors that inhibit acid production by parietal cells⁵. A switch in membrane polarity provides an electrical barrier that prevents the entry of protons (H⁺). A positive cell interior can be created by the active extrusion of anions or by a proton diffusion potential. The latter model appears more likely as no clear mechanism for electrogenic anion efflux is apparent in the genome. A proton diffusion potential would require the anion permeability of the cytoplasmic membrane to be low and, thus far, only three anion transporters have been identified. However, it remains to be determined whether anion conductances are associated with other proteins: the MDR-like transporters (HP600, HP1082 and HP1206) or hypotheticals. Although it has been suggested that proton-translocating P-type ATPases could mediate survival in acid conditions by the extrusion of protons from the cytoplasm³⁸, this idea is not supported by the identified transporter

Table 3 Hom	opolymeric tracts a	nd dinucleotide	repeats in <i>H. pylori</i>					
HP no.	ID		No. of repeats	G	ene status	Poly(A) or Poly(Γ) tracts in 5' interg	genic region
starting at the CCAAAAATOT T ATG AAAAAŌ Y E K I M K K	designated methioning the state of the state	oo ng of HP0722 sho ne leads to a trun GAAATCCAATAA ICTCTCTCTCTC S L S L A L S L S	11 CT 11 AG 6 CT 8 CT 6 CT 9 AG 11 CT 9 AG wing the CT dinucleotide cated product. The addition ATTTATGGTAAAGT-37bp. GCTTCATCACTCCTTTGCAC S S L L H L H R S C T	((() ((con or deletion of b-TTTACAATAAA	two CT repeats, by ' AAAATTACTTTAAG	slipped-strand mispair GAACATTT		
(b) Homopolyr HP no. 58 217 379 464 619 651 1353 1471 1522	neric poly(C) and poly	Hyp Hyp fucc Type glyc Hyp Hyp	ID o o o syl transf. bl R os. transf.		Tract lengr C15 G12 C13 C15 C13 C13 C15 G14 G12	th		Gene status Off On On On Truncated On Truncated On Truncated
Genes possib HP no. 9 227 350 722 876 1342	ly regulated by homor ID OMP OMP IMP OMP frpB OMP	oolymeric poly(A) Tract A14 T14 A15 T16 T16 A14	or poly(T) tracts in 5' inte HP no. 25 228 547 725 896 1400	ergenic regions ID OMP IMP cagA OMP OMP fecA	Tract T15 A14 A14 T14 A14 A16	HP no. 208 349 629 733 912	ID rfaJ pyrG Hypo Hypo OMP	Tract A11 T15 T15 T13 T13

genes. The P-type ATPase sequences in *H. pylori* (*copAP*, HP791, and HP1503) are more closely related to divalent cation transporters than to ATPases with specificity for protons or monovalent cations. One of them, HP0791, is involved in Ni²⁺ supply, an essential component of urease activity³⁹. The others may be involved in the elimination of toxic metals from the cytoplasm and not in pH regulation.

Additional mechanisms of pH homeostasis may well contribute to *H. pylori* survival. A change in protein content observed in response to a shift of extracellular pH from 7.5 to 3.0 suggests the presence of an acid-inducible response⁴⁰. Although *H. pylori* lacks most orthologues of the genes that are acid-induced in *E. coli* and *Salmonella typhimurium*, including the amino-acid decarboxylases and formate hydrogen lyase, certain virulence factors, outer membrane

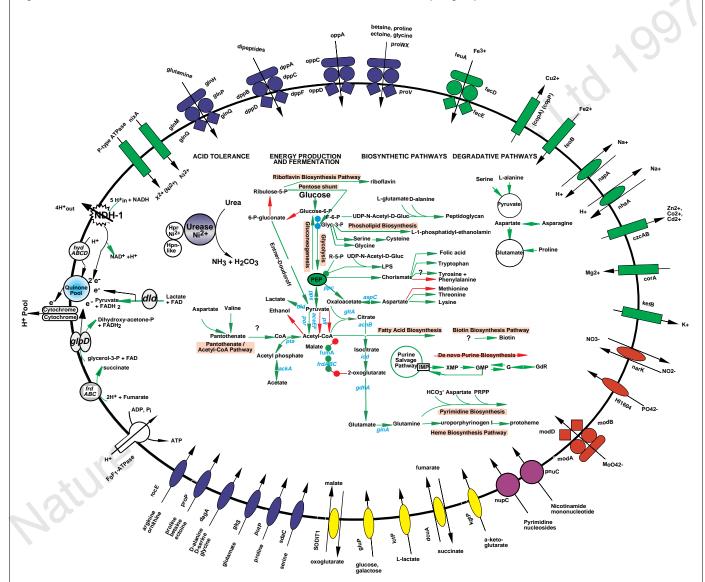


Figure 6 Solute transport and metabolic pathways of Helicobacter pylori. Transporters identified by sequence comparisons are characterists of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley¹⁵: blue, amino acids, peptides and amines; red, anions; yellow, carbohydrates, organic alcohols and acids; green, cations; and purple, nucleosides, purines and pyrimidines. Numerous permeases (ovals) with specificity for amino acids (recE, proP, dagA, gltS, putP and sdaC) or carbohydrates (SODiTI, gluP, lactP, cduA, kgtP) import organic nutrients. Structurally related permease proteins maintain ionic homeostasis by transporting HPO₄²⁻ (HI1604), NO₃²⁻ (narK), and Na+ (nhA, napA). Primary active-transport systems, independent of the proton cycle, are also apparent. Included in this group are ATP-binding proteincassette (ABC) transporters (composite figures of 2 diamonds, 2 circles, 1 oval) for the uptake of oligopeptides (oppACD), dipeptides (dppABCDF), proline (proVWX), glutamine (glnHMPQ), molybdenum (modABD), and iron III (fecED), Ptype ATPases that extrude toxic metals from the cell (copAP and cadA), and the glutathione-regulated potassium-efflux protein (kefB). Transporters for the accumulation of ionic cofactors are encoded by nixA (Ni²⁺ for urease activation), corA (Mg²⁺ for phosphohydrolases, phosphotransferases, ATPases) and feoB (Fe²⁺

import under anaerobic conditions for cytochromes, catalase). An integrated view of the main components of the central metabolism of *H. pylori* strain 26695 is presented. The use of glucose as the sole carbohydrate source is emphasized. Urease, a multisubunit Ni2+-binding enzyme, is crucial for colonization and for survival of H. pylori at acid pH, and is indicated as a complex (purple circle) with Hpn, a Ni²⁺-binding cofactor, and a newly identified Hpn-like protein (HP1432). A question mark is attached to pathways that could not be completely elucidated. Pathways or steps for which no enzymes were identified are represented by a red arrow. Pathways for macromolecular biosynthesis (RNA, DNA and fatty acids) have been omitted. ackA, acetate kinase; acnB, aconitase B; aspC, aspartate aminotransferase; dld, p-lactate dehydrogenase; gdhA, glutamate dehydrogenase; glnA, glutamine synthetase; gltA citrate synthase; HydABC, hydrogenase complex; icd, isocitrate dehydrogenase; pfl, pyruvate formate lyase; por, pyruvate ferredoxin oxidoreductase; ppc, phosphoenolpyruvate carboxylase; pps, phosphoenolpyruvate synthase; pta, phosphate acetyltransferase; gldD, glycerol-3-phosphate dehydrogenase; NDH-1, NADH-ubiquinone oxidoreductase complex.

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proteins, sensor-regulator pairs and other proteins may be acidinduced.

Regulation of gene expression

Bacteria regulate the transcription of their genes in response to many environmental stimuli, such as nutrient availability, cell density, pH, contact with target tissue, DNA-damaging agents, temperature and osmolarity. In the case of pathogens, the regulated expression of certain key genes is essential for successful evasion of host responses and colonization, adaptation to different body sites, and survival as the pathogen passes to new hosts. In H. pylori, global regulatory proteins are less abundant than in *E. coli*. For example, orthologues of many DNA-binding proteins that regulate the expression of certain operons such as OxyR (oxidative stress), Crp (carbon utilization), RpoH (heat shock), and Fnr (fumarate and nitrate regulation) are absent. Only four H. pylori proteins have a perfect match to helix-turn-helix (HTH) motifs, a signature of transcription factors; a putative heat-shock protein (HspR), two proteins with no database match (HP1124 and HP1349) and SecA, a component of the general secretory machinery. In contrast, 34 proteins containing an HTH motif were found in H. influenzae and 148 in E. coli. We identified several other putative regulatory functions, including SpoT and CstA for 'stringent response' to amino-acid starvation and to carbon starvation, respectively.

Environmental response requires sensing changes and transmission of this information to cellular regulatory networks. Two-component regulator systems, consisting of a membrane histidine kinase sensor protein and a cytoplasmic DNA-binding response regulator, provide a well studied mechanism for such signal transduction. Four sensor proteins and seven response regulators were found in *H. pylori*, similar to the number found in *H. influenzae*⁷. This is approximately one third the number found in *E. coli* which, in contrast to *H. pylori* and *H. influenzae*, may be exposed to more environments.

Metabolism

Metabolic pathway analysis of the H. pylori genome suggests the following features. H. pylori uses glucose as the only source of carbohydrate and the main source for substrate-level phosphorylation. It also derives energy from the degradation of serine, alanine, aspartate and proline. The glycolysis-gluconeogenesis metabolic axis constitutes the backbone of energy production and the start point of many biosynthetic pathways. The biosynthesis of peptidoglycan, phospholipids, aromatic amino acids, fatty acids and cofactors is derived from acetyl-CoA or from intermediates in the glycolytic pathway (Fig. 6). The metabolism of pyruvate reflects the microaerophilic character of this organism. Neither the aerobic pyruvate dehydrogenase (aceEF) nor the strictly anaerobic pyruvate formate lyase (pfl) associated with mixed-acid fermentation are present. The conversion of pyruvate to acetyl CoA is performed by the pyruvate ferrodoxin oxidoreductase (POR), a four-subunit enzyme thus far only described in hyperthermophilic organisms⁴¹. The tricarboxylic acid cycle (TCA) is incomplete and the glyoxylate shunt is absent. The analysis of degradative pathways, uptake systems and biosynthetic pathways for pyrimidine, purine and haem suggests that H. pylori uses several substrates as nitrogen source, including urea, ammonia, alanine, serine and glutamine. The assimilation of ammonia, an abundant product of urease activity, is achieved by the glutamine synthase enzyme and α ketoglutarate is transformed into glutamate by glutamate dehydrogenase rather than by the glutamate synthase enzyme.

In *H. pylori*, proton translocation is mediated by the NDH-1 dehydrogenase and the different cytochromes, including the primitive-type cytochrome cbb3 (Table 2). Four respiratory electron-generating deydrogenases have been identified, glycerol-3-phosphate dehydrogenase (GlpD), D-lactate dehydrogenase, NADH-ubiquinone oxidoreductase complex (NDH-1), and a hydrogenase complex (HydABC). Our analysis also suggests that

H. pylori is not able to use nitrate, nitrite, dimethylsulphoxide, trimethylamine N-oxide or thiosulphate as electron acceptors. Much of our metabolic analysis is supported by experimental evidence^{41,42}.

Evolutionary relationships of *H. pylori*

H. pylori is currently classified in the Proteobacteria, a large, diverse division of Gram-negative bacteria which includes two other completely sequenced species, H. influenzae and E. coli. Given this taxonomic placement, based primarily on 16S rRNA sequence comparisons, one might expect the proteins of *H. pylori* more closely to resemble their H. influenzae and E. coli homologues rather than those in other genomes such as Synechocystis sp., M. genitalium, M. pneumoniae, M. jannaschii, and Saccharomyces cerevisae. This is indeed the case for many proteins. There are, however, many examples of H. pylori proteins in amino-acid biosynthesis, energy metabolism, translation and cellular processes that have greater sequence similarity to those found in non-Proteobacteria. For example, Dhs1, the initial enzyme in the chorismate biosynthesis pathway is 75.5% similar to Arabidopsis thaliana chloroplast Dhs1 gene product, and has minimal sequence similarity to the equivalent E. coli AroH, AroF or AroG gene products. The remaining enzymes in this pathway have strong sequence similarity to their E. coli counterpart. Similarly, the H. pylori prephenate dehydrogenase (TyrA), which converts chorismate to tyrosine, and six out of 15 enzymes in the aspartate amino acid biosynthetic pathways, resemble those from B. subtilis. A similar pattern can be seen in a different functional category. Nearly all H. pylori tRNA synthetases have eubacterial homologues, mostly with best matches to Proteobacteria species. However, histidyl-tRNA synthetase shows several amino-acid sequence signatures in common with eukaryotic and archaeal (M. jannaschii)

Such observations of discordant sequence similarity are often interpreted as evidence of lateral gene transfer in the evolutionary history of an organism. It is also possible that *H. pylori* diverged early from the lineage that led to the gamma Proteobacteria, and retained more ancient forms of enzymes that have been subsequently replaced or have diverged extensively in *H. influenzae* and *E. coli*.

Conclusion

Our whole-genome analysis of *H. pylori* gives new insight into its pathogenesis, acid tolerance, antigenic variation and microaerophilic character. The availability of the complete genome sequence will allow further assessment of *H. pylori* genetic diversity. This is an important aspect of *H. pylori* epidemiology as allelic polymorphism within several loci has already been associated with disease outcome^{5,21,31}. The extent of molecular mimicry between *H. pylori* and its human host, an underappreciated topic, can now be fully explored⁴³. The identification of many new putative virulence determinants should allow critical tests of their roles and thus new insight into mechanisms of initial colonization, persistence of this bacterium during long-term carriage, and the mechanisms by which it promotes various gastroduodenal diseases.

Methods

H. pylori strain 26695 (ref. 44) was originally isolated from a patient in the United Kingdom with gastritis (K. Eaton, personal communication) and was chosen because it colonizes piglets and elicits immune and inflammatory responses. It is also toxigenic, and transformable, and thus amenable to mutational tests of gene function.

The *H. pylori* genome sequence was obtained by a whole-genome random sequencing method previously applied to genomes of *Haemophilus influenzae*⁷, *Mycoplasma genitalium*⁸, and *Methanococcus jannaschii*⁹. Ninety-two per cent of the genome was covered by at least one λ clone and only 0.56% of the genome had single-fold coverage.

Open reading frames (ORFs) and predicted coding regions were identified using three methods. The predicted protein-coding regions were initially defined by searching for ORFs longer than 80 codons. Coding potential analysis of the entire genome was performed with a version of GeneMark⁴⁵ trained with a set of H. pylori ORFs longer than 600 nucleotides. Coding sequences and potential starts of translation were also determined using GeneSmith (H.S., unpublished), a program that evaluates ORF length, separation of ORFs and overlap and quality of ribosome binding site. ORFs with low GeneMark coding potential, no database match, and not retained by GeneSmith were eliminated. GeneSmith identified 25 ORFs that are smaller than 100 codons, had no database match and were GeneMark negative. Frameshifts were detected by inspecting pairwise alignments, families of orthologues (similar proteins derived from different species) and paralogues (similar proteins from within the same organism), and regions containing homopolymer stretches and dinucleotide repeats. Ambiguities were resolved by an alternative sequencing chemistry (terminator reactions), and by sequencing PCR products obtained using the genomic DNA as template. Frameshifts that remain in the genome are considered authentic and not sequencing artefacts.

To determine their identity, ORFs were searched against a non-redundant amino-acid database as previously described⁹. ORFs were also analysed using 175 hidden Markov models constructed for a number of conserved protein families (pfam v1.0) using hmmer⁴³. In addition, all ORFs were searched against the prosite motif database using MacPattern⁴⁶. Families of paralogues were constructed by pairwise searches of proteins using FASTA. Matches that spanned at least 60% of the smaller of the protein pair were retained and visually inspected.

A unix version of the program TopPred⁴⁷ was used to identify membrane-spanning domains (MSD) in proteins. Six hundred and sixty three proteins containing at least one MSD were found; of these, 300 had 2 potential MSDs or more. The presence of signal peptides and the probable position of the cleavage site in secreted proteins were detected using Signal-P, a neural net program that had been trained on a curated set of secreted proteins from Gram-negative bacteria⁴⁸. 367 proteins were predicted to have a signal peptide. Lipoproteins were identified by scanning for the presence of a lipobox in the first 30 amino acids of every protein; 20 lipoproteins were identified, eighteen of which were Signal-P positive. Outer-membrane proteins were found by searching for aromatic amino acids at the end of the proteins.

Homopolymer and dinucleotide repeats were found by using RepScan (H.O.S., unpublished) which finds direct repeats of any length. All features identified using these programs were validated by visual inspection to remove false positives. Metabolic pathways were curated by hand and by reference to EcoCyc⁴⁹.

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Correspondence and requests for materials should be addressed to J.-F.T. (e-mail: ghp@tigr.org). The annotated genome sequence and gene family alignments are available on the World-Wide Web site at http://www.tigr.org/tdb/mdb/hpdb/hpdb.html. The sequence has been deposited with GenBank under accession number AE000511.

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Table 2. List of *H.* pylori genes with putative identifications. Gene numbers correspond to those in Fig. 1. Each identified gene has been assigned a putative role category adapted from ref. 15. Percentages represent per cent identities.

	D BIOSYNTHESIS		HP0841	pantothenate metabolism flavoprotein (dfp)	31.3%	HP0855		41.8%
General HP0695	hudantain utilization protoin A (huuA)	28.6%	Pvridoxine			HP0326	CMP-N-acetylneuraminic acid synthetase (neuA)	31.9%
	hydantoin utilization protein A (hyuA)	20.0%		pyridoxal phosphate biosynthetic protein		HP0230	CTP:CMP-3-deoxy-D-manno-octulosonate-	
	nino-acid family 3-dehydroquinase type II (aroQ)	99.4%		A (pdxA)	34.2%			36.2%
	3-dehydroquinate synthase (aroB)	38.1%		pyridoxal phosphate biosynthetic protein J		HP1392 HP0379		25.7% 39.2%
HP0134	3-deoxy-D-arabino-heptulosonate		Riboflavin	(pdxJ)	42.6%	HP0651	fucosyltransferase fucosyltransferase	39.2%
HP0401	7-phosphate synthase (dhs1) 3-phosphoshikimate	54.6%		GTP cyclohydrolase II (ribA)	47.2%			62.1%
HFU4U1	1-carboxyvinyltransferase (aroA)	53.6%		GTP cyclohydrolase II/3,4-dihydroxy-2-butar		HP0867	lipid A disaccharide synthetase (lpxB)	32.0%
HP1279	anthranilate isomerase (trpC)	47.0%		4-phosphate synthase (ribA, ribB)	44.0%	HP0159	lipopolysaccharide 1,2-glucosyltransferase	20.00/
HP1282	anthranilate synthase component I (trpE)	47.9%		riboflavin biosynthesis protein (ribG)	33.1%	HP0208	(rfaJ) lipopolysaccharide 1,2-glucosyltransferase	28.9%
HP1280		42.5%		riboflavin biosynthesis regulatory protein (ribC)	28.9%			26.7%
	anthranilate synthase component II (trpD) chorismate synthase (aroC)	40.2% 47.2%		riboflavin synthase alpha subunit (ribC)	32.8%	HP0805	lipooligosaccharide 5G8 epitope biosynthes	
	prephenate dehydrogenase (tyrA)	30.2%		riboflavin synthase beta chain (ribE)	52.4%	LIDOOOO		36.9%
HP1249	shikimate 5-dehydrogenase (aroE)	36.6%		glutaredoxin and glutathione		HP0826	lipooligosaccharide 5G8 epitope biosynthes associated protein (lex2B)	39.2%
	shikimic acid kinase I (aroK)	36.1%		gamma-glutamyltranspeptidase (ggt)	53.2%	HP1416	lipopolysaccharide 1,2-glucosyltransferase	00.E /0
HP1277 HP1278	tryptophan synthase, alpha subunit (trpA) tryptophan synthase, beta subunit (trpB)	46.5% 66.1%		thioredoxin thioredoxin (trxA)	38.3% 51.5%		(rfaJ)	29.2%
		00.170		thioredoxin (trxA)	28.5%	HP0679	lipopolysaccharide biosynthesis protein	
	amily aspartate ammonia-lyase (aspA)	55.5%	Thiamine	anorodoxiii roddolado (iixb)	20.0 10	HP1475	(wbpB) lipopolysaccharide core biosynthesis proteir	42.8%
HP1189	aspartate-semialdehyde dehydrogenase	00.070		thiamin biosynthesis protein (thiF)	34.6%	HF 1475	(kdtB)	49.0%
	(asd)	45.7%		thiamin phosphate pyrophosphorylase/		HP0279	lipopolysaccharide heptosyltransferase-1	
HP1229	aspartokinase (lysC) 48.0%	4770/		hyroxyethylthiazole kinase (thiB)	35.7%		(rfaC)	31.7%
HP0106 HP0290	cystathionine gamma-synthase (metB) diaminopimelate decarboxylase	47.7%		thiamin phosphate pyrophosphorylase/ hyroxyethylthiazole kinase (thiM)	37.9%	HP0619	lipopolysacharide biosynthesis glycosyl	2720
111 0230	(dap decarboxylase) (lysA)	42.7%		thiamine biosynthesis protein (thi)	41.0%	HP1105	transferase (lic2B) LPS biosynthesis protein	37.2% 28.7%
HP0566	diaminopimelate epimerase (dapF)	30.0%	Pyridine nuc					28.1%
	dihydrodipicolinate reductase (dapB)	95.3%			37.5%	HP1581		29.2%
HP1013	dihydrodipicolinate synthetase (dapA)	39.5%		nicotinate-nucleotide pyrophosphorylase		HP0857	phosphoheptose isomerase (gmhA)	44.5%
	homoserine dehydrogenase (metL) homoserine kinase (thrB)	37.7% 27.7%		(nadC)	36.3%	HP1275	phosphomannomutase (algC)	00.00/
	solute-binding signature and mitochondrial	21.1 10	HP1356	quinolinate synthetase A (nadA)	34.2%	HP1429	{Pseudomonas aeruginosa}	39.6%
111 0072	signature protein (aspB)	47.3%	CELL ENVE	OPE		FIF 1429	polysialic acid capsule expression protein (kpsF)	46.0%
HP0212	succinyl-diaminopimelate desuccinylase			, lipoproteins and porins		HP0366	spore coat polysaccharide biosynthesis	
LIDOCCO	(dapE)	42.3%		60 kDa inner-membrane protein	40.0%		protein C	35.3%
HP0626	tetrahydrodipicolinate N-succinyltransferase	36.1%	HP0180	apolipoprotein N-acyltransferase (cute)	28.0%	HP0178	spore coat polysaccharide biosynthesis	00.00/
HP0098	(dapD) threonine synthase (thrC)	32.9%	HP0175	cell binding factor 2	34.9%	HP0421	protein E type 1 capsular polysaccharide biosynthesis	36.2%
Glutamate f		OL.0 70		Hypothetical protein	28.4%	MFU421	protein J (capJ)	29.0%
HP0380	glutamate dehydrogenase (gdhA)	59.0%			26.4% 98.9%	HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine	20.070
HP0512	glutamine synthetase (glnA)	48.6%		membrane-associated lipoprotein (lpp20) outer membrane protein	39.9%		N-acyltransferase (lpxD)	39.5%
HP1158	pyrroline-5-carboxylate reductase (proC)	28.9%			0.0%	HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylas	se
Pyruvate fai	mily				0.0%	LIDAGRE	(envA)	44.6%
HP0941	alanine racemase, biosynthetic (alr)	32.4%		outer membrane protein (omp11)		HP1375	UDP-N-acetylglucosamine acyltransferase (lpxA)	41.8%
HP1468	branched-chain-amino-acid	00.50	HP0477		0.0%	Curfoso oto		41.070
HP0330	aminotransferase (ilvE) ketol-acid reductoisomerase (ilvC)	63.5% 48.1%		outer membrane protein (omp13)	0.0% 36.0%	Surface stru HP0840		60.2%
Serine famil		40.170		outer membrane protein (omp14) outer membrane protein (omp15)	33.5%			32.7%
	cysteine synthetase (cysK)	45.7%		outer membrane protein (omp16)	43.3%	HP0351		34.4%
	phosphoglycerate dehydrogenase	31.0%	HP0725	outer membrane protein (omp17)	43.3%	HP0246		37.9%
HP0397		32.5%	HP0796	outer membrane protein (omp18)				37.0%
HP0736	phosphoserine aminotransferase (serC)	30.7%		outer membrane protein (omp19)	36.6%	HP1559	flagellar basal-body rod protein (flgB)	31.0%
HP0652	phosphoserine phosphatase (serB)	36.5%	HP0025 HP0912	outer membrane protein (omp2) outer membrane protein (omp20)	0.0%	HP1558	(proximal rod protein) flagellar basal-body rod protein (flgC)	31.0%
	serine acetyltransferase (cysE) serine hydroxymethyltransferase (glyA)	98.2% 54.0%		outer membrane protein (omp21)	38.2%	111 1000	(proximal rod protein)	46.0%
111-0100	serille riyuroxymetriyittarisierase (giyA)	34.070			0.0%	HP1092		35.5%
BIOSYNTHE	SIS OF COFACTORS, PROSTHETIC GROUP	PS,		outer membrane protein (omp23)		HP1585		47.7%
AND CARRI	ERS			outer membrane protein (omp24)	36.0%	HP1041		43.1%
General				outer membrane protein (omp25)	0.0% 23.0%	HP1035 HP0684		35.5% 43.4%
HP0220	synthesis of [Fe-S] cluster (nifS)	48.0%		outer membrane protein (omp26) outer membrane protein (omp27)	37.0%	HP0770		38.7%
Biotin				outer membrane protein (omp28)	0.0%	HP0685	flagellar biosynthetic protein (fliP)	55.6%
		34.9%	HP1342	outer membrane protein (omp29)	0.0%	HP1419	flagellar biosynthetic protein (fliQ)	52.3%
HP0976	adenosylmethionine-8-amino-7-oxononanoa	te			0.0%	HP0173		26.4%
HP1140	aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz	49.2%			0.0%	HP0353	flagellar export protein (fliH)	29.1%
TF 1140		36.9%		outer membrane protein (omp31)	0.0%	HP1420 HP0870	flagellar export protein ATP synthase (flil) flagellar hook (flgE)	47.6% 98.9%
HP0407	biotin sulfoxide reductase (bisC)	42.7%		outer membrane protein (omp32) outer membrane protein (omp4)	0.0%	HP0908	flagellar hook (flgE)	30.5%
HP1254	biotin synthesis protein (bioC)	32.1%		outer membrane protein (omp5)	36.8%	HP1119	flagellar hook-associated protein 1	00.070
	biotin synthetase (bioB)	36.2%	HP0229	outer membrane protein (omp6)	38.4%		(HĂP1) (flgK)	27.6%
	dethiobiotin synthetase (bioD)	36.0%		outer membrane protein (omp7)	30.6%	HP0752		28.9%
Folic acid				outer membrane protein (omp8)	37.6%	HP0815 HP0816		32.9% 29.7%
HP1036	7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (folK)	34.6%		outer membrane protein (omp9) outer membrane protein P1 (ompP1)	36.3% 23.3%	HP0352		37.0%
HP0587	aminodeoxychorismate lyase (pabC)	32.4%	HP0955	prolipoprotein diacylglyceryl transferase (lgt	1)34.4%	HP1031	flagellar motor switch protein (fliM)	34.4%
HP1232	dihydropteroate synthase (foIP)	34.5%		protective surface antigen D15	27.5%	HP0753	flagellar protein (fliS)	32.3%
	folylpolyglutamate synthase (folC)	35.2%		rare lipoprotein A (rlpA)	37.6%	HP0327	flagellar protein G (flaG)	23.3%
HP0928	GTP cyclohydrolase I (folE)	50.9%		toxin-like outer membrane protein	26.3%	HP0797 HP0584	flagellar sheath adhesin hpaA	98.5% 39.7%
HP0577	methylene-tetrahydrofolate dehydrogenase (foID)	48.4%		toxin-like outer membrane protein toxin-like outer membrane protein	29.5% 30.6%	HP0684 HP0601	flagellar switch protein (fliN) flagellin A (flaA)	39.7% 99.8%
HP0293	para-aminobenzoate synthetase (pabB)	35.1%			30.070	HP0115	flagellin B (flaB)	99.0%
Haem and p				amidase	40.6%	HP0295	flagellin B homologue (fla)	32.9%
	delta-aminolevulinic acid dehydratase		HP0738	D-alanine:D-alanine ligase A (ddlA)	28.5%	HP1575	flhB protein (flhB)	40.5%
	(hemB)	50.5%	HP0549	glutamate racemase (glr)	36.6%	HP1030 HP0907	fliY protein (fliY) Hook assembly protein, flagella (flgD)	29.3% 25.5%
HP0376	ferrochelatase (hemH)	33.4%	HP0772	N-acetylmuramoyl-L-alanine amidase (amiA)26.8%		paralysed flagella protein (pflA)	23.9%
HP0306	glutamate-1-semialdehyde 2,1-aminomutase (hemL)	51.3%		penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 2 (pbp2)	33.7% 35.0%	HP0751	polar flagellin (flaG)	21.9%
HP0239	glutamyl-tRNA reductase (hemA)	32.7%	HP1125	peptidoglycan associated lipoprotein precui	rsor	HP0410	putative neuraminyllactose-binding	
HP0665	oxygen-independent coproporphyrinogen III	l		(omp18)	42.6%	HP1192	haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility	24.2%
	oxidase (hemN)	42.4%	HP0493	phospho-N-acetylmuramoyl-pentapeptide-		HP1192 HP1462	secreted protein involved in flagellar motility	
HP1226	oxygen-independent coproporphyrinogen III		HP0743	transferase (mraY) rod shape-determining protein (mreB)	45.2% 37.7%		secreted protein involved in flagellar motility	/99.2%
HP0237	oxidase (hemN) porphobilinogen deaminase (hemC)	37.9% 45.7%	HP1373	rod shape-determining protein (mreB)	51.9%		,	,
HP0381	protoporphyrinogen oxidase (hemK)	35.9%	HP1372	rod shape-determining protein (mreC)	33.6%	CELLULAR	PROCESSES	
HP0604	uroporphyrinogen decarboxylase (hemE)	46.3%	HP0645	soluble lytic murein transglycosylase (slt)	32.2%	General		
HP1224	uroporphyrinogen III cosynthase (hemD)	27.6%		toxR-activated gene (tagE)	37.2%			26.8%
	ne and ubiquinone			toxR-activated gene (tagE)	31.2%	HP0393		31.7%
HP1360	4-hydroxybenzoate octaprenyltransferase	00.00		transferase, peptidoglycan synthesis (murG)	28.2%	HP0616 HP1067		27.9% 99.2%
HP0929	(ubiA) geranyltranstransferase (ispA)	26.6% 39.8%		UDP-MurNac-pentapeptide presynthetase				95.6%
		31.6%		(murF)	25.7%	HP1490	haemolysin	39.2%
Molybdopte					36.0%	HP1086		40.2%
	molybdenum cofactor biosynthesis			UDP-N-acetylenolpyruvoylglucosamine	22.70/	HP0599	haemolysin secretion protein precursor	45.4%
	protein A (moaA)	31.4%		reductase (murB) UDP-N-acetylglucosamine enolpyruvyl	32.7%	HP0392	(hylB) histidine kinase (cheA)	45.4%
HP0798	molybdenum cofactor biosynthesis protein	C		transferase (murZ)	46.7%	HP0099	methyl-accepting chemotaxis protein (tlpA)	
	(moaC)	97.9%		UDP-N-acetylmuramate-alanine ligase		HP0103	methyl-accepting chemotaxis protein (tlpB)	30.7%
HP0172	molybdopterin biosynthesis protein (moeA)			(murC)	37.3%	HP0082	methyl-accepting chemotaxis transducer	
	molybdopterin biosynthesis protein (moeB)		HP0494	UDP-N-acetylmuramoylalanine-D-glutamate			(tlpC)	28.2%
HP0799 HP0801	molybdopterin biosynthesis protein (mog) molybdopterin converting factor, subunit 1	50.8%		ligase (murD)	31.1%	HP0391		34.3%
0001	(moaD)	31.1%	Surface poly	saccharides, lipopolysaccharides and antig		Cell division		E0.001
HP0800	molybdopterin converting factor, subunit 2			3-deoxy-d-manno-octulosonic acid 8-phosph	nate 52.4%			50.2% 25.7%
	(moaE)	31.1%		synthetase (kdsA) 3-deoxy-d-manno-octulosonic-acid transfera	53.4%			25.7% 31.9%
HP0769	molybdopterin-guanine dinucleotide biosynt			3-deoxy-d-manno-octulosonic-acid transfera (kdtA)	se 35.9%			37.6%
D	protein A (mobA)	28.3%		ADP-heptose synthase (rfaE)	40.6%	HP0286	cell division protein (ftsH)	41.2%
Pantothenai		eforaço	HP1191	ADP-heptose-lps heptosyltransferase II		HP1069	cell division protein (ftsH)	98.6%
	3-methyl-2-oxobutanoate hydroxymethyltran (panB)	sterase 43.7%		(rfaF)	33.2%	HP1556	cell division protein (ftsl)	30.6%
HP0034	aspartate 1-decarboxylase (panD)	50.0%		ADP-L-glycero-D-mannoheptose-6-epimeras	se 32.7%			39.8% 32.7%
	pantoate-beta-alanine ligase (panC)	44.2%		(rfaD)	JE./70			46.6%
						0,00	zz zoon proton (tot)	.0.0 /0

HP0332	cell division topological specificity factor				-1.0%		(devB)	29.2%
HP0979	(minE) cell divison protein (ftsZ)	33.8% 43.3%	HP1270	NADH-ubiquinone oxidoreductase, NQO11 subunit (NQO11) ({Paracoccus denitrificans}	42.6%		glucose-6-phosphate dehydrogenase (g6pD)	36.7%
HP1159 Cell killing	cell filamentation protein (fic)	63.2%	HP1271	NADH-ubiquinone oxidoreductase, NQO12 subunit (NQO12)	43.2%	HP1495 HP1088	transaldolase (tal) transketolase A (tktA)	33.5% 46.7%
HP0887	vacuolating cytotoxin 94.7%		HP1272	NADH-ubiquinone oxidoreductase, NQO13		HP0354	transketolase B (tktB)	39.7%
Chaperones		00.60	HP1273	NADH-ubiquinone oxidoreductase,	40.2%	Sugars HP0574	galactosidase acetyltransferase (lacA)	41.0%
HP0109	chaperone and heat shock protein 70		HP1266	NQO14 subunit (NQO14) NADH-ubiquinone oxidoreductase, NQO3	31.2%	HP0360	UDP-glucose 4-epimerase	43.1%
HP0210	(dnaK) chaperone and heat shock protein C62.5	63.4%		subunit (NQO3)	31.6%	TCA cycle HP0779	aconitase B (acnB)	64.0%
HP0011	(htpG) co-chaperone (groES)	46.5% 99.2%	HP1263	NADH-ubiquinone oxidoreductase, NQO4 subunit (NQO4){Triticum aestivum}	44.6%	HP0026	citrate synthase (gltA) fumarase (fumC)	47.8% 63.7%
HP1332	co-chaperone and heat-shock protein		HP1262	NADH-ubiquinone oxidoreductase, NQO5 subunit (NQO5)	-1.0%	HP0509	glycolate oxidase subunit (glcD)	98.0%
HP0110	(dnal) co-chaperone and heat-shock protein	42.7%	HP1261	NADH-ubiquinone oxidoreductase, NQO6		HP0027	isocitrate dehydrogenase (icd)	70.7%
HP1024	(grpE) co-chaperone-curved DNA-binding protein	33.0%	HP1260	NADH-ubiquinone oxidoreductase, NQO7	62.2%		AND PHOSPHOLIPID METABOLISM	
11111024		37.7%	HP1267	subunit (NQO7) NADH-ubiquinone oxidoreductase, NQO8	40.7%	General HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein)	
	ne-associated protein plasmid replication-partition related protein	40.4%		subunit (NQO8)	42.4%		dehydratase (fabZ) 1-acyl-glycerol-3-phosphate acyltransferase	47.4%
Detoxification	n		HP1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	41.2%		(plsC) (Escherichia coli)	32.0%
HP1563 HP0875	alkyl hydroperoxide reductase (tsaA)	98.5% 99.4%	Amino acida HP1398	s and amines	39.6%		3-ketoacyl-acyl carrier protein reductase (fabG)	45.7%
HP0267	chlorohydrolase	42.6%	HP0294	aliphatic amidase (aimE)	75.4%		acetyl coenzyme A acetyltransferase (thiolase) (fadA)	52.0%
HP0243	neutrophil activating protein (napA) (bacterioferritin)	95.8%	HP1238 HP1399		37.2% 31.8%	HP0950	acetyl-CoA carboxylase beta subunit	
HP0389 HP1452	superoxide dismutase (sodB) thiophene and furan oxidizer (tdhF)	98.6% 37.6%	HP0943	D-amino acid dehydrogenase (dadA)	26.2%		(accD) acetyl-CoA synthetase (acoE)	49.4% 52.3%
	peptide secretion		HP0056		32.2%	HP0557	acetyl-coenzyme A carboxylase (accA) acyl carrier protein (acpP)	50.3% 55.3%
HP0355 HP0074	GTP-binding membrane protein (lepA) lipoprotein signal peptidase (lspA)	57.3% 97.0%	HP0723 HP0132		54.1% 45.8%	HP0962	acyl carrier protein (acpP)	56.3%
HP0786	preprotein translocase subunit (secA)	54.0%	Anaerobic				beta ketoacyl-acyl carrier protein synthase (fabF)	II 50.0%
HP1300 HP1255	preprotein translocase subunit (secY) protein translocation protein, low temperatu	41.2% ire	HP0666	anaerobic glycerol-3-phosphate dehydrogen subunit C (glpC)	ase, 27.2%		beta-ketoacyl-acyl carrier protein synthase I (fabH)	III 44.4%
HP1550	(secG) protein-export membrane protein (secD)	30.6% 38.9%	HP0589	ferredoxin oxidoreductase, alpha subunit	42.7%	HP0371	biotin carboxyl carrier protein (fabE)	30.8%
HP1549	protein-export membrane protein (secF)	35.1%	HP0590 HP0591	ferredoxin oxidoreductase, beta subunit ferredoxin oxidoreductase, gamma subunit			biotin carboxylase (accC) CDP-diglyceride hydrolase (cdh)	52.1% 73.9%
HP0576 HP1152	signal peptidase I (lepB) signal recognition particle protein (ffh)	40.3% 41.4%	HP0193	fumarate reductase, cytochrome b subunit (frdC)	58.8%	HP0215	CDP-diglyceride synthetase (cdsA)	42.4%
	trigger factor (tig)	27.6%	HP0192	fumarate reductase, flavoprotein subunit		HP0700	cyclopropane fatty acid synthase (cfa) diacylglycerol kinase (dgkA)	39.7% 45.8%
Transforma: HP0520	tion cag pathogenicity island protein (cag1)	96.5%	HP0191	(frdA) fumarate reductase, iron-sulfur subunit	69.4%	HP0195	enoyl-(acyl-carrier-protein) reductase (NADH (fabl)	H) 45.8%
HP0530	cag pathogenicity island protein (cag10)	98.4%		(frdB)	70.8%	HP0201	fatty acid/phospholipid synthesis protein	
HP0531 HP0532	cag pathogenicity island protein (cag11) cag pathogenicity island protein (cag12)	97.2% 98.9%	HP1110	pyruvate ferredoxin oxidoreductase, alpha subunit	41.0%		(plsX) Holo-acp synthase (acpS)	37.8% 29.1%
HP0534 HP0535	cag pathogenicity island protein (cag13)	98.0% 97.6%	HP1111	pyruvate ferredoxin oxidoreductase, beta subunit	43.7%	HP0090	malonyl coenzyme A-acyl carrier protein	
HP0536	cag pathogenicity island protein (cag14) cag pathogenicity island protein (cag15)	96.4%	HP1109	pyruvate ferredoxin oxidoreductase, delta			transacylase (fabD) phosphatidylglycerophosphate synthase	35.4%
HP0537 HP0538	cag pathogenicity island protein (cag16) cag pathogenicity island protein (cag17)	98.9% 95.3%	HP1108	subunit pyruvate ferredoxin oxidoreductase, gamma	47.0%		(pgsÅ) phosphatidylserine decarboxylase proenzyr	35.4%
HP0539	cag pathogenicity island protein (cag18)	98.7%		subunit	37.2%		(psd)	33.2%
HP0540 HP0521	cag pathogenicity island protein (cag19) cag pathogenicity island protein (cag2)	99.5% 92.5%	ATP-protoni HP0828	motive force interconversion ATP synthase FO, subunit a (atpB)	37.7%		phosphatidylserine synthase (pssA) phospholipase A1 precursor	99.6%
HP0541	cag pathogenicity island protein (cag20)	97.8%	HP1136	ATP synthase FO, subunit b (atpF)	28.3%		(DR-phospholipase A)	33.8%
HP0542 HP0543	cag pathogenicity island protein (cag21) cag pathogenicity island protein (cag22)	97.9% 95.5%	HP1137 HP1212		32.5% 41.2%	PURINES. P	YRIMIDINES, NUCLEOSIDES AND NUCLEO	TIDES
HP0544 HP0545	cag pathogenicity island protein (cag23)	99.0% 98.5%	HP1134	ATP synthase F1, subunit alpha (atpA)	62.7%	General		
HP0546	cag pathogenicity island protein (cag24) cag pathogenicity island protein (cag25)	95.7%	HP1132 HP1135		85.6% 24.6%		beta-alanine synthetase homologue	40.0%
HP0547 HP0522		92.9% 98.1%	HP1131	ATP synthase F1, subunit epsilon (atpC)	32.7%		nonucleotide metabolism	
						111 0372	deoxycytidine triphosphate deaminase	
HP0523	cag pathogenicity island protein (cag3) cag pathogenicity island protein (cag4)	95.7%	HP1133 Electron tra		37.8%		(dcd)	28.2%
HP0523 HP0524	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5)		HP1133 Electron tra HP0146	nsport cbb3-type cytochrome c oxidase subunit Q		HP0865	(dcd) deoxyuridine 5Õ-triphosphate nucleotidohydr (dut)	rolase 41.4%
HP0523 HP0524 HP0526 HP0527	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7)	95.7% 99.1% 97.5% 94.6%	Electron tra HP0146 HP0265	nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA)	44.2% 35.4%	HP0865 HP0364	(dcd) deoxyuridine 5Ō-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta	rolase 41.4%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9%	Electron tra HP0146 HP0265 HP0378	nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5)	44.2%	HP0865 HP0364 HP0680	(dcd) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alp	rolase 41.4% a 39.0% oha
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence lipoprotein (comL)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5%	Electron tra HP0146 HP0265 HP0378 HP0147	nsport cbb3-type cytochrome c oxidase subunit Q (CccQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP)	44.2% 35.4% 37.5%	HP0865 HP0364 HP0680	(dcd) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB)	rolase 41.4% a 39.0%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag9) competence ilicoprotein (com1) competence locus E (comE3) conjugal transfer protein (traG)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3%	Electron tra HP0146 HP0265 HP0378	nsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper-	44.2% 35.4% 37.5% 33.0%	HP0865 HP0364 HP0680 HP0825 Purine ribon	(dcd) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alg subunit (nrdA) thioredoxin reductase (trxB) uucleotide biosynthesis	rolase 41.4% a 39.0% bha 28.4% 45.9%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence iliopprotein (com), competence iliopprotein (com), conjugal transfer protein (traG) conjugalty transfer protein (traG)	95.7% 99.1% 99.15% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7%	Electron tra HP0146 HP0265 HP0378 HP0147	nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixN) cytochrome c oxidase, noheme subunit,	44.2% 35.4% 37.5% 33.0%	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321	(dod)	rolase 41.4% a 39.0% bha 28.4% 45.9%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0333 HP0042	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag9) cag pathogenicity island protein (cag9) competence liciporotein (comp.) competence liciporotein (com.) conjugal transfer protein (traG) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein	95.7% 93.1% 97.5% 94.6% 99.0% 99.9% 25.5% 26.7% 27.73% 30.7% 32.9% 31.4%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461	Insport chb3-type cytochrome c oxidase subunit Q (Coc0) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixA) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO)	44.2% 35.4% 37.5% 33.0%	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321 HP0618 HP1112	(dod) " (dot) " deoxyuridine 5Ö-triphosphate nucleotidohydri (dut) " ribonucleoside diphosphate reductase, bets subunit (nrdB) ribonucleoside-diphosphate reductase 1 alp subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis 5Ö-gurnylate kinase (gmk) adernylate kinase (adk) adernylate kinase (duck)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0333	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cap pathogenicity island protein (cag8) competence locus E (comE3) competence locus E (comE3) conjugal transfer protein (trac1) conjugal transfer protein (trac1) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein vir811 homologue	95.7% 99.1% 94.6% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227	Insport chib3-type cytochrome c oxidase subunit Q (Cocol) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c551 peroxidase cytochrome c553	44.2% 35.4% 37.5% 33.0% 	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321 HP0618 HP1112 HP0255	(dcd) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alp subunit (hrdA) thioredoxin reductase (trxB) uucleotide biosynthesis 5Ö-gunylate kinase (gmk) adenylate kinase (adk) adenylate kinase (purB) adenylosuccinate lyxase (purB) adenylosuccinate synthetase (purA)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1006 HP1421 HP0333 HP0042 HP0525 HP0441 HP0017	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence locus E (comE3) competence locus E (comE3) conjugative transfer regulori protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue VirB4 homologue VirB4 homologue	95.7% 99.1% 97.5% 94.6% 99.0% 98.3% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277 HP0588	Insport chb3-type cytochrome c oxidase subunit Q (Coc0) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c561 peroxidase cytochrome c563 ferredoxin ferrodoxin-like protein	44.2% 35.4% 37.5% 33.0% 43.9% 45.7% 48.5% 38.4% 52.5%	HP0865 HP0364 HP0680 HP0825 <i>Purine ribon</i> HP0321 HP0618 HP1112 HP0255 HP1434 HP1218	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr, subunit (hrdA) thioredoxin reductase (trxB) tucleotide biosynthesis 6Ö-gusnylate kinase (gmk) adenylate kinase (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formyltetrahydrofolate hydrofase (purU) glycinamider irbonucleotide synthetase	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 49.1%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0333 HP0042 HP0525 HP0441 HP0017 HP0459	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence ilouse 1 (comE3) competence ilouse 1 (comE3) conjugative transfer regulori protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue (virB4) cag6 virB4 homologue (virB4) virB4 homologue (virB4)	95.7% 91.1% 97.5% 94.6% 99.0% 99.9% 25.5% 26.7% 30.7% 32.9% 32.9% 31.4% 100.0%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277 HP0588 HP1508	Insport Coco) Ottochrome c biogenesis protein (codA) oytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (yot5) cytochrome c biogenesis protein (yot5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper binding subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, membrane-bound (fixN) cytochrome c551 peroxidase cytochrome c551 ferredoxin-like protein ferrodoxin-like protein	44.2% 35.4% 35.4% 33.0% 43.9% 45.7% 48.5% 33.4% 52.5% 42.6%	HP0865 HP0364 HP0680 HP0825 <i>Purine ribon</i> HP0321 HP0618 HP1112 HP0255 HP1434 HP1218 HP0854	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr, subunit (hrdA) hiboratoria (hrdB) hiboratoria reductase (trxB) nucleotide biosynthesis 6Ö-gusnyiate kinase (gmk) adenylate kinase (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formyitetrahydrofolate hydrolase (purU) glycinamider irbonucleotide synthetase (purD) GMP reductase (guaC)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 31.8%
HP0523 HP0524 HP0527 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0033 HP0042 HP0525 HP0441 HP0017 HP0459 CENTRAL II	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence locus E (comE3) competence locus E (comE3) conjugative transfer regulori protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue VirB4 homologue VirB4 homologue	95.7% 99.1% 97.5% 94.6% 99.0% 98.3% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277 HP0277 HP0588 HP1508 HP1161 HP1642	Insport Coco) Great State St	44.2% 35.4% 37.5% 33.0% - 45.7% 45.7% 48.5% 38.4% 52.5% 42.6% 29.4% 47.0% 46.1%	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321 HP0618 HP1112 HP0255 HP1434 HP1218 HP0854 HP0854 HP0409	(ded) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) deoxyuridine 5Ö-triphosphate reductase, beta subunit (nrdB) diphosphate reductase 1 alra subunit (nrdB) diphosphate reductase 1 alra subunit (nrdA) thioredoxin reductase (trxB) <i>nucleotide biosynthesis</i> 5O-ganylate kinase (gmk) adenylate kinase (adk) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formylterahydrofolate hydrolase (purU) glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC)	rolase 41.4% 39.0% 59.0% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8%
HP0523 HP0526 HP0527 HP0529 HP0529 HP1378 HP1361 HP106 HP1421 HP006 HP1421 HP0042 HP0042 HP0047 HP0047 HP055 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP0141 HP0141 HP1014	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence liceprotein (comL) competence locus E (comE3) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trbI protein virB1 homologue virB4 homologue virB4 homologue virB4 homologue virB4 homologue (virB4) virB4	95.7% 91.1% 97.5% 94.6% 93.0% 93.9% 25.5% 26.7% 30.7% 30.7% 30.7% 31.4% 100.0% 23.5% 23.5% 23.5%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277 HP0588 HP1508 HP1161	Insport Chb3-type cytochrome c oxidase subunit Q (CocQ) (CocQ) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixA) cytochrome c oxidase, monoheme subunit, membrane-bound (fixC) cytochrome c551 peroxidase cytochrome c551 ferredoxin ferrodoxin-like protein	44 2% 37.5% 33.0% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 29.4% 47.0% 46.1%	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321 HP0318 HP1112 HP0254 HP1218 HP0854 HP0409 HP0829	(ded) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, bete subunit (nrdB) ribonucleoside-diphosphate reductase 1 alg subunit (nrdA) thioredoxin reductase (trxB) uculeotide biosynthesis 5Ö-gusnylate kinase (gmk) adenylate kinase (adk) adenylate kinase (gmk) adenylate kinase (adk) adenylosuccinate byase (purB) adenylosuccinate byase (purB) (ormyltetrahydrofolate hydrolase (purU) glychamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) inosine-5O-monophosphate dehydrogenase (guaB)	rolase 41.4% a 33.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 56.1% 56.1% 58.5%
HP0523 HP0526 HP0527 HP0527 HP0529 HP0529 HP1381 HP1381 HP1381 HP1381 HP0333 HP0452 HP0454 HP0459 CENTRAL II General HP1186	eag pathogenichi siland protein (eag4) eag pathogenichi siland protein (eag6) eag pathogenichi siland protein (eag6) eag pathogenichi siland protein (eag6) eag pathogenichi siland protein (eag7) eag pathogenichi siland protein (eag8) eag pathogenichi siland protein (eag8) eag pathogenichi siland protein (eag8) competence lipoprotein (comL) competence licous E (comE2) eag pathogenichi siland protein (eag8) eag pathogenichi siland protein (eag8) eag pathogenichi siland eag pathogenic	95,7% 991.9% 991.9% 975.9% 991.9% 975.9% 994.59% 999.0% 999.0% 983.9% 25.59% 27.39% 30.7% 32.99% 314.49% 100.0% 25.29% 25.39% 37.79% 37	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277 HP0277 HP058 HP1161 HP1508 HP1161 HP16082 HP10642 HP0642 HP0642	Ispoor chb3-type cytochrome c oxidase subunit Q (CcoQ) (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycd5) cytochrome c biogenesis protein (ycd5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copperbinding subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c561 persoxidase cytochrome c561 persoxidase cytochrome c561 persoxidase (cytochrome c561 persoxidase) ferredoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein errodoxin-like protein errodoxin-like protein errodoxin-like protein ferrodoxin-like protein errodoxin-like errodoxin-like protein errodoxin-like errodoxin-like errodoxin-like errodoxin-like errodoxin-like errodoxin-like errodoxin-like e	44.2% 33.0% 33.0% 43.9% 45.7% 45.7% 42.6% 52.5% 42.6% 52.5% 44.6% 52.5% 45.7% 56.5% 45.7% 56.5% 45.7% 56.5%	HP0865 HP0364 HP0680 HP0825 Purine ribon HP0321 HP0321 HP0255 HP1424 HP128 HP1434 HP128 HP0854 HP0409 HP0829	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr, subunit (hrdA) hiboredoxin reductase (trxB) hucleotide biosynthesis 5Ö-gurnylate kinase (gmk) adenylate kinases (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formylaterahydrofolate hydrolase (purU) glychamidie ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) GMP reductase (guaC) GMP synthase (guaC) mosine-5O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk)	rolase 41.4% a 33.90% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 56.1% 56.1% 58.5% 67.7%
HP0523 HP0526 HP0527 HP0529 HP0529 HP1378 HP1361 HP106 HP1421 HP006 HP1421 HP0042 HP0042 HP0047 HP0047 HP055 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP017 HP0441 HP0141 HP0141 HP1014	eag pathogenicity island protein (eag4) eag pathogenicity island protein (eag6) eag pathogenicity island protein (eag6) eag pathogenicity island protein (eag6) eag pathogenicity island protein (eag7) eag pathogenicity island protein (eag8) eag pathogenicity island protein (eag8) eag pathogenicity island protein (eag8) competence lipoprotein (comL) competence licours E (comE2) eag pathogenicity island protein (traG1) conjugative transfer eputhon (traG1) exclusive transfer protein (traG1) exclusive transfer protein (traG1) exclusive transfer eputhor protein (traG1) exclusive transfer eputhor exclusive tradition (traG1) exclusive tradition (traG1) exclusive transfer eputhor exclusive tradition (traG1) exclusive tradition (traG1) exclusive tradition (traG1) exclusive transfer eputhor exclusive tradition (traG1) exclusive tradition (tr	95,7% 991.9% 97.5% 97.5% 97.5% 99.0% 99.0% 99.0% 99.9% 25.5% 25.7% 27.3% 32.2% 32.9% 31.4% 100.0% 25.5% 25.3% 32.3% 33.2% 33.2% 37.0% 33.3%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP0277 HP0588 HP1508 HP1508 HP1508 HP160842 HP0634	Insport Chb3-type cytochrome c oxidase subunit Q (CcoQ) (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycd5) cytochrome c biogenesis protein (ycd5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper- briding subunit, membrane-bound (fixR) cytochrome c boxidase, monoheme subunit, membrane-bound (fixC) cytochrome c561 forerodxidase cytochrome c563 ferredoxin-fike protein ferrodoxin-fike protein ferrodoxin-fike-fike-fike-fike-fike-fike-fike-fike	44 2% 33 4% 37.5% 33.0% 43.9% 45.7% 48.5% 45.7% 48.5% 42.6% 52.5% 42.6% 49.3% 46.1% 52.7% 54.7% 64.7% 64.7%	HP0865 HP0364 HP0860 HP0825 Purine ribon HP0321 HP0618 HP112 HP0255 HP1218 HP0424 HP1218 HP0854 HP0409 HP0829 HP0329	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr, subunit (hrdA) hiboredoxin reductase (trxB) hucleotide biosynthesis 5Ö-gurnylate kinase (gmk) adenylate kinases (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formylaterahydrofolate hydrofase (purU) glychamidie ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) GMP reductase (guaC) GMP synthase (guaA) phosphoribosyloprophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosyloprophosphate synthetase (prsA)	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 56.1% 56.1% 56.1% 56.5%
HP0523 HP0524 HP0526 HP0527 HP0529 HP1378 HP1381 HP1064 HP10333 HP0042 HP0333 HP0042 HP0491 HP0491 HP0491 HP0491 HP0491 HP0491 HP0491 HP186 HP186 HP186 HP186 HP186 HP186 HP186 HP186 HP186 HP186 HP186	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) completence locus E (comE3) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue VirB4 homologue CirbA1 VirBMEDIARY METABOLISM 7-x-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase	95,7% 991.9% 991.9% 975.9% 991.9% 975.9% 994.59% 999.0% 999.0% 983.9% 25.59% 27.39% 30.7% 32.99% 314.49% 100.0% 25.29% 25.39% 37.79% 37	Electron tra HP0146 HP0268 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0588 HP1508 HP1508 HP1508 HP160842 HP0634 HP0634 HP0633 HP0632	Insport Chib3-type cytochrome c oxidase subunit Q (Coc0) Cytochrome c biogenesis protein (codA) Cytochrome c biogenesis protein (codA) Cytochrome c biogenesis protein (ydfs) Cytochrome c oxidase, diheme subunit, membrane-bound (fixP) Cytochrome c oxidase, heme b and copper binding subunit, membrane-bound (fixA) Cytochrome c oxidase, monoheme subunit, membrane-bound (fixA) Cytochrome c 651 peroxidase Cytochrome c 651 peroxidase Cytochrome c 653 ferredoxin ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fidA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H rehydrogenase, (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG)	44.2% 35.4% 37.5% 33.0% -43.9% 45.7% 48.5% 38.4% 52.5% 52.5% 42.6% 52.5% 46.1% 52.7% 64.7% 67.7%	HP0865 HP0364 HP0826 Purine ribon HP0321 HP0618 HP1112 HP0255 HP1218 HP0424 HP1218 HP0854 HP0409 HP0829 HP0884 HP0429 HP0884 HP0429 HP0884 HP0429 HP0884 HP0429 HP0884 HP0429 HP0884 HP0484 HP0484 HP0484 HP0484 HP0484 HP0484	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr, subunit (hrdA) hiboredoxin reductase (trxB) hucleotide biosynthesis 5Ö-gurnylate kinase (gmk) adenylate kinases (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formylaterahydrofolate hydrofase (purU) glychamidie ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) GMP reductase (guaC) GMP synthase (guaA) phosphoribosyloprophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosyloprophosphate synthetase (prsA)	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 56.1% 58.5% 67.7%
HP0523 HP0526 HP0526 HP0527 HP0528 HP0529 HP0529 HP1378 HP1361 HP1378 HP1361 HP1421 HP0032 HP0032 HP0032 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0469 HP164 HP0044 HP1689 HP0004 HP0089	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) completence locus E (comE3) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue VirB4 homologue VirB4 homologue VirB4 homologue (virB4) virB4 homol	95,7% 991.9% 97.5% 97.5% 97.5% 99.0% 99.0% 99.0% 99.9% 25.5% 25.7% 27.3% 32.2% 32.9% 31.4% 100.0% 25.5% 25.3% 32.3% 33.2% 33.2% 37.0% 33.3%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0588 HP1508 HP1508 HP1608 HP1608 HP0634 HP0634 HP0632 HP0632	Insport Chib3-type cytochrome c oxidase subunit Q (Coc0) Cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (ydfs) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper binding subunit, membrane-bound (fixA) cytochrome c oxidase, monoheme subunit, membrane-bound (fixA) cytochrome c 651 peroxidase cytochrome c 653 ferredoxin ferrodoxin-like protein ferrodo	44.2% 35.4% 37.5% 33.0% -43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 42.6% 47.0% 46.1% 32.7% 54.7% 56.5% 68.5% 68.5%	HP0865 HP0864 HP0680 HP0825 Purine ribon HP0321 HP0618 HP1112 HP0255 HP1434 HP1218 HP0854 HP0409 HP0829 HP0874 HP0188 HP0742 HP0188 HP0742 HP1530 Pyrimidine n	(dod) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, bete subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdA) thioredoxin reductase (trxB) uculeotide biosynthesis 5Ö-gurnylate kinase (gmk) adenylate kinase (adk) adenylate kinase (adk) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA) formylaterahydrofolate hydrolase (purU) glychamider irbonucleotide synthetase (purU) GMP eynthase (guaA) inosine-5O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosyloyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ibonucleotide biosynthesis aspartate transcarbamolylase (pvrB)	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 56.1% 56.1% 56.1% 56.5%
HP0523 HP0524 HP0526 HP0526 HP0527 HP0528 HP0529 HP1378 HP1006 HP1421 HP1006 HP1421 HP00042 HP0033 HP0041 HP0459 CENTRAL II General HP049	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag7) competence locus E (comE3) conjugal transfer protein (resc) conjugal transfer protein (resc) conjugal transfer protein (resc) conjugative transfer regulon protein (rbB) DNA processing chain A (dprA) trbl protein virB4 homologue (virB4) virB4 homo	95,7% 991.9% 991.9% 975.9% 991.9% 975.9% 994.89% 999.09% 998.99% 25.59% 27.39% 30.7% 32.99% 31.44% 100.0% 25.29% 25.39% 33.39% 28.19% 33.29% 33.39% 28.19%	Electron tra HP0146 HP0268 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0588 HP1508 HP1508 HP1508 HP160842 HP0634 HP0634 HP0633 HP0632	Insport Chb3-type cytochrome c oxidase subunit Q (CcoQ) (44.2% 35.4% 37.5% 33.0% -43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 42.6% 47.0% 46.1% 32.7% 54.7% 56.5% 68.5% 68.5%	HP0865 HP0864 HP0825 Putine ribon HP0321 HP0321 HP0321 HP0321 HP1218 HP0255 HP1434 HP0459 HP0854 HP049 HP0829 HP0884 HP042 HP0894 HP0894 HP0899	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdA) thioredoxin reductase (trxB) uucleotide biosynthesis 5Ö-gunylate kinase (gmk) adenylate kinase (adk) adenylate kinase (adk) adenylatesionate synthetase (purA) formylatetrahydrofolate hydrofase (purU) glycinamide ribonucleotide synthetase (purD) GMP synthase (guaA) inosine-5O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphates synthese (glutamine- hydrolysing) (pyrAb)	rolase 41.4% 43.39.0% 0ha 28.4% 45.9% 44.8% 43.33% 49.5% 44.6% 49.1% 56.1% 58.5% 67.7% 66.5% 20.7% 48.6% 48.6%
HP0523 HP0526 HP0526 HP0527 HP0528 HP0529 HP0529 HP1378 HP1361 HP1378 HP1361 HP1421 HP0032 HP0032 HP0032 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0469 HP164 HP0044 HP1689 HP0004 HP0089	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cap pathogenicity island protein (cag8) competence lipoprotein (comL) competence licours E (comE3) conjugal transfer protein (traG1) conjugalive transfer regulon protein (trbB) DNA processing chain A (dprA) virB4 homologue (virB4)	95,7% 991.9% 991.9% 975.9% 991.9% 975.9% 994.89% 999.09% 993.99% 25.59% 26.79% 32.99% 31.44% 100.0% 23.55% 25.29% 25.39% 33.29% 33.29% 33.29% 33.29% 33.29% 34.49% 100.0% 24.49% 25.39% 33.29%	Electron tra HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0588 HP1508 HP1508 HP1608 HP1608 HP0634 HP0634 HP0632 HP0632	Insport Chb3-type cytochrome c oxidase subunit Q (CcoQ) (CcoQ) (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, differen subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper briding subunit, membrane-bound (fixA) cytochrome c 561 cytochrome c 563 ferredoxin ferrodoxin-like protein ferrodoxin-like	44.2% 35.4% 37.5% 33.0% 443.9% 45.7% 48.5% 42.6% 42.6% 52.5% 42.6% 52.5% 45.7% 55.7% 56.7% 66.5% 68.5% 68.5%	HP0865 HP0864 HP0860 HP0825 Purine ribon HP0815 HP0816 HP0815 HP0816 HP0	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdA) thioredoxin reductase (trxB) uucleotide biosynthesis 5Ö-gunylate kinase (gmk) adenylate kinase (adk) adenylatesinate synthetase (purA) formylaterahydrofolate hydrolase (purA) formylaterahydrofolate hydrolase (purA) formylaterahydrofolate synthetase (purA) formylaterahydrofolate hydrolase (purA) purboniosphosphosphate dehydrogenase (pusB) phosphoribosylpyrophosphate synthetase (prsA) prime nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purime nucleoside phosphorylase (purB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb)	rolase 41.4% a 39.0% oha 28.4% 45.9% 45.9% 44.8% 33.3% 49.5% 441.6% 49.1% 31.8% 56.1% 66.7% 56.5% 20.7% 38.7%
HP0523 HP0524 HP0526 HP0526 HP0527 HP0528 HP0529 HP1378 HP1006 HP1421 HP1006 HP1421 HP00042 HP0033 HP0041 HP0459 CENTRAL II General HP049	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cap pathogenicity island protein (cag8) competence lipoprotein (comL) competence lipoprotein (comL) competence lipoprotein (rag1) conjugative transfer epution protein (trbB) DNA processing chain A (dprA) virB4 homologue (virB4) vi	95,7% 991.9% 991.9% 97.5% 991.9% 97.5% 994.69% 99.0% 99.0% 99.0% 99.39% 25.5% 26.79% 27.39% 30.79% 32.99% 31.44% 100.0% 23.55% 25.29% 25.39% 33.29% 33.29% 33.29% 33.29% 33.29% 33.5% 28.19% 41.4% 38.5% 47.89%	Electron tra HP0146 HP0245 HP0378 HP0147 HP0144 HP0144 HP0145 HP1461 HP1227 HP0277 HP0277 HP0277 HP0688 HP1508 HP1508 HP1684 HP0684 HP0683 HP0683 HP0683 HP0683 HP0683 HP0683 HP0681 HP0681 HP0681 HP0681 HP0681	Insport Chb3-type cytochrome c oxidase subunit Q (CcoQ) (44.2% 33.4% 37.5% 43.9% 443.9% 45.7% 48.5% 52.5% 42.6% 45.7% 52.7% 54.7% 17.0% 68.5% 68.5% 68.5% 68.5% 68.5%	HP0865 HP0864 HP0860 HP0825 Purine ribon HP0815 HP0816 HP0815 HP0816 HP0818 HP0816 HP0818	(ded) deoxyuridine 5Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr subunit (hrdA) hioredoxin reductase (trxB) nucleotide biosymthasis 50-gunylate kinase (gmk) adenylate kinase (adk) adenylate kinase (adk) adenylosuccinate lyase (purB) adenylosuccinate symthetase (purA) formytterahydrofolate hydroitase (purU) glychamider ribonucleotide symthetase (purD) GMP reductase (guaC) GMP synthase (guaB) GMP reductase (guaC) GMP synthase (guaB) purine nucleoside diphosphate kinase (ndk) phosphoribosylprophosphate synthetase (pusA) purine nucleoside phosphorylase (punB) ibonucleotide biosymthasis aspartate transcarbamoylase (purB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC)	rolase 41.4% 43.39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 56.1% 56.5% 67.7% 58.5% 67.7% 48.6% 49.7% 58.7% 58.7% 48.6% 49.7% 50.7%
HP0523 HP0524 HP0526 HP0526 HP0527 HP0528 HP0529 HP1378 HP1006 HP1421 HP1006 HP1421 HP00042 HP0033 HP0041 HP0459 CENTRAL II General HP049	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) competence locus E (comE3) conjugative transfer regulor protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue (virB4) virB4 homolo	95.7% 99.1% 99.1% 99.1% 99.1% 99.5% 99.1% 99.5%	Electron tra HP0146 HP0378 HP0147 HP0147 HP0144 HP0145 HP1461 HP1461 HP1461 HP0458 HP1681 HP0684 HP1681 HP0684 HP0683 HP0683 HP0683 HP0683 HP1681 HP0683 HP1681 HP0683 HP1683	Ispoor Chb3-type cytochrome c oxidase subunit Q (Coco) (Co	44.2% 35.4% 37.5% 33.0% 443.9% 45.7% 48.5% 42.6% 42.6% 52.5% 42.6% 52.5% 45.7% 55.7% 56.7% 66.5% 68.5% 68.5%	HP0865 HP0864 HP0825 Purine ribon HP0321 HP0321 HP0321 HP0321 HP0255 HP1434 HP0499 HP0285 HP0349 HP0349 HP0349 HP0349 HP0399 HP1530 Pyrimidine ri HP1084 HP0999 HP1237 HP1237 HP0266 HP0266	(dcd) deoxyuridine 6Ö-triphosphate nucleotidohydr (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdA) thioredoxin reductase (trxB) uucleotide biosynthesis 5Ö-gunylate kinase (gmk) adenylate kinase (adk) adenylate kinase (adk) adenylatesionate synthetase (purA) formylaterahydrofolate hydrofase (purU) glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-5O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (purA) purine nucleoside phosphorylase (purB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrF)	rolase 41.4% 3 39.0% 39.0% 39.0% 44.8% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 56.1% 56.5% 67.7% 56.5% 67.7% 48.6% 39.7% 48.6% 39.7% 48.6% 59.7%
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НР0523 НР0524 НР0526 НР0526 НР0527 НР0528 НР0529 НР1378 НР1381 НР1039 НР1381 НР1031 НР0333 НР0333 НР041 НР0313 НР041	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cap can cap	95.7% 99.1% 99.1% 99.1% 99.1% 99.1% 99.1% 99.1% 99.5% 99.5% 99.0% 99.5%	Electron re Electron tra Electron tra HP0146 HP0378 HP0147 HP0144 HP0144 HP0145 HP1461 HP1227 HP0583 HP161 HP0583 HP161 HP0683 HP0631 HP0695 HP0905 HP0905 HP0905 HP0905 HP0905 Gluconeoge HP0385 Gluconeoge HP0905 Gluconeoge HP0905 Gluconeoge HP0905 HP0905 Gluconeoge HP0905 HP0905 Gluconeoge HP0905 HP0905 HP0905 Gluconeoge HP0905 HP0905 Gluconeoge Glycolysis	insport chb3-type cytochrome c oxidase subunit Q (CcoQ) (44.2% 35.4% 37.5% 33.0% 44.2% 43.9% 44.5% 45.7% 45.7% 45.7% 45.6% 42.6% 42.6% 42.1% 46.1% 68.5% 68.5% 68.5% 68.9% 39.3% 52.8% 50.7% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 67.7%	HP0865 HP0865 HP0869 HP0825 Purine ribon HP0825 Purine ribon HP0826 HP0868 HP1112 HP0686 HP1434 HP0085 HP1434 HP0086 HP0829 HP0889 HP0889 HP0889 HP0899 HP188 HP0899 HP188 HP0899 HP1984 HP0899 HP1984 HP0899 HP1984 HP0899 HP1987 HP0896 HP1987 HP0896 HP0899 HP188 HP0896 HP188 HP0898	(ded) deoxyuridine 6Ö-triphosphate nucleotidohydri (dut) ribonucleoside diphosphate reductase, beta subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdB) ribonucleoside-diphosphate reductase 1 alr subunit (nrdA) hibrodeoxin reductase (trxB) ucleotide biosynthesis 6Ö-guanylate kinase (gmk) adenylate kinase (adk) adenylate kinase (adk) adenylosuccinate synthetase (purA) formyltetrahydrofolate hydrofase (purU) glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-5O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) carbamoyl-phosphate synthetase (prsA) purine nucleoside synthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotate dehydrogenase (pyrE) orotate phosphoribosyltransferase (pyrE) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoC) xanthine guanine phosphoribosyl transferase (ppt) uncleosides and nucleotides 200-phosphate (deoC) xanthine guanine phosphoribosyltransferase (pri) phosphopentomutase (deoB) xanthine guanine phosphoribosyltransferase (pri) phosphoribosyltransferase (pri) phosphopentomutase (deoB) xanthine guanine phosphoribosyltransferase (pri)	rolase (14.9) 41.496 43.30.9% 44.896 33.33% 44.596 44.596 44.596 44.596 44.596 44.596 44.596 44.596 44.596 44.596 44.596 44.596 45.596 56.596
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HP0523 HP0524 HP0524 HP0526 HP0526 HP0527 HP0528 HP0527 HP0528 HP0527 HP0528 HP1378 HP1381 HP1381 HP1381 HP1381 HP0333 HP0042 HP0333 HP00441 HP0333 HP00441 HP0481 HP0482 HP0481 HP0482 HP0481 HP0482 HP0481 HP0482 HP0481 HP0482 HP04832 HP04832 HP06834 HP06835 HP06854 HP06854 HP06854 HP06854 HP06854 HP06854 HP06854 HP06854 HP06854 HP06855 HP06854 HP06855 HP06856 HP0685	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lipoprotein (comL) competence lipoprotein (rag3) conjugative transfer epution (rag4) virB4 homologue (virB4) wirB4 homologue (virB4) virB4 homo	95.7% 991.9% 991.9% 97.5% 97.5% 98.6% 98.9%	Electron re Electron tra HP0146 HP01378 HP0147 HP0141 HP01	insport chb3-type cytochrome c oxidase subunit Q (CcoQ) (44 296 33 .096 43 .996 44 .996 45 .796 33 .096 45 .796 45 .796 45 .796 46 .796 46 .996	HP0865 HP0865 HP0869 HP0825 Purine ribon HP0825 Purine ribon HP0821 HP0861 HP1112 HP0864 HP0864 HP0864 HP0869 HP087 HP0864 HP0869 HP0866 HP086	(ded) (ded) (ded) (ded) (ded) (dev)	10 (a) 26 (a) 27 (b) 27 (b) 27 (c) 27
НР0523 НР0523 НР0524 НР0526 НР0526 НР0527 НР0528 НР0527 НР0528 НР0527 НР0528 НР1378 НР10529 НР1378 НР1381 НР1033 НР0041 НР0333 НР0042 НР0333 НР0041 НР041	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) campetence lipoprotein (comL) competence lipoprotein (comP) competence accessory protein (comP) comp	95.7% 991.9% 991.9% 97.5% 97.5% 98.6% 98.9%	Electron re Electron tra HP0146 HP01378 HP0147 HP0144 HP0145 HP0146 HP0146 HP0146 HP0146 HP0158 HP01	insport cobb3-type cytochrome c oxidase subunit Q (CcoQ) (44 296 33 496 37.596 33.096 45.796 43.996 45.796 48.596 48.596 52.596 42.696 54.706 68.596 68.596 68.596 65.596 73.296 65.596 73.296 65.596 73.296 65.596 73.296 65.596 65.596 65.596 65.596 66.596 66.596 66.596 66.596 66.596	HP0865 HP0869 HP0826 Purine ribon HP0825 Purine ribon HP0825 Purine ribon HP0825 HP0818 HP0321 HP0818 HP0321 HP0818 HP0322 HP018 HP0328 HP0328 HP0329 HP0328 HP0329 HP0329 HP0329 HP0329 HP1237 HP0349 HP0329 HP1237 HP0349 HP0329 HP1237 HP0349 HP0329 HP1237 HP0349 HP0349 HP1237 HP0349 HP0349 HP0349 HP0349 HP0349 HP0358 HP0349 HP0358	(dod) deoxyuridine 6Ö-triphosphate nucleotidohydri (dut) ribonucleoside diphosphate reductase, beta subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr subunit (hrdB) ribonucleoside-diphosphate reductase 1 alr subunit (hrdA) hibroedoxin reductase (trxB) nucleotide biosynthesis 50-ganylate kinase (gmk) adenylate kinase (gurB) adenylate kinase (gurB) adenylate kinase (gurB) adenylate kinase (gurB) adenylate kinase (purD) glychamide ribonucleotide synthetase (purU) glychamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaB) GMP reductase (guaC) GMP synthase (guaB) phosphoribosylprophosphate synthetase (purB) phosphoribosylprophosphate synthetase (purB) purine nucleoside phosphorylase (purB) irbonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) crp synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) protate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) phosphorenomulase (deaB) purine-nucleosides and nucleotides 200-gclic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (pt) phosphopentomulase (deaB) purine-nucleoside phosphoribosyl transferas (gpt) purine-nucleoside phosphoribosyl transferas (gpt) purine-nucleoside phosphoribosyl transferas (gpt) purine-nucleoside phosphoribosyl transferas (gpt) adenine guanine phosphoribosyl transferas (gpt) purine-nucleoside phosphoribosyl transferas (gpt) adenine phosphoribosyltransferase (pmi) or (algA) NUPP-lucose pryophosphoribosyl transferas (gpt) adenine phosphoribosyltransferase (pmi) or (algA) carbon storage regulator (csrA)	rolase (14.96 4.4.96 4.59% 44.896 33.3.9% 44.896 33.3.9% 44.896 33.3.9% 56.596 67.796 31.896 33.796 44.896 33.796 44.896 33.796 44.896 33.796 56.596
НР0523 НР0523 НР0524 НР0526 НР0526 НР0527 НР0527 НР0528 НР0529 НР1381 НР1052 НР1381 НР1034 НР1381 НР0333 НР0419 НР04	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lipoprotein (comL) completence lipoprotein (rinG3) conjugality transfer protein (traG3) conjugality transfer protein (traG3) conjugality transfer protein (traG4) rivB4 homologue virB4 homologue (virB4) v	95.7% 991.9% 991.9% 97.5% 97.5% 98.6% 99.0% 99.0% 99.9% 25.5% 25.5% 27.3% 32.2% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.6% 37.0% 33.3% 41.4% 50.0% 41.4% 33.5% 47.8% 33.5% 47.8% 33.5% 41.4% 41.7% 50.0% 33.3% 41.4% 50.0% 50.	Electron tra HP0146 HP0378 HP0147 HP0147 HP0145 HP0147 HP0145 HP0146 HP1227 HP0278 HP0278 HP0278 HP0388 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1539 HP0632 HP0631 HP0632 HP0631 HP1538 HP1540 Enther-Dow HP1538 HP1540 Enther-Dow HP1699 HP1699 HP1699 HP1090 HP1090 HP1090 HP0090	insport chb3-type cytochrome c oxidase subunit Q (CcoQ) (44.2% 35.4% 37.5% 33.0% 44.2% 45.7% 45.7% 45.7% 42.6% 29.4% 44.6% 39.3% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 66.5% 73.2% 65.5% 73.2% 65.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.2% 66.5% 75.6%	HP0865 HP0865 HP08680 HP0825 Purine ribon HP0825 Purine ribon HP0826 HP0868 HP1112 HP0681 HP0184 HP0266 HP1218 HP0854 HP049 HP0869 HP0889 HP089 HP089 HP089 HP189 HP089 HP189 HP088	(ded) (ded) (ded) (ded) (dev)	rolase (14.9%) a 30,9% b 14.8% a 31.8% a 30.9% a 30.9% a 31.8% a 30.9% a 30.9% a 31.8% a 30.9% a 30.9% a 31.8% a 30.9% a 31.8% a 30.9% a 31.8% a 30.9% a 30.9% a 31.8% a 30.9%
НР0523 НР0523 НР0524 НР0526 НР0526 НР0527 НР0528 НР0527 НР0528 НР0527 НР0528 НР1378 НР10529 НР1378 НР1381 НР1033 НР0041 НР0333 НР0042 НР0333 НР0041 НР041	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) campetence lipoprotein (comL) competence lipoprotein (comL) carbonic anhydrase (cidA) hydrogenase expression/formation protein (hypA) compounds inorganic prophosophates (ppA) carboxynorspermidine decarboxylase (ppA) carboxynorspermidine decarboxylase (ppA) carboxynorspermidine decarboxylase (ppA) carboxynorspermidine synthase (ppA) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureH) urease accessory protein (ure	95.7% 991.9% 991.9% 97.5% 97.5% 98.6% 99.0% 99.0% 99.9% 25.5% 25.5% 27.3% 32.2% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 41.4% 61.00 41.4% 63.5% 47.8% 47.8% 47.8% 47.8% 47.8% 48.6% 48.	Electron tra HP0146 HP0147 HP0147 HP0147 HP0147 HP0147 HP0147 HP0148 HP1048 HP1048 HP1048 HP1058 HP1068 HP1068 HP1068 HP1638 HP1638 HP1638 HP1638 HP1638 HP1638 HP1639 HP1639 HP1639 HP1639 HP1639 HP1639 HP1639 HP1639 HP100 Fermentatic HP0681 HP0681 HP0681 HP0681 HP0681 HP0681 HP109 HP10 HP1	insport chb3-type cytochrome c oxidase subunit Q (CcoQ) (44 296 33 496 37.596 33.096 44 3.996 45.796 48.596 48.596 48.596 48.196	HP0865 HP0865 HP0825 Purine ribon HP0825 Purine ribon HP0825 Purine ribon HP0826 HP0826 HP1821 HP0826 HP0827 HP084 HP084 HP084 HP084 HP084 HP085 HP0868 HP0868 HP0868 HP0868 HP0868 HP0868 HP0868 HP0888 HP0986 HP0888 HP0986 HP0888 HP0986 HP0888 HP1888 HP0888 HP1888	(ded) (ded) (ded) (ded) (dev)	rolase 14.496 3 3 3 9 9 9 9 9 9 9

HP0775	penta-phosphate guanosine-3Õ-pyrophospho		1104404			LIDOGGG	olle and an annual and an analysis of the analysis	30.5%
	hydrolase (spoT)	36.7%	HP1471	type IIS restriction enzyme R protein (BCGIB)	28.2%			58.2%
HP0224	peptide methionine sulphoxide reductase		HP1366	type IIS restriction enzyme R protein		HP1295		56.2%
	(msrA)	66.8%		(MBOIIR)	37.1%	HP1197		79.0%
HP1025 HP1572		46.2% 31.9%	HP1208	ulcer associated adenine specific DNA methyltransferase	93.4%			55.8% 68.3%
HP0703		44.2%	HP1209	ulcer-associated gene restriction endonucle				57.8%
HP1021	response regulator	28.7%		(iceA)	95.5%	HP1151	ribosomal protein S16 (rpS16)	46.8%
HP1043		26.8%	HP1347	uracil-DNA glycosylase (ung)	43.1%			55.4%
HP1365 HP0166	response regulator response regulator (ompR)	32.4% 51.0%	TRANSCRIF	PTION				55.2% 61.1%
HP0714		37.1%	Degradation					49.6%
HP0088	RNA polymerase sigma-70 factor (rpoD)	43.5%	HP1213	polynucleotide phosphorylase (pnp)	38.9%	HP0076	ribosomal protein S20 (rps20)	41.4%
HP0792 HP0164	sigma-54 interacting protein	97.7%		DNA-dependent RNA polymerase				42.4% 56.7%
HP1364	signal-transducing protein, histidine kinase signal-transducing protein, histidine kinase	24.9%	HP1293	DNA-directed RNA polymerase, alpha subu	ınit 35.3%			51.2%
HP0244	signal-transducing protein, histidine kinase		HP1198	(rpoA) DNA-directed RNA polymerase, beta subur		HP1302		65.5%
		30.0%		(rpoB)	47.8%			32.1%
HP0048 HP1287	transcriptional regulator (hypF) transcriptional regulator (tenA)	34.5% 34.7%	Transcriptio					62.2% 45.0%
HP0727		33.3%	HP0866	transcription elongation factor GreA (greA)	50.3%			50.4%
			HP1514	transcription termination factor NusA (nusA)	39.1%	HP1047		26.3%
REPLICATION			HP0001	transcription termination factor NusB (nusB		tRNA modifi	ication	
Degradatio	n of DNA ATP-dependent nuclease (addB)	2720	HP1203	transcription termination factor NusG				37.5%
HP0275 HP0259		27.2% 37.6%	HP0550	(nusG) transcription termination factor Rho (rho)	41.0% 56.6%		peptidyl-tRNA hydrolase (pth) pseudouridylate synthase I (hisT)	46.6% 32.2%
	eation, restriction, modification, recombination		HFU00U	transcription termination factor kno (mo)	00.0%	HP1448		29.3%
HP0142	A/G-specific adenine glycosylase (mutY)	38.2%	RNA proces			HP1062	S-adenosylmethionine:tRNA	00.00/
HP0050	adenine specific DNA methyltransferase	07.40/	HP0640	poly(A) polymerase (papS)	37.4%	HP1513		39.3% 36.2%
HP0910	(dpnA) adenine specific DNA methyltransferase	37.4%	HP0662	ribonuclease III (rnc)	37.3%	HP1148	tRNA (guanine-N1)-methyltransferase (trmD)	
111 0010	(HINDIIM)	33.4%	TRANSLATI	ON		HP1415	tRNA delta(2)-isopentenylpyrophosphate	
HP1352	adenine specific DNA methyltransferase		General					30.7% 45.6%
HP0263	(HINFIM) adenine specific DNA methyltransferase	62.5%	HP0944	translation initiation inhibitor, putative	45.6%	Translation		45.0%
HFU203		33.9%	Aminoacyl 1	RNA synthetases		HP0247	ATP-dependent RNA helicase, DEAD-box	
HP0481	adenine specific DNA methyltransferase		HP1241 HP0319	alanyl-tRNA synthetase (alaS) arginyl-tRNA synthetase (argS)	44.9% 35.8%		family (deaD)	37.7%
1150000		29.3%	HP0617		50.1%		peptide chain release factor RF-1 (prfA)	52.6%
HP0260	adenine specific DNA methyltransferase (mod)	33.9%	HP0886	cysteinyl-tRNA synthetase (cysS)	97.3%	HP0171 HP1256		49.6% 43.7%
HP0593	adenine specific DNA methyltransferase	33.570	HP0476	glutamyl-tRNA synthetase (gltX)	43.1%	HP1195	translation elongation factor EF-G (fusA)	67.5%
	(mod)	38.5%	HP0643 HP0960	glutamyl-tRNA synthetase (gltX) glycyl-tRNA synthetase, alpha subunit	39.8%			45.1%
HP1522	adenine specific DNA methyltransferase	10.00	111 0300	(glyQ)	60.1%			43.1%
HP0478	(mod) adenine specific DNA methyltransferase	42.2%	HP0972	glycyl-tRNA synthetase, beta subunit (glyS)	33.6%			89.5% 65.3%
111 0470	(VSPIM)	42.1%	HP1190	histidyl-tRNA synthetase (hisS)	32.4%			45.4%
HP0054	adenine/cytosine DNA methyltransferase	32.1%	HP1422 HP1547	isoleucyl-tRNA synthetase (ileS) leucyl-tRNA synthetase (leuS)	49.7% 45.9%		translation initiation factor IF-3 (infC)	43.4%
HP0790		42.9%	HP0182	lysyl-tRNA synthetase (lysS)	58.6%	TDANIODOD	T AND BINDING PROTEINS	
HP1529	chromosomal replication initiator protein (dnaA)	34.9%	HP0417	methionyl-tRNA synthetase (metS)	42.4%	General	I AND BINDING PROTEINS	
HP1121	cytosine specific DNA methyltransferase		HP0403	phenylalanyl-tRNA synthetase, alpha subun (pheS)			ABC transporter, ATP-binding protein	66.7%
	(BSP6IM)	37.0%	HP0402	phenylalanyl-tRNA synthetase, beta subunit	48.7%		ABC transporter, ATP-binding protein	31.1%
HP0051	cytosine specific DNA methyltransferase (DDEM)	39.0%	111 0 102	(pheT)	30.0%	HP0715	ABC transporter, ATP-binding protein	52.3%
HP0483	cytosine specific DNA methyltransferase	39.0%	HP0238	prolyl-tRNA synthetase (proS)	39.8%			48.2%
	(HPHIMC)	38.7%	HP1480 HP0123	seryl-tRNA synthetase (serS) threonyl-tRNA synthetase (thrS)	48.3% 42.1%	111 1400	ABC transporter, ATP-binding protein (HI1087)	37.8%
HP0701		97.4%	HP1253	tryptophanyl-tRNA synthetase (triS)	52.6%	HP1220	ABC transporter, ATP-binding protein (yhcG))31.5%
HP0501 HP1478		46.0% 35.3%	HP0774	tyrosyl-tRNA synthetase (tyrS)	54.7%		ABC transporter, ATP-binding protein (yheS)	
HP0548		38.8%	HP1153	valyl-tRNA synthetase (valS)	43.7%			43.1% 29.7%
HP0615	DNA ligase (lig)	40.1%		of proteins, peptides and glycopeptides	00.50/			50.0%
HP0621 HP1470		32.6% 40.0%	HP0570 HP0033	aminopeptidase a/i (pepA) ATP-dependent C1p protease (clpA)	38.5% 40.3%	HP1427	histidine-rich, metal binding polypeptide	
HP1460		42.0%	HP0794	ATP-dependent clp protease proteolytic				100.0% 26.2%
HP0500		26.0%		component (clpP)	64.6%			32.4%
HP1231	DNA polymerase III delta prime subunit	10.00	HP1379 HP0223	ATP-dependent protease (Ion) ATP-dependent protease (sms)	43.9% 41.0%	HP0600	multidrug-resistance protein (spaB)	29.7%
HP1387	(holB) DNA polymerase III epsilon subunit (dnaQ)	48.6% 35.1%	HP1374	ATP-dependent protease (Sms)	41.070			29.1%
HP0717	DNA polymerase III gamma and tau subuni			(clpX)	56.3%	HP0497 HP0498	sodium- and chloride-dependent transporter sodium- and chloride-dependent trans-	r31.7%
	(dnaX)	39.0%	HP0264	ATP-dependent protease binding subunit	0770	111 0430		30.8%
HP0012		36.6%	HP0169	(clpB) collagenase (prtC)	97.7% 40.1%	HP0214		36.6%
HP1523 HP1393		32.7% 28.3%	HP0516		98.4%		s, peptides and amines	
HP0116	DNA topoisomerase I (topA)	45.1%	HP0515	heat-shock protein (hslV)	57.1%		amino acid ABC transporter, periplasmic	44.50/
HP0440		31.7%	HP0470 HP0657		97.9% 24.2%	HP0939	binding protein (yckK) amino acid ABC transporter, permease	41.5%
HP0602 HP0585	endonuclease III endonuclease III (nth)	36.6% 40.1%	HP1485	processing protease (ymxG) proline dipeptidase (pepQ)	35.2%		protein (yckJ)	46.9%
HP0705		53.4%	HP1350	protease	40.6%			41.7%
HP1114	excinuclease ABC subunit B (uvrB)	53.1%	HP1012	protease (pqqE)	29.6%		D-alanine glycine permease (dagA) dipeptide ABC transporter, ATP-binding	44.5%
HP0821			HP1435	protease IV (PspA) protein kinase C inhibitor (SP:P16436)	41.7% 40.2%	111 0301		59.5%
		31.5%	LIDOAGA				dipeptide ABC transporter, ATP-binding	
HP1526 HP0213	exodeoxyribonuclease (lexA)	31.5% 58.9%	HP0404 HP1019		52.9%			
HP1526 HP0213 HP1063	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA)	31.5%	HP1019 HP1584	serine protease (htrA) sialoglycoprotease (gcp)	35.7%			54.8%
HP0213 HP1063 HP1553	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase	31.5% 58.9% 48.5% 32.9% 33.0%	HP1019 HP1584 HP0382	serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YJR117W)		HP0298	dipeptide ABC transporter, periplasmic	
HP0213 HP1063 HP1553 HP0883	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0%	HP1019 HP1584 HP0382 Nucleoprote	serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YJR117W) sins	35.7% 36.2%	HP0298	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease	39.8%
HP0213 HP1063 HP1553 HP0883 HP1059	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB)	31.5% 58.9% 48.5% 32.9% 33.0%	HP1019 HP1584 HP0382 Nucleoprote HP0835	serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YJR117W) sins histone-like DNA-binding protein HU (hup)	35.7% 36.2%	HP0298 HP0299	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB)	39.8% 49.3%
HP0213 HP1063 HP1553 HP0883 HP1059 HP0877	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase helicase helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodeoxyribonuclease (ruvC)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod	serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YJR117W) sins histone-like DNA-binding protein HU (hup) liffication	35.7% 36.2% 44.6%	HP0298 HP0299	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein	39.8% 49.3% in
HP0213 HP1063 HP1553 HP0883 HP1059 HP0877	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC)	31.5% 58.9% 58.9% 32.9% 33.0% 39.0% 54.6% 34.7% 31.8%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363	serine protease (htrA) sialoglycoprotease (cpc) zinc-metalloprotease (YIR117W) zins histone-like DNA-binding protein HU (hup) diffication L-isoaspartyl-protein carboxyl methyltransfe (pcm)	35.7% 36.2% 44.6% erase 43.0%	HP0298 HP0299 HP0300 HP1506	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) de ABC transporter, permease protein (dppC) glutamate permease (gliS)	39.8% 49.3%
HP0213 HP1063 HP1553 HP0883 HP1059 HP0877 HP0675 HP0995	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase helicase (muR) Holliday junction DNA helicase (muR) Holliday junction DNA helicase (muR) Holliday junction endodexyribonuclease (muC) integrase/recombinase (xerC) integrase/recombinase (xerC)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6% 34.7% 31.8% 27.896	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299	serine protease (htrA) sialoglycoprotease (acp) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) histone-like DNA-binding protein HU (hup) lification Lisoaspartyl-protein carboxyl methyltransfe (pcm) methionine amino peptidase (map)	35.7% 36.2% 44.6%	HP0298 HP0299 HP0300 HP1506 HP1171	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding	39.8% 49.3% in 52.5% 56.9%
HP0213 HP1063 HP1553 HP0883 HP1059 HP0877	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine	31.5% 58.9% 48.5% 32.9% 32.9% 33.0% 54.6% 34.7% 31.8% 27.8% 31.1%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363	serine protease (htr.A) sialoglycoprotease (cp) zinc-metalloprotease (YIR117W) zins histone-like DNA-binding protein HU (hup) tification L-isoaspartyl-protein carboxyl methyltransfe (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B,	35.7% 36.2% 44.6% rase 43.0% 43.0%	HP0298 HP0299 HP0300 HP1506 HP1171	dipeptide ABC transporter, peripleasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiate permease (gttS) glutamiae ABC transporter, ATP-binding protein (glinO)	39.8% 49.3% in 52.5%
HP0213 HP1063 HP1653 HP0883 HP069 HP0877 HP0675 HP0995 HP0323 HP0676	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase holiday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1)	31.5% 58.39% 48.5% 32.9% 32.9% 33.0% 33.0% 34.7% 34.7% 31.8% 27.89 31.1%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299	serine protease (htr.A) sialoglycoprotease (acp) zinc-metalloprotease (YIR117W) zins histone-like DNA-binding protein HU (hup) sification L-isoaspartyl-protein carboxyl methyltransfe (pcm) methionline amino peptidase (map) peptidyl-prolyl cis-trans isomerase B,	35.7% 36.2% 44.6% trase 43.0% 43.0% 58.1% pe	HP0298 HP0299 HP0300 HP1506 HP1171	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (glIS) glutamine ABC transporter, ATP-binding protein (glnQ) glutamine ABC transporter, periplasmic	39.8% 49.3% in 52.5% 56.9% 51.9%
HP0213 HP1063 HP1553 HP0883 HP1059 HP0877 HP0675 HP0995 HP0323 HP0676	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA)	31.5% 58.9% 48.5% 32.9% 32.9% 53.0% 54.6% 34.7% 31.8% 27.8% 31.1% 41.0%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299 HP1441 HP1123	serine protease (IntrA) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (Number of the Communication of the Communica	35.7% 36.2% 44.6% rase 43.0% 43.0% 58.1% pe	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, periplasmic dipeptide-bindring protein (dppA) dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamine ABC transporter, ATP-bindring protein (glnQ) glutamine ABC transporter, periplasmic glutamine-bindring protein (glhH) glutamine-bindring protein (glhH) glutamine-bindring protein (glhH)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2%
HP0213 HP1063 HP1653 HP0883 HP069 HP0877 HP0675 HP0995 HP0323 HP0676	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodexyribonuclease (ruvC) Holliday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNANprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA)	31.5% 58.9% 48.5% 32.9% 33.0% 33.0% 54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 99.1%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793	serine protease (htrA) sialoglycoprotease (acp) zinc-metalloprotease (yIR117W) zinc-metalloprotease (YIR117W) zinc-metalloprotease (YIR117W) zinc-metalloprotease (YIR117W) zinc-metalloprotease (YIR117W) zinc-metalloprote	35.7% 36.2% 44.6% trase 43.0% 43.0% 58.1% pe	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, peripleamic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gtS) glutamite ABC transporter, ATP-binding protein (glnG) glutamine ABC transporter, periplasmic glutamine-binding protein (glnG) glutamine-binding protein (glnH) glutamine-binding protein (glnH) grotein (glnF) protein (glnF)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6%
HP0213 HP1063 HP1063 HP1063 HP0883 HP1069 HP0877 HP0676 HP0323 HP0676 HP0387 HP0153	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction DNA helicase (ruvB) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrahe bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende	31.5% 58.9% 48.5% 32.9% 33.0% 33.0% 33.0% 33.0% 33.0% 34.7% 31.8% 27.89% 31.19 41.0% 36.3% 39.9% 36.5% 11.5% 36.5% 11.5% 36.5% 11.5% 36.5% 11.5%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal J	serine protease (htrA) sialoglycoprotease (acp) zinc-metalloprotease (YIR117W) zinc histone-like DNA-binding protein HU (hup) tification L-isoaspartyl-protein carboxyl methyltransfe (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-proly cis-trans isomerase, FKBP-ty, rotamase (slyD) polypeptide deformylase (def)	35.7% 36.2% 44.6% rrase 43.0% 43.0% 58.1% pe 40.4% 41.8%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gltS) glutamine ABC transporter, ATP-binding protein (glnA) glutamine ABC transporter, periplasmic glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine ABC transporter, permease protein (glnA)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein
HP0213 HP1063 HP1063 HP1063 HP0883 HP1069 HP0877 HP0675 HP0323 HP0676 HP0323 HP0676 HP0323 HP0676	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (helicase (helicase) punction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvA) Holiiday junction endodeoxyribonuclease (ruvC) helicase (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/fyrotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep.)	31.5% 58.9% 48.5% 32.9% 53.9% 54.6%	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal	serine protease (htrA) sialoglycoprotease (acp.) zinc-metalloprotease (yJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zins zinc-zinc-zinc-zinc-zinc-zinc-zinc-zinc-	35.7% 36.2% 44.6% rase 43.0% 43.0% 58.1% pe	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gltS) glutamine ABC transporter, ATP-binding protein (glnA) glutamine ABC transporter, periplasmic glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine ABC transporter, permease protein (glnA)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6%
HP0213 HP1063 HP1063 HP0883 HP0883 HP0877 HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0153 HP0911 HP1362	exodeoxyribonuclesse (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase fundhibited division protein (gidB) helicase flutA) helicase flutA) helicase flutA) helicase flutA) floridisary junction endodeoxyribonuclease (ruxC) helididay junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep)	31.5% 58.9% 48.5% 32.9% 33.0% 33.0% 33.0% 33.0% 33.0% 34.7% 31.8% 27.89% 31.1% 41.0% 36.5%	HP1019 HP1584 HP0382 Nucleoprote HP0885 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal HP1201 HP1200	serine protease (IntrA) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (Intra-metalloprotease (In	35.7% 36.2% 44.6% rasse 43.0% 43.0% 55.1% pe 40.4% 41.8%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gltS) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) oligopeptide ABC transporter, ATP-binding protein (oppD)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein
HP0213 HP1063 HP1063 HP0883 HP0883 HP0877 HP0675 HP0995 HP0387 HP0183 HP0183 HP0911 HP1362 HP1383 HP06661	exodéxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase funda, plucose-inhibited division protein (gidB) helicase holiday junction DNA helicase (ruxA) Holiday junction endodexyribonuclease (ruxC) integrase / recombinase (xerC) integrase / recombinase (xerC) integrase / recombinase (xerC) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease H (mhA)	31.5% 58.9% 48.5% 32.9% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 34.7% 31.8% 27.89% 31.1% 41.0% 31.8% 27.89% 31.1% 41.0% 33.8% 39.9% 33.5	HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal / HP1201 HP1200	serine protease (htrA) sialoglycoprotease (acp) zinc-metalloprotease (YR117W) sins histone-like DNA-binding protein HU (hup) sification L-isoasparty-protein carboxyl methyltransfe (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-ty rotamase (slyD) proteins: synthesis and modification ribosomal protein L1 (pft) ribosomal protein L10 (rpl10) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl10)	35.7% 36.2% 44.6% 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 30.4% 63.8%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, perplasmic	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1%
HP0213 HP1063 HP1663 HP1683 HP0883 HP0877 HP0675 HP0323 HP0676 HP0323 HP0153 HP0925 HP0925 HP0921 HP1383 HP0661 HP1383 HP0661 HP1383 HP0661 HP1383	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (quad) helicase (quad) helicase (quad) helidasy junction DNA helicase (quad) Holiday junction DNA helicase (quad) heliday junction endodeoxyribonuclease (quad) heliday junction endodeoxyribonuclease (quad) heliday junction endodeoxyribonuclease (quad) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNANprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) repenicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6%	HP1019 HP1584 HP0382 Nucleoprote HP0885 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1201 HP1201 HP1202 HP1202 HP1202 HP1068	serine protease (IntrA) sialoglycoprotease (acp.) zinc-metalloprotease (yJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-zinc-zinc-zinc-zinc-zinc-zinc-zinc-	35.7% 36.2% 44.6% 143.0% 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 30.4% 53.9%	HP0298 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (ghaC) glutamine ABC transporter, periplasmic glutamine-binding protein (ginH) glutamine ABC transporter, permease protein (ginH) glutamine ABC transporter, permease protein (ginH) glutamine ABC transporter, permease protein (ginHP) oligopeptide ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, periplasmic	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9%
HP0213 HP1063 HP1063 HP1063 HP0883 HP00877 HP00877 HP0323 HP0076 HP0323 HP0076 HP0387 HP0153 HP0911 HP1362 HP1383 HP0661 HP1323 HP0661 HP1323 HP0661 HP1323 HP1323 HP0661 HP1323 HP1323 HP1323 HP1324	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase [huA] glucose-inhibited division protein (gidB) helicase holiday junction DNA helicase (ruxA) Holiday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinate (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) residented bNA-depende HTPase (rep) residented bNA-depende HTPase (rep) residented DNA-belicase (dnaB) restriction modification system S subunit ribonuclease H (rinA) ribonuclease H (rinA) ribonuclease BH (rinB) single-strand DNA-binding protein (ssb)	31.5% 58.9% 48.5% 32.9% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 34.7% 31.8% 27.89% 31.1% 41.0% 31.8% 27.89% 31.1% 41.0% 33.8% 39.9% 33.5	HP1019 HP1584 HP0382 Nucleoprote HP0385 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1201 HP1200 HP1202 HP1202 HP1084 HP0084 HP1099	serine protease (IntrA) sialoglycoprotease (acp.) zinc-metalloprotease (yJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (pornometalloprotease (pornometalloprotease (pornometalloprotease (pornometalloprotease (pornometalloprotease (sylV)) polypeptidy-protyl zinc-trans isomerase, FKBP-tyloprotease (sylV) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (rpt11) ribosomal protein L11 (rpt11) ribosomal protein L11 (rpt11) ribosomal protein L11 (rpt11) ribosomal protein L13 (rpt13) ribosomal protein L14 (rpt13) ribosomal protein L14 (rpt14)	36.7% 36.2% 44.6% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 58.1% 52.0% 30.4% 30	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (ghO) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppA) oligopeptide ABC transporter, permease protein (oppA) oligopeptide ABC transporter, permease protein (oppA)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1%
HP0213 HP1063 HP1063 HP1065 HP0877 HP0677 HP0676 HP0926 HP0926 HP0927 HP0183 HP0926 HP0911 HP1362 HP1983 HP0984 HP1988 HP1988 HP	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (qua) helicase heliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease HII (rnhB) single-stranded-DNA-specific exonuclease (recd)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6%	HP1019 HP10382 Nucleoprote HP0382 Nucleoprote HP0385 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1068 HP0084 HP1309 HP1088	serine protease (htrA) sialoglycoprotease (acp) zinc-metalloprotease (yz) zinc-metalloprotease (YiR117W) sin-sialoglycoprotease (YiR117W) sin-sialoglycoprotease (YiR117W) sin-sialoglycoprotease (YiR117W) sin-sialoglycoprotease (YiR117W) sin-sialoglycoprotease (ycolospoin-type rotamase (ppi) peptidyl-prolyl cis-trans isomerase FKBP-tyrotamase (siyD) poptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (rp111) ribosomal protein L11 (rp111) ribosomal protein L11 (rp111) ribosomal protein L11 (rp113) ribosomal protein L13 (rp113) ribosomal protein L13 (rp114) ribosomal protein L13 (rp115) ribosomal protein L13 (rp114) ribosomal protein L15 (rp115) ribosomal protein L17 (rp116) ribosomal protein L18 (rp116) ribosomal protein L19 (rp116)	36.7% 36.2% 44.6% rrase 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 30.4% 63.8% 53.4% 663.9% 65.9%	HP0298 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1262 HP1251 HP0251	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) dipeptide ABC transporter, ATP-binding protein (glnA) glutamiae ABC transporter, ATP-binding protein (glnA) glutamine ABC transporter, periplasmic glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-binding protein (glnA) glutamine-ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) oligopeptide ABC transporter, ATP-binding protein (oppD) digopeptide ABC transporter, permease protein (oppB)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1% 28.7% 59.6%
HP0213 HP1053 HP1053 HP10583 HP0087 HP0087 HP0087 HP0087 HP0087 HP0086 HP0087 HP0086 HP0081 HP0081 HP1083 HP0681 HP1083 HP1083 HP10881	exodeoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase helicase helicase helicase representation of the protein gidB) helicase helicase (nuch and protein glucose funda punction divideose (nuch and protein endodeoxyribonuclease (nuch methyribase fundamentation) helicase (nuch methyribase (nuch methyribase) helicase (nuch methyribas	31.5% 58.9% 48.5% 32.9% 53.0% 54.6%	HP1019 HP10382 Nucleoprote HP0385 Protein mod HP1383 HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1309 HP1309 HP1301 HP1301 HP1301	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (DAC) zinc-metalloprotease (pompoptidy-prolyl cis-trans isomerase B, cyclospoint-ype rotamase (pai) peptidy-prolyl cis-trans isomerase, FKBP-ty potyloprotease (siyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (pril1) ribosomal protein L11 (pril1) ribosomal protein L11 (pril1) ribosomal protein L13 (pril3) ribosomal protein L14 (pril4) ribosomal protein L14 (pril4) ribosomal protein L14 (pril4) ribosomal protein L14 (pril4) ribosomal protein L16 (pril5) ribosomal protein L16 (pril5) ribosomal protein L16 (pril6)	35.7% 36.2% 44.6% 44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 52.0% 63.8% 33.4% 63.8% 38.4% 60.0% 65.9% 42.5%	HP0298 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine ABC transporter, permease protein (glnF) glutamine ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) oligopeptide ABC transporter, permease protein (oppC) orderotein (oppC)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% in 30.9% 39.1% 59.6% 31.4%
HP0213 HP1063 HP1063 HP1069 HP0877 HP0677 HP0676 HP0323 HP00676 HP0323 HP0965 HP0911 HP1382 HP0961 HP1382 HP0984 HP0984 HP0984 HP0984 HP0984 HP0984 HP1382 HP1382 HP1384 H	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (qua) helicase heliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease HII (rnhB) single-stranded-DNA-specific exonuclease (recl) single-stranded-DNA-specific exonuclease (recl) site-specific recombinase transcription-repair coupling factor (trcF)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6%	HP1019 HP10382 Nucleoprote HP0385 Protein mod HP10383 HP1299 HP1201 HP1201 HP1201 HP1200 HP1200 HP1200 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309 HP1309	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (Intional Commentary) protein carboxyl methyltransfe (pcm) methionine amino peptidase (map) peptidy-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppt) peptidy-prolyl cis-trans isomerase, FKBP-tyr ortamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (prtl1) ribosomal protein L11 (prtl1) ribosomal protein L11 (prtl1) ribosomal protein L13 (prtl3) ribosomal protein L14 (prtl4) ribosomal protein L14 (prtl4) ribosomal protein L16 (prtl5) ribosomal protein L16 (prtl6) ribosomal protein L16 (prtl6) ribosomal protein L16 (prtl6) ribosomal protein L17 (prtl7) ribosomal protein L18 (prtl6) ribosomal protein L18 (prtl6) ribosomal protein L19 (prtl6) ribosomal protein L19 (prtl8)	36.7% 36.2% 44.6% 44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 50.0% 63.8% 50.0% 63.8% 42.6% 42.6% 43.9% 44.5%	HP0298 HP0300 HP1506 HP1170 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0251 HP0819 HP0819	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnP) glutamine-ABC transporter, permease protein (glnP) glutamine-ABC transporter, permease protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein (proVV) osmoprotection protein (proVV)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% in 30.9% 39.1% 59.6% 31.4% 38.3% 30.4%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0077 HP0075 HP00323 HP00323 HP00323 HP00323 HP0091 HP1332 HP0911 HP1332 HP0945 HP1332 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941 HP10941	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (quuA) helicase (helicase (quuA) helicase (quuA) helicase (quuA) helicase (quuA) helidasy junction endodexyribonuclease (quuC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine methylated-DNA/protein-cysteine (recA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (freA) respirated DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease HII (rnhB) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdS) type I restriction enzyme S protein (fisdS) type I restriction enzyme S protein (fisdS)	31.5% 58.9% 48.5% 32.9% 33.0% 39.0% 54.6%	HP1019 HP10382 Nucleoprote HP0385 Protein mod HP1293 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1200 HP1309 HP1309 HP1301 HP1309	serine protease (IntrA) sialoglycoprotease (acp) zinc-metalloprotease (yIR117W) zinc-methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppt) peptidyl-protyl cis-trans isomerase, FKBP-tyrotamase (sly1) poptidyl-protyl cis-trans isomerase, FKBP-tyrotamase (sly1) proteins: synthesis and modification ribosomal protein L11 (rp111) ribosomal protein L11 (rp111) ribosomal protein L11 (rp111) ribosomal protein L11 (rp111) ribosomal protein L13 (rp113) ribosomal protein L14 (rp114) ribosomal protein L15 (rp116) ribosomal protein L15 (rp116) ribosomal protein L17 (rp117) ribosomal protein L17 (rp117) ribosomal protein L18 (rp118) ribosomal protein L19 (rp119)	36.7% 36.2% 44.6% 44.6% 43.0% 43.0% 43.0% 58.1% 58.1% 59.2% 40.4% 41.8% 50.0% 63.8% 65.8% 65.9% 65.9% 62.4% 45.5% 62.9%	HP0298 HP0299 HP0300 HP1506 HP1771 HP1172 HP1170 HP0250 HP1262 HP1261 HP0251 HP0819 HP0819 HP0818	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiate permease (gltS) glutamiate permease (gltS) glutamiae ABC transporter, ATP-binding protein (glnG) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine ABC transporter, permease protein (glnP) glutamiae ABC transporter, permease protein (glnP) glutamiae ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, permease protein (oppB) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline permease (putP)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% sin 30.9% 39.1% 59.6% 31.4% 38.3% 30.4% 51.4%
HP0213 HP1053 HP1053 HP10583 HP0059 HP0077 HP00576 HP00376 HP00376 HP00376 HP0153 HP00376 HP0153 HP0225 HP0911 HP1323 HP1023 HP1023 HP10245 HP1034 HP1049 HP	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase helicase helicase helicase helicase helicase helicase helicase helicase heliday junction DNA helicase (ruvA) helicase (ruvB) helicase heliday junction endodeoxyribonuclease (ruvB) helicase helica	31.5% 56.3%	HP1019 HP10382 Nucleoprote HP03836 Nucleoprote HP03836 HP1299 HP1441 HP1123 HP0793 HP1201 HP1200 HP1201 HP1200 HP1301 HP1	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR118W) zinc-metalloprotease (pompose (pompos	36.2% 44.6% 44.6% 44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 52.0% 30.4% 63.8% 38.4% 50.0% 63.8% 42.6% 42.6% 42.6% 43.5% 43.5% 45.5% 50.9%	HP0298 HP0300 HP1506 HP1170 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0251 HP0819 HP0818 HP0818 HP0936	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (ghBC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine-binding protein (ghB) glutamine ABC transporter, permease protein (ghBC) glutamine ABC transporter, permease protein (ghBC) dipopeptide ABC transporter, permease protein (ppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betainet transporter (proP)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% sin 30.9% 39.1% 59.6% 51.4% 30.4% 51.4% 29.1%
HP0213 HP1063 HP1063 HP1069 HP0877 HP0677 HP0676 HP0323 HP0065 HP0323 HP0065 HP0911 HP1362 HP1368 HP1245 HP1245 HP1245 HP10944 HP10944 HP10948	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (quuA) Helicase (helicase (quuA) Helicase (quuA) Helicase (quuA) Helidasy junction DNA helicase (quuA) Holiday junction endodexyribonuclease (quuC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease HII (rnhB) single-stranded-DNA-specific exonuclease (recl) single-stranded-DNA-specific exonuclease (recl) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdS) type I restriction enzyme R protein (fisdR)	31.5% 58.9% 48.5% 32.9% 31.7% 33.6% 21.3% 37.7% 37.7% 31.7% 48.0% 58.9% 37.7% 37.7% 31.7% 48.0% 58.9% 31.7% 37.7% 37.7% 31.7% 48.0% 58.9%	HP1019 HP10382 Nucleoprote HP0385 Protein mod HP1293 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1200 HP1309 HP1309 HP1301 HP1309	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR118W) zinc-metalloprotease (pompose (pompos	36.7% 36.2% 44.6% 44.6% 43.0% 43.0% 43.0% 58.1% 58.1% 59.2% 40.4% 41.8% 50.0% 63.8% 65.8% 65.9% 65.9% 62.4% 45.5% 62.9%	HP0298 HP0300 HP1506 HP1170 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0251 HP0819 HP0818 HP0818 HP0936	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (ghBC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine-binding protein (ghB) glutamine ABC transporter, permease protein (ghBC) glutamine ABC transporter, permease protein (ghBC) dipopeptide ABC transporter, permease protein (ppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betainet transporter (proP)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% sin 30.9% 39.1% 59.6% 31.4% 38.3% 30.4% 51.4%
HP0213 HP1053 HP1053 HP10583 HP0059 HP0077 HP00576 HP00376 HP00376 HP00376 HP0153 HP00376 HP0153 HP0225 HP0911 HP1323 HP1023 HP1023 HP10245 HP1034 HP1049 HP	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase [quanda] publicase-inhibited division protein (gidB) helicase helidasy junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodeoxyribonuclease (ruvB) Holliday junction endodeoxyribonuclease (ruvB) helicase (recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrahe bound endonuclease (nuc) methylated-DNA/picrotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) report (recR) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA) ribonuclease H (mhA) ribonuclease H (mhA) ribonuclease H (mhA) ribonuclease (recI) single-stranded-DNA-specific exonuclease (recI) yel restriction enzyme S protein (fisdM) type I restriction enzyme M protein (fisdM) type I restriction enzyme R protein (fisdM) type I restriction enzyme R protein (fisdM) type I restriction enzyme R protein (fisdR)	31.5% 58.9% 48.5% 32.9% 54.6%	HP1019 HP10382 Nucleoprote HP0835 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1088 HP0084 HP1301 HP1301 HP1301 HP1301 HP1301 HP1303 HP1303 HP1303 HP1303 HP1303 HP1303 HP1303 HP1304 HP1305 HP1305 HP1305 HP1305 HP1306 HP1306 HP1307 HP1307 HP1307 HP1307 HP1307 HP1307 HP1307 HP1307 HP1308	serine protease (IntrA) sialoglycoprotease (acp) zinc-metalloprotease (yIR117W) zinc-methionine amino peptidase (map) peptidy-protyl cis-trans isomerase B, cyclosporin-type rotamase (pi) peptidy-protyl cis-trans isomerase, FKBP-tyrotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (pri10) ribosomal protein L11 (pri10) ribosomal protein L11 (pri10) ribosomal protein L14 (pri14) ribosomal protein L14 (pri14) ribosomal protein L15 (pri16) ribosomal protein L16 (pri16) ribosomal protein L17 (pri17) ribosomal protein L18 (pri18) ribosomal protein L19 (pri19) ribosomal protein L19 (pri19) ribosomal protein L19 (pri19) ribosomal protein L20 (pri20) ribosomal protein	36.7% 36.2% 44.6% 136.2% 44.6% 1396 43.0% 43.0% 58.1% 58.1% 58.1% 58.4% 58.6%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0251 HP0319 HP0319 HP0319 HP0313 HP0313 Anions	dipeptide ABC transporter, peripleasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, ATP-binding protein (glnC) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnF) glutamine-ABC transporter, ATP-binding protein (ppD) oligopeptide-ABC transporter, ATP-binding protein (ppD) oligopeptide-ABC transporter, periplasmic oligopeptide-binding protein (ppA) oligopeptide-ABC transporter, permease protein (oppD) oligopeptide-ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline permease (putF) proline-betaine transporter (proP) serine transporter (glaC)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iii 30.9% 39.1% 59.6% 31.4% 39.3% 30.4% 51.4% 29.1% 44.6%
HP0213 HP1053 HP1053 HP0583 HP0089 HP00875 HP00896 HP00876 HP0323 HP00876 HP10387 HP10	exodexyribonuclesse (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase [quuA] helicase (hura) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA) ribonuclease transcription-repair coupling factor (trcF) type I restriction enzyme S protein (hsdN) type I restriction enzyme M protein (hsdN) type I restriction enzyme R protein (hsdN) type I restriction enzyme R protein (hsdN) type I restriction enzyme R protein (hsdN) type I restriction enzyme M protein (hsdN) type I restriction enzyme M protein (hsdN) type I restriction enzyme M protein (hsdM)	31.5% 56.39% 48.5% 32.9% 54.6%	HP1019 HP10382 Nucleoprote HP03836 Nucleoprote HP03836 HP1299 HP1441 HP1233 HP0793 HP1201 HP1200 HP1201 HP1200 HP1301 HP1309 HP1301 HP1	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR118W) zinc-metalloprotease (pompetalloprotease (pompetalloprotease (pompetalloprotease (pompetalloprotease (sylon)) peptidyl-prolyl cis-trans isomerase R, cyclosporin-type rotamase (sylon) polypeptide deformylase (def) protease (sylon) polypeptide deformylase (def) protease (sylon) protein L1 (prit) ribosomal protein L1 (prit) ribosomal protein L1 (prit) ribosomal protein L11 (prit) ribosomal protein L11 (prit) ribosomal protein L14 (prit) ribosomal protein L15 (prit) ribosomal protein L16 (prit) ribosomal protein L16 (prit) ribosomal protein L18 (prit) ribosomal protein L18 (prit) ribosomal protein L19 (prit) ribosomal protein L2 (prit)	36.7% 36.296 44.696 FIRSE 43.096 43.096 58.196 69.694 41.896 52.096 30.496 63.896 63.896 38.496 65.096 42.596 65.096 42.596 65.0996 42.596 65.996 44.598	HP0298 HP0300 HP1300 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0819 HP0819 HP00818 HP0035 HP0033 Anions HP0475	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (dpnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-baBC transporter, periplasmic glutamine-baBC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppA) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline /betaine transporter (proP) serine transporter (groP) serine transporter (groP) serine transporter (proP) serine transporter (proP) serine transporter (ABC transporter, ATP-binding protein (modD)	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% sin 30.9% 39.1% 59.6% 51.4% 30.4% 51.4% 29.1%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0675 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP0975 HP10975 HP10975 HP10975 HP1098	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase (quuA) Holicase inhibited division protein (gidB) helicase Holiday junction DNA helicase (quuA) Holiday junction endodexyribonuclease (quuC) integrase /recombinase (xerC) integrase /recombinase (xerC) integrase /recombinase (xerC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane pound endonuclease (quuC) membrane protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase; single-stranded DNA-depende Al Pase (rep) restriction modification system S subunit ribonuclease HI (rnhA) ribonuclease HI (rnhB) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme R protein (fisdR) type I restriction enzyme R protein fisdR)	31.5% 58.9% 32.9% 33.0% 31.5% 34.7% 31.5% 34.7% 31.5%	HP1019 HP10382 Nucleoprote HP0383 HP0383 HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1200 HP1200 HP1309 HP1301 HP1200 HP1309 HP1301 HP1309 HP1301 HP1303 HP1303 HP1303 HP1303 HP1303 HP1303 HP1316 HP1316 HP1316 HP1316 HP1316 HP1317 HP1317 HP1317 HP1317	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (yJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (protease	36.7% 36.2% 44.6% rrase 43.0% 43.0% 58.1% 58.1% 59.2% 40.4% 51.9% 52.0% 53.4% 63.8% 65.8% 65.9% 65.9% 65.9% 45.5% 65.9% 45.5% 65.9% 45.5% 65.9% 45.5% 65.9% 65.4% 45.5% 65.9% 65.4% 65.9% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.4% 65.5% 65.5% 65.4% 65.4% 65.4% 65.5%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0319 HP0319 HP0333 Anions HP0473	dipeptide ABC transporter, periplasmic dipeptide-binding protein (appA) dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, perplasmic glutamine ABC transporter, perplasmic glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (ppD) oligopeptide ABC transporter, perplasmic oligopeptide ABC transporter, perplasmic oligopeptide ABC transporter, perplasmic oligopeptide ABC transporter, perplasmic oligopeptide ABC transporter, permease protein (ppD) oligopeptide ABC transporter, permease protein (ppD) osmoprotection protein (proV) osmoprotecti	39.8% 49.3% in 52.5% 56.9% 56.9% 51.9% 32.2% 27.6% iin 30.9% 39.1% 59.6% 31.4% 38.3% 30.4% 51.4% 29.1% 44.6%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0089 HP0877 HP00896 HP00876 HP0387 HP1025 HP0387 HP1025 HP10383 HP1025 HP10383 HP1025 HP10383 HP1025 HP10383 HP1024 HP10384 HP10384 HP10384 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10484 HP10846 HP1086 HP1086 HP1086 HP1086 HP1086 HP1086 HP1086 HP1086 HP108	exodexyribonuclesse (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase (nuA) helicase (nuA) helicase (nuA) helicase (nuC) protein (gidB) heliday junction DNA helicase (nuC) Holliday junction DNA helicase (nuC) heliday junction DNA helicase (nuC) heliday junction endodeoxyribonuclease (nuC) methylated-buANprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rephilicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA) ribonuclease transcription-repair coupling factor (rcF) type I restriction enzyme S protein (hsdN) type I restriction enzyme S protein (hsdN) type I restriction enzyme R protein (hsdN) type I restriction enzyme R protein (hsdN) type I restriction enzyme M protein (hsdM)	31.5% 58.9% 48.5% 32.9% 54.6%	HP1019 HP10382 Nucleoprote HP0835 Protein mod HP1293 HP1441 HP1123 HP0793 Ribosomal J HP1200 HP1200 HP1200 HP1200 HP1200 HP1301 HP1302 HP1302 HP1302 HP1303 HP1302 HP1303 HP1302 HP1303 HP1302	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (yJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (poincease (poince	36.7% 36.296 44.696 FIRSE 43.096 43.096 58.196 69.694 41.896 52.096 30.496 63.896 63.896 38.496 65.096 42.596 65.096 42.596 65.0996 42.596 65.996 44.598	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0819 HP0819 HP0818 HP00818 HP00938 HP10133 Anions HP0475	dipeptide ABC transporter, periplasmic dipeptide-binding protein (appA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (ppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proV) osmoprotection protein	39.8% 49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iii 30.9% 39.1% 59.6% 31.4% 39.3% 30.4% 51.4% 29.1% 44.6%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0095 HP0877 HP0095 HP0076 HP0376 HP0376 HP0376 HP0376 HP10376 HP1037 HP1037 HP1037 HP1037 HP1037 HP1037 HP1037 HP1038 H	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase (quuA) Holicase inhibited division protein (gidB) helicase Holiday junction DNA helicase (quuA) Holiday junction endodexyribonuclease (quuC) integrase /recombinase (xerC) integrase /recombinase (xerC) integrase /recombinase (xerC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane bound endonuclease (quuC) membrane pound endonuclease (quuC) membrane protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase; single-stranded DNA-depende Al Pase (rep) restriction modification system S subunit ribonuclease HI (rnhA) ribonuclease HI (rnhB) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme R protein (fisdR) type I restriction enzyme R protein fisdR)	31.5% 58.9% 48.5% 32.9% 54.6%	HP1019 HP10382 Nucleoprote HP0836 Nucleoprote HP0836 HP1299 HP1441 HP1123 HP1231 HP1231 HP1201 HP1201 HP1201 HP1201 HP1201 HP1201 HP1202 HP1301 HP1308	serine protease (IntA) sialoglycoprotease (apr.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-zinc-metalloprotease (PJR117W) zinc-zinc-zinc-zinc-zinc-zinc-zinc-zinc-	36.7% 36.296 44.696 44.696 44.696 43.096 43.096 58.196 99 40.496 41.896 52.096 53.496 63.896 38.496 50.096 65.996 42.596 62.496 448.396 45.596 50.996 52.496 448.396 45.596 50.996 54.698 45.596 54.896 44.996 44.1796 44.1796 44.796 41.796	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0819 HP0819 HP0818 HP0035 HP0338 HP0475 HP0475 HP0473 HP0473	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (ppB) digopeptide ABC transporter, permease protein (ppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline / betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdenum ABC transporter, periplasmic molybdenum ABC transporter, periplasmic molybdenum ABC transporter, periplasmic molybdenum ABC transporter, permease protein (modD) molybdenum ABC transporter, permease protein (modA)	39.8% 49.3% in 56.5% 56.5% 56.5% 51.9% 32.2% 27.6% in 30.9% 39.1% 28.7% 39.1%
HP0213 HP1053 HP1053 HP1059 HP0087 HP0097 HP0097 HP0097 HP0097 HP0097 HP0097 HP0097 HP0097 HP0097 HP0097 HP1097 HP1097 HP1098 HP	exodexyribonuclease (lexA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase (quuA) Holicase inhibited division protein (gidB) helicase Holiday junction DNA helicase (quuA) Holiday junction endodexyribonuclease (quuC) integrase /recombinase (xerC) integrase /recombinase (xerC) integrase /recombinase (xerC) membrane bound endonuclease (quuC) membrane bround endonuclease (quuC) membrane bround factor (priA) recombinase (recA) respective (recA) respective (recA) recombinase (recA) respective (recA) respe	31.5% 58.9% 32.9% 33.0% 34.7% 31.8% 54.6% 34.7% 31.8% 54.6% 56.6% 57.7%	HP1019 HP10382 Nucleoprote HP0835 Protein mod HP0835 HP1299 HP1441 HP1123 HP0793 Ribosomel J HP1200 HP1200 HP1200 HP1200 HP1200 HP1088 HP0084 HP0084 HP0084 HP1089 HP1301 HP1200 HP1301 HP1200 HP1301 HP1311 HP1311 HP1311 HP1311	serine protease (Int'A) sialoglycoprotease (acp.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (promptification technological popularity in the protein carboxyl methyltransfe (pcm) peptidy-prolyl cis-trans isomerase B, cyclosporin-type roteanse (pt)) peptidy-prolyl cis-trans isomerase, FKBP-tyroteanse (styl)) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (pri10) ribosomal protein L1 (pri10) ribosomal protein L1 (pri10) ribosomal protein L1 (pri11) ribosomal protein L14 (pri14) ribosomal protein L15 (pri15) ribosomal protein L16 (pri16) ribosomal protein L16 (pri16) ribosomal protein L19 (pri19) ribosomal protein L19 (pri20) ribosomal protein L20 (pri20) ribosomal	36.7% 36.2% 44.6% 136.2% 44.6% 1396 43.0% 43.0% 58.1%	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0261 HP0319 HP0318 HP0318 HP0318 HP0474 HP0473 HP0474 HP0474 HP0474	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dippA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (pppM) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline /betainc transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, permease protein (modd) molybdenum	39.8% 49.3% in 56.59% 56.99% 51.99% 32.2% 27.6% in 33.2% 39.1% 59.6% 31.4% 38.3% 59.6% 31.4% 38.3% 44.6% 38.4%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0095 HP0877 HP0095 HP0373 HP0376 HP10376	exodexyribonuclesse (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase flutA) plucose-inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mrhA) ribonuclease (recA) system S sordein (hadS) yiel estriction enzyme S protein (hadS) yiel restriction enzyme M protein (hadN) yiel restriction enzyme M protein (mod) yiel literatiction enzyme M protein (mod) yiel literatiction enzyme M protein (mod) yiel literatiction enzyme M protein (mod)	31.5% 56.3% 59% 32.9% 54.6% 55.5% 55.5% 55.7% 55	HP1019 HP10382 Nucleoprote HP0836 Nucleoprote HP0836 HP1299 HP1441 HP1123 HP1293 HP1291 HP1201 HP1201 HP1202 HP1202 HP1203 HP1201 HP1202 HP1303 HP1301	serine protease (IntA) sialoglycoprotease (apr.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR117W) zinc-metalloprotease (pompetalloprotease (pompetalloprotease (pompetalloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotealloprotease (pompetalloprotealloprotealloprotealloprotease (pompetalloprotease (36.7% 36.296 44.696 rass 44.696 rass 64.3.096 43.096 43.096 55.196 62.496 43.896 63.896 38.496 50.096 65.996 42.596 62.496 43.396 65.996 42.596 62.496 43.397 45.596 62.496 43.397 45.596 62.496 44.996 31.796 54.696 44.996 31.796 55.296 64.796 44.996 41.896	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0819 HP0819 HP0818 HP0133 Anions HP0475 HP0475 HP0477 HP0473	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (pppB) dlamine ABC transporter, permease protein (pppB) dispensible ABC transporter, (pppB) serine transporter (sdaC) molybdenum ABC transporter, perplasmic molybdenum ABC transporter, permease protein (modD) molybdenum ABC t	39.8% 49.3% in 56.5% 56.5% 56.5% 51.9% 32.2% 27.6% in 30.9% 39.1% 28.7% 39.1%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0975 HP0975 HP0976 HP0387 HP0976 HP0387 HP0976 HP0987 HP0976 HP0987 HP0987 HP0987 HP0987 HP0987 HP0988 HP1088 HP	exodexyribonuclesse (lexA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase (nuA) Holicase inhibited division protein (gidB) helicase Holiday junction DNA helicase (nuA) Holiday junction endodexyribonuclease (nuC) Holiday junction endodexyribonuclease (nuC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuC) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) rep helicase, single-stranded DNA-depende ATPase (rep) helicase, single-stranded DNA-depende ATPase (rep) helicase, single-stranded DNA-binding protein (recI) rep helicase DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rmAA) ribonuclease H (rmAAA	31.5% 58.9% 32.9% 33.0% 34.7% 31.8% 54.6% 34.7% 31.8% 54.6% 56.6% 57.7%	HP1019 HP10382 Nucleoprote HP0835 Nucleoprote HP0835 HP1299 HP1441 HP1123 HP1293 HP1291 HP1201 HP1202 HP1202 HP1203 HP1201 HP1202 HP1303 HP1309 HP1301 HP1301 HP1309 HP1301	serine protease (IntA) sialoglycoprotease (apr.) sialoglycoprotease (apr.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (pr.) populoprotease (pr.) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (pp.) peptidyl-prolyl cis-trans isomerase, FKBP-tyrotamase (sply) polypeptid efformylase (del) proteins: synthesis and modification ribosomal protein L10 (rpl10) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl11) ribosomal protein L13 (rpl3) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl18) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl2) ribosomal protein L21 (rpl21) ribosomal protein L21 (rpl22) ribosomal protein L23 (rpl22) ribosomal protein L23 (rpl23) ribosomal protein L23 (rpl23) ribosomal protein L29 (rpl23) ribosomal protein L29 (rpl23) ribosomal protein L29 (rpl23) ribosomal protein L29 (rpl24) ribosomal protein L29 (rpl25) ribosomal protein L29 (rpl27) ribosomal protein L29 (rpl29) ribosomal protein L31 (rpl31) ribosomal protein L31 (rpl31) ribosomal protein L33 (rpl33)	36.2% 36.2% 44.6% 1789 1789 1789 1789 1789 1789 1789 1789	HP0298 HP0299 HP0300 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1261 HP0251 HP0251 HP0313 HP0313 HP0474 HP0373 HP0474 HP0313 HP0474 HP0313 HP0474	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betainer transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, ATP-binding protein (modD) molybdenum ABC transporter, permease protein (modD) molybdenum ABC transporter, permease protein (modD) molybdenum ABC transporter, permease protein (modB) molybdenum ABC transporter permease protein (modB) m	39.8% 49.9% in 52.5 £9% 56.99% 51.99% 32.2% 27.69% ii) 39.1% 59.6% 31.4% 38.3% 59.6% 31.4% 38.3% 44.6% 38.4% 59.69% 38.4%
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HP0213 HP1053 HP1053 HP1059 HP0877 HP0895 HP0877 HP0325 HP0323 HP0256 HP0327 HP1337 HP1323 HP1223 HP1223 HP1223 HP1224 HP1338 HP1099 HP154 HP094 HP1099 HP154 HP094 HP1095 HP1095	exodeoxyribonuclesse (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase flutA) helicase Holiday junction DNA helicase (rutA) Holiday junction DNA helicase (rutA) Holiday junction endodeoxyribonuclease (rutC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA) ribonuclease (recA) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (troF) type I restriction enzyme S protein (hsdS) type I restriction enzyme R protein (hsdR) type II restriction enzyme R protein (hsdR) type III restriction enzyme R protein (hsdR) type III restriction enzyme R protein (hsdR) type III restriction enzyme R protein (hsdR) t	31.5% 58.9% 32.9% 33.0% 39.0% 54.6% 54.6% 55.3% 55.0% 55.0% 54.6%	HP1019 HP10382 Nucleoprote HP0836 Nucleoprote HP0836 HP1299 HP1441 HP1123 HP1293 HP1291 HP1201 HP1202 HP1202 HP1202 HP1203 HP1201 HP1202 HP1303 HP1301 HP1309 HP1301 HP1309 HP1301 HP1401 HP1401 HP1401 HP1401 HP1401	serine protease (IntA) sialoglycoprotease (apr.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR117W) zinc-metalloprotease (pompetalloprotease	36.2% 36.2% 44.6% 1789 1789 189 189 189 189 189 189 189 189 189 1	HP0298 HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0318 HP0251 HP0318 HP0473 Anions HP0473 HP0473 HP0473 HP0474 HP0313 HP0474 HP0313 HP1913 HP0313 HP1913 HP0474 HP1913 HP0474 HP1913 HP1914 HP1913 HP1914 HP1916 HP	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dippA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnG) glutamine ABC transporter, ATP-binding protein (glnG) glutamine-binding protein (glnG) glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnF) glutamine-ABC transporter, permease protein (glnF) glutamine-ABC transporter, ATP-binding protein (ppDI) oligopeptide-ABC transporter, periplasmic morbided protein (protein (prote	39.8% 49.3% in 52.5% 56.9% 56.9% 51.9% 32.2% 27.6% in 30.9% 39.1% 59.6% 30.4% 59.6% 33.34% 95.9% 38.4% 95.9% 38.4% 38.4% 38.4% 38.4% 38.4% 38.4% 38.4% 38.4%
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HP0213 HP1053 HP1053 HP1059 HP0877 HP0895 HP0877 HP0325 HP0323 HP0256 HP0327 HP1337 HP1323 HP1223 HP1223 HP1223 HP1224 HP1338 HP1099 HP154 HP094 HP1099 HP154 HP094 HP1095 HP1095	exodexyribonuclease (lexA) glucoseinhibited division protein (gidA) glucoseinhibited division protein (gidA) glucoseinhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (ruc) methydate-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) repositions (recA) recombinase (recA) repositions divided by the combinational DNA repair protein (recI) repositions of the protein factor (priA) recombinase (recA) repositions of the protein factor (priA) recombinase (recA) reposition divided by the protein factor (priA) recombinational DNA repair protein (recA) reposition modification system S subunit ribonuclease H (rmAA) ribonuclease	31.596 58.996 48.596 32.996 33.096 33.096 33.096 34.796 31.896 27.896 31.196 46.596 46.596 47.796 31.896 31.196 32.896 33.196 33.996 39.196 33.896 33.7796 37.796 37.796 37.796 37.796 37.796 37.796 37.796 37.796 37.796 37.796 37.796 37.896	HP1019 HP1019 HP1084 HP0382 Nucleoprote HP0383 Nucleoprote HP0383 HP1299 HP1441 HP1123 HP0793 Ribosomal J HP1201 HP1200 HP1201 HP1200 HP1301 HP1200 HP1301 HP1201 HP1200 HP1301	serine protease (Int'A) sialoglycoprotease (acp) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (promote (pcm) methionine amino peptidase (map) peptidy-protyl cis-trans isomerase B, cyclosporin-type rotamase (pn) peptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (rpf11) ribosomal protein L1 (rpf11) ribosomal protein L1 (rpf11) ribosomal protein L14 (rpf14) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf15) ribosomal protein L16 (rpf16) ribosomal protein L18 (rpf18) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L29 (rpf29) ribosomal protein L39 (rpf39) ribosomal protein L3	36.7% 36.2% 44.6% rrase 43.0% 43.0% 43.0% 58.1% 69 69 40.4% 43.0% 58.1% 60.8% 63.8% 63.8% 65.0% 65.9% 66.7% 64.7% 45.6% 45.5% 65.9% 64.7% 64.7% 64.7% 64.7% 64.7% 65.6% 64.7% 64.7% 65.6% 65.9% 66.9%	HP0298 HP0300 HP1300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0251 HP0338 HP0475 HP0473 HP0474 HP0474 HP0474 HP1074 HP1091	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) dipeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA	39,8% 49,3% in 52,5 £ 9% 56,99% 51,99% 32,2% 27,69% in 33,1% 28,7% 59,6% 31,4% 38,3% 44,6% 38,3% 44,6% 38,4% 44,6% 53,8% 53,6%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0895 HP0877 HP0325 HP0323 HP1025 HP1323 HP1323 HP1323 HP1223 HP1223 HP1223 HP1224 HP133 HP1094 HP1095 HP1	exodexyribonuclease (lexA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase flutA) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mhA) repair m (mhA) ribonuclease h (mhA) ribonuclea	31.5% 58.9% 48.5% 32.9% 54.7% 31.5% 55.3% 55.0%	HP1019 HP10382 Nucleoprote HP10836 Nucleoprote HP0836 Nucleoprote HP10836 HP1299 HP1441 HP1123 HP1238 HP1297 HP1201 HP1202 HP1202 HP1202 HP1203 HP1201 HP1202 HP1203 HP1201 HP1203 HP1201 HP1202 HP1303 HP1301	serine protease (IntA) sialoglycoprotease (apr.) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (PJR117W) zinc-metalloprotease (pompetition zinc-metallo	36.2% 44.6% 1789 189 189 44.6% 1819 189 1819 189 1819 189 18189	HP0298 HP0300 HP1300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0251 HP0338 HP0475 HP0473 HP0474 HP0474 HP0474 HP1074 HP1091	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) dipeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA	33.8% 49.3% in 55.9% 56.9% 56.9% 51.9% 32.2% 27.6% in 30.9% 33.1% 59.6% 33.1% 59.6% 33.1% 33.3%
HP0213 HP1053 HP1053 HP1059 HP0877 HP0895 HP0877 HP0323 HP0255 HP0323 HP0256 HP0323 HP10325 HP1333 HP1025 HP1333 HP1025 HP1333 HP1025 HP1333 HP1025 HP1034 HP1035 HP1035 HP1036 HP1036 HP1036 HP1037 HP1037 HP1037 HP1037 HP1037	exodexyribonuclease (lexA) glucoseinhibited division protein (gidA) glucoseinhibited division protein (gidA) glucoseinhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction endodexyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (ruc) methydate-DNA/protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) repositions (recA) recombinase (recA) repositions divided by the combinational DNA repair protein (recI) repositions of the protein factor (priA) recombinase (recA) repositions of the protein factor (priA) recombinase (recA) reposition divided by the protein factor (priA) recombinational DNA repair protein (recA) reposition modification system S subunit ribonuclease H (rmAA) ribonuclease	31.5% 58.9% 48.5% 32.9% 54.7% 31.5% 55.3% 55.0%	HP1019 HP1019 HP10382 Nucleoprote HP0383 Nucleoprote HP0383 HP1299 HP1441 HP11293 HP1441 HP11293 HP1290 HP1441 HP1202 HP1202 HP1202 HP1202 HP1203 HP1301 HP1311	serine protease (Int'A) sialoglycoprotease (acp) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (YJR117W) zinc-metalloprotease (promote (pcm) methionine amino peptidase (map) peptidy-protyl cis-trans isomerase B, cyclosporin-type rotamase (pn) peptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptidy-protyl cis-trans isomerase, FKBP-tyl potylopeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (rpf11) ribosomal protein L1 (rpf11) ribosomal protein L1 (rpf11) ribosomal protein L14 (rpf14) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf15) ribosomal protein L16 (rpf16) ribosomal protein L18 (rpf18) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L29 (rpf29) ribosomal protein L39 (rpf39) ribosomal protein L3	36.2% 44.6% 136.2% 44.6% 136.2% 44.6% 136.2% 43.0% 58.1%	HP0298 HP0300 HP1300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0251 HP0338 HP0475 HP0473 HP0474 HP0474 HP0474 HP1074 HP1091	dipeptide ABC transporter, periplasmic dipeptide ABC transporter, permease protein (dppA) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) dipeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modP) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (periplasmic molybdate-binding protein (modA	39,8% 49,3% in 52,5 £ 9% 56,99% 51,99% 32,2% 27,69% in 33,1% 28,7% 59,6% 31,4% 38,3% 44,6% 38,3% 44,6% 38,4% 44,6% 53,8% 53,6%

Cations HP0791								
111 0/31	cadmium-transporting ATPase, P-type		HP0258	conserved hypothetical integral membrane protein			conserved hypothetical protein	29.3%
	(cadA)	975%	HP0284	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	31.0% 30.2%
HP0969		37.3%	111 0201	protein	29.2%	HP0745	conserved hypothetical protein	33.7%
HP1328	cation efflux system protein (czcA)	28.9%	HP0362	conserved hypothetical integral membrane		HP0747	conserved hypothetical protein	32.4%
HP1329		31.3%	1100445	protein			conserved hypothetical protein	36.1%
HP1503		30.3% 92.4%	HP0415	conserved hypothetical integral membrane		HP0810	conserved hypothetical protein	31.0%
HP1073 HP1072	copper ion binding protein (copP) copper-transporting ATPase, P-type (copA)		HP0467	protein conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	32.5% 27.8%
HP0471	glutathione-regulated potassium-efflux syste		111 0107	protein			conserved hypothetical protein	52.1%
	protein (kefB)	99.3%	HP0571	conserved hypothetical integral membrane			conserved hypothetical protein	32.2%
HP0687		33.6%		protein			conserved hypothetical protein	33.8%
HP1561	iron(III) ABC transporter, periplasmic iron-	27.5%	HP0644	conserved hypothetical integral membrane protein		HP0892	conserved hypothetical protein	39.1%
HP1562	binding protein (ceuE) iron(III) ABC transporter, periplasmic iron-	27.0%	HP0677	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	39.8% 30.7%
111 1002	binding protein (ceuE)	28.2%	111 0077	protein			conserved hypothetical protein	33.6%
HP0888	iron(III) dicitrate ABC transporter, ATP-bindir		HP0693	conserved hypothetical integral membrane			conserved hypothetical protein	36.2%
		34.4%		protein		HP0959	conserved hypothetical protein	31.1%
HP0889	iron(III) dicitrate ABC transporter, permease	00.00/	HP0718	conserved hypothetical integral membrane			conserved hypothetical protein	29.1%
HP0686		38.3% 29.7%	HP0737	protein conserved hypothetical integral membrane	33.5%		conserved hypothetical protein	25.0% 31.5%
HP0807		28.5%	11110131	protein	33.3%		conserved hypothetical protein conserved hypothetical protein	95.9%
HP1400		26.3%	HP0758	conserved hypothetical integral membrane		HP1046	conserved hypothetical protein	32.6%
HP1344	magnesium and cobalt transport protein			protein		HP1049	conserved hypothetical protein	39.7%
1104400	(corA)	26.3%	HP0759	conserved hypothetical integral membrane			conserved hypothetical protein	41.3%
HP1183 HP1552	NA+/H+ antiporter (napA) Na+/H+ antiporter (nhaA)	26.6% 49.2%	HP0787	protein conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	24.7% 34.7%
HP1077		98.7%	111 0/0/	protein	25.2%		conserved hypothetical protein	34.6%
HP0490	putative potassium channel protein,		HP0851	conserved hypothetical integral membrane		HP1214	conserved hypothetical protein	21.5%
	putative	25.7%		protein		HP1221	conserved hypothetical protein	42.4%
	es, purines and pyrimidines		HP0920	conserved hypothetical integral membrane		HP1240	conserved hypothetical protein	22.5%
HP1290	nicotinamide mononucleotide transporter		LIDOOAO	protein	36.3%		conserved hypothetical protein	42.3%
LID4400		28.0%	HP0946	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	44.6% 36.8%
HP1180	pyrimidine nucleoside transport protein (nupC)	32.9%	HP0952	conserved hypothetical integral membrane			conserved hypothetical protein	26.3%
Other	(Hupe)	32.570		protein	38.5%	HP1335	conserved hypothetical protein	33.9%
HP0876	iron-regulated outer membrane protein		HP0983	conserved hypothetical integral membrane			conserved hypothetical protein	27.2%
111 0070		27.6%		protein			conserved hypothetical protein	36.2%
HP0915	iron-regulated outer membrane protein		HP1044	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	33.6% 27.5%
		28.1%	HP1061	conserved hypothetical integral membrane	30.0%		conserved hypothetical protein	41.6%
HP0916	iron-regulated outer membrane protein	00.00	111 1001	protein	35.0%		conserved hypothetical protein	27.4%
HP1129		28.8% 29.7%	HP1080	conserved hypothetical integral membrane		HP1417	conserved hypothetical protein	23.7%
HP1130		33.5%		protein			conserved hypothetical protein	40.3%
HP1339		46.8%	HP1162	conserved hypothetical integral membrane			conserved hypothetical protein	40.0%
HP1340	biopolymer transport protein (exbD)	35.8%	LID447E	protein	27.6%		conserved hypothetical protein	37.8%
HP1445	biopolymer transport protein (exbB)	45.5%	HP1175	conserved hypothetical integral membrane protein	40.6%		conserved hypothetical protein	37.9% 39.0%
HP1446		36.2%	HP1184	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	26.8%
HP1512	iron-regulated outer membrane protein	00.00		protein			conserved hypothetical protein	30.1%
LIDOGEO		26.6% 99.4%	HP1185	conserved hypothetical integral membrane		HP1504	conserved hypothetical protein	23.9%
HP0653 HP1341	nonheme iron-containing ferritin (pfr) siderophore-mediated iron transport protein	99.4%		protein	55.5%		conserved hypothetical protein	30.6%
111 10-11		37.2%	HP1225	conserved hypothetical integral membrane			conserved hypothetical protein	25.4%
	(tone)	07.2 10	LIDAGOA	protein	31.6%		conserved hypothetical protein	40.5%
OTHER CA	TEGORIES		HP1234	conserved hypothetical integral membrane protein	29.0%		conserved hypothetical protein	42.2%
General			HP1235	conserved hypothetical integral membrane	23.070		conserved hypothetical protein conserved hypothetical protein	39.0% 32.0%
HP0924		37.7%	111 1200	protein	30.9%	HP1589	conserved hypothetical protein	35.1%
HP1034		36.3%	HP1330	conserved hypothetical integral membrane			conserved hypothetical protein	
HP1000 HP1139		29.7% 47.4%		protein	41.7%		(plasmid pHPM180)	41.8%
HP0827		46.8%	HP1331	conserved hypothetical integral membrane	00.00/		conserved hypothetical secreted protein	42.1%
	s and atypical conditions	40.070	HP1343	protein conserved hypothetical integral membrane	33.6%		conserved hypothetical secreted protein	37.1% 30.6%
HP1496		26.5%	111 10-10	protein	49.1%		conserved hypothetical secreted protein conserved hypothetical secreted protein	31.4%
HP1483		33.3%	HP1363	conserved hypothetical integral membrane			conserved hypothetical secreted protein	24.3%
HP0927	heat shock protein (htpX)	32.8%		protein	33.1%		conserved hypothetical secreted protein	31.5%
HP0280		27.2%	HP1407	conserved hypothetical integral membrane		HP0257	conserved hypothetical secreted protein	29.2%
HP1228	invasion protein (invA)	38.2%		protein	22.4%	HP0320	conserved hypothetical secreted protein	36.4%
HP0970	nickel-cobalt-cadmium resistance protein	0440	HP1466	conserved hypothetical integral membrane	00.00/		conserved hypothetical secreted protein	29.8%
HP1444		21.1% 42.1%	HP1484	protein conserved hypothetical integral membrane	30.9%		conserved hypothetical secreted protein conserved hypothetical secreted protein	96.9% 26.6%
HP0930		37.7%	111 1404	protein	41.2%		conserved hypothetical secreted protein	39.7%
HP0315		70.2%	HP1486	conserved hypothetical integral membrane	TILE 10		conserved hypothetical secreted protein	29.4%
HP0967		28.9%		protein	23.8%	HP0980	conserved hypothetical secreted protein	57.4%
HP1248	virulence associated protein homolog			conserved hypothetical integral membrane		HP1075	conserved hypothetical secreted protein	42.9%
			HP1487		30.7%	HP1098	conserved hypothetical secreted protein	27.0%
		36.0%		protein				
HP0885	virulence factor mviN protein (mviN)	36.0% 33.5%	HP1487 HP1509	protein conserved hypothetical integral membrane		HP1117	conserved hypothetical secreted protein	32.3%
HP0885 Colicin-rela	virulence factor mviN protein (mviN) sted functions	33.5%	HP1509	protein conserved hypothetical integral membrane protein	34.3%	HP1117 HP1216	conserved hypothetical secreted protein	31.9%
HP0885 Colicin-rela HP1126	virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB)			protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane	34.3%	HP1117 HP1216 HP1285	conserved hypothetical secreted protein conserved hypothetical secreted protein	31.9% 38.0%
HP0885 Colicin-rela	virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster	33.5% 25.7%	HP1509	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein	34.3%	HP1117 HP1216 HP1285	conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein	31.9%
HP0885 Colicin-rela HP1126 HP0428	virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (toIB) phage/colicin/tellurite resistance cluster terY protein	33.5%	HP1509 HP1548 HP0138 HP1438	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein	34.3% 30.6%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488	conserved hypothetical secreted protein conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4% 29.8%
HP0885 Colicin-rela HP1126 HP0428 Drug and a	virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein analog sensitivity	33.5% 25.7%	HP1509 HP1548 HP0138 HP1438 HP0151	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein	34.3% 30.6% 41.2% 32.0% 21.8%	HP1117 HP1216 HP1285 HP1286 HP1464	conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4%
HP0885 Colicin-rela HP1126 HP0428	virulence factor mviN protein (mviN) red functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein analog sensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl-	33.5% 25.7%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551	conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4% 29.8%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606	virulence factor mviN protein (mviN) teed functions colicin tolerance-like protein (toIB) phage /colicin /fellunter resistance cluster tery 'protein etry' protein analog sensitivity (185 rRNA (adenosine-N6,N6)-dimethyltransferase (ksgA) membrane fusion protein (mtrC)	33.5% 25.7% 25.6% 35.5% 24.2%	HP1509 HP1548 HP0138 HP1438 HP0151	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial	34.3% 30.6% 41.2% 32.0% 21.8% 38.8%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN	conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4% 29.8%
HP0885 Colicin-rela HP1126 HP0428 Drug and & HP1431 HP0606 HP0630	virulence factor mviN protein (mviN) teted functions collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster tery 'protein analog sensitivity 168 rRNA (adenosine-N6,N6-)-dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66)	33.5% 25.7% 25.6% 35.5% 24.2% 62.3%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN General	conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476	virulence factor mviN protein (mviN) teed functions collicin tolerance-like protein (toIB) phage /collicin /fellunter resistance cluster tee*/ protein rete*/ protein /fast /collicin /fellunter resistance cluster tee*/ protein /fast /collicin /fellunter /fast /collicin /fellunter /fast /f	33.5% 25.7% 25.6% 35.5% 24.2%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein full-like protein conserved hypothetical protein conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2% 48.2% 37.0%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN General HP0390	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7%
HP0885 Colicin-rela HP1126 HP0428 Drug and & HP1431 HP0606 HP0630	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (toIB) phage/colicin/tellulrite resistance cluster tety' protein arailog sensitivity 165 rRNA (adenosine-N6,N6-)-dimethyltransferase (ksgA) protein (mtrC) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA[P],	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 33.7%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032 HP0035	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical rotein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.6% 23.2% 48.2% 37.0% 34.1%	HP1117 HP1216 HP1285 HP1286 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0872	conserved hypothetical secreted protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1185	virulence factor mviN protein (mviN) tete functions colicin tolerance-like protein (toIB) phage/colicin/tellurité resistance cluster terv' protein etrv' protein analog sensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl-transférase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative	33.5% 25.7% 25.6% 35.5% 24.2% 62.3%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032 HP0032 HP0035 HP0086	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein intuitive protein conserved hypothetical protein	34.3% 30.6% 412% 32.0% 21.8% 38.8% 23.2% 48.2% 37.0% 34.1% 34.1%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0872 HP0207	conserved hypothetical secreted protein debetween secretary and protein (gap) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1185	virulence factor mviN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage /colicin /telluprite resistance cluster tery /ptctein /telluprite resistance cluster tery /ptctein /telluprite resistance cluster tery /ptctein /tellupriteransferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacnylic acid decarboxylase tetracycline resistance protein tetA(P), putative membrane functions	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 33.7%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032 HP0035 HP0035 HP0094	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2% 48.2% 37.0% 34.1% 24.2% 34.2% 24.2% 34.2% 24.2% 34.2% 34.3%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0872 HP0136	conserved hypothetical secreted protein (phnA) adhesin-thiol peroxidase (tagD) addo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertinic nomigratory protein (bcp)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0663 HP0630 HP1476 HP165 Transposo HP1008 HP00414	virulence factor mviN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage/colicin/telluprife resistance cluster terY protein (talB) phage/colicin/telluprife resistance cluster terY protein (talB) phage/colicin/telluprife resistance protein (mtrC) maillog sensitivity (mds66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative protein sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 33.9%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032 HP0032 HP0035 HP0086	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein intuitive protein conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2% 43.2% 37.0% 34.1% 28.7% 28.7%	HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0872 HP0207 HP0136 HP0485	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp) catalase-like protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9%
HP0885 Collicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1165 Transposo HP1008 HP0414 HP0988	virulence factor mviN protein (mviN) teted functions collect horizons collect horizons collect horizons collect horizons collect horizons have collect horizons have collect here. The factor has been seen such that have been su	33.5% 25.7% 26.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 33.9%	HP1509 HP1548 HP0138 HP0138 HP0151 HP0675 HP1258 HP1492 HP0032 HP0035 HP0094 HP0100 HP0100 HP0100	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipogratein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2% 48.2% 43.7% 23.7% 28.7% 28.7% 29.9% 39.9%	HP1117 HP1216 HP1285 HP1286 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0207 HP0136 HP0485 HP1104	conserved hypothetical secreted protein (phnA) ATP-binding protein (mpr) bacteriofertinic consignatory protein (bcp) catalase-like protein conserved hypothetical secreted protein conserved hypothetical secreted hypothetical secreted hypothetical secreted hypothetical secreted hypothetica	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1165 Transposo HP1008 HP0414 HP0988 HP0414 HP0988 HP0998	virulence factor mviN protein (mviN) tede functions collect tolerance-like protein (tolB) phage/collicin /tellunite resistance cluster terY protein saidous sensitivity. Its FiRN (adenosine-N6,N6)-dimethyl-transferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylici acid decarboxylase tetracycline resistance protein tetA(P), putative modulativity insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 irransposase (tnpA) IS005 transposase (tnpA)	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0032 HP0032 HP0086 HP0094 HP0100 HP0102 HP0107	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical inpoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical mitochondrial conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 41.2% 33.2.0% 48.2% 37.0% 34.1% 32.8% 32.0% 48.2% 37.0% 34.1% 32.0% 32.0% 32.0% 32.0% 32.0% 32.0% 32.0% 32.0% 32.0% 32.0% 33.0	HP1117 HP1216 HP1285 HP1286 HP1464 HP1464 HP1551 UNKNOWN General HP0390 HP0390 HP0193 HP0872 HP0207 HP0196 HP0485 HP1104	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp) catalase-like protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1165 Transposo HP1008 HP0084 HP0988 HP09414 HP0988 HP0988 HP1098	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (toIB) phage/colicin/tellulrite resistance cluster tety protein (toIB) phage/colicin/tellulrite resistance cluster tety protein saralog sensitivity 165 (RNA (adenosine-N6,N6-)-dimethyl-transferase (ksgA) meimbrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative prelated functions 1S200 insertion sequence from SARA17 1S200 insertion sequence from SARA17 1S005 transposase (tnpA) 1S605 transposase (tnpA) 1S605 transposase (tnpA)	33.5% 25.7% 26.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 39.2% 97.2% 97.2%	HP1509 HP1548 HP0138 HP0131 HP0151 HP0575 HP1258 HP1032 HP0035 HP0035 HP0094 HP0100 HP0100 HP0100 HP0105 HP0105 HP0105	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 protein demonserved hypothetical mitochondrial protein demonserved hypothetical protein conserved hypothetical protein	34.3% 30.6% 41.2% 32.0% 21.8% 38.8% 23.2% 48.2% 37.0% 34.1% 28.7% 32.0% 32.0% 32.0% 32.0% 33.7% 34.7%	HP1117 HP1216 HP1285 HP1286 HP1288 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0372 HP0136 HP0485 HP0136 HP0485 HP10869	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpn bacteriofermitin comigratory protein (bcp) catalase-like protein cinnamyl-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (gtp1)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1165 Transposo HP1008 HP0988 HP0988 HP1098 HP1098 HP1098	virulence factor mviN protein (mviN) tede functions collect tolerance-like protein (tolB) phage/collicin /tellunite resistance cluster terY protein saidous sensitivity. Its FixNa (adenosine-N6,N6)-dimethyl-transferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylici acid decarboxylase tetracycline resistance protein tetA(P), putative protein sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 irsertion	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0035 HP0086 HP0094 HP0100 HP0102 HP0102 HP0107 HP0117 HP0162	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical inportein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein conserved hypothetical prot	34.3% 30.6% 41.2% 41.2% 21.8% 38.8% 21.8% 38.8% 48.2% 48.2% 48.2% 48.2% 48.2% 37.0% 34.1% 28.7% 32.0% 32.0% 32.0% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7%	HP1117 HP1218 HP1285 HP1286 HP1286 HP1484 HP1484 HP1488 HP1581 HP0390 HP193 HP0390 HP193 HP0485 HP0485 HP0485 HP1048 HP0486 HP04	conserved hypothetical secreted protein (alkylhosphonate uptake protein (phnA) ATP-binding protein (mpn protein (mpn pataleselike protein cinnamy-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (fgb1) GTP-binding protein (fbg)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5%
HP0885 Colicin-rela HP1126 HP0426 HP0431 HP0606 HP0630 HP1476 HP165 Transposo HP1008 HP0018 HP0098 HP0098 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP1998	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (tolB) phage /colicin/tellulrite resistance cluster tety /protein /tellulrite resistance cluster tety /protein /tellulrite resistance cluster tety /protein /tellulrite sensitivity 168 rRNA (adenosine-N6,N6-)-dimethyltransferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative prelated functions 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15005 transposase (tnpA) 15005 transposase (tnpA) 15005 transposase (tnpA) 15605 transposase (tnpA)	33.5% 25.7% 25.6% 35.5% 36.5% 36.2% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2%	HP1509 HP1548 HP0138 HP0151 HP0675 HP1258 HP0032 HP0032 HP0036 HP0094 HP0100 HP0107 HP0107 HP0117 HP0162 HP0233	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 your protein description of the protein conserved hypothetical protein conserved hypothetica	34.3% 30.6% 41.2% 32.0% 32.0% 38.8% 38.8% 42.2% 37.0% 34.1% 28.7% 32.9% 32.0% 32.0% 32.0% 32.0% 33.9% 30.0% 33.9%	HP1117 HP1285 HP1285 HP1286 HP1286 HP1488 HP1551 UNKNOWN General HP0390 HP193 HP0207 HP0306 HP193 HP0485 HP104 HP0485 HP104 HP0481 HP0599 HP0503 HP10834	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpna) bacterioferritin comigratory protein (bcp) catalase-like protein cinnamy-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (ptp.) GTP-binding protein (bcg) GTP-binding protein hypothemical protein (ptp.) GTP-binding protein nowlogue (yphC) GTP-binding protein mologue (yphC) GTP-binding protein mologue (yphC) GTP-binding protein mologue (yphC)	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7%
HP0885 Collicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP1436 HP1456 HP165 Transposo HP10988 HP0988 HP0988 HP0988 HP0988 HP0988 HP0986 HP1096 HP1437 HP0988 HP1956 HP1437 HP0988	virulence factor mviN protein (mviN) teted functions collect total collect functions collect functions collect functions collect functions for the function for the function for the function fu	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2%	HP1509 HP1548 HP0138 HP01438 HP0151 HP0576 HP0258 HP10932 HP0032 HP0032 HP0094 HP0100 HP0100 HP01010 HP01010 HP01010 HP01017 HP0105 HP017 HP0162 HP0233	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 41.2% 21.8% 38.8% 23.2% 48.2% 48.2% 48.2% 23.2% 48.2% 24.8% 37.0% 34.1% 29.8% 32.0% 32.0% 32.0% 32.0% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7%	HP1117 HP1216 HP1285 HP1286 HP1286 HP1464 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0485 HP0485 HP1046 HP0485 HP1040 HP0903 HP10903 HP10903 HP0903 HP0903 HP0903 HP0903 HP0903 HP0903 HP0903 HP0903 HP0903 HP0903	conserved hypothetical secreted protein alkylphosphonate uptake protein (phnA) ATP-binding protein (mgratory protein (bcp) catalase-like protein companyl-alcohol dehydrogenase ELI3-2 (cad) exonuclease VI-like protein (xseA) GTP-binding protein (bgt) GTP-binding protein (bgt-hypothetical protein) (bgt-hypothetical	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 611.1% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1%
HP0885 Collicin-rela HP1128 HP0428 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP165 HP1050 HP00414 HP0998 HP0414 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998 HP0998	virulence factor mviN protein (mviN) tede functions collect tolerance-like protein (tolB) phage /collect hellunter resistance cluster ted* protein (tolB) phage /collect hellunter resistance cluster ted* protein (tref*) pro	33.5% 25.7% 25.6% 26.6% 36.5% 24.2% 62.3% 39.7% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4%	HP1509 HP1548 HP0138 HP0151 HP0675 HP1258 HP0032 HP0032 HP0036 HP0094 HP0100 HP0107 HP0107 HP0117 HP0162 HP0233	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 your protein description of the protein conserved hypothetical protein conserved hypothetica	34.3% 30.6% 41.2% 32.0% 32.0% 32.18% 38.8% 38.8% 48.2% 37.0% 34.1% 528.7% 32.9% 32.9% 32.9% 32.9% 32.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9%	HP1117 HP1285 HP1286 HP1286 HP1286 HP1488 HP1488 HP1481 HP0390 HP0390 HP0390 HP0372 HP0372 HP0361 HP0381 HP0381 HP0383 HP0383 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpna) bacterioferritin comigratory protein (bcp) catalase-like protein cinnamy-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (bg) GTP-binding protein hypothetin (gtp1) GTP-binding protein hypothetin	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 36.7% 54.1%
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP1476 HP1476 HP1008 HP0414 HP0088 HP0944 HP0989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0997 HP09989 HP0998 HP098 HP098 HP0998 HP0998 HP0998 HP098	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (tolB) phage /colicin/telluprite resistance cluster tety / protein salega sensitivity membrane fusion protein (mtr.C) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative prelated functions S200 insertion sequence from SARA17 S200 insertion sequence from SARA17 S200 insertion sequence from SARA17 S200 istansposase (tnpA) S205 transposase (tnpA) S205 transposase (tnpA) S205 transposase (tnpA) S205 transposase (tnpB)	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 33.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0035 HP0086 HP0094 HP0100 HP0100 HP0107 HP0162 HP017 HP0162 HP0216 HP0226 HP0228 HP0248 HP0248	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein conserved hypothetical prote	34.3% 30.6% 41.2% 41.2% 52.6% 53.8% 53.8% 53.8% 53.8% 53.8% 53.7% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9% 53.9%	HP1117 HP1216 HP1226 HP1226 HP1426 HP1464 HP1488 HP1488 HP1393 HP0393 HP0393 HP0872 HP0393 HP04872 HP0495 HP1049 HP0393 HP0393 HP0494 HP0393 HP0494 HP0393 HP0494 HP0393 HP0494 HP049	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mgratory protein (bcp) catalase-like protein (cinnamyl-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (hypothetical protein (pgt-1) GTP-binding protein homologue (yphC) GTP-binding protein, fusA-homolog (yihK) lipase-like protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 54.1% 54.1% 54.1%
HP0885 Collicin-rela HP1126 HP0428 HP0428 Drug and a HP1431 HP0606 HP0606 HP0606 HP1476 HP165 HP108 HP0144 HP0988 HP0414 HP0988 HP0988 HP0988 HP0988 HP0988 HP1086 HP1086 HP10969 HP1086 HP10969 HP1087 HP0988	virulence factor mviN protein (mviN) teted functions collect foreign from the first functions collect foreign foreign from the first function foreign from the first function function function function for first function	33.5% 25.7% 25.6% 26.6% 35.5% 24.2% 62.3% 37.7% 37.7% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4% 93.4%	HP1509 HP1548 HP0138 HP1438 HP0157 HP1258 HP14258 HP1032 HP0035 HP0036 HP0094 HP0100 HP0102 HP0106 HP0107 HP0162 HP0164 HP017 HP0162 HP017 HP0162 HP017 HP0162 HP017 HP0164 HP017 HP0165 HP017 HP0165 HP017 HP0166 HP017 HP0166 HP017 HP0167 HP017 HP0168 HP017 HP0169 HP017 HP0169 HP017 HP0169 HP017 HP0169 HP017 HP017 HP0180 HP017 HP0180 HP0180 HP0180 HP0180 HP0180 HP0180 HP0180 HP0180	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical ipoprotein conserved hypothetical lipoprotein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein conserved hypothetical protein conserved hypot	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 41,2% 38,8% 38,8% 32,0% 48,2% 37,0% 34,1% 32,0% 32,0% 32,0% 32,0% 32,0% 33,7% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5%	HP1117 HP1285 HP1286 HP1286 HP1286 HP1488 HP1488 HP1488 HP0390 HP0390 HP0390 HP0390 HP0495 HP0495 HP0495 HP0334 HP0334 HP0334 HP0334 HP0495 HP0495	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpna) bacterioferritin comigratory protein (bcp) catalase-like protein cinnamy-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (bg) GTP-binding protein in (bg) GTP-binding protein in (bg) GTP-binding protein in fusA-homolog (yihK) lipase-like protein	31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 36.7% 54.1%
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP1476 HP1060 HP1476 HP1008 HP0414 HP0988 HP0988 HP0989 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1044 HP1098 HP10	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (tolB) phage /colicin/telluprite resistance cluster tety* protein saracy colicin tolerance-like protein (tolB) phage /colicin/telluprite resistance cluster tety* protein from 1885 rRNA (adenosine-N6,N6)-dimethyl-transferase (kspA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative protein tetA(P), putative protein sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS205 transposase (tnpA) IS205 transposase (tnpA) IS205 transposase (tnpA) IS205 transposase (tnpA) IS205 transposase (tnpB) IS205 transposas	33.5% 25.7% 25.6% 35.5% 36.5% 37.0% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.4% 93.4% 93.4% 93.4%	HP1609 HP1648 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0032 HP0032 HP0036 HP0019 HP0100 HP0101 HP0101 HP0101 HP0101 HP0102 HP0102 HP0102 HP0102 HP0103 HP0218 HP0238 HP0248 HP0274 HP0289 HP0310 HP0310	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 41.2% 32.0% 32.0% 48.2% 38.8% 48.2% 37.7% 34.1% 28.7% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 33.9% 33.9% 30.5% 30.5% 30.5% 30.5% 30.5% 30.5% 30.5%	HP1117 HP1216 HP12285 HP12464 HP14864 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0207 HP0207 HP0207 HP0207 HP0308 HP0485 HP0485 HP0485 HP0485 HP0480 HP04	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (phnA) artP-binding protein (mpn) bacteriofermin comigratory protein (bcp) cataliase-like protein (mpn) bacteriofermin comigratory protein (bcp) cataliase-like protein (mpn) secretin (ptn) diff-binding protein hypothetical protein (ptn) GTP-binding protein hypothetical protein nilS-like protein nilS-like protein ptn lil-like protein ptn ptopin ptn protein ptn lil-like protein ptn protein ptn ptn protein ptn ptn protein ptn ptn protein ptn ptn ptn ptn ptn ptn ptn ptn ptn pt	31,9% 38,0% 38,0% 27,4% 29,8% 42,7% 38,3% 46,6% 61,1% 38,9% 41,1% 48,1% 42,5% 48,1% 48,1% 54,1%
HP0885 Collicin-rela HP1426 HP0428 Drug and 4 HP1431 HP0606 HP1476 HP1676 Transposo HP1088 HP0414 HP0988 HP0998 HP0998 HP0998 HP1096 HP1535 HP047 HP0989 HP0981 HP0414 HP0438 HP0998 HP0998 HP1096 HP1535 HP047 HP0989 HP047 HP	virulence factor mviN protein (mviN) teted functions collect foreign from the first functions collect foreign foreign from the first function foreign from the first function function function function for first function	33.5% 25.7% 25.6% 26.6% 35.5% 24.2% 62.3% 37.7% 37.7% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4% 93.4%	HP1509 HP1548 HP0138 HP1438 HP0157 HP1258 HP1258 HP1035 HP0035 HP0035 HP00036 HP00094 HP0100 HP0102 HP0102 HP0104 HP0104 HP0105 HP017 HP0162 HP0216 HP0218 HP0228 HP0228 HP0228 HP0238 HP0238 HP0238	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein and protein and conserved hypothetical protein conserved hypoth	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 32,0% 48,2% 32,0% 34,1% 32,0% 33,0% 33,0% 33,0% 33,0% 33,0% 33,0% 31,3% 33,0% 47,2% 31,0% 31,3% 33,0% 47,2% 31,0% 31,0% 31,0% 31,0% 31,3% 31,0% 31,3% 31,0% 31,3% 31,0% 31,3% 31,0%	HP1117 HP1216 HP12265 HP12265 HP1464 HP1468 HP1468 HP1468 HP1468 HP1030 HP193 HP0207 HP0305 HP193 HP0405 HP193 HP0405 HP193 HP0405 HP194 HP0405 HP0405 HP0405 HP0405 HP0405 HP0405 HP0405 HP0405 HP0405 HP04069 HP0406	conserved hypothetical secreted protein (alkylhosphonate uptake protein (phnA) ATP-binding protein (mpnA) bacterioferritin comigratory protein (bcp) catalase-like protein (mpnyl-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (bdg) GTP-binding protein (bdg) GTP-binding protein (bdg) GTP-binding protein (bdg) GTP-binding protein (mpsa-like protein mill-like protein hypothetin protein (psp.) protein (psp.) Periolin (psp.) protein (psp.) Periolin (psp.)	31,9% 38,0% 37,5% 27,4% 29,8% 42,7% 38,3% 42,7% 38,3% 44,0% 44,0% 42,5% 48,1% 48,2% 54,1% 41,1% 48,2% 54,1% 48,2% 54,1%
HP0885 Colicin-rela HP1128 HP0428 Drug and a HP1431 HP0626 HP0630 HP1476 HP10081 HP0041 HP0041 HP0041 HP0047 HP0088 HP1096 HP109	virulence factor mviN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage/colicin/telluprife resistance cluster terV protein (talB) phage/colicin/telluprife resistance cluster terV protein (talB) phage/colicin/telluprife resistance cluster terV protein (talB) phage/colicin/telluprife resistance protein (mtrC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA(P), putative protein sequence from SARA17 is putative protein sequence from SARA17 is protein sequence fr	33.5% 25.7% 25.6% 35.5% 36.5% 37.0% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.4% 93.4% 93.4% 93.4%	HP1609 HP1648 HP0138 HP1438 HP0431 HP0575 HP1258 HP0032 HP0032 HP0032 HP0016 HP0100 HP0102 HP01016 HP01016 HP0107 HP0108 HP0218 HP0218 HP0218 HP0228 HP0310 HP0310 HP0310 HP0310 HP0318 HP0328	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 41.2% 32.2% 48.2% 38.8% 48.2% 37.7% 34.1% 28.7% 28.7% 32.9% 32.9% 32.9% 32.9% 33.7% 33.9% 30.5% 30.7% 38.6% 30.5% 31.3% 31.3% 33.37% 33.37%	HP1117 HP1216 HP12285 HP12464 HP1464 HP1468 HP1651 UNKNOWN General HP0390 HP193 HP0390 HP193 HP047 HP0304 HP0485 HP0485 HP0485 HP0485 HP0480 H	conserved hypothetical secreted protein secretary secret	31,996 33,7596 37,596 27,496 29,896 42,796 38,396 42,796 38,996 35,596 30,896 44,096 42,596 48,196 4
HP0885 Collicin-rela HP1426 HP0428 Drug and 4 HP1431 HP0606 HP1476 HP1676 Transposo HP1088 HP0414 HP0988 HP0998 HP0998 HP0998 HP1096 HP1535 HP047 HP0989 HP0981 HP0414 HP0438 HP0998 HP0998 HP1096 HP1535 HP047 HP0989 HP047 HP	virulence factor mviN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage colicin fellurife resistance cluster terV protein (mviN) tedev protein (tolB) phage colicin fellurife resistance cluster terV protein (mviN) and committee sensitivity (mviN) transferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA[P], putative mviN (mviN) transferate functions (s200 insertion sequence from SARA17 (s200 insertion seque	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2%	HP1609 HP1648 HP0138 HP1438 HP0161 HP0575 HP1258 HP0035 HP0035 HP0036 HP0094 HP0100 HP0102 HP01017 HP0102 HP0104 HP0104 HP0105 HP0105 HP0107 HP0108 HP0285 HP0238 HP0238 HP0238 HP0238 HP0238 HP0339 HP0318 HP0318 HP0334 HP0334	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein at conserved hypothetical protein conserved hypothetical p	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 32,0% 48,2% 32,0% 48,2% 32,0% 34,1% 32,0% 34,1% 32,0% 32,0% 32,0% 32,0% 32,0% 33,0%	HP1117 HP1216 HP1285 HP1484 HP1488 HP1481 HP1551 UNKNOWN General HP0392 HP1039 HP1039 HP1039 HP0495 HP0495 HP0495 HP0495 HP0495 HP0495 HP0495 HP0495 HP0495 HP0495 HP0496	conserved hypothetical secreted protein (alkylinosphonate uptake protein (phnA) ATP-binding protein (mapprotein (phnA) ATP-binding protein (phnA) atprotein (phnA) atpr	31,9% 38,0% 37,5% 27,4% 29,8% 42,7% 38,3% 42,7% 38,3% 44,0% 44,0% 42,5% 48,1% 48,2% 54,1% 41,1% 48,2% 54,1% 48,2% 54,1%
HP0885 Colicin-rela HP1128 HP0428 Drug and a HP1431 HP0626 HP0630 HP1476 HP10081 HP0041 HP0041 HP0041 HP0047 HP0088 HP1096 HP109	virulence factor mviN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage colicin fellurife resistance cluster terV protein (mviN) tedev protein (tolB) phage colicin fellurife resistance cluster terV protein (mviN) and committee sensitivity (mviN) transferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA[P], putative mviN (mviN) transferate functions (s200 insertion sequence from SARA17 (s200 insertion seque	33.5% 25.7% 25.6% 35.5% 36.5% 37.0% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.4% 93.4% 93.4% 93.4%	HP1609 HP1648 HP0138 HP1438 HP0161 HP0575 HP1258 HP1032 HP0035 HP0035 HP00036 HP00102 HP01010 HP01102 HP01107 HP0102 HP0108 HP0108 HP01094 HP01096 HP0	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 37,0% 34,1% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 33,0% 33,0% 33,0% 33,0% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 33,5% 31,5% 33,5% 33,5% 31,5% 31,5% 33,5% 31,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1651 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0390 HP0495 HP0495 HP0495 HP0495 HP0495 HP0490 HP1499 HP0490 HP1499 HP0490 HP1499 HP0490 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphorate uptake protein (ppn alkylphosphorate uptake protein (ppn alkylphosphorate uptake protein (ppn bacteriofermin comigratory protein (bcp) catalase-like protein (mpr) secretalase-like protein (ppn alkylphosphorate uptake protein (xseA) GTP-binding protein (ppn alkylphosphorate) (ppn alkylphosphorated) (ppn alkylphosphorate	31,9% 38,0% 37,5% 27,4% 29,8% 42,7% 38,3% 46,6% 611,9% 38,9% 35,5% 42,5% 44,0% 42,5% 48,1% 48,1% 54,1%
HP0885 Colicin-rela HP1128 HP0428 Drug and a HP1431 HP0626 HP0630 HP1476 HP10081 HP0041 HP0041 HP0041 HP0047 HP0088 HP1096 HP109	virulence factor, mivN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage colicin fellunite resistance cluster ted functions colicin tolerance-like protein (tolB) phage colicin fellunite resistance cluster ted protein (miscon phenylacy)tic acid decarboxylase tetracycline resistance protein tetA[P], putative protein sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS205 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpB) IS805 transpos	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2%	HP1609 HP1648 HP0138 HP1438 HP01431 HP0575 HP1258 HP0032 HP0032 HP0032 HP0096 HP0100 HP0100 HP0100 HP0100 HP0101 HP0102 HP0102 HP01034 HP0104 HP0104 HP0105 HP0107	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchcondrial protein 4 conserved hypothetical protein	34.3% 30.6% 41.2% 41.2% 32.2% 48.2% 38.8% 48.2% 37.7% 34.1% 28.7% 32.9% 32.9% 32.9% 32.9% 32.9% 33.7% 32.9% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7% 33.7%	HP1117 HP1216 HP1285 HP1484 HP1488 HP1481 HP1551 UNKNOWN General HP0393 HP183 HP0393 HP0393 HP0393 HP0494 HP0394 HP049 HP049 HP	conserved hypothetical secreted protein disk-protein conserved hypothetical secreted protein (phn A) ATP-binding protein (ppn bacterioferritin comigratory protein (bcp) catalase-like protein cinnamyl-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (bcb) GTP-binding protein (bcb) GTP-binding protein (psn) GTP-binding protein (psn) milG-like protein hilG-like protein protein protein (psn) F-TIIZ-like protein gsp8) signature protein (asp8)	31,996 33,7596 37,596 27,496 29,896 42,796 38,396 42,796 38,996 35,596 30,896 44,096 42,596 48,196 4
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0436 HP1436 HP1476 HP1476 HP1088 HP0414 HP0988 HP0998 HP0998 HP0998 HP0998 HP1096 HP1535 HP0437 HP0988	virulence factor, mivN protein (mviN) tede functions colicin tolerance-like protein (tolB) phage colicin fellunite resistance cluster ted functions colicin tolerance-like protein (tolB) phage colicin fellunite resistance cluster ted protein (miscon phenylacy)tic acid decarboxylase tetracycline resistance protein tetA[P], putative protein sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS205 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpA) IS805 transposase (mpB) IS805 transpos	33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2%	HP1609 HP1648 HP0138 HP1438 HP0431 HP0575 HP1258 HP1032 HP0032 HP0035 HP00035 HP0004 HP0100 HP01010 HP01010 HP01010 HP01017 HP0106 HP0107 HP0108 HP0231 HP0238 HP02348 HP02348 HP02348 HP02348 HP0330 HP0310	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protei	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 37,0% 34,1% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 33,7% 32,0% 33,7% 33,7% 33,7% 33,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0495 HP0490 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphorate uptake protein (ppn alkylphosphorate uptake protein (ppn alkylphosphorate uptake protein (ppn bacteriofermin comigratory protein (bcp) catalase-like protein (mpr) secretalase-like protein (ppn alkylphosphorate uptake protein (xseA) GTP-binding protein (ppn alkylphosphorate) (ppn alkylphosphorated) (ppn alkylphosphorate	31,9% 38,0% 37,5% 27,4% 29,8% 42,7% 38,3% 46,6% 611,9% 38,9% 35,5% 42,5% 44,0% 42,5% 48,1% 48,1% 54,1%
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1436 HP165 Transposo HP1008 HP0414 HP0988 HP0098 HP0414 HP0998 HP0417 HP0989 HP0998 HP0013 HP1007 HP0739 HYPOTHET General	virulence factor mviN protein (mviN) teted functions collicin tolerance-like protein (toIB) phage collicin tolerance-like protein (toIB) phage collicin reliament for the first phage collicin tellurite resistance cluster tery protein files (risNA (adenosine-N6,N6)-dimethyltransferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putalive n-related functions 15200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 transposase (tnpA) IS305 transposase (tnpB) Iransposase-like protein, PS3IS transposase-like protein, PS3IS Iransposase-like protein, PS3IS Iranspos	33.5% 25.7% 25.6% 26.6% 36.5% 24.2% 62.3% 39.7% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4% 93.4% 33.6% 34.3% 30.1%	HP1609 HP1648 HP0138 HP1438 HP01431 HP0675 HP1258 HP0032 HP0032 HP0032 HP00032 HP0006 HP0100 HP0100 HP0100 HP0100 HP0102 HP0102 HP0102 HP0103 HP0103 HP0103 HP0103 HP0103 HP0103 HP0248 HP0248 HP0248 HP0248 HP0248 HP0248 HP0248 HP0347	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein c	34.3% 30.6% 41.2% 41.2% 21.8% 38.8% 48.2% 48.3%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0495 HP0490 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) (ppn alkylphosph	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP0430 HP1476 HP1063 HP044 HP044 HP044 HP048 HP0494 HP0498 HP0989 HP0989 HP0989 HP1037 HP1098 HP1037 HP1098 HP0438 HP0438 HP0438 HP0438 HP047 HP059 HP059 HP059 HP059 HP059 HP059 HP059 HP059 HP051 HP079	virulence factor mivil protein (mivil) teef functions colicin tolerance-like protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein in fills (fill fill fill fill fill fill fill fil	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4%	HP1509 HP1548 HP0138 HP1438 HP0431 HP0575 HP1258 HP0032 HP0035 HP0035 HP00035 HP00094 HP0100 HP0100 HP0117 HP0107 HP0107 HP0107 HP0107 HP0107 HP0107 HP0238 HP0238 HP0239 HP0310	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein conserved hypothetical	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 37,0% 34,1% 32,3% 32,0% 42,2% 33,0% 32,0% 33,0%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0495 HP0490 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) (ppn alkylphosph	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06050 HP1436 HP1655 Transposo HP1008 HP0414 HP0988 HP0098 HP0414 HP0998 HP098 HP008 HP013 HP1007 HP073 HP1014 HP073 HP1007 HP073 HP006 HP078 HP0066 HP088 HP0066	virulence factor mivN protein (mivN) teted functions collicin tolerance-like protein (toIB) phage collicin tolerance-like protein (toIB) phage collicin fellurite resistance cluster tety' protein (ref) protein files (rsNA (adenosine-N6,N6)-dimethyltransferase (ksgA) membrane (usion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putalive n-related functions 15200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS305 transposase (tnpA) IS305 transposase (tnpB) Iransposase-like protein, PS3IS transposase-like protein, PS3IS Iransposase-like protein, PS3IS Iransposase-like protein, PS3IS Iransposase-like protein protein conserved hypothetical ATP-binding protein conserved hypothetical	33.5% 25.7% 25.6% 26.6% 36.5% 24.2% 62.3% 39.7% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4% 93.4% 93.4% 93.4% 33.6% 34.3% 30.1%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0575 HP1258 HP0032 HP0032 HP0032 HP0096 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0248 HP0248 HP0248 HP0248 HP0274 HP0285 HP0285 HP0285 HP0285 HP0373 HP0278 HP0373 HP0373 HP0373 HP0373 HP0373 HP0374 HP0387 HP0374 HP0387 HP0388 HP0396 HP0419	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein c	34.3% 30.6% 41.2% 32.2% 42.2% 32.2% 42.2% 32.2% 42.2% 37.7% 32.2% 42.2% 37.7% 32.5% 42.2% 32.7% 32.5% 42.2% 32.7% 32.5% 32.5% 32.5% 32.5% 32.5% 32.5% 33.3% 33.5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0495 HP0490 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) (ppn alkylphosph	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP0430 HP1476 HP0630 HP1476 HP0630 HP0484 HP0494 HP0494 HP0494 HP0494 HP0498 HP0998 HP0998 HP0998 HP0998 HP0098 HP1037 HP1098 HP1037 HP1098 HP0438 HP0418 HP0438 HP0438 HP0438 HP0418 HP041	virulence factor, mivil protein (mivil) teef functions colicin tolerance-like protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein in fills (fill phage/colicin /fellunite resistance cluster ter/ protein in fills (fill phage sensitivity) (misseriase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative modulator (fill protein fill protein sequence from SARA17 is 200 insertion sequence from SARA17 insertion sequence from SARA	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4%	HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0035 HP0035 HP00036 HP0109 HP0100 HP0110 HP01107 HP0107 HP0107 HP0107 HP0107 HP0238 HP0238 HP0238 HP0238 HP0398 HP0310 HP0398 HP0310 HP0410	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical proprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 protein description of the protein descri	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 32,0% 48,2% 37,0% 34,1% 32,3% 32,0% 42,2% 33,0% 32,0% 33,0%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) (ppn alkylphosph	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1436 HP1655 Transposo HP1008 HP0414 HP09988 HP0098 HP0417 HP0998 HP0098 HP0181 HP0011 HP0739 HPP0THET General HP0066 HP0299 HP0312 HP00312	virulence factor mviN protein (mviN) teted functions collicin tolerance-like protein (toIB) phage collicin folerance-like protein (toIB) phage collicin folerance-like protein (toIB) phage collicin fellurite resistance cluster tety' protein in the factor of the factor	33.5% 25.7% 25.6% 26.6% 35.5% 24.2% 62.3% 33.9% 33.9% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4% 93.4% 93.4% 33.6% 34.3% 35.6% 34.3% 30.1%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0575 HP1258 HP0032 HP0032 HP0032 HP0096 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0248 HP0248 HP0248 HP0248 HP0274 HP0285 HP0285 HP0285 HP0285 HP0373 HP0278 HP0373 HP0373 HP0373 HP0373 HP0373 HP0374 HP0387 HP0374 HP0387 HP0388 HP0396 HP0419	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein c	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 37,0% 32,0% 48,2% 37,0% 34,1% 32,0% 48,2% 37,0% 39,1% 39,1% 39,1% 30,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP0430 HP1476 HP1008 HP0081 HP0088 HP0018 HP0088	virulence factor, mivil protein (mivil)) tied functions colicin tolerance-like protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein nailog sensitivity inailog sensitivity insideriase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 152	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0151 HP0575 HP0032 HP0032 HP0036 HP0096 HP0016 HP0190 HP0190 HP0190 HP0190 HP0191 HP0192 HP0191 HP01933 HP0244 HP0274 HP0374 HP0466 HP0466 HP0468	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein conserved hypothetical prote	34.3% 30.6% 41.2% 41.2% 41.2% 538.8% 538.8% 54.2% 537.0% 54.1% 55.3% 56.	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1436 HP1655 Transposo HP1008 HP0414 HP09988 HP0098 HP0417 HP0998 HP0098 HP0181 HP0011 HP0739 HPP0THET General HP0066 HP0299 HP0312 HP00312	virulence factor mviN protein (mviN) teted functions collicin tolerance-like protein (toIB) phage collicin fellurite resistance cluster tet protein fellurite	33.5% 25.7% 25.6% 26.6% 35.5% 24.2% 62.3% 33.9% 27.0% 33.9% 33.9% 97.2%	HP1609 HP1648 HP0138 HP1438 HP0151 HP06756 HP1258 HP0032 HP0035 HP0035 HP0036 HP00102 HP0102 HP01017 HP0102 HP01017 HP0102 HP0103 HP0104 HP0105 HP0117 HP0168 HP0231 HP0248 HP0234 HP0234 HP0234 HP0234 HP0234 HP0234 HP0347 HP0359 HP0310 HP0416 HP0416 HP04166 HP04169	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical propretial conserved hypothetical propretial conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein conserved hypothetical prote	34,3% 30,6% 31,0% 32,0% 32,0% 32,0% 32,0% 34,1% 32,0% 34,1% 32,0% 34,1% 32,0% 34,1% 32,0% 32,0% 34,1% 32,0% 32,0% 32,0% 33,0%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1431 HP06030 HP1476 HP165 Transposo HP1008 HP0414 HP0988 HP0989 HP0389 HP0389 HP0389 HP0389 HP0389 HP0389 HP0399 HP0319 HP1031 HP0071 DP1086 HP0739 HP10966 HP0289 HP0312 HP1430 HP14567	virulence factor, mivil protein (mivil)) tied functions colicin tolerance-like protein (tolB) phage/colicin /fellunite resistance cluster ter/ protein nailog sensitivity inailog sensitivity insideriase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 152	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.4% 94.6% 95.6% 96.6%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0151 HP0575 HP0032 HP0032 HP0036 HP0096 HP0016 HP0190 HP0190 HP0190 HP0190 HP0191 HP0192 HP0197 HP0198 HP01996 HP0469 HP0469 HP0469 HP0469 HP0469	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein c	34.3% 30.6% 41.2% 41.2% 52.2% 48.2% 53.7% 48.2% 53.7% 53.2% 54.5% 53.2% 54.5% 53.2% 54.5% 55.5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1426 HP0428 Drug and a HP1431 HP0626 HP0630 HP1476 HP1030 HP1038 HP0414 HP0884 HP0988 HP0988 HP0988 HP0988 HP1935 HP0988 HP1935 HP0988 HP0413 HP097 HP097 HP097 HP0981 HP047 HP0988 HP0413 HP047 HP0413 HP047 HP0413 HP047 HP0413 HP0413 HP0414 HP0414 HP0414 HP0414 HP0415 HP0415 HP0415 HP0415 HP0415 HP0416 HP041	virulence factor miviN protein (mviN) tede functions collect total collect functions collect functions collect functions collect functions collect functions function	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.3% 93.4% 93.3% 93.4% 93.4% 93.5% 93.4% 93.5% 93.5% 93.6% 93.5% 93.6%	HP1609 HP1648 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0035 HP0035 HP0036 HP00102 HP0102 HP01017 HP0102 HP01017 HP0102 HP0103 HP0104 HP0105 HP0117 HP0162 HP0216 HP0216 HP0217 HP0216 HP0216 HP0217 HP0228 HP0239 HP0310	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical propretial conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein conserved hyp	34,3% 30,6% 31,0% 32,0% 33,0%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1431 HP06030 HP1476 HP165 Transposo HP1008 HP0414 HP0988 HP0989 HP0389 HP0989 HP0381 HP0089 HP0381 HP0071 HP0739 HYPOTHET General HP0739 HP1971 HP07312 HP1971 HP19	virulence factor mviN protein (mviN) teted functions collicin tolerance-like protein (toIB) phage collicin fellurite resistance cluster tet for functions collicin tolerance-like protein (toIB) phage collicin fellurite resistance cluster tet for protein (mric for function) and conserved function for function	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.4% 94.6% 95.6% 96.6%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0151 HP0575 HP0032 HP0032 HP0036 HP0096 HP0016 HP0190 HP0190 HP0190 HP0191 HP0192 HP0191 HP01933 HP0244 HP0234 HP0234 HP0234 HP0248 HP0274 HP0284 HP0284 HP0284 HP0284 HP0284 HP0284 HP0286 HP0286 HP0386 HP0386 HP0386 HP0386 HP0386 HP0386 HP0486 HP0486 HP0486 HP0486 HP0468 HP0469	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein conserved hypothetical protei	34,3% 30,6% 41,2% 41,2% 32,2% 48,2% 33,8% 48,2% 37,7% 48,2% 37,7% 32,5% 32,7% 33,7% 33,7% 33,9% 30,5% 30,5% 30,5% 30,5% 31,3% 31,3% 33,7% 47,2% 30,5% 30,5% 30,5% 30,5% 30,5% 31,3% 30,5% 31,3% 31,3% 32,7% 47,2% 30,5% 30,5% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 31,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1431 HP06030 HP1476 HP165 Transposo HP1008 HP0414 HP0988 HP0989 HP0389 HP0389 HP0389 HP0389 HP0389 HP0389 HP0399 HP0319 HP1031 HP0071 DP1086 HP0739 HP10966 HP0289 HP0312 HP1430 HP14567	virulence factor, mivil protein (mivil) tede functions colicin tolerance-like protein (tolB) phage/colcin/fellurité resistance cluster ter/ protein (1876) phage/colcin/fellurité resistance cluster ter/ protein (1851 fiNA (adenosine-N6,N6)-dimethyl-transférase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative membrane tusion protein tetA(P), putative membrane tusion protein tetA(P), putative membrane tusion for significant functions (1800 insertion sequence from SARA17 18200 insertion sequence from SARA17 18200 insertion sequence from SARA17 18206 transposase (tnpA) 1806 transposase (tnpA) 1806 transposase (tnpA) 1806 transposase (tnpA) 1806 transposase (tnpB) 1	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.3% 93.5%	HP1609 HP1648 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0032 HP0035 HP0036 HP0094 HP0100 HP0102 HP01017 HP0102 HP01017 HP0102 HP0103 HP0103 HP0104 HP0105 HP0107 HP0107 HP0108 HP0216 HP0230 HP0310 HP0310 HP0330 HP03310 HP0337 HP0337 HP03374 HP03374 HP03374 HP0354 HP0365 HP0466 HP0466 HP0466 HP0466 HP0466 HP0466 HP0466 HP0469	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein described in the protein conserved hypothetical protein conser	34,3% 30,6% 31,0% 32,0% 33,0%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1431 HP06030 HP1476 HP165 Transposo HP1008 HP0414 HP0988 HP0989 HP0359 HP1534 HP0637 HP1635 HP1634 HP0739 HP1634 HP10739 HP1637 HP1666 HP0026 HP0026 HP0021 HP1830 HP1667 HP1666 HP0022	virulence factor mviN protein (mviN) teted functions colicin tolerance-like protein (toIB) phage colicin fellunite resistance cluster ter y protein (mile) phage colicin fellunite resistance cluster ter y protein (mile) phage colicin fellunite resistance cluster ter y protein (mile) protein (mile) phage colicin fellunite resistance protein (mtrC) modulator of drug activity (mda66) phenylacyricia caid decarboxylase tetracycline resistance protein tetA[P], putative protein general protein sequence from SARA17 IS200 insertion sequence from SARA17 IS205 transposase (mpA) IS205 transposase (mpB) IS205 transposase	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.3% 93.4% 93.3% 93.4% 93.4% 93.5% 93.4% 93.5% 93.5% 93.6% 93.5% 93.6%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0151 HP0575 HP0032 HP0032 HP0036 HP0096 HP0016 HP0190 HP0190 HP0190 HP0191 HP0192 HP0191 HP01933 HP0244 HP0234 HP0234 HP0234 HP0248 HP0274 HP0284 HP0284 HP0284 HP0284 HP0284 HP0284 HP0286 HP0286 HP0386 HP0386 HP0386 HP0386 HP0386 HP0386 HP0486 HP0486 HP0486 HP0486 HP0468 HP0469	protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein conserved hypothetical protei	34,3% 30,6% 41,2% 41,2% 32,2% 48,2% 33,8% 48,2% 37,7% 48,2% 37,7% 32,5% 32,7% 33,7% 33,7% 33,9% 30,5% 30,5% 30,5% 30,5% 31,3% 31,3% 33,7% 47,2% 30,5% 30,5% 30,5% 30,5% 30,5% 31,3% 30,5% 31,3% 31,3% 32,7% 47,2% 30,5% 30,5% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 31,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06030 HP1431 HP06030 HP1476 HP165 Transposo HP1008 HP0414 HP0988 HP0989 HP0389 HP0989 HP0381 HP0089 HP0381 HP0071 HP0739 HYPOTHET General HP0739 HP1971 HP07312 HP1971 HP19	virulence factor, mivil protein (mivil) teef functions colicin tolerance-like protein (tolB) phage/colcin/fellurité resistance cluster ter/ protein (1876) phage/colcin/fellurité resistance cluster ter/ protein (1851 fiNA (adenosine-N6,N6)-dimethyl-transférase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative membrane tusion protein tetA(P), putative membrane tusion protein tetA(P), putative membrane tusion for significant functions (1800 insertion sequence from SARA17 18200 insertion sequence from SARA17 18200 insertion sequence from SARA17 18206 transposase (tnpA) 1806 transposase (tnpB) 1	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.4% 93.5% 93.5%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0575 HP0032 HP0032 HP0036 HP0086 HP0096 HP0190 HP0190 HP0190 HP0190 HP0190 HP0218 HP0234 HP0234 HP0244 HP0240 HP0240 HP0240 HP0240 HP0250 HP0250 HP0250 HP0260 HP0260 HP0270 H	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein cons	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 41,2% 33,2% 48,2% 32,0% 48,2% 37,0% 32,0% 48,2% 37,0% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 33,0% 32,0% 33,0% 36,2% 30,5% 31,3% 30,5% 31,3% 32,0% 41,2% 30,5% 31,3% 32,0% 41,2% 30,5% 31,3% 31,3% 32,0% 41,2% 30,5% 31,3% 31,3% 32,0% 41,2% 30,5% 31,3% 31,3% 32,0% 41,2% 30,5% 31,3% 31,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0490 HP0495 HP0495 HP0495 HP0495 HP0496 HP049	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4
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HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP06050 HP1437 HP165 Transposo HP1008 HP0414 HP0988 HP0098 HP0414 HP0988 HP0098 HP0417 HP055 HP155 HP156 HP075 HP156 HP075 HP156 HP075 HP156 HP066 HP067 HP166 HP066 HP067 HP166 HP067 HP166 HP067 HP166 HP067 HP166 HP0628	virulence factor, mivil protein (mivil) teef functions colicin tolerance-like protein (tolB) phage/colcin/fellurité resistance cluster ter/ protein (1878) phage/colcin/fellurité resistance cluster ter/ protein (1851 RNA (adenosine-N6,N6)-dimethyl-transférase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacylice acid decarboxylase tetracycline resistance protein tetA(P), putative membrane tusion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS200 fransposase (tnpA) IS200 fransposase (tnpB) IS200 f	33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.4% 93.5% 93.5% 93.5% 93.5% 93.5% 93.5% 93.6%	HP1509 HP1548 HP0138 HP1438 HP01431 HP0575 HP0032 HP0032 HP0032 HP0036 HP0096 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0318 HP0244 HP0240 HP0334 HP0247 HP0386 HP0387 HP0387 HP0387 HP0388 HP0388 HP0388 HP0389 HP0391 HP0496 HP06503 HP0659 HP0659 HP0659 HP0659 HP0659 HP0659 HP0659 HP0659 HP0659	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein conserved hypothetical	34,3% 30,6% 41,2% 32,0% 41,2% 32,0% 48,2% 37,0% 32,0% 48,2% 37,0% 32,0% 48,2% 37,0% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 32,0% 33,0% 32,0% 33,0% 36,0% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,3% 30,5% 31,5% 31,5% 30,5% 31,5% 30,5% 31,5% 30,5% 31,5% 30,5% 31,5% 30,5% 31,5% 31,5% 30,5% 31,5% 31,5% 30,5% 31,5%	HP1117 HP1216 HP12285 HP12464 HP1486 HP1464 HP1561 UNKNOWN General HP0390 HP1193 HP0390 HP1193 HP0470 HP0485 HP0485 HP0485 HP0485 HP0485 HP0480 HP048	conserved hypothetical secreted protein secreted protein conserved hypothetical secreted protein alkylphosphonate uptake protein (ppn alkylphosphonate) protein (ppn alk	31.996. 37.596 37.596 37.596 42.796 38.396 46.696 46.696 46.696 38.396 46.696 42.296 4