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

RNA

tibosomal RNA	Coordinates
23S-5S	445,306-448,642 bp
23S-5S	1,473,557-1,473,919 b
16S	1,209,082-1,207,584 b
16S	1,511,138-1,512,635 bp
58	448,041-448,618 bp

Transfer RNA

36 species (7 clusters, 12 single genes)

Structural RNA

1 species (ssrD)

629,845-630,124 bp

Associated genes

DNA

Insertion sequences

IS605 13 copies (5 full-length, 8 partial) IS606 4 copies (2 full-length, 2 partial)

$\hbox{Distinct } G+C \hbox{ regions}$

region 1 (33% \dot{G} + C) 452-479 kb region 2 (35% \dot{G} + C) 539-579 kb region 3 (33% \dot{G} + C) 1,049-1,071 kb region 4 (43% \dot{G} + C) 1,264-1,276 kb region 5 (33% \dot{G} + C) 1,590-1,602 kb

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

Coding sequences

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

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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

540

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).

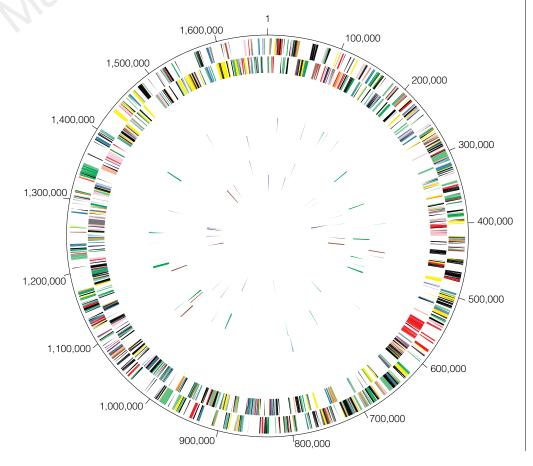
Adhesion and adaptive antigenic variation

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.



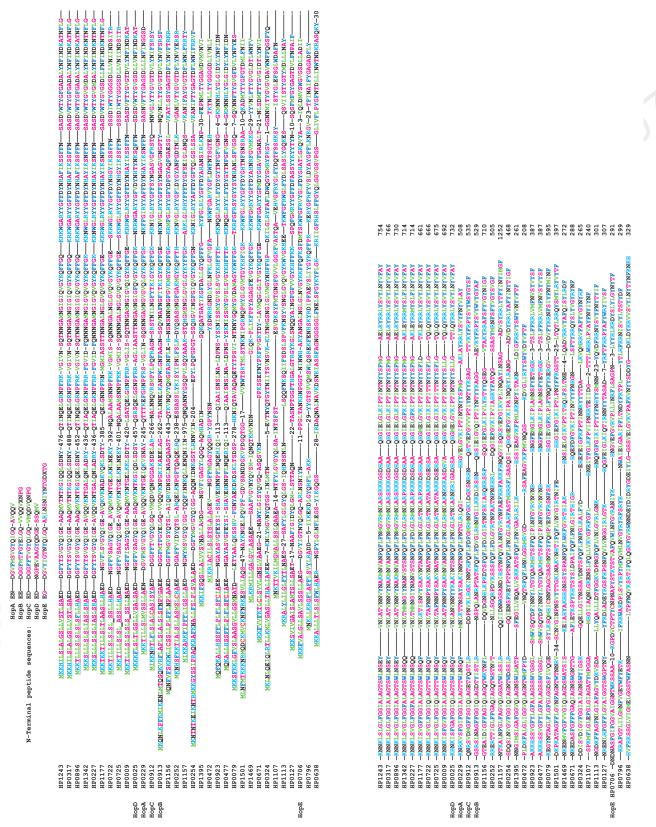


Figure 3 Multiple sequence alignment of members of the outer membrane protein family of *H. pylori*. These proteins were identified as OMPs based on the characteristic alternating hydrophobic residues at their carboxy termini. All members of this family have one domain of similarity at the amino-terminal 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

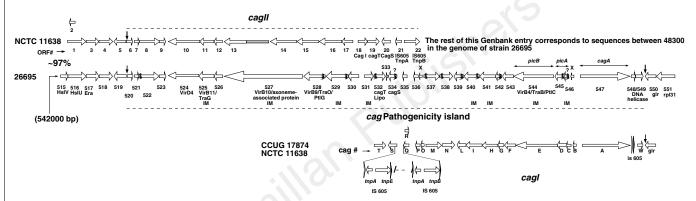


Figure 4 Comparison between the Cag pathogenicity islands of the sequenced strain, 26695 and the NCTC11638 strain. The twenty nine ORFs of the contiguous PAI in strain 26695 are represented together with the corresponding ORFs from the PAI present in NCTC11638 (AC000108 and U60176). The PAI in NCTC11638 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.

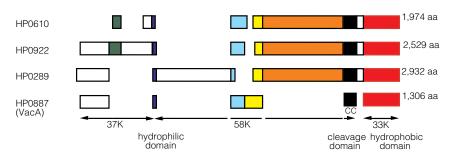


Figure 5 Conserved domains of VacA and related proteins. HP887 is the vacuolating cytotoxin (vacA) gene from *H. pylori* 26695 strain. HP610, HP922 and HP289 are related proteins. Blocks of aligned sequence and the length of each protein are shown. Arrows designate the extents of each VacA domain. The 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 and	d dinucleotide	repeats in H. pylori					
HP no.	ID		No. of repeats	Ger	ne status	Poly(A) or Poly(T) tracts in 5' interg	enic region
starting at the CCAAAAATC T ATG AAAAA	designated methionine) g of HP0722 sho leads to a trunc AAATCCAATAA	11 CT 11 AG 6 CT 8 CT 6 CT 9 AG 11 CT 9 AG wing the CT dinucleotide sated product. The additi ATTTATGGTAAAGT-37b; GCTTCATCGCTCTTGCA S S L L H L H R S C T	On Off Off Tru On Tru repeat and the pol on or deletion of tw p-TTTACAATAAAA	incated incated incated ly T tract. The puta vo CT repeats, by ' AAATTACTTTAAG	slipped-strand mispair GAACATTT		
(b) Homopoly HP no. 58 217 379 464 619 651 1353 1471 1522	meric poly(C) and poly((Hypi Hypi fuco Type glyci Hypi Hypi Type	ID o o o syl transf. al R os, transf. o		Tract leng	th		Gene status Off On On On Truncated On Truncated On Truncated
Genes possib HP no. 9 227 350 722 876 1342	oly regulated by homopo ID OMP OMP IMP OMP frpB OMP	olymeric 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 <i>cagA</i> OMP OMP <i>fecA</i>	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

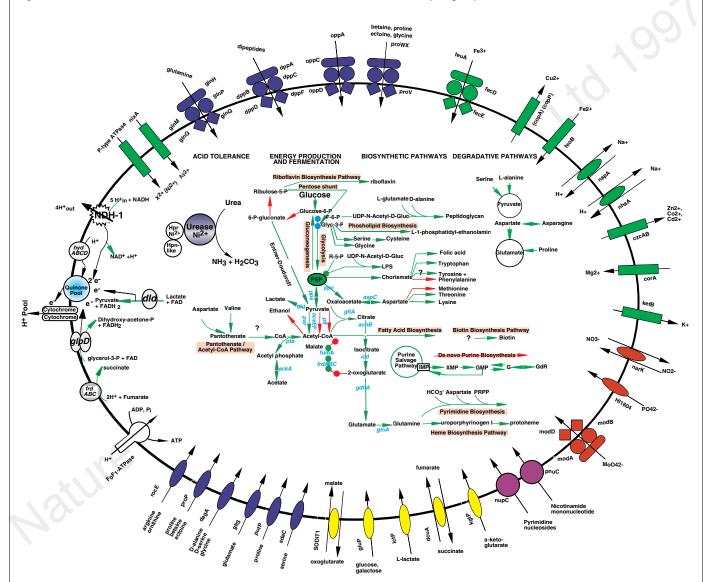


Figure 6 Solute transport and metabolic pathways of Helicobacter pylori. Transporters identified by sequence comparisons are characterists of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley¹⁵: blue, amino acids, peptides and amines; red, anions; yellow, carbohydrates, 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.

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.

AMINO-ACID BIOSYNTHESIS		HP0841	pantothenate metabolism flavoprotein (dfp)		HP0855		41.8%
General					HP0326	CMP-N-acetylneuraminic acid synthetase	
HP0695 hydantoin utilization protein A (hyuA)	28.6%	Pyridoxine	nuridoual abacabata bioquathatic arotain		LIDOGGO		31.9%
Aromatic amino-acid family		HP1583	pyridoxal phosphate biosynthetic protein A (pdxA)	34.2%	HP0230	CTP:CMP-3-deoxy-D-manno-octulosonate- cytidylyl-transferase (kdsB)	36.2%
HP1038 3-dehydroquinase type II (aroQ)	99.4%	HP1582	pyridoxal phosphate biosynthetic protein J	34.270	HP1392		25.7%
HP0283 3-dehydroquinate synthase (aroB)	38.1%	111 1002	(pdxl)		HP0379		39.2%
HP0134 3-deoxy-D-arabino-heptulosonate	E 4 00V	Riboflavin	(1-2-2)		HP0651		39.2%
7-phosphate synthase (dhs1) HP0401 3-phosphoshikimate	54.6%		GTP cyclohydrolase II (ribA)	47.2%	HP0044	GDP-D-mannose dehydratase (rfbD)	62.1%
1-carboxyvinyltransferase (aroA)	53.6%	HP0804	GTP cyclohydrolase II/3,4-dihydroxy-2-butar		HP0867		32.0%
HP1279 anthranilate isomerase (trpC)	47.0%		4-phosphate synthase (ribA, ribB)	11.070	HP0159	lipopolysaccharide 1,2-glucosyltransferase	00.00/
HP1282 anthranilate synthase component I (trpE)	47.9%		riboflavin biosynthesis protein (ribG)	33.1%	HP0208	(rfaJ) lipopolysaccharide 1,2-glucosyltransferase	28.9%
HP1280 anthranilate synthase component II (trpD)	TL.U /U	HP1087	riboflavin biosynthesis regulatory protein		111-0200		26.7%
HP1281 anthranilate synthase component II (trpD)	40.2%	HP1574	(ribC)	28.9% 32.8%	HP0805	lipooligosaccharide 5G8 epitope biosynthes	
HP0663 chorismate synthase (aroC)	T1.L 10		riboflavin synthase alpha subunit (ribC) riboflavin synthase beta chain (ribE)	52.4%	0000		36.9%
HP1380 prephenate dehydrogenase (tyrA)	00.L /0			JZ.470	HP0826	lipooligosaccharide 5G8 epitope biosynthes	
HP1249 shikimate 5-dehydrogenase (aroE) HP0157 shikimic acid kinase I (aroK)	36.6% 36.1%	HP1118	glutaredoxin and glutathione gamma-glutamyltranspeptidase (ggt)	53.2%			39.2%
HP1277 tryptophan synthase, alpha subunit (trpA)		HP1458	thioredoxin	38.3%	HP1416	lipopolysaccharide 1,2-glucosyltransferase	
HP1278 tryptophan synthase, beta subunit (trpB)	66.1%		thioredoxin (trxA)	61 606	1100000		29.2%
Aspartate family			thioredoxin reductase (trxB)	28.5%	HP0679	lipopolysaccharide biosynthesis protein	40.00/
HP0649 aspartate ammonia-lyase (aspA)	55.5%	Thiamine			HP1475	(wbpB) lipopolysaccharide core biosynthesis proteil	42.8%
HP1189 aspartate-semialdehyde dehydrogenase			thiamin biosynthesis protein (thiF)	34.6%	1111 1475	(kdtB)	49.0%
(asd)			thiamin phosphate pyrophosphorylase/		HP0279	lipopolysaccharide heptosyltransferase-1	10.070
HP1229 aspartokinase (lysC) 48.0%			hyroxyethylthiazole kinase (thiB)	35.7%			31.7%
HP0106 cystathionine gamma-synthase (metB)	47.7%	HP0845	thiamin phosphate pyrophosphorylase/		HP0619	lipopolysacharide biosynthesis glycosyl	
HP0290 diaminopimelate decarboxylase	42.7%	HP0844	hyroxyethylthiazole kinase (thiM)	37.9%			37.2%
(dap decarboxylase) (lysA) HP0566 diaminopimelate epimerase (dapF)	30.0%		thiamine biosynthesis protein (thi)		HP1105		28.7%
HP0510 dihydrodipicolinate reductase (dapi)	0.5.001	Pyridine nuc			HP1578 HP1581		28.1% 29.2%
HP1013 dihydrodipicolinate synthetase (dapA)			NH(3)-dependent NAD+ synthetase (nadE) nicotinate-nucleotide pyrophosphorylase		HP0857		44.5%
HP0822 homoserine dehydrogenase (metL)	37.7%	111 1000	(nadC)		HP1275	phosphomannomutase (algC)	11.070
HP1050 homoserine kinase (thrB)	27.7%	HP1356	quinolinate synthetase A (nadA)	34.2%			39.6%
HP0672 solute-binding signature and mitochondria	ıl		, , , , , , , , , , , , , , , , , , , ,		HP1429	polysialic acid capsule expression protein	
signature protein (aspB)	47.3%	CELL ENVE	LOPE			(kpsF)	46.0%
HP0212 succinyl-diaminopimelate desuccinylase	40.00	Membranes	, lipoproteins and porins		HP0366	spore coat polysaccharide biosynthesis	
(dapE) HP0626 tetrahydrodipicolinate N-succinyltransferas	42.3% ie	HP1450	60 kDa inner-membrane protein	40.0%	UD0170		35.3%
(dapD) tetranydrodipicolinate N-succinyitransieras	e 36.1%		apolipoprotein N-acyltransferase (cute)	20.070	HP0178	spore coat polysaccharide biosynthesis protein E	36.2%
HP0098 threonine synthase (thrC)	22.00%	HP0175	cell binding factor 2	34.9%	HP0421	type 1 capsular polysaccharide biosynthesis	
Glutamate family			Hypothetical protein	20.470	. 11 0421	rype i capsular polysaccharide biosynthesis protein J (capJ)	s 29.0%
HP0380 glutamate dehydrogenase (gdhA)			membrane protein	26.4%	HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine	/0
HP0512 glutamine synthetase (glnA)	10.00		membrane-associated lipoprotein (lpp20) outer membrane protein	39 9%		N-acyltransferase (lpxD)	39.5%
HP1158 pyrroline-5-carboxylate reductase (proC)	00.00			0.0%	HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylas	se
Pyruvate family			outer membrane protein (omp10)	0.0%		(envA)	44.6%
HP0941 alanine racemase, biosynthetic (alr)	32.4%	HP0472	outer membrane protein (omp10)	99.5%	HP1375	UDP-N-acetylglucosamine acyltransferase	
HP1468 branched-chain-amino-acid		HP0477	outer membrane protein (omp12)	0.0%		(IpxA)	41.8%
aminotransferase (ilvE)	63.5%	HP0638	outer membrane protein (omp13)		Surface stru		
HP0330 ketol-acid reductoisomerase (ilvC)	48.1%	HP0671	outer membrane protein (omp14)		HP0840		60.2%
Serine family		HP0706	outer membrane protein (omp15)		HP0325		32.7%
HP0107 cysteine synthetase (cysK)	45.7%		outer membrane protein (omp16)		HP0351		34.4%
HP0096 phosphoglycerate dehydrogenase	31.0%		outer membrane protein (omp17)		HP0246		37.9%
HP0397 phosphoglycerate dehydrogenase (serA)			outer membrane protein (omp18)		HP1557		37.0%
HP0736 phosphoserine aminotransferase (serC)	30.7%		outer membrane protein (omp19)		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%
HP1210 serine acetyltransferase (cysE)	98.2%	HP0913	outer membrane protein (omp21)	38.2%	111-1006	(proximal rod protein)	46.0%
HP0183 serine hydroxymethyltransferase (glyA)		HP0923	outer membrane protein (omp21)	0.0%	HP1092		35.5%
BIOSYNTHESIS OF COFACTORS, PROSTHETIC GROU		HP1107	outer membrane protein (omp23)		HP1585		47.7%
AND CARRIERS	10,	HP1113	outer membrane protein (omp24)	36.0%	HP1041		43.1%
		HP1156	outer membrane protein (omp25)	0.0%	HP1035	flagellar biosynthesis protein (flhF)	35.5%
General HP0220 synthesis of [Fe-S] cluster (nifS)	48.0%	HP1157	outer membrane protein (omp26)		HP0684		43.4%
	48.0%	HP1177	outer membrane protein (omp27)		HP0770		38.7%
Biotin	04.00/	HP1243	outer membrane protein (omp28)		HP0685		55.6%
HP0598 8-amino-7-oxononanoate synthase (bioF)	34.9%	HP1342	outer membrane protein (omp29)		HP1419		52.3%
HP0976 adenosylmethionine-8-amino-7-oxononano			outer membrane protein (omp3)		HP0173		26.4%
aminotransferase (bioA) HP1140 biotin operon repressor/biotin acetyl coen			outer membrane protein (omp30)		HP0353		29.1%
A carboxylase synthetase (birA)	36.9%	HP1469	outer membrane protein (omp31)		HP1420		47.6%
HP0407 biotin sulfoxide reductase (bisC)		HP1501	outer membrane protein (omp32)		HP0870 HP0908		98.9% 30.5%
HP1254 biotin synthesis protein (bioC)		HP0127 HP0227	outer membrane protein (omp4) outer membrane protein (omp5)		HP1119	flagellar hook-associated protein 1	30.5%
HP1406 biotin synthetase (bioB)	36.2%	HP0229	outer membrane protein (omp6)	38.4%	111 1113	(HAP1) (flgK)	27.6%
HP0029 dethiobiotin synthetase (bioD)	36.0%		outer membrane protein (omp7)		HP0752		28.9%
Folic acid			outer membrane protein (omp8)		HP0815		32.9%
HP1036 7, 8-dihydro-6-hydroxymethylpterin-			outer membrane protein (omp9)		HP0816		29.7%
pyrophosphokinase (folK)						flagellar motor switch protein (fliG)	37.0%
HP0587 aminodeoxychorismate lyase (pabC)	34.6%	HP0839	outer membrane protein P1 (ompP1)	23.3%	HP0352		
HP1232 dihydropteroate synthase (foIP)	32.4%	HP0839 HP0955	outer membrane protein P1 (ompP1) prolipoprotein diacylglyceryl transferase (lgt	23.3% t)34.4%	HP1031		34.4%
HP1545 folylpolyglutamate synthase (folC)	32.4% 34.5%	HP0839 HP0955 HP0655	outer membrane protein P1 (ompP1) prolipoprotein diacylglyceryl transferase (lgt protective surface antigen D15	23.3% t)34.4% 27.5%	HP1031 HP0753	flagellar protein (fliS)	32.3%
HP0928 GTP cyclohydrolase I (folE)	32.4% 34.5% 35.2%	HP0839 HP0955 HP0655 HP1571	outer membrane protein P1 (ompP1) prolipoprotein diacylglyceryl transferase (lgt protective surface antigen D15 rare lipoprotein A (rlpA)	23.3% t)34.4% 27.5% 37.6%	HP1031 HP0753 HP0327	flagellar protein (fliS) flagellar protein G (flaG)	32.3% 23.3%
	32.4% 34.5% 35.2% 50.9%	HP0839 HP0955 HP0655 HP1571 HP0610	outer membrane protein P1 (ompP1) prolipoprotein diacy/glyceryl transferase (Igt protective surface antigen D15 rare lipoprotein A (rfpA) toxin-like outer membrane protein	23.3% ()34.4% 27.5% 37.6% 26.3%	HP1031 HP0753 HP0327 HP0797	flagellar protein (fliS) flagellar protein G (flaG) flagellar sheath adhesin hpaA	32.3% 23.3% 98.5%
HP0577 methylene-tetrahydrofolate dehydrogenase	32.4% 34.5% 35.2% 50.9%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922	outer membrane protein P1 (ompP1) prolipoprotein diacylglyceryl transferase (lgt protective surface antigen D15 rare lipoprotein A (rfpA) toxin-like outer membrane protein toxin-like outer membrane protein	23.3% ()34.4% 27.5% 37.6% 26.3% 29.5%	HP1031 HP0753 HP0327 HP0797 HP0584	flagellar protein (fliS) flagellar protein G (flaG) flagellar sheath adhesin hpaA flagellar switch protein (fliN)	32.3% 23.3% 98.5% 39.7%
HP0577 methylene-tetrahydrofolate dehydrogenase (foID)	32.4% 34.5% 35.2% 50.9%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289	outer membrane protein P1 (ompP1) prolipoprotein diacylglyceyl transferase (gt protective surface antigen D15 rare lipoprotein A (fpA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein	23.3% t)34.4% 27.5% 37.6% 26.3% 29.5%	HP1031 HP0753 HP0327 HP0797	flagellar protein (fliS) flagellar protein G (flaG) flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA)	32.3% 23.3% 98.5%
HP0577 methylene-tetrahydrofolate dehydrogenase (foID) HP0293 para-aminobenzoate synthetase (pabB)	32.4% 34.5% 35.2% 50.9%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc	outer membrane protein P1 (ompP1) prolipoprotein diacy/glycen/ transferase (Igt protective surface antigen D15 rare lipoprotein A (fpA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein such-like outer membrane protein subus and peptidoglycan	23.3%)34.4% 27.5% 37.6% 26.3% 29.5% 30.6%	HP1031 HP0753 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295	flagellar protein (fils) flagellar protein G (flaG) flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB)	32.3% 23.3% 98.5% 39.7% 99.8%
HP0577 methylene-tetrahydrofolate dehydrogenase (folD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin	32.4% 34.5% 35.2% 50.9% 48.4% 35.1%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0830	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like out	23.3% 134.4% 27.5% 37.6% 26.3% 29.5% 30.6%	HP1031 HP0753 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575	flagellar protein (fils) flagellar protein G (flaG) flagellar switch protein (fliN) flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flbB protein (flhB)	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5%
HP0577 methylene-tetrahydrofolate dehydrogenase (foID) HP0293 para-aminobenzoate synthetase (pabB)	32.4% 34.5% 35.2% 50.9% 48.4% 35.1%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0830	outer membrane protein P1 (ompP1) prolipoprotein diacy/glycen/ transferase (Igt protective surface antigen D15 rare lipoprotein A (fpA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein usuks and peptidoglycan	23.3% 1)34.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5%	HP1031 HP0753 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030	flagellar protein (flis) flagellar protein (flisd) flagellar sheath adhesin hpaA flagellar switch protein (flink) flagellin S (flida) flagellin B (flida) flagellin B (flida) flagellin B homologue (fla) flhB protein (flinb) fly protein (fliry)	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5% 29.3%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH)	32,4% 34,5% 35,2% 50,9% 35,1% 50,5% 33,4%	HP0839 HP0955 HP0665 HP1671 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772	outer membrane protein P1 (ompP1) proflopportein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like out	23.3% 134.4% 134.4% 27.5% 37.6% 26.3% 29.5% 40.6% 40.6% 40.6% 40.6% 36.6%	HP1031 HP0753 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar switch protein (flin) flagellin (flagellin	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH)	32,4% 34,5% 35,2% 50,9% 35,1% 50,5% 30,4%	HP0839 HP0955 HP19571 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0549 HP0772 HP0597	outer membrane protein P1 (ompP1) profiloprotein diacylglyceryl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like outer membrane protein D-alanine:D-alanine ligase A (ddIA) glutamate racemase (gir) N-acetylmuramoyl-L-alanine amidase (amiA penicillin-binding protein 14 (PBP-1A)	23.3%)34.4% 27.5% 37.6% 28.3% 29.5% 30.6% 40.6% 36.6% 36.6%	HP1031 HP0763 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP0907 HP1274	flagellar protein (flis) flagellar protein (flisd) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar with protein (fliN) flagellin M (flaA) flagellin B (flaB) flagellin B (maB) flagellin B homologue (fla) flagellin B homologue (fla) flinB protein (flinB) fly protein (fliTy) Hook assembly protein, flagella (flgD) paralysed flagella protein (fnfA)	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9%
HP0577 methylene-tetrahydrofolate dehydrogenase (folD) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL)	32.4% 34.5% 35.2% 50.9% 48.4% 35.1% 50.5% 33.4% 6	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772 HP0549 HP0772 HP0597 HP1565	outer membrane protein P1 (ompP1) profloporotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (rfpA) toxin-like outer membrane protein sulus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddIA) glutamiate racemase (gir) N-acetylmuramyl-t-allanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A)	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 40.6% 40.6% 40.6% 40.6% 33.7% 33.7% 33.7%	HP1031 HP0753 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751	flagellar protein (flis) flagellar protein (flis) flagellar rotein (flisd) flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin (flidA) flagellin (flidA) flagellin (flidA) flagellin (flidA) flagellin (flidA) flagellin (flidB) fliB protein (flitB) fliY protein (flitP) Hook assembly protein, flagella (flgD) paralysed flagella protein (pfiA) polar flagellin (flidG)	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
HP0577 methylene-terrahydrofolate dehydrogenase (folD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0396 glutamytet-1-semialdehyde 2,1-aminomutas (hemL) HP0299 glutamytet-1-semialdehyde (hemA)	32.4% 34.5% 35.2% 50.99 48.4% 35.1% 50.5% 60.5% 36.1% 60.5% 32.7%	HP0839 HP0955 HP19571 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0549 HP0772 HP0597	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein amiddase D-alanine-D-alanine ligase A (ddIA) glutamate racemase (gir) N-acetylmuramoyl-Lalanine amiddase (emiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) peptidoglycan associated lipoprotein precu	23.3%)34.4% 27.5% 37.6% 26.3% 50.6% 40.6% 36.6% 36.6%)26.8% 36.7% 36.7% 36.7% 36.7%	HP1031 HP0763 HP0327 HP0797 HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP0907 HP1274	flagellar protein (fils) flagellar protein (filsd) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin B (filaB) flagellin B homologue (fla) flinB protein (filiN) fly protein (filiN) flook assembly protein, flagella (flgD) paralysed flagellar protein (filA) polar flagellin (filaG) putative neureminyllactose-binding	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9%
HP0577 methylene-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 errorchelatase (hemH) glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) HP0685 oxygen-independent coproporphyrinogen	32.4% 34.5% 50.9% 50.9% 148.4% 35.1% 50.5% 50.5% 33.4% 6 61.3% 11.3% 32.7%	HP0839 HP0955 HP0655 HP1671 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772 HP0597 HP1565 HP1125	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (rfpA) toxin-like outer membrane protein sulus and peptidoglycan amidase D-alanineiD-alanine ligase A (ddlA) giutamate racemase (glr) N-acety/muramoyl-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) peptidoglycan associated lipoprotein precu (omp18)	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 40.6% 40.6% 36.6% 36.6% 33.7% 35.0% 50.5% 40.6% 28.6% 36.7% 50.5% 5	HP1031 HP0753 HP0327 HP0797 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1576 HP1030 HP0907 HP1274 HP0751 HP0410	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar switch protein (flin) flagellar (flin) flagellin (flia) flagellin (flia) flagellin (flia) flagellin (flia) flagellin (flia) flagellin (flia) fly protein (flih) fly protein (fliy) Hook assembly protein, flagella (flgD) paralysed flagella protein (fliA) polar flagellin (fliaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA)	32.3% 23.3% 98.5% 99.5% 99.9% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0293 glutamyl-tRNA reductase (hemA) HP0365 oxygen-independent coproporphyrinogen oxidase (hemN)	32.4% 34.5% 35.2% 50.9% 48.4% 35.1% 60.5% 33.4% 6 61.3% 32.7% III 42.4%	HP0839 HP0955 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772 HP0549 HP0772 HP0597 HP1565	outer membrane protein P1 (ompP1) profiloprotein diacy/glycen/ transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein brown of the control of the contr	23.3% 334.4% 27.5% 27.5% 26.3% 26.3% 29.5% 40.6% 40.6% 40.6% 36.6% 36.6% 35.0% 35.0% 35.0% 35.0% 35.0% 42.6%	HP1031 HP0753 HP0753 HP0797 HP0797 HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP1030 HP0907 HP1274 HP0751 HP0410 HP192	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin B (filaB) flagellin (filaB) flagellin (filaC) pratiyed flagellin (filaC) polar flagellin (filaG) potative neureminyllactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility	32.3% 23.3% 98.5% 39.7% 99.8% 99.0% 40.5% 40.5% 29.3% 22.9% 23.9% 21.9% 24.2% 772.5%
HP0577 methylene-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen	32.4% 34.5% 50.9% 50.9% 31.45% 50.9% 32.1% 50.5% 50.5% 33.4% 61.3% 32.7% 11.1% 42.4%	HP0839 HP0965 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0738 HP0738 HP0738 HP0749 HP0772 HP0597 HP1565 HP1125 HP0493	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein sulus and peptidoglycan amidase D-alaninei-D-alanine ligase A (ddiA) glutamater accemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A) peptidoglycan associated lipoprotein precu (omp18) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)	23.3% 334.4% 27.596 37.6% 26.3% 29.5% 40.6% 40.6% 40.6% 33.7% 33.7% 33.7% 33.7% 33.7% 44.6% 44.6% 44.6% 45.2%	HP1031 HP0753 HP0753 HP0797 HP0797 HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar switch protein (flink) flagellar flagellar (flink) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) fly protein (flifty) fly protein (flifty) fly protein (fliry) flook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (fliad) putative neuraminyflactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	32.3% 23.3% 98.5% 99.7% 99.8% 99.0% 32.9% 40.5% 25.5% 21.9% 24.2% 7/2.5% 9/6.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0366 ferrochelatase (hemH) HP0299 glutamyt-RNA reductase (hemA) HP0660 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN)	32.4% 34.5% 50.9% 50.9% 60.9% 60.5% 35.1% 60.5% 33.4% e 61.3% 61.3% 62.7% III 32.7% III 37.9%	HP0839 HP0955 HP0655 HP1671 HP0610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0772 HP0549 HP0772 HP1665 HP1125 HP0493 HP0743	outer membrane protein P1 (ompP1) profiloprotein diacy/glycen/ transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dustal and peptidoglycan amidase (adiA) gilutamate racemase (glr) N-acety/muramoyl-Lalanine amidase (amiA penicillin-binding protein 2 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (omp18) phospho-N-acety/muramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB)	23.3% 33.4 4% 27.5% 27.5% 26.3% 26.3% 26.9% 40.6% 40.6% 40.6% 30.6% 40.6% 35.0% 35.0% 35.0% 42.6% 45.2% 37.7%	HP1031 HP0753 HP0753 HP0797 HP0797 HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP1030 HP0907 HP1274 HP0751 HP0410 HP192	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin B (filaB) flagellin (filaB) flagellin (filaC) pratiyed flagellin (filaC) polar flagellin (filaG) potative neureminyllactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility	32.3% 23.3% 98.5% 99.7% 99.8% 99.0% 32.9% 40.5% 25.5% 21.9% 24.2% 7/2.5% 9/6.2%
HP0577 methylene-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0336 glutamate-1-semialdehyde 21-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC)	32.4% 34.5% 50.2% 50.9% 60.9% 18.4% 35.1% 50.5% 33.4% 61.3% 31.7% 11.3% 42.4% 11.37.9% 44.45,7%	HP0839 HP0655 HP1671 HP0665 HP1671 HP0610 HP0922 HP0289 Murein sacc HP0330 HP0738 HP0749 HP0574 HP0549 HP0772 HP0697 HP1125 HP06937 HP1125 HP06937 HP1125 HP1125 HP0493 HP0743 HP1373	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein sulla protein a (dIA) glutamater accemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (pSP-1A) penicillin-binding protein 1A (pSP-1A) penicillin-binding protein (poprotein precu (omp18) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rotei shape-determining protein (mreB)	23.3% 334.4% 27.596 37.696 26.3% 26.3% 26.3% 26.5% 40.6% 28.5% 40.6% 36.6% 36.6% 36.6% 36.6% 36.7% 36.7% 40.6% 37.7% 40.6% 40.	HP1031 HP0753 HP0797 HP0797 HP0797 HP0684 HP0681 HP015 HP0295 HP1030 HP0907 HP1030 HP0907 HP0907 HP10410 HP1172 HP1462 HP1462 HP1462 HP1462 HP1462	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar switch protein (flink) flagellar flagellar (flink) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) flagellin (fliad) fly protein (flifty) fly protein (flifty) fly protein (fliry) flook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (fliad) putative neuraminyflactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	32.3% 23.3% 98.5% 99.7% 99.8% 99.0% 32.9% 40.5% 25.5% 21.9% 24.2% 7/2.5% 9/6.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 [hermC] glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-tRNA reductase (hemA) Oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxyden-independent coproporphyrinogen oxidase (hemN) HP0237 protoporphyrinogen didase (hemN) HP0331 protoporphyrinogen didase (hemN)	32.4% 34.5% 50.9% 50.9% 50.9% 50.5% 35.1% 60.5% 33.4% 61.13% 32.7% III 37.9% 45.7% 35.9%	HP0839 HP0656 HP1671 HP0666 HP1671 HP0610 HP0822 HP0289 HP0289 HP0380 HP0738 HP0579 HP1566 HP1126 HP0493 HP0741 HP0493 HP0743 HP1372	outer membrane protein P1 (ompP1) profloprotein diacy/glycen/ transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta and peptidoglycan amidase (adiA) glutamate racemase (glr) N-acety/muramoyl-lalanine amidase (amiA penicillin-binding protein 2 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicogho-N-acety/muramoyl-pentapeptid-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB)	23.3% j34.4% 27.5% 31.6% 27.5% 31.6% 26.3% 29.5% 29.5% 40.6% 28.5% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 50.5% 27.5% 37.7% 55.9% 37.7% 51.9% 33.6% 60.6% 40.2% 37.7% 51.9% 33.6% 60.6% 40.3% 37.7% 51.9% 33.6% 60.6% 40.3% 37.7% 51.9% 33.6% 60.6% 40.3% 37.7% 51.9% 33.6% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.3% 31.5% 60.6% 40.5% 31.5% 40.5%	HP1031 HP0753 HP0327 HP0797 HP0797 HP0601 HP0115 HP0605 HP1575 HP1030 HP1575 HP1030 HP0907 HP1274 HP0907 HP1274 HP0410 HP0410 HP1462 HP04232 CELLULAR	flagellar protein (flis) flagellar protein (flisd) flagellar sheath adhesin hpaA flagellar switch protein (flink) flagellar switch protein (flink) flagellin B (flasl) protein (flist) fly protein (flist) fly protein (flist) fly protein (flist) protein (flist) fly protein (flist) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility	32.3% 23.3% 98.5% 99.7% 99.8% 99.0% 32.9% 40.5% 25.5% 21.9% 24.2% 7/2.5% 9/6.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0336 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0331 protoporphyrinogen oxidase (hemS)	32.4% 34.5% 50.9% 6 50.5% 50.5% 6 50.5% 50.5% 6 50.5% 33.4% 6 61.3% 32.7% 1 11.37.9% 45.7% 35.9% 46.3% 6	HP0839 HP0955 HP1571 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0380 HP0772 HP0549 HP0772 HP0597 HP1125 HP1125 HP0493 HP1373 HP1373 HP1373 HP1373	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein amidase D-alanine:D-alanine ligase A (ddIA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 2 (pbp2) penicollin-binding protein 2 (pbp2) penicollin-binding protein 2 (pbp2) penicollin-binding protein 2 (pbp2) prospho-N-acetylmuramoyl-pentapeptide-transferase (mra*) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transflycosylase (slt)	23.3% 134.4% 27.5% 318.4 318.4 318.4 318.4 318.4 318.5 218.5% 26.3% 28.5% 28.5% 40.6% 26.3% 40.6% 28.5% 31.5	HP1031 HP0753 HP0797 HP0797 HP0797 HP0684 HP0681 HP015 HP0295 HP1030 HP0907 HP1030 HP0907 HP0907 HP10410 HP1172 HP1462 HP1462 HP1462 HP1462 HP1462	flagellar protein (flis) flagellar protein (flisd) flagellar sheath adhesin hpaA flagellar switch protein (flisd) flagellar switch protein (flist) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B (flaG) flagellin flagellin g (flaG) protein (flnB) fly protein (flnB) fly protein (flnB) fly protein (flnB) protein (flaG) polar flagellin (flaG) polar flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES	32.3% 23.3% 98.5% 99.7% 99.8% 99.0% 32.9% 40.5% 25.5% 21.9% 24.2% 7/2.5% 9/6.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 [ferrochelatase (hemH)] HP0239 [lutamate-1-semialdehyde 2,1-aminomutas (hemL)] HP0239 [sutamyl-tRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) oxygen-independent coproporphyrinogen oxidase (hemN) HP1261 oxygen-independent coproporphyrinogen oxidase (hemN) profipobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen lili cosynthase (hemE)	32.4% 34.5% 50.9% 60.9% 60.9% 35.1% 60.5% 33.4% e 61.3% 32.7% III 32.7% III 37.9% 45.7% 35.9% 46.3% 27.6%	HP0839 HP0955 HP1571 HP0655 HP1571 HP0610 HP0922 HP0289 Murein sacc HP0380 HP0772 HP0549 HP0772 HP0597 HP1125 HP1125 HP0493 HP1373 HP1373 HP1373 HP1373	outer membrane protein P1 (ompP1) profloprotein diacy/glycen/ transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta and peptidoglycan amidase (adiA) glutamate racemase (glr) N-acety/muramoyl-lalanine amidase (amiA penicillin-binding protein 2 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicogho-N-acety/muramoyl-pentapeptid-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB)	23.3% j34.4% j34.4% j34.4% j34.4% j34.4% j34.4% j37.6% j46.2% j36.6% j46.6% j46	HP1031 HP0753 HP0327 HP0397 HP0397 HP0584 HP06801 HP0295 HP1575 HP10295 HP1576 HP1030 HP0907 HP1924 HP0410 HP1924 HP1462 HP1462 HP1462 HP1462 HP1462 HP0410 General	flagellar protein (flis) flagellar protein (flisd) flagellar sheath adhesin hpaA flagellar switch protein (flisd) flagellar switch protein (flist) flagellar switch protein (flist) flagellar A (flaA) flagellar B (flaB) flagellar B (hab) flagellar B (hab) flagellar B (hab) flagellar B (hab) flagellar protein (flaB) flagellar protein (flaB) polar flagellar protein (flAB) polar flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility escreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV)	32.3% 98.5% 39.7% 99.8% 99.9% 99.9% 40.5% 29.3% 21.9% 24.2% 772.5% 99.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0283 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0366 ferrochelatase (hemH) HP0367 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP02381 protoporphyrinogen oxidase (hemB) HP0236 uroporphyrinogen deamosylase (hemE) HP0247 uroporphyrinogen decarboxylase (hemE) HP0248 uroporphyrinogen decarboxylase (hemE) HP0269 Menaeuinone and ubiquinone	32.4% 34.5% 50.9% 6 50.9% 6 60.9% 6 60.5% 6 50.5% 6 50.5% 6 33.4% 6 61.3% 32.7% 1 11 42.4% 1 11 37.9% 45.7% 59.9% 46.3% 27.6% 6	HP0839 HP0855 HP16571 HP0655 HP1571 HP0610 HP0922 HP0322 HP0329 Murein sacx HP0830 HP0738 HP0549 HP0772 HP0549 HP0772 HP1665 HP1125 HP0433 HP0743 HP1373 HP1373 HP1373 HP1374 HP1645 HP0645 HP1373	outer membrane protein P1 (ompP1) profloprotein diacylglyceny transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gf) N-acetylmuramoyl-t-alanine amidase (amiA penicillin-binding protein 1 A (PBP-1A) penicillin-bind	23.3% j34.4% j34.4% j34.4% j34.4% j34.4% j34.4% j34.6% j34.6% j36.6% j36.6% j36.6% j36.6% j36.6% j37.7% j36.6% j37.7% j36.6% j37.7% j38.6% j38	HP1031 HP0353 HP0327 HP0327 HP0654 HP06601 HP0654 HP06601 HP0155 HP0235 HP1030 HP10307 HP10307 HP0237 HP0410 HP1462 HP0410 HP1462 HP0410 HP1462 HP0410 HP1462 HP0410 HP1463 HP0410 HP1463 HP0410 HP1463 HP0410 HP1463 HP0410 HP1463 HP0410 HP1463 HP0410 HP1463 HP1663 HP1463 HP166	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin A (filaA) flagellin B (filaB) flagellin B homologue (flaB) flagellin (filaB) flip protein (filt) flip protein (filt) flook assembly protein, flagella (figD) paralysed flagella protein (pfIA) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	32.3% 32.3% 98.5% 39.7% 99.8% 99.0% 39.7% 99.0% 40.5% 40
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-tRNA reductase (hemA) MP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP1261 profopolingen deaminase (hemC) HP0331 profopolingen deaminase (hemC) HP0361 uroporphyrinogen deachoxylase (hemE) HP1264 uroporphyrinogen didase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase	32.4% 34.5% 50.9% 6 50.9% 6 60.9% 6 60.5% 6 50.5% 6 50.5% 6 50.5% 6 33.4% 6 61.3% 6 32.7% 1 11 42.4% 1 11 37.9% 45.7% 59.9% 46.3% 6 27.6% 6	HP0839 HP0955 HP0965 HP0965 HP067 HP0321 HP0321 HP0289 HP0289 HP038 HP0772 HP0587 HP1125 HP0493 HP1373 HP1373 HP1373 HP1373 HP1374 HP1374 HP1374 HP1374 HP1374 HP1375 HP13	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane protein protein dipartition oxin-like outer membrane protein protein protein protein protein protein (mida protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp) phospho-N-acetylmuramoyl-pentapeptide-transferase (mrxY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-like protein protein (mreB) toxin-like dipen (mraB) toxin-like dipen (mraB) toxin-like dipen (mraB) transferase, peptidoglycan synthesis (murG)	23.3% 1334.4% 27.5% 27.5% 27.5% 27.5% 27.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 28.5% 29.5% 27.5% 28.5% 29.5% 27.5% 28.5% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 28.2% 29.5% 27.2% 28.2% 29.5% 27.5% 28.2% 29.5% 27.5% 29.5	HP1031 HP0327 HP0327 HP0397 HP0597 HP0597 HP0598 HP0596 HP1576 HP10296 HP1576 HP1030 HP0907 HP1192 HP0410 HP1192 HP0410 HP1192 HP04232 CELLULAR General HP0039 HP0039 HP0039 HP0039 HP0039 HP0039	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin (flaG) fly protein (flify) flook assembly protein, flagella (flgD) paralysed flagellar protein (pflA) polar flagellin (flaG) polar flagellin (flaG) patative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	32.3% 23.3% 98.5% 98.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 29.5% 25.5% 22.3% 25.5% 22.3% 25.5% 23.9% 21.9% 24.2% 772.5% 99.2% 26.8% 31.7% 27.9% 26.8% 31.7% 27.9%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folD) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0336 ferrochelatase (hemH) glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1260 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0240 uroporphyrinogen decarboxylase (hemE) HP0360 4-hydroxybenzoate octaprenyltransferase (ubiA)	32.4% 34.5% 50.2% 50.9% 60.9% 48.4% 35.1% 50.5% 33.4% 6 61.3% 32.7% 11.3% 42.4% 11.37.9% 44.57% 35.9% 44.9% 11.37.9% 44.57% 27.6% 26.6%	HP0839 HP0965 HP0965 HP10610 HP0922 HP0289 Murein sacc HP0830 HP0772 HP0587 HP0772 HP0597 HP1125 HP0493 HP0743 HP1373 HP1373 HP1373 HP1373 HP1373 HP1374 HP1565 HP1543	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta amidase (amidase D-alanine:D-alanine ligase A (ddlA) gilutamate racemase (girl) N-acetylmuramoyl-Jalanine amidase (amidapenicillin-binding protein 1 A (PSP-1A) penicillin-binding protein (pppp) priospho-N-acetylmuramoyl-pentapeptide-transferase (mary) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) tox-Ractivated gene (tagE) transferase, peptidoglycan synthesis (murd)	23.3% j34.4% j34.4% j34.4% j34.4% j34.4% j37.5% j37.6% j36.5% j36.6% j37.7% j36.7% j36.7% j36.6% j36.7% j36.6% j36	HP1031 HP0753 HP0327 HP0327 HP0684 HP0601 HP0615 HP0015 HP1015 HP10295 HP1030 HP1030 HP0274 HP0751 HP0410 HP1192 HP1462 HP0410 HP1033 HP0033 HP0033 HP0033 HP0033 HP0031 HP1031 H	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin A (filaA) flagellin B (filaB) flagellin B homologue (fla) flibB protein (filtS) fliV protein (filtS) fliV protein (filtS) flook assembly protein, flagella (figD) paralysed flagella protein (filaA) polar flagellin (filaC) putative neuraminyllactose-binding haemagglutnin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV)	32.3% 23.3% 98.5% 98.5% 99.6% 99.9% 40.5% 22.3% 22.3% 22.3% 21.9% 24.2% 772.5% 99.2% 24.2% 31.7% 31.7% 99.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-tRNA reductase (hemA) MP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP1267 portpobliniogen deaminase (hemC) HP0381 protpoorphyrinogen deaminase (hemC) HP0381 uroporphyrinogen dearboxylase (hemE) HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0929 geranytransferase (ispA)	32.4% 34.5% 35.2% 50.9% 9 148.4% 35.1% 9 15.3%	HP0839 HP0955 HP09655 HP09655 HP06656 HP0610 HP0289 Murein sacc HP0289 HP0378 HP0378 HP0579 HP1565 HP0743 HP1373 HP1373 HP1373 HP1373 HP1373 HP1374 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1647 H	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane protein protein discription of the protein discription of the protein discription of protein protein protein protein protein protein (mpB) protein protein dispendentermining protein (mreB) rod shape-determining protein (mreB) rod shape-determi	23.3% 334.4% 27.5% 37.6% 26.3% 28.5% 28.5% 40.6% 28.5% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 35.0% 35.0% 35.0% 35.0% 35.2%	HP1031 HP0753 HP0327 HP0584 HP06801 HP0681 HP0681 HP0381 HP0381 HP1375 HP1300 HP19274 HP0410 HP1922 HP1482 CELLULAR General HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP19393 HP0393 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellin A (filaA) flagellin B (filaB) flagellin B (filaB) flagellin (filaB) flagellin flagellin (filaG) poralysed flagellar protein (finB) polar flagellin (filaG) polar flagellin (filaG) patative neureminyllactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV)	32.3% 23.3% 98.5% 39.7% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 29.5% 22.9% 25.5% 23.9% 21.9% 24.2% 772.5% 26.5% 99.2% 26.6% 99.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 [ferrochelatase (hemH)] HP0239 glutamyt-HRNA reductase (hemA) HP0239 glutamyt-HRNA reductase (hemA) HP0260 oxygen-independent coproporphyrinogen oxidase (hemN) HP1260 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 proftpoliniogen deaminase (hemC) HP0381 protoporphyrinogen didase (hemE) HP0604 uroporphyrinogen didase (hemE) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0290 octaprenyltransferase (spB)	32.4% 34.5% 55.2% 50.9% 48.4% 35.1% 50.5% 33.4% 8 11.3% 32.7% 11.3% 42.4% 11.3% 45.7% 45.7% 46.3% 27.6% 26.6% 39.8% 31.6%	HP0839 HP0965 HP0965 HP0665 HP06610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0573 HP0573 HP0665 HP0743 HP0743 HP1372 HP0493 HP1372 HP0645 HP1372 HP0645 HP1372 HP0645 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP	outer membrane protein P1 (ompP1) profloprotein diacylglyceny transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta and peptidoglycan protein outer protein (amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gri) N-acetylmuramoyl-Jeanidase (amidapenicillin-binding protein 1 A (PBP-1A) penicillin-binding protein 1 A (PBP-1A) penicillin-binding protein 1 A (PBP-1A) penicillin-binding protein (pppp) priosopho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-tripeptide synthetase (murF)	23.3% j34.4% j34.4% j34.4% j34.4% j34.4% j34.4% j34.6% j34.6% j36.6% j36	HP1031 HP0753 HP0327 HP0397 HP0584 HP0801 HP0115 HP0156 HP1675 HP1675 HP1675 HP1675 HP0292 CELLULAR General/ HP0319 HP0333 HP0333 HP067 HP067 HP067 HP067 HP1067 HP1067 HP1067 HP1067 HP1068	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (filiN) flagellin A (filaA) flagellin A (filaA) flagellin B (filaB) flagellin B homologue (flaB) flagellin B flagellin (filaB) flagellin (filaB) flix protein (filx) flook assembly protein, flagella (figD) paralysed flagella protein (pfIA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) flagelling protein (era) haemolysin flagenosyin (fily)	32.3% 23.3% 98.5% 98.5% 99.6% 99.9% 40.5% 22.3% 22.3% 22.3% 21.9% 24.2% 772.5% 99.2% 24.2% 31.7% 31.7% 99.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) HP0239 glutamyl-IRNA reductase (hemA) HP0239 coxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphoblinogen deaminase (hemC) HP0237 porphoblinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0381 uroporphyrinogen decarboxylase (hemE) HP124 uroporphyrinogen decarboxylase (hemD) Managuinone and ubiquinone HP1360 4hydroxyberzoate octaprenyltransferase (ubiA) HP0239 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB)	32.4% 34.5% 55.2% 50.9% 48.4% 35.1% 50.5% 33.4% 8 11.3% 32.7% 11.3% 42.4% 11.3% 45.7% 45.7% 46.3% 27.6% 26.6% 39.8% 31.6%	HP0839 HP0955 HP09655 HP09655 HP06656 HP0610 HP0289 Murein sacc HP0289 HP0378 HP0378 HP0579 HP1565 HP0743 HP1373 HP1373 HP1373 HP1373 HP1373 HP1374 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1647 H	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like oxin-lik	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 35.0% 42.6% 45.2% 35.0% 32.2% 37.7% 51.9% 32.2% 37.2% 37.2% 37.2% 37.2% 37.2% 37.2% 37.2% 38.0%	HP1031 HP0753 HP0327 HP0584 HP06801 HP0681 HP0681 HP0381 HP0381 HP1375 HP1300 HP19274 HP0410 HP1922 HP1482 CELLULAR General HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP0393 HP19393 HP0393 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939 HP1939	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar sheith protein (filiN) flagellin A (filaA) flagellin A (filaA) flagellin A (filaA) flagellin B homologue (fla) flispellin B homologue (fla) flisperin (filiY) Hook assembly protein, flagella (flgD) prarlysed flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) secreted protein involved in flagellar motility s	32.3% 23.3% 98.5% 99.5% 99.5% 99.5% 99.5% 99.0% 32.9% 40.5% 22.9% 22.3% 22.5% 22.5% 23.5% 23.5% 23.5% 23.5% 24.2% 77.2.5% 99.2% 24.2% 77.2.5% 99.2% 24.2% 99.2% 99.2% 26.8% 31.7% 31.7% 31.279% 99.2% 40.2% 40.2% 40.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 [ferrochelatase (hemH)] HP0239 [lutamate-1-semialdehyde 2,1-aminomutas (hemL)] HP0239 [sutamyl-tRNA reductase (hemA)] HP0269 coxygen-independent coproporphyrinogen oxidase (hemN) HP1260 coxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0804 uroporphyrinogen III cosynthase (hemD) Menaquinone and ubiquinone HP1380 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0404 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis	32.4% 34.5% 55.2% 50.9% 48.4% 35.1% 50.5% 33.4% 6 61.3% 32.7% 1111 42.4% 1111 47.4% 1111 37.9% 46.3% 27.6% 26.6% 39.8% 31.6%	HP0839 HP0965 HP0965 HP0665 HP06610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0573 HP0573 HP0665 HP0743 HP0743 HP1372 HP0645 HP1372 HP0645 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1546 HP1544 HP1546 HP156 HP15	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dusta and peptidoglycan protein outer protein formed prenicilini-brinding protein 2 (pbp2) penicililin-brinding protein 12 (pbp2) penicililin-brinding protein 12 (pbp2) penicililin-brinding protein 12 (pbp2) penicililin-brinding protein (pppp) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE)	23.3% j34.4% j31.4% j31.4% j31.4% j31.4% j31.6% j31	HP1031 HP0753 HP0327 HP07597 HP0584 HP0801 HP0115 HP0295 HP1575 HP1274 HP0307 HP1274 HP0307 HP1274 HP0410 HP1192 HP0232 CELLULAR General HP031 HP0333 HP0333 HP067 HP067 HP1067 HP1067 HP1069 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (flis) flagellar switch protein (flis) flagellin A (flaA) flagellin B (flaB) flagellin B flagellin B flaB flagellin B homologue (fla flisB protein (flis) fliy protein (flis') flook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) flagellar protein (reh) flagellar protein (ren) flagellar prote	32.3% 23.3% 98.5% 99.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 detta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP0269 oxygen-independent coproporphyrinogen oxidase (hemN) HP0279 porphoblinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0381 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdopterin HP0788 protein A (moaA)	32.4% 34.5% 55.2% 50.9% 148.4% 345.7% 150.5% 33.4% 189.5% 150.5% 32.7% 189.5% 1	HP0839 HP0965 HP0965 HP0665 HP06610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0573 HP0573 HP0665 HP0743 HP0743 HP1372 HP0493 HP1372 HP0645 HP1372 HP0645 HP1372 HP0645 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP165 HP1646 HP	outer membrane protein P1 (ompP1) profiloprotein diacylglyceny transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 30.6% 30.7% 35.0%	HP1031 HP0753 HP0327 HP0327 HP0584 HP0601 HP0105 HP1050 HP1050 HP10575 HP10575 HP10575 HP00751 HP0410 HP0410 HP1122 HP1462 HP0410 HP1039 HP0639 HP0639 HP0686 HP1086 HP1086 HP1086 HP1086 HP1086 HP1089 HP1086 HP1089	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar sheith protein (filiN) flagellin A (filaA) flagellin A (filaB) flagellin B (filaB) flagellin (filaC) polar flagellin molility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) flagellin	32.3% 23.3% 98.5% 98.5% 98.5% 99.8% 99.8% 99.9% 40.5% 23.9% 40.5% 22.9% 42.5% 25.5% 22.9% 22.9% 24.2% 23.9% 27.25% 27.9% 27.25% 99.2% 24.2% 99.2% 24.2% 40.2
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0306 [ferrochelatase (hemH)] HP0239 [lutamate-1-semialdehyde 2,1-aminomutas (hemL)] HP0239 [sutamyl-tRNA reductase (hemA)] HP0269 coxygen-independent coproporphyrinogen oxidase (hemN) HP1260 coxygen-independent coproporphyrinogen oxidase (hemN) HP0237 profipobiliniogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0804 uroporphyrinogen III cosynthase (hemD) Menaquinone and ubiquinone HP1380 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis	32.4% 34.5% 55.2% 50.9% 148.4% 345.7% 150.5% 33.4% 189.5% 150.5% 32.7% 189.5% 1	HP0839 HP0965 HP0965 HP0665 HP0665 HP0628 HP0289 Murein sacc HP0830 HP0738 HP0578 HP0578 HP0577 HP1666 HP0743 HP0743 HP1372 HP0648 HP1372 HP0648 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1658 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1546 HP156	outer membrane protein P1 (ompP1) profipoprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein toxin-like outer membrane grotein toxin-like outer membrane grotein toxin-like outer membrane grotein lipa protein lipa protein lipa protein lipa protein protein (omp18) membrane grotein protein (omp18) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) sof shape-determining protein (mreB) toxin-like lipa grotein synthesis (murG) (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE)	23.3% j 334.4% j 27.5% j 37.6% j 26.3% j 26.5% j 40.6% j 30.6% j 40.6% j 36.6% j	HP1031 HP0753 HP0327 HP07597 HP0584 HP0691 HP0115 HP0295 HP10575 HP1274 HP0397 HP1274 HP0397 HP0232 CELLULAR General HP0393 HP039 HP0393 HP039 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (flis) flagellar switch protein (flis) flagellin A (flaA) flagellin B (flaB) flagellin B flagellin B flaB flagellin B homologue (fla flisB protein (flis) fliy protein (flis) fliy protein (flist) flook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagolutinin homologue (hpaA) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) flaemolysin protein (reh) flaemolysin (fly) haemolysin secretion protein precursor (ryfB) histdine kinase (cheA) methy-faceopting chemotaxis protein (flpA)	32.3% 23.3% 98.5% 99.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0336 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 porphobilnogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0230 carphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP0380 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (moaC)	32.4% 34.5% 55.2% 55.9% 50.9% 48.4% 35.1% 50.5% 33.4% 61.3% 32.7% 11.37.9% 44.5.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.6% 31.4% 1 C 97.9%	HP0839 HP0965 HP0965 HP0665 HP06610 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0573 HP0573 HP0665 HP0743 HP0743 HP1372 HP0645 HP1372 HP0645 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1546 HP1544 HP1546 HP156 HP15	outer membrane protein P1 (ompP1) profiloprotein diacylglycery transferase (Igt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like outer membrane (gir) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein (1 (PBP-1	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0%	HP1031 HP0753 HP0327 HP0327 HP0584 HP0601 HP0105 HP1050 HP	flagellar protein (fils) flagellar protein (fils) flagellar sheath adhesin hpaA flagellar protein (fifs) polar flagellin (flaG) polar flagellar protein (fpfA) polar flagellar protein (fpfA) polar flagellar motility secreted protein involved in flagellar motility chemotaxis protein (cheV) flagellar flagellar flagellar flagellar motility flagellar motility flagellar flagellar flagellar motility flagellar flagellar flagellar motility flagellar fla	32.3% 23.3% 98.5% 99.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0336 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 porphobilnogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0230 carphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP0380 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (moaC)	32.4% 34.5% 35.2% 50.9% \$1.4% \$2.4% \$3.4% \$3.4% \$3.4% \$3.2.7% \$3.4% \$4.5.7% \$3.2.7% \$3.5.9% \$4.5.7% \$3.5.9% \$4.5.7% \$3.5.9% \$4.6.3% \$2.7.6% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9% \$3.6.9%	HP0839 HP09656 HP09656 HP09656 HP09676 HP0922 HP0289 Murein sacc HP0830 HP0738 HP0578 HP0577 HP1666 HP0743 HP0743 HP1372 HP0648 HP1372 HP0645 HP1444 HP1418 HP0740 HP1494 HP149 H	outer membrane protein P1 (ompP1) profipoprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein subus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (girl) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (pppp) protein procu (omp18) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE)	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0%	HP1031 HP0753 HP0327 HP07597 HP0584 HP0691 HP0115 HP0295 HP10575 HP1274 HP0397 HP1274 HP0397 HP0232 CELLULAR General HP0393 HP039 HP0393 HP039 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (flis) flagellar switch protein (flis) flagellin A (flaA) flagellin B (flaB) flagellin B flagellin B flaB flagellin B homologue (fla) flibB protein (flis) fliV protein (flis) fliV protein (flis) fliv protein (flis) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility processes chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) flagellin fligellin fligel	32.3% 23.3% 98.5% 99.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0293 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-t-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-tRNA reductase (hemA) HP0239 glutamyl-tRNA reductase (hemA) HP0239 glutamyl-tRNA reductase (hemA) HP0237 porphobilinogen deaminase (hemC) protoporphyrinogen deaminase (hemC) protoporphyrinogen deaminase (hemE) HP0371 porphobilinogen deaminase (hemE) HP0404 uroporphyrinogen diecarboxylses (hemE) HP0405 uroporphyrinogen ill cosynthase (hemE) HP0406 deaminase deaminase (hemE) HP0407 geranytranstransferase (ispA) Octaprenyl-diphosphate synthase (ispB) Molybdotpterin HP0788 molybdenum cofactor biosynthesis protein (moaC) HP0120 molybdopterin biosynthesis protein (moaC)	32.4% 34.5% 50.5% 50.9% 51.3% 33.4% 65.1% 65.1% 33.4% 65.13% 32.7% 111111111111111111111111111111111111	HP0839 HP0965 HP0965 HP0665 HP0665 HP0628 HP0289 Murein sacc HP0830 HP0738 HP0578 HP0578 HP0577 HP1666 HP0743 HP0743 HP1372 HP0648 HP1372 HP0648 HP1373 HP1544 HP1544 HP1544 HP1544 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1658 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1544 HP1545 HP1546 HP156	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (Igt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane (gri) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1 (PSP-1A) penicillin-binding protein 1 (PSP-1A) penicillin-binding protein 1 (PSP-1A) penicillin-binding protein 1 (PSP-1A) penicillin-binding protein (pppprotein procu (omp18) prospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murC) UDP-MurNac-tripeptide synthetase (murE) UDP-Nacetyliocosamine enolopyruvyl transferase (murZ) UDP-Nacetylinuramate-alanine ligase (murC) UDP-Nacetylinuramate-alanine ligase (murC) UDP-Nacetylinuramoylalanine-D-glutamate	23.3% 334.4% 27.5% 37.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 37.7%	HP1031 HP0783 HP0327 HP0327 HP0584 HP0601 HP0105 HP10576 HP10576 HP10576 HP10576 HP00751 HP0410 HP0410 HP1224 HP0410 HP1032 HP10616 HP1039 HP0681 HP0681 HP1088 HP0681 HP1088 HP0681 HP1088 HP1088 HP0689	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch portein (fliiN) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaG) polar flagellin mologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motilit	32.3% 23.3% 98.5% 98.5% 98.5% 99.5% 99.5% 99.5% 99.0% 32.9% 40.5% 23.3% 22.9% 40.5% 23.3% 23.5% 24.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0336 glutamate-1-semialdehyde 21-aminomutas (hemB) HP0337 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 porphobilnogen deaminase (hemC) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0331 porphobilnogen deaminase (hemC) HP0331 protoporphyrinogen oxidase (hemN) HP0331 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterini HP0788 molybdopterini blosynthesis protein (moaC) HP0172 molybdopterin blosynthesis protein (moaC) HP0775 molybdopterin blosynthesis protein (moaC)	32.4% 34.5% 55.2% 55.2% 55.9% 3.1% 50.5% 33.4% 6.13% 33.4% 6.13% 32.7% 1111 42.4% 1111 37.9% 45.7% 35.9% 46.3% 27.6% 31.6% 31.6% 31.4% 0 C 97.9% 31.6% 31.4% 0 C 97.9% 31.4% 0 C 97.9% 31.6% 50.8%	HP0839 HP09656 HP09656 HP09656 HP09656 HP09670 HP0829 Murein sacc HP0829 HP0289 HP0722 HP0289 HP0722 HP0837 HP0737 HP0749 HP0125 HP0493 HP0743 HP0742 HP0493 HP0744 HP1474 HP0494 HP1474 HP0484 HP0740 HP1494 HP1478 HP0648 HP0648 HP0648	outer membrane protein P1 (ompP1) profipoprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (rjpA) toxin-like outer membrane protein butus and peptidoglycan amidase D-telanineD-alanine ligase A (ddlA) glutamate racemase (gr) Nacetylmuramoyl-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 2 (pbp2) peptidoglycan associated lipoprotein precu (omp18) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (lagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murC) UDP-MurNac-tripeptide synthe	23.3% 1334.4% 27.5% 27.5% 27.5% 28.2% 28.2% 28.2% 29.5% 28.2% 29.5% 28.2% 29.5	HP1031 HP0783 HP0327 HP0787 HP0584 HP0801 HP0115 HP0801 HP1015 HP0295 HP1575 HP10751 HP0410 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellar switch protein (fliN) flagellin B flagellar protein (flagellar protein (flagellar motifity secreted protein involved in flagellar motifity secreted pro	32.3% 23.3% 98.5% 99.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-tRNA reductase (hemA) MP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0381 porphobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemK) HP0404 uroporphyrinogen decarboxylase (hemE) Menaquinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdotperin HP0788 molybdenum cofactor biosynthesis protein (moeC) HP0795 molybdopterin biosynthesis protein (moeC) HP0795 molybdopterin biosynthesis protein (moeA) HP0801 molybdopterin biosynthesis protein (moeA) HP0801 molybdopterin ocnverting factor, subunit 1 (moaD)	32.4% 34.5% 55.2% 50.9% 48.4% 35.1% 50.5% 50.5% 33.4% 6 51.3% 32.7% 11 42.4% 11 37.9% 45.7% 50.9% 46.3% 31.6% 31.4% 22.6% 30.8% 31.6% 31.4% 31.4% 31.4% 31.4% 31.5% 31.4% 31.5%	HP0839 HP0965 HP0965 HP0965 HP0965 HP0967 HP097	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein surface of the control of	23.3% j34.4% 27.5% 31.2% 31.2% 32.2% 31.2% 32.2% 31.2% 32.2%	HP1031 HP0753 HP0327 HP0327 HP0584 HP0397 HP0584 HP0601 HP0115 HP0295 HP1576 HP1576 HP1576 HP1576 HP1930 HP0907 HP1930 HP0907 HP0410 HP1192 HP1462 HP0410 HP1933 HP0619 HP0393 HP0619 HP10393 HP0619 HP10393 HP0619 HP10393 HP1069 HP108 HP108	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (fliin) flagellar switch protein (fliin) flagellar skitch protein (fliin) flagellar flagellar fligellar flagellar fligellar flagellar fligellar flagellar fligellar flagellar fligellar flagellar fligellar protein (flix) hoka sasembly protein, flagellar (flgD) paralysed flagellar protein (flqA) polar flagellin (flaG) polar flagellin (flaG) potative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagelar motility secreted protein involved in flagelar motility carected protein involved in flagelar motility PROCESSES chemotaxis protein (cheV) haemolysin flagellar heamolysin (fly) haemolysin secretion protein precursor (hylB) histidine kinase (cheA) methyl-accepting chemotaxis protein (tlpA) methyl-accepting chemotaxis transducer (flyC) purine-binding chemotaxis protein (cheW)	32.3% 23.3% 98.5% 39.7% 98.5% 39.7% 99.5% 39.7% 99.8% 99.9% 32.9% 40.5% 29.3% 22.5.5% 22.9% 40.5% 29.9% 27.2% 56.5% 32.2% 42.2% 27.25% 99.2% 26.6% 31.7% 59.2% 42.
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0366 ferrochelatase (hemH) HP0367 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0368 oxygen-independent coproporphyrinogen oxidase (hemN) HP0268 oxygen-independent coproporphyrinogen oxidase (hemN) HP1260 oxygen-independent coproporphyrinogen oxidase (hemN) HP0267 porthobilinogen deaminase (hemC) HP0381 prothoporphyrinogen oxidase (hemB) HP0381 uroporphyrinogen decarboxylase (hemB) HP1224 uroporphyrinogen decarboxylase (hemB) HP1360 4-hydroxybenzoate octaprenyltransferase (ublA) HP0929 geranyltranstransferase (ispA) HP0381 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdopterin biosynthesis protein (moaC) HP0172 molybdopterin biosynthesis protein (moaC) HP0799 molybdopterin biosynthesis protein (moaC) HP0810 molybdopterin oonverting factor, subunit 2 (moaD) HP0800 molybdopterin converting factor, subunit 2 (molphopterin converting factor, subunit 2 (molphop	32.4% 34.5% 50.2% 50.9% 1 8.48.4% 35.1% 50.5% 33.4% 6 61.3% 32.7% 1111 42.4% 1111 37.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.6% 31.4% C 29.79% 31.4% C 31.4%	HP0839 HP0965 HP0965 HP0965 HP0965 HP0967 HP097 HP097 HP097 HP0987 HP0988	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane (grote) litansierase (grote) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (23.3% 334.4% 27.5% 37.6% 26.3% 28.5% 28.5% 28.5% 40.6% 28.5% 40.6% 28.5% 30.6% 40.6% 33.7% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.2% 35.3%	HP1031 HP0783 HP0327 HP0787 HP0584 HP0601 HP0115 HP0601 HP1015 HP0295 HP1575 HP10751 HP0407 HP0407 HP0407 HP0409 HP040 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellar switch protein (fliN) flagellar switch protein (fliN) flagellin A (flaA) flagellin B flagellar flagellin B flagellar flagellin B homologue (fla flagellin B homologue (fla flagellin B flagellar flagellar flagellar floot assembly protein, flagellar (flgD) paralysed flagellar protein (pflA) polar flagellar (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein (flaC) putal motility secreted protein involved in flagellar motility secreted protein involved in flagell	32.3% 32.3% 98.5% 99.5% 39.7% 99.5% 99.5% 32.9% 40.5% 29.3% 22.9% 40.5% 23.3% 22.55% 23.3% 22.55% 23.3% 25.55% 23.9% 21.9% 29.5% 20.5% 23.9% 21.9% 29.5% 20.5% 23.9% 21.9% 29.5% 20.
HP0577 methyleine-tetrahydrofolate dehydrogenase (foliD) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0369 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0376 savgen-independent coproporphyrinogen oxidase (hemN) HP0239 glutamyl-tRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP0381 profhoblinogen deaminase (hemC) HP0381 uroporphyrinogen deachoxylase (hemE) HP0404 uroporphyrinogen deachoxylase (hemD) Menaquinone and ubiquinone HP1360 d-hydroxyberzoate octaprenyltransferase (ubiA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdotperin molybdenum cofactor biosynthesis protein (moeC) HP0775 molybdopterin biosynthesis protein (moeC) HP0785 molybdopterin biosynthesis protein (moeC) HP0801 molybdopterin converting factor, subunit 1 (moaD) HP0800 molybdopterin converting factor, subunit 2 (moaE)	32.4% 34.5% 35.2% 50.9% 48.4% 35.1% 50.5% 50.5% 33.4% 8 50.5% 32.7% 11 42.4% 11 37.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.6% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4% 31.4%	HP0839 HP0965 HP0965 HP0965 HP0965 HP0967 HP0810 HP0972 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0738 HP0772 HP0649 HP0740 HP0649 HP0743 HP157 HP1665 HP1125 HP0494 HP0740 HP1494 HP1418 HP0740 HP0648 HP0623 HP0648 HP06494 Surface poly	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dividus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein (rippprotein procu (omp18) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-M-acetylenolpyruxoylglucosamine enolpyruxyl transferase (murE) UDP-M-acetylmuramoylalanine-D-glutamate ligase (murD) UDP-M-acetylmuramoylalanine-D-glutamate ligase (murD) saccharides, lipopolysaccharides and antig 3-deoxyd-manno-octulosonic acid 8-phospi synthetase (KdsA)	23.3% j34.4% 27.5% 37.6% 40.6% 26.3% 29.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 30.6% 40.6% 28.5% 30.7% 35.0% 50.6% 50.6% 20.6% 20.6% 30.6% 40.6% 20.6% 30.6% 40.6% 30.6% 40.6% 30.6%	HP1031 HP0753 HP0327 HP0327 HP0584 HP0397 HP0686 HP1057 HP0691 HP1015 HP0295 HP1576 HP1030 HP19097 HP1930 HP0907 HP1924 HP0751 HP0410 HP1928 HP1462 HP1462 HP1462 HP0393 HP0697 HP0393 HP0697 HP1097 HP1099 HP109 HP10 HP10 HP10 HP10 HP10 HP10 HP10 HP10	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (flit) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaG) poralysed flagella protein (flAI) polar flagellin (flaG) potative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemotysin protein protein precursor (ry/B) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis transducer (flpC) purine-binding chemotaxis protein (fleW) cell division inhibitor (minD) cell division inhibitor (minD)	32.3% 23.3% 98.5% 39.7% 98.5% 39.7% 99.5% 39.7% 99.5% 29.3% 29.6% 29.3% 22.9% 40.5% 29.3% 22.5.5% 23.9% 21.9
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0366 ferrochelatase (hemH) HP0367 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0368 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0269 oxygen-independent coproporphyrinogen oxidase (hemN) HP1260 oxygen-independent coproporphyrinogen oxidase (hemN) HP0261 profoporphyrinogen oxidase (hemC) HP0381 profoporphyrinogen oxidase (hemE) HP0381 uroporphyrinogen decarboxylase (hemE) HP1264 uroporphyrinogen decarboxylase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (bibA) HP0929 geranyltranstransferase (spA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdenum cofactor biosynthesis protein (moaC) HP0172 molybdenum cofactor biosynthesis protein (moaC) HP01739 molybdopterin biosynthesis protein (moaC) HP0399 molybdopterin biosynthesis protein (moaC) HP0800 molybdopterin ocoverting factor, subunit 1 (moaC) HP0800 molybdopterin converting factor, subunit 2 (moaE) HP0800 molybdopterin converting factor, subunit 2 (moaE) HP0800 molybdopterin converting factor, subunit 2 (moaE)	32.4% 34.5% 50.2% 50.5% 60.9% 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	HP0839 HP0965 HP0965 HP0965 HP0965 HP0965 HP0969 Murein sacc HP0329 HP0329 HP0328 HP0328 HP0328 HP0738 HP0549 HP0772 HP1566 HP05772 HP1566 HP0493 HP0740 HP157 HP1564 HP157 HP1564 HP157 HP1648 HP0648 HP0653 HP0657	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like	23.3% 1334.4% 275% 37.3% 312.5% 32.2% 33.7% 34.6% 25.5% 32.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 35.6% 25.5% 37.7% 51.9% 36.6% 32.2% 37.7% 51.9% 32.5% 31.2% 31.2% 32.5% 31.2% 31.5% 28.2% 31.2% 31.5% 28.2% 31.2% 31.5% 28.2% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.7% 31.5% 25.5% 31.5% 25.5	HP1031 HP0783 HP0327 HP0787 HP0584 HP0601 HP0115 HP0601 HP1015 HP0295 HP1575 HP10751 HP0470 HP1087 HP0470 HP0487 HP0482 HP1462 HP0482 HP1462 HP0482 H	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar A (fliaA) flagellin A (fliaA) flagellin B (flaB) flagellin B (flaB) flagellin (fliaG) prarlysed flagellar protein (flagellar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) paralysed flagellar protein (fnA) polar flagellin (flaG) polar flagellin (flaG) paralysed flagellar protein (fpA) secreted protein involved in flagellar motility secreted protein (fleV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (ren) haemolysin (ty) haemolysin secretion protein proteins flagellar motility secreted protein flagellar m	32.3% 23.3% 98.5% 99.5% 99.5% 99.5% 99.5% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 40.5% 22.9% 40.5% 22.9% 24.2% 77.25% 24.2% 77.25% 99.2% 24.2% 40.5% 31.7% 32.2% 40.2% 40.2% 40.5% 31.7% 32.2% 40.2
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HP0577 methyleine-tetrahydrofolate dehydrogenase (folD) HP0230 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0336 flemante i-semialdehyde 2,1-aminomutas (hemB) HP0336 glutamyl-RNA reductase (hemA) Gygen-independent coproporphyrinogen oxidase (hemN) HP0237 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porthobilinogen deaminase (hemC) HP03381 protphobilinogen deaminase (hemC) HP03381 protphobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemB) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (bibA) HP0229 geranyltranstransferase (ispA) HP0329 geranyltranstransferase (ispA) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (mosC) HP0712 molybdopterin biosynthesis protein (mosC) HP0712 molybdopterin biosynthesis protein (mosC) HP0719 molybdopterin biosynthesis protein (mosC) HP0719 molybdopterin onoverting factor, subunit 2 (mosE) HP072 molybdopterin converting factor, subunit 2 (mosE) HP072 molybdopterin converting factor, subunit 2 (mosE) HP0730 molybdopterin converting factor, subunit 2 (mosE) HP0740 molybdopterin converting factor, subunit 2 (mosE) HP0750 molybdopterin quanine dinucleotide biosy protein A (mobA)	32.4% 34.5% 50.2% 50.9% 6 60.59% 31.4% 6 60.59% 33.4% 6 61.3% 31.79% 11 77.9% 42.4% 11 37.99% 44.57% 35.99% 46.39% 36.39% 31.6% 31.4% 6 0 0 37.99% 31.4% 6 0 0 37.99% 31.4% 6 0 0 31.4% 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	HP0839 HP0955 HP09655 HP09655 HP09655 HP09656 HP0967 HP0370 HP037	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane grotein oxin-like oxin	23.3% 1334.4% 27.5% 23.3% 1334.4% 27.5% 23.3% 13.44% 28.5% 2	HP1031 HP0783 HP0327 HP0787 HP0584 HP0601 HP0115 HP0601 HP1015 HP0285 HP1575 HP10751 HP0402 HP10751 HP0410 HP0401 HP040 HP0401 HP040 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP040 HP040 HP04	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin (flaG) prarlysed flagellar protein (flaF) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) paralysed flagellar protein (fhaA) polar flagellin (flaG) polar flagellin (flaG) polar flagellar motility secreted protein involved in flagellar motility secreted protein fla	32.3% 23.3% 98.5% 99.5% 99.5% 99.5% 99.5% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 40.5% 22.9% 40.5% 22.9% 24.2% 26.5% 24.2%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0366 letta-aminolevulinic acid dehydratase (hemB) HP0367 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 porphobilinogen deaminase (hemC) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen oxidase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0239 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdopterin ofactor biosynthesis protein HP0788 molybdopterin biosynthesis protein (moaC) HP0172 molybdopterin biosynthesis protein (moaC) HP0799 molybdopterin converting factor, subunit 1 (moaD) HP0890 molybdopterin converting factor, subunit 1 (moaB) HP0890 molybdopterin converting factor, subunit 1 (moaB) HP0890 3-methyl-2-oxobutanoate hydroxymethyltra	32.4% 34.5% 35.2% 50.9% \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	HP0839 HP0965 HP0965 HP0965 HP0965 HP0967 HP0810 HP0910 HP0928 HP0289 HP0289 HP0289 HP0738 HP0378 HP0572 HP0494 HP0772 HP0493 HP0772 HP0649 HP0772 HP1665 HP0493 HP0743 HP1373 HP1373 HP1544 HP147 HP1655 HP0648 HP0740 HP1494 HP1418 HP0648 HP0623 HP0648 HP0623 HP06494 Surface poly	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dividus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gfr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp-phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transglycosylase (stl) toxR-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murS) UDP-MurNac-tripeptide synthetase (toXa) 3-deoxyd-manno-octulosonic acid 8-phospi synthetase (toXa) 3-deoxyd-manno-octulosonic-acid transferase (toXa) ADP-heptose synthese (toXa) ADP-heptose synthese (toXa) ADP-heptose synthese (toXa)	23.3% 1334.4% 125.5% 25.7% 25.7% 25.7% 31.2% 25.7% 32.7% 31.2% 26.7% 32.	HP1031 HP0783 HP0327 HP0787 HP0584 HP0601 HP0115 HP0601 HP1015 HP0295 HP1575 HP16029 HP10751 HP0410 HP0401 HP0410	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellar sheath adhesin hpaA flagellar switch protein (flis) flagellar switch protein (flis) flagellar switch protein (flis) flagellar skitch protein (flis) flagellar skitch protein (flis) flagellar skitch glagellar sheath flagellar skitch flagellar skitch flagellar skitch flagellar skitch flagellar protein (flis) polar flagellar protein (flis) polar flagellar protein (flis) polar flagellar motility secreted protein involved in flagellar motility secreted protein flagellar motility secreted protein flagellar motility secreted protein (fleX) secreted protein flagellar motility secreted protein flagellar motility secreted protein flagellar motility secreted prote	32.3% 32.3% 98.5% 39.7% 98.5% 39.7% 98.5% 39.7% 98.5% 39.7% 32.9% 40.5% 29.3% 22.5.5% 29.3% 22.5.5% 32.9% 21
HP0577 methyleine-tetrahydrofolate dehydrogenase (folD) HP0230 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0336 flerrochelatase (hemH) HP0336 glutamyt-RNA reductase (hemA) HP0339 glutamyt-RNA reductase (hemA) HP0239 glutamyt-RNA reductase (hemA) Oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porthobilinogen deaminase (hemC) HP0381 prothobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemB) HP0381 uroporphyrinogen oxidase (hemB) HP0380 deaminase (hemC) HP0390 geranytranstransferase (ispA) HP0390 geranytranstransferase (ispA) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (mosC) HP0795 molybdopterin biosynthesis protein (mosC) HP0799 molybdopterin biosynthesis protein (mosC) HP0799 molybdopterin biosynthesis protein (mosC) HP0800 molybdopterin onoverting factor, subunit 2 (mosE) HP0780 molybdopterin converting factor, subunit 2 (mosE) HP0780 s-molybdopterin converting factor, subunit 2 (mosE) HP0780 molybdopterin converting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE)	32.4% 34.5% 50.2% 50.9% 6 60.5% 60.5% 33.4% 6 61.3% 632.7% 11.3% 12.7% 12.7% 13.79% 14.2.4% 11.37.9% 13.19% 13.14% 10.1 13.19% 13.14% 10.1 13.19% 13.14% 10.1 13.19% 13.13% 13.19% 13.11% 13.11% 13.11% 13.11% 13.11% 13.11%	HP0839 HP0965 HP0665 HP0665 HP0665 HP0665 HP0667 HP087 HP087 HP087 HP087 HP087 HP087 HP087 HP087 HP088 HP0648 HP0658 HP0658	outer membrane protein P1 (ompP1) profiloprotein diacylglycenyl transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein oxin-like outer membrane grotein oxin-like outer membrane (girl N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein (pppplospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-like oxide	23.3% 1334.4% 125.5% 25.7% 25.7% 25.7% 31.2% 25.7% 32.7% 31.2% 26.7% 32.	HP1031 HP0783 HP0327 HP0787 HP0584 HP0601 HP0115 HP0601 HP1015 HP0295 HP1575 HP16029 HP10751 HP0410 HP0401 HP0410	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin (flaG) prarlysed flagellar protein (flaP) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) polar flagellin (flaG) polar flagellin motived in flagellar motility secreted protein involved in flagellar motility secreted protein flagellar motility secreted protein flagellar motility secreted protein involved in flagellar motility secreted protein flagellar motil	32.3% 23.3% 98.5% 39.7% 98.5% 39.7% 98.5% 39.7% 99.8% 99.9% 32.9% 40.5% 29.3% 22.5.5% 23.9% 27.5.5% 99.2% 26.5% 30.7% 24.2% 47.5% 30.7% 24.2% 47.5% 30.7% 28.2% 47.5% 30.7% 28.2% 30.7% 28.2% 30.7% 28.2% 30.7% 28.2% 30.7% 28.2% 30.7% 28.2% 31.9% 31.9% 30.7% 30.7% 28.2% 30.7% 29.2% 30.2% 30.2% 29.2% 29
HP0577 methyleine-tetrahydrofolate dehydrogenase (folio) HP0233 para-aminobenzoate synthetase (pabB) Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase (hemB) HP0376 ferrochelatase (hemH) HP0360 glutamate-1-semialdehyde 2,1-aminomutas (hemB) HP0376 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP0236 porphobinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen oxidase (hemN) HP0381 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0239 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdopterin converting stote (moaC) HP0172 molybdopterin biosynthesis protein (moaC) HP0799 molybdopterin biosynthesis protein (moaC) HP0799 molybdopterin converting factor, subunit 1 (moaD) HP0800 molybdopterin converting factor, subunit 1 (moaD) HP0700 molybdopterin converting factor, subunit 2 (moaE) HP0700 molybdopterin converting factor, subunit 2 (moaE) HP0700 molybdopterin converting factor, subunit 2 (moaE) HP0700 molybdopterin converting factor, subunit	32.4% 34.5% 35.2% 50.9% \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	HP0839 HP0965 HP0965 HP0965 HP0965 HP0965 HP0967 HP0810 HP0929 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772 HP0840 HP0772 HP0840 HP0773 HP0647 HP0597 HP1565 HP0743 HP1373 HP1373 HP1373 HP1374 HP0648 HP0740 HP1494 HP1418 HP0648 HP0623 HP0623 HP0668 HP0623 HP0967 HP0688 HP0967 HP0868	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (lgt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein dividus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gfr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp-phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transglycosylase (stl) toxR-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murS) UDP-MurNac-tripeptide synthetase (toXa) 3-deoxyd-manno-octulosonic acid 8-phospi synthetase (toXa) 3-deoxyd-manno-octulosonic-acid transferase (toXa) ADP-heptose synthese (toXa) ADP-heptose synthese (toXa) ADP-heptose synthese (toXa)	23.3% 334.4% 27.596 37.696 26.3% 29.596 30.6% 40.6% 28.5% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 36.0% 37.7% 31.2% 32.2% 37.7% 37	HP1031 HP0783 HP0327 HP0787 HP0584 HP0691 HP0161 HP0116 HP0295 HP1575 HP1627 HP1482 HP1482 HP1482 HP0410 HP	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellin B (flaB) flagellin G (flagellar flagellar (flaG) polar flagellin motived in flagellar motility secreted protein involved in flagellar motility flagellar motility secreted protein involved in flagellar motility flagellar motili	32.3% 23.3% 98.5% 98.5% 98.5% 99.5% 99.5% 99.5% 99.5% 99.0% 32.9% 40.5% 25.5%
HP0577 methyleine-tetrahydrofolate dehydrogenase (folD) HP0230 para-aminobenzoate synthetase (pabB) Haem and porphyrin delta-aminolevulinic acid dehydratase (hemB) HP0336 flerrochelatase (hemH) HP0336 glutamyt-RNA reductase (hemA) HP0339 glutamyt-RNA reductase (hemA) HP0239 glutamyt-RNA reductase (hemA) Oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porthobilinogen deaminase (hemC) HP0381 prothobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemB) HP0381 uroporphyrinogen oxidase (hemB) HP0380 deaminase (hemC) HP0390 geranytranstransferase (ispA) HP0390 geranytranstransferase (ispA) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (mosC) HP0795 molybdopterin biosynthesis protein (mosC) HP0799 molybdopterin biosynthesis protein (mosC) HP0799 molybdopterin biosynthesis protein (mosC) HP0800 molybdopterin onoverting factor, subunit 2 (mosE) HP0780 molybdopterin converting factor, subunit 2 (mosE) HP0780 s-molybdopterin converting factor, subunit 2 (mosE) HP0780 molybdopterin converting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin overting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE) HP0780 s-molybdopterin averting factor, subunit 2 (mosE)	32.4% 34.5% 50.2% 50.9% 6 60.5% 60.5% 33.4% 6 61.3% 632.7% 11.3% 12.7% 12.7% 13.79% 14.2.4% 11.37.9% 13.19% 13.14% 10.1 13.19% 13.14% 10.1 13.19% 13.14% 10.1 13.19% 13.13% 13.19% 13.11% 13.11% 13.11% 13.11% 13.11% 13.11%	HP0839 HP0965 HP0965 HP0965 HP0965 HP0965 HP0967 HP0810 HP0929 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0772 HP0840 HP0772 HP0840 HP0773 HP0647 HP0597 HP1565 HP0743 HP1373 HP1373 HP1373 HP1374 HP0648 HP0740 HP1494 HP1418 HP0648 HP0623 HP0623 HP0668 HP0623 HP0967 HP0688 HP0967 HP0868	outer membrane protein P1 (ompP1) profloprotein diacylglycery transferase (Igt protective surface antigen D15 rare lipoprotein A (ripA) toxin-like outer membrane protein subus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gfr) N-acetylmuramoyi-L-alanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 14 (PBP-1A) penicillin-binding protein 14 (PBP-1A) penicillin-binding protein (ppp) prospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transglycosylase (slt) toxR-activated gene (tagE) transferase, peptidoglycan synthesise (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murS) UDP-MurNac-pentapeptide presynthetase (murS) UDP-MurNac-pentapeptide presynthetase (murS) UDP-MurNac-pentapeptide presynthetase (tasA) 3-deoxyd-manno-octulosonic acid 8-phospi synthetase (tasA) 3-deoxyd-manno-octulosonic-acid transferas (tafA) ADP-heptose synthesase (faEA) ADP-heptose synthesase GAPP-Leptoce-D-mannoheptose-6-epimeras	23.3% 334.4% 27.596 37.696 26.3% 29.596 30.6% 40.6% 28.5% 40.6% 28.5% 30.6% 40.6% 28.5% 33.7% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 35.0% 36.0% 37.7% 31.2% 32.2% 37.7% 37	HP1031 HP0753 HP0327 HP0757 HP0584 HP0397 HP0586 HP1576 HP10576 HP10576 HP115776 HP11576 HP115776 HP115776 HP115776 HP115776 HP115776 HP11577776 HP1157776 HP1157776 HP11577777777777777777777777777777777777	flagellar protein (flis) flagellar protein (flis) flagellar sheath adhesin hpaA flagellin B (flaB) flagellin G (flagellar flagellar (flaG) polar flagellin motived in flagellar motility secreted protein involved in flagellar motility flagellar motility secreted protein involved in flagellar motility flagellar motili	32.3% 23.3% 98.6% 99.5%

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 filamentation protein (fic)	63.2%	HP1271	NADH-ubiquinone oxidoreductase, NQO12	43.2%	HP1495	transaldolase (tal) transketolase A (tktA)	33.5% 46.7%
Cell killing HP0887	vacuolating cytotoxin 94.7%		HP1272	NADH-ubiquinone oxidoreductase, NQO13		HP0354	transketolase B (tktB)	39.7%
Chaperones HP0010		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	(dnaJ) 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	
111 1024		37.7%	HP1267	subunit (NQO7) NADH-ubiquinone oxidoreductase, NQO8	40.7%	General HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein)	
Chromoson HP1138	ne-associated protein plasmid replication-partition related protein	10.4%		subunit (NQO8)	42.4%		dehydratase (fabZ) 1-acyl-glycerol-3-phosphate acyltransferase	47.4%
Detoxification	on		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 acid	s and amines	39.6%		3-ketoacyl-acyl carrier protein reductase (fabG)	45.7%
HP0267	chlorohydrolase	42.6%	HP1398 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 (fabH)	III 44.4%
HP1550	(secG) protein-export membrane protein (secD)	30.6% 38.9%	HP0589	ferredoxin oxidoreductase, alpha subunit	42.7% 43.2%	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		HP0370 HP0871	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%
HP0795	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 (NADI-	H) 45.8%
HP0530	cag pathogenicity island protein (cag10)	98.4%		(frdB)	70.8%		(fabl) 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	cag pathogenicity island protein (cag13)	98.0%	HP1111	pyruvate ferredoxin oxidoreductase, beta		HP0090	malonyl coenzyme A-acyl carrier protein	
HP0535 HP0536	cag pathogenicity island protein (cag14) cag pathogenicity island protein (cag15)	97.6% 96.4%	HP1109	subunit pyruvate ferredoxin oxidoreductase, delta	43.7%		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%		(pgsA)	35.4%
HP0539		98.7%	HF IIU6		37.2%		phosphatidylserine decarboxylase proenzyr (psd)	me 33.2%
HP0540 HP0521	cag pathogenicity island protein (cag19) cag pathogenicity island protein (cag2)	99.5% 92.5%		motive force interconversion	37.7%	HP1071	phosphatidylserine synthase (pssA)	99.6%
HP0541	cag pathogenicity island protein (cag20)	97.8%	HP0828 HP1136		28.3%		phospholipase A1 precursor (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%	PLIBINES P	YRIMIDINES, NUCLEOSIDES AND NUCLEC	TIDES
HP0544	cag pathogenicity island protein (cag23)	99.0%	HP1134	ATP synthase F1, subunit alpha (atpA)	62.7%	General	THINIBINES, NOCEEGOIDES 744D NOCEEG	/IIDEO
HP0545 HP0546	cag pathogenicity island protein (cag24) cag pathogenicity island protein (cag25)	98.5% 95.7%	HP1132 HP1135		85.6% 24.6%		beta-alanine synthetase homologue	40.0%
HP0547 HP0522	cag pathogenicity island protein (cag26) cag pathogenicity island protein (cag3)	92.9% 98.1%	HP1131	ATP synthase F1, subunit epsilon (atpC)	32.7%		onucleotide metabolism deoxycytidine triphosphate deaminase	
HP0523	cag pathogenicity island protein (cag4)	95.7%	HP1133 Electron tra		37.8%		(dcd)	28.2%
HP0524 HP0526	cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6)	99.1% 97.5%	HP0146	cbb3-type cytochrome c oxidase subunit Q			deoxyuridine 5Ō-triphosphate nucleotidohydi (dut)	41.4%
HP0527	cag pathogenicity island protein (cag7)	94.6%	HP0265		44.2% 35.4%		ribonucleoside diphosphate reductase, beta subunit (nrdB)	a 39.0%
HP0528 HP0529	cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9)	99.0% 98.9%	HP0378	cytochrome c biogenesis protein (ycf5)	37.5%	HP0680	ribonucleoside-diphosphate reductase 1 alp	pha
HP1378	competence lipoprotein (comL)	25.5%	HP0147	cytochrome c oxidase, diheme subunit, membrane-bound (fixP)	33.0%	HP0825	subunit (nrdA) thioredoxin reductase (trxB)	28.4% 45.9%
HP1361 HP1006	competence locus E (comE3) conjugal transfer protein (traG)	26.7% 27.3%	HP0144	cytochrome c oxidase, heme b and copper-	- 43.9%		nucleotide biosynthesis	
HP1421 HP0333	conjugative transfer regulon protein (trbB) DNA processing chain A (dprA)	30.7% 32.9%	HP0145	cytochrome c oxidase, monoheme subunit,			5Ö-guanylate kinase (gmk) adenylate kinase (adk)	44.8% 33.3%
HP0042	trbl protein	31.4%	HP1461		45.7% 48.5%	HP1112	adenylosuccinate lyase (purB)	49.5%
HP0525 HP0441	virB11 homologue VirB4 homologue	100.0% 23.5%	HP1227	cytochrome c553	38.4%		adenylosuccinate synthetase (purA) formyltetrahydrofolate hydrolase (purU)	44.6% 49.1%
HP0017	virB4 homologue (virB4)	25.2%	HP0277 HP0588		52.5% 42.6%	HP1218	glycinamide ribonucleotide synthetase	
HP0459	virB4 homologue (virB4)	25.3%	HP1508	ferrodoxin-like protein	29.4%		(purD) GMP reductase (guaC)	31.8% 31.8%
	NTERMEDIARY METABOLISM		HP1161 HP0642		47.0% 46.1%	HP0409	GMP synthase (guaA)	56.1%
General HP1014	7-α-hydroxysteroid dehydrogenase (hdhA)	33.2%	HP0954 HP0634	oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD)	32.7%		inosine-5Ö-monophosphate dehydrogenase (guaB)	58.5%
HP1186	carbonic anhydrase	37.0%	HP0633	quinone-reactive Ni/Fe hydrogenase, cytoch		HP0198	nucleoside diphosphate kinase (ndk)	67.7%
HP0004 HP0869	carbonic anhydrase (icfA) hydrogenase expression/formation protein	33.3%		b subunit (hydC)				
HP0900	(hypA)		HP0632	guinone-reactive Ni/Fe hydrogenase, large	51.4%	HP0742	phosphoribosylpyrophosphate synthetase (prsA)	56.5%
111 0300		28.1%	HP0632	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB)	51.4%	HP0742 HP1530	(prsA) purine nucleoside phosphorylase (punB)	56.5% 20.7%
	hydrogenase expression/formation protein (hypB)	28.1% 41.4%	HP0631	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA)	51.4%	HP0742 HP1530 Pyrimidine r HP1084	(prsA) purine nucleoside phosphorylase (punB) ribonucleotide biosynthesis aspartate transcarbamoylase (pyrB)	
HP0899	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein	41.4%		quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase,	51.4% 68.5% 68.9%	HP0742 HP1530 Pyrimidine ri HP1084 HP0919	(prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-	20.7%
HP0899 HP0898	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein	41.4% 38.5%	HP0631	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase,	51.4% 68.5% 68.9% 39.3%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa)	20.7% 38.7% 48.6% 39.7%
	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD)	41.4%	HP0631 HP1539 HP1538	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (fbcH)	51.4% 68.5% 68.9%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarmoylase (pyrB) carbarmoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbarmoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrG)	20.7% 38.7% 48.6%
HP0898 HP0047	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE)	41.4% 38.5% 47.8% 39.7%	HP0631 HP1539	quinone-reactive NI/Fe hydrogenase, large subunit (hydB) ille hydrogenase, small subunit (hydA) quinone-reactive NI/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (tbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (tbcH) ubiquinol cytochrome c3 subunit (tbcH) ubiquinol cytochrome c oxidoreductase,	51.4% 68.5% 68.9% 39.3%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349 HP0349 HP0266 HP0581	(prsA) purine nucleoside phosphorylase (punB) ribonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5%
HP0898 HP0047 HP0197	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX)	41.4% 38.5% 47.8% 39.7%	HP0631 HP1539 HP1538 HP1540 Entner-Doub	quinone-reactive NI/Fe hydrogenase, large subunit (hydl) quinone-reactive NI/Fe hydrogenase, small subunit (hydl) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome coxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome coxidoreductase, Rieske 27e-28 subunit (fbcF) drorff	51.4% 68.5% 68.9% 39.3% 28.8%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcartamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydrorotase (pyrC)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0%
HP0898 HP0047	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) S-ademosylmethionine synthetase 2 (metX) 378 gilucosamine fructose-6-phosphate	41.4% 38.5% 47.8% 39.7% 62.1%	HP0631 HP1539 HP1538 HP1540 Entner-Double	quinone-reactive Ni/Fe hydrogenase, large subunit (hydl) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (flbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (flbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (flbcF) doraff 2-keto-3-deoxy-6-phosphogluconate aldolase	51.4% 68.5% 68.9% 39.3% 28.8%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1257 HP0005	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcribamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 5)39.0%
HP0898 HP0047 HP0197 <i>Amino suga</i> HP1532	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) 373 glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	41.4% 38.5% 47.8% 39.7%	HP0631 HP1539 HP1538 HP1540 Entner-Double HP1099 HP1100	quinone-reactive NI/Fe hydrogenase, large subunit (hydd) quinone-reactive NI/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) droff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase	51.4% 68.5% 68.9% 39.3% 28.8% 39.2%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1257 HP0005 HP0474	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) czrbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrE)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% -39.0% 33.9%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypB) seamond formation protein (hypB) seamond formation protein (hypB) glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa)	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0%	HP0631 HP1539 HP1538 HP1540 Entner-Double	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n	51.4% 68.5% 68.9% 39.3% 28.8% 39.2%	HP0742 HP1530 Pyrimidine r. HP1084 HP1084 HP0237 HP0236 HP0266 HP0581 HP1011 HP1011 HP1257 HP0005 HP1474 HP0777	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcariamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotidine 50-phosphate decarboxylase (pyrF hymidylate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 539.0%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) argueosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9%	HP0631 HP1539 HP1538 HP1540 Entner-Double HP1099 HP1100 Fermentation HP0691	quinone-reactive Nii/Fe hydrogenase, large subunit (hydl) quinone-reactive Nii/Fe hydrogenase, small subunit (hydl) vibiquinol cytochrome to oxidoreductase, cytochrome to subunit (fboH) ubiquinol cytochrome to subunit (fboF) 24ceto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase no-3-oxoadipate coA-transferase subunit A (vyiD)	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 50.3%	HP0742 HP1530 Pyrimidine r. HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1257 HP0005 HP1474 HP0777 Salvage of r.	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) thymidylate kinase (rmk) uridine 50-monophosphate (UMP) kinase	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% (39.0%) 33.9% 50.4%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-mettyhydantoinase polyphosphate kinase (ppk) biosynthesis	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 38.5%	HP0631 HP1539 HP1538 HP1540 Entner-Dour HP1099 HP1109 Fermentation HP0691 HP0692	quinone-reactive Nii/Fe hydrogenase, large subunit (hydi) quinone-reactive Nii/Fe hydrogenase, small subunit (hydi) ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fboH) ubiquinol cytochrome to subunit (fboH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fboH) ubiquinol cytochrome ci subunit (fboF) doroff celebrate subunit (fboF) doroff celebrate subunit (fboF) doroff celebrate subunit (fboF) doroff celebrate subunit delayore subu	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 9 50.3% 50.7% 65.5%	HP0742 HP1530 Pyrimidine r. HP1084 HP1084 HP0919 HP1237 HP0349 HP0266 HP1011 HP1057 HP0056 HP1474 HP0777 Salvage of r	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotale phosphoribosyltanisferase (pyrE) orotale phosphoribosyltanisferase (pyrE) orotale incomposphate decarboxyliase (pyrF thymidylate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH) urucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pdB)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 41.5% 31.5% 41.5% 33.9% 50.4%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I HP0422	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydratoriasepolyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA)	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9%	HP0631 HP1539 HP1538 HP1540 Entner-Dour HP100 Fermentatio HP0691 HP0692 HP0903	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) a bubunit (hydd) bubunit (hydd) bubunit (hydd) bubunit (hydd) bubunit (hydd) bubunit (behl) bubunit (behl) bubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) bubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n 3-oxoadipate coA-transferase subunit A (yxiD) 3-oxoadipate coA-transferase subunit B (yxiE) acetate kinase (ackA) (Escherichia coli)	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 50.3% 65.5% 65.5%	HP0742 HP1530 Pytimidine r. HP1084 HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1257 HP0474 HP00777 Salvage of r. HP0104 HP0572 HP0179	(prsA) purine nucleoside phosphorylase (punB) ithorucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAs) carbamoyl-phosphate synthetase (pyrAs) CTP synthetase (pyrG) dihydroorotase (pyrG) dihydroorotase (pyrG) dihydroorotase (pyrC) dihydroorotase (pyrD) orotate phosphorobytransferase (pyrE) orotate phosphorobytransferase (pyrE) orotate phosphorobytransferase (pyrE) thymidylate kinase (tmk) urdine 60-monophosphate (UMP) kinase (pyrH) wide bytransferase (pyrE) orotate phosphorobytransferase (pyrE) orotate phosphorobytransferase (apt) phosphopentomutase (decB)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 33.9% 50.4% 31.8% 50.3% 55.9%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I HP0422 HP0020	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) S-ademosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC)	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9% 33.3% 45.6% 45.6%	HP0631 HP1539 HP1538 HP1540 Entner-Dou HP1099 HP1100 Fermentatic HP0691 HP0692 HP0903 HP0904 HP0905	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome c oxidoreductase, cytochrome of subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) cytochrome c oxidoreductase (eda) 6-phosphogluconate dehydratase oxidoreductase (pa) 3-oxoadipate co-A-transferase subunit B (yxiE) accetate kinase (ackA) (Escherichia coli) phosphate acetyltransferase (pla)	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 50.3% 65.5% 65.5% 65.5% 65.5% 65.5%	HP0742 HP1530 Pyrimidine r HP1084 HP1081 HP1037 HP0379 HP0379 HP0379 HP0581 HP0058 HP0058 HP1474 HP0077 HP0104 HP0572 HP1178	(prsA) purine nucleoside phosphorylase (punB) ilbonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrG) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) urdine 50-monophosphate (UMP) kinase (pyrH) urdine 50-monophosphate (UMP) kinase (pyrH) urdine 50-monophosphate (UMP) kinase (pyrH) urdine 50-monophosphate (deptides 20-phosphodiesterase (cpdB) addenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) purine-nucleoside phosphorylase (deoD)	20.7% 38.7% 48.6% 39.7% 50.7% 50.7% 51.0% 31.5% 41.5% 35.5% 53.9% 50.4% 31.8% 50.3% 55.9% 55.9%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I HP0422 HP0020 HP0832	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) scadenosylmethionine synthetase 2 (metX) as glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidline decarboxylase	41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.0% 38.5% 33.3%	HP0631 HP1539 HP1538 HP1540 Entner-Dou HP109 HP1100 Fermentatic HP0692 HP0903 HP0904 HP0905 HP0905 HP0905 HP0905 HP0905	quinone-reactive NII/Ee hydrogenase, large subunit (hydig) quinone-reactive NII/Ee hydrogenase, small subunit (hydid), ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome to subunit (fbcF) cytochrome to subunit (fbcF) doroff 2-kete-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase (rd) 3-oxoadipate co-A-transferase subunit A (yxiDi) 3-oxoadipate co-A-transferase subunit B (yxiE) acetate kinase (ackA) [Escherichia coli) phosphotransacelylase (pta) short-chiai alcohol dehydrogenase	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 9 50.3% 50.7% 65.5% 73.2% 42.3% 51.0%	HP0742 HP1630 Pyrimidine r. HP1084 HP1084 HP0919 HP1237 HP0237 HP02681 HP10911 HP1097 HP0005 HP1474 HP0007 HP0104 HP0177 Salvage of r. HP0174 HP0175 HP0175 HP0176 HP0177	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) corbamoyl-phosphate synthetase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) urdine 60-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-phosphodiesterase (pdB) addenine phosphoribosyltransferase (apt) phosphorentomutase (decB) phosphorpentomutase (decB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (pdpI)	20.7% 38.7% 48.6% 39.7% 50.7% 50.7% 51.0% 31.5% 41.5% 35.5% 53.9% 50.4% 31.8% 50.3% 55.9% 55.9%
HP0898 HP0047 HP0197 Amino suga HP1632 Phosphorus HP0690 HP0696 HP1010 HP0422 HP0020 HP0832 Other HP0070	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypE) scadenosylmethionine synthetase 2 (metX) as scadenosylmethionine synthetase 2 (metX) as scanpounds inorganic pyrophosphatase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspC) spermidine synthase (speE) urease accessory protein (ureE)	41.4% 43.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9% 33.3% 45.6% 26.5% 97.1%	HP0631 HP1539 HP1540 Entner-Dou HP1090 HP1090 HP1090 HP0692 HP0903 HP0904 HP0905 HP0367 Gluconeoge HP1385	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) disquinone-reactive Ni/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n 3-xoxadipate coA-transferase subunit A (yxiD) 3-xoxadipate coA-transferase subunit B (yxiE) accetate kinase (ackA) (Escherichia coli) phosphate acetyltransferase (pta) phosphortasecytiase (pta) short-chain alcohol dehydrogenase nessis	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 50.3% 50.7% 66.5% 73.2% 51.0% 51	HP0742 HP1703 HP1703 HP1703 HP1084 HP1084 HP0919 HP1237 HP0266 HP0268 HP0266 HP1057 HP0005 HP1127 HP00777 Salvage of rl HP1179 HP1179 HP1179 HP1179 HP1179 Sugarnucle	(prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoylasela transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrG) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate sChonophosphate decarboxylase (pyrF) urdine sChonophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 2x30-cyclic-nucleoside 2x30-phosphodiesterase (cpdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) yntine-nucleoside phosphoribosyl transferase (apt) phosphopentomutase (deoB) xanthine guanine phosphoribosyl transferase (apt) gunine-nucleoside phosphoribosyl transferase (apt) control purine-nucleoside phosphoribosyl transferase (apt) control princip yntine-nucleoside phosphoribosyl transferase (apt) control purine-nucleoside phosphoribosyl transfera	20.7% 38.7% 48.6% 39.7% 50.7% 50.7% 51.5% 41.5% 41.5% 31.5% 50.3% 50.4% 31.8% 50.3% 55.9% 55.5% se
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine 1 HP0422 HP0020 HP0832 Other HP0079	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) 373 (glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glimS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE)	41.4% 47.8% 47.8% 62.1% 41.7% 60.0% 62.9% 38.5% 33.3% 45.6% 97.1% 94.5%	HP0631 HP1539 HP1538 HP1540 Entner-Dou HP1090 HP1100 Fermentatic HP0691 HP0903 HP0904 HP0905 HP0905 HP1385 Gluconeoge HP1385	quinone-reactive Nii/Fe hydrogenase, large subunit (hydl) quinone-reactive Nii/Fe hydrogenase, small subunit (hydl) with the properties of	51.4% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 2 50.3% 50.7% 65.5% 73.2% 42.3% 51.0% 26.9% 67.6% 56.4% 65.4%	HP0742 HP1530 Pyrimidine r. HP1084 HP1084 HP0919 HP1237 HP0248 HP0266 HP0266 HP1027 HP0005 HP1127 HP0007 HP1474 HP0777 Salvage of r. HP178 HP178 HP178 HP178 HP178 HP178 Sugar-nucle HP0043	(prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis asparatae transcariamoylase (pyrB) carbamoylasela transcariamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) uridine 50-monophosphate (UMP) kinase (pyrFl uridine 50-monophosphate (UMP) kinase (pyrFl uridine 50-monophosphate (dipMP) kinase (cpdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferase (apt) phosphosphosphase (deoD) xanthine guanine phosphoribosyl transferase (apt) cuide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 41.5% 35.5% 67.39.0% 33.9% 50.4% 31.8% 50.3% 55.5% se 27.1%
HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0896 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070 HP0069 HP0069 HP0068	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) 373 glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rispC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureG) urease accessory protein (ureG) urease accessory protein (ureH)	41.4% 47.8% 47.8% 47.8% 62.1% 41.7% 50.0% 52.9% 38.5% 33.3% 45.6% 97.1% 94.5% 95.0% 96.2%	HP0631 HP1539 HP1540 Entner-Dou HP1090 HP1090 HP1090 HP0692 HP0903 HP0904 HP0905 HP0367 Gluconeoge HP1385	quinone-reactive Nii/Fe hydrogenase, large subunit (hydl) quinone-reactive Nii/Fe hydrogenase, small subunit (hydl) which will be have been considered to the considered to th	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 9 50.3% 50.7% 65.5% 73.2% 42.3% 51.0% 26.9% 57.6% 36.4% 47.3%	HP0742 HP1630 Pyrimidine r. HP1084 HP0919 HP1237 HP0249 HP0248 HP0268 HP1058 HP1077 HP0077 Salvage of r. HP0174 HP0174 HP0174 HP0175 Sugar-nucle HP0043 HP0045	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) orotate phosphoribosyttansferase (pyrE) orotate phosphoribosyttansferase (pyrE) orotate phosphoribosyttansferase (pyrE) thymidylate kinase (trnk) uridine 50-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 20-opolic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyttansferase (apt) phosphopentomutase (deoB) prine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyt transferat (gpt) colide biosynthesis and conversions manose-6-phosphate isomerase (pmi) or (algA) nodulation protein (noIK)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 41.5% 50.3% 50.4% 33.9% 50.4% 31.8% 50.3% 55.9% 55.5% 8e 27.1%
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0696 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070 HP0088 HP0068 HP0068 HP0068 HP0067	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) srs gliucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydrantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH)	41.4% 47.8% 47.8% 47.8% 49.7% 62.1% 41.7% 50.0% 28.9% 33.3% 46.6% 97.1% 94.5% 94.5%	HP0631 HP1539 HP1538 HP1540 Entner-Dout HP1009 HP1000 HP0692 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1385 HP0121 HP1385 HP0121 HP1385 HP0154	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome to subunit (hydd) ubiquinol cytochrome to subunit (hydd) ubiquinol cytochrome to subunit (hydd) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (hydd) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (hydd) cytochrome c2 subunit (hydd) cytochrome c3 subunit (hydd) cytochrome c3 subunit (hydd) cytochrome c3 cytochrome c3 cytochrome c3 cytochrome c4 suborome c3 cytochrome c4 subcquid (hydrome) cytochrome c4 subcquid cytochrome c5 subunit (hydrome) c4 cytochrome c5 subunit (hydrome) c4 cytochrome c5 subcquid c4 cytochrome c5	51.4% 68.5% 68.9% 68.9% 39.3% 28.8% 39.2% 50.3% 50.7% 65.5% 65.5% 42.3% 51.0% 52.4% 47.3% 56.9%	HP0742 HP1630 HP1630 HP1084 HP0919 HP1237 HP0266 HP0266 HP0267 HP0077 HP0077 Salvage of t HP1077 HP017 HP179 HP178 HP178 HP179 HP178	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) cTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) widne 50-monophosphate (UMP) kinase (pyrHymidylate kinase (trnk) undine 50-monophosphate (UMP) kinase (pyrHymidylate kinase (pyrHy	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 31.5% 50.4% 50.3% 50.4% 50.3% 55.9% 55.5% se 27.1% 42.8% 44.3% 65.6% ise
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP1010 Polyamine I HP0422 HP0020 HP0832 HP0070 HP0088 HP0068 HP0068 HP0068 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) ss gliucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydrationiase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureG) urease accessory protein (ureG) urease accessory protein (ureH) urease alpha subunit (ureA) (urea midolydrolase)	41.4% 47.8% 47.8% 47.8% 62.1% 41.7% 50.0% 52.9% 38.5% 33.3% 45.6% 97.1% 94.5% 95.0% 96.2%	HP0631 HP1539 HP1538 HP1540 Entner-Dou HP1009 HP1000 HP0692 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1385 HP0121 HP1345 HP0154 HP0154 HP0154 HP0176 HP0176	quinone-reactive Ni/Fe hydrogenase, large subunit (hydd) quinone-reactive Ni/Fe hydrogenase, small subunit (hydd) ubiquinol cytochrome to subunit (hydd) ubiquinol cytochrome to subunit (hydd) ubiquinol cytochrome extra subunit (fbeH) cytochrome extra subunit A (xyiD) axoxoadipate coA-transferase subunit B (xyiE) axoxoadipate coA-transferase subunit B (xyiE) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) short-chain alcohol dehydrogenase intesis fructose-1&-bisphosphatase phosphoenolpyruvate synthase (ppsA) phosphoglycerate kinase enolase (eno) fructose-bisphosphate aldolase (tsr) glucokinase (glk)	51.4% 68.5% 68.9% 68.9% 39.3% 28.8% 39.2% 50.3% 65.7% 65.5% 42.3% 51.0% 22.9% 42.3% 51.0% 52.4% 47.3%	HP0742 HP1630 HP1630 HP1084 HP0919 HP1237 HP0266 HP0266 HP0267 HP0077 HP0077 Salvage of t HP1077 HP017 HP179 HP178 HP178 HP179 HP178	(prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis aspartale transcartamoylase (pyrB) carbamoylase lateranscartamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) urdine 50-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 20-phosphodiesterase (cpdB) purine-nucleoside phosphoribosyltransferase (apt) phosphopentomutase (deoB) yntine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (gpt) olide biosynthesis and conversions mannose-6-phosphate isomerase (pmI) or (algA) nodulation protein (noIK) UDP-glucose pyrophosphorylase (galU)	20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 50.3% 50.4% 31.8% 55.5% 58.2 27.1% 42.8% 44.3%
HP0898 HP0047 HP0197 Amino suga HP1632 Phosphorus HP0620 HP0698 HP1010 Polyamine I HP0042 HP0020 HP0832 Other HP0070 HP0069 HP0070 HP0073 HP0073 HP0073	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) as glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biologymthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureI) urease alpha subunit (ureI)	41.4% 38.5% 47.8% 47.8% 62.1% 41.7% 50.0% 50.9% 38.5% 33.3% 45.6% 94.5% 94.5% 95.0% 96.2% 96.2% 98.5%	HP0631 HP1538 HP1540 Entner-Dou HP1099 HP1100 Fermentatic HP0691 HP0903 HP0904 HP0905 HP0905 HP0905 HP09121 HP09121 HP1385 Glycolysis HP0154 HP0176 H	quinone-reactive Ni/Fe hydrogenase, large subunit (hydl) quinone-reactive Ni/Fe hydrogenase, small subunit (hydl) which will be have been considered to the	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 65.3% 65.5% 73.2% 65.5% 73.2% 42.3% 51.0% 52.4% 47.3% 56.9% 47.3% 66.9% 48.0% 41.5% 53.3%	HP0742 HP1084 HP1080 Pyrimidine r. HP1084 HP0919 HP1084 HP0919 HP0237 HP0349 HP0266 HP0086 HP1087 HP0087 HP1087 HP1087 HP107 HP107 HP007 HP007 HP007 HP007 HP007 HP007 HP008 HP0083 REGULATOF	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) cTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) widne 50-monophosphate (UMP) kinase (pyrHymidylate kinase (trnk) undine 50-monophosphate (UMP) kinase (pyrHymidylate kinase (pyrHy	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 31.5% 50.4% 50.3% 50.4% 50.3% 55.9% 55.5% se 27.1% 42.8% 44.3% 65.6% ise
HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP1010 Polyamine I HP0422 HP0020 HP0832 HP0070 HP0088 HP0068 HP0068 HP0068 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070 HP0070	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) 3r3 glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methyhlydantoinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureA) (urea amidohydrolase) urease alpha subunit (ureA) (urea amidohydrolase)	41.4% 38.5% 47.8% 47.8% 62.1% 41.7% 50.0% 52.9% 38.5% 33.3% 45.6% 94.5% 94.5% 95.0% 96.2% 96.5% 100.0%	HP0631 HP1538 HP1540 Entner-Dou HP1099 HP1100 Fermentatic HP0691 HP0903 HP0904 HP0905 HP0905 HP0905 HP0121 HP0905 HP0121 HP0135 HP0121 HP014 HP0905 HP0154 HP0154 HP0176 H	quinone-reactive Ni/Fe hydrogenase, large subunit (hydi) quinone-reactive Ni/Fe hydrogenase, small subunit (hydi) quinone-reactive Ni/Fe hydrogenase, small subunit (hydi) ubiquinol cytochrome to subunit (fbort) discrete to subunit (fbort) cytochrome to subunit (fbort) cytochrome to subunit (fbort) cytochrome to subunit (bort) cytochrome to subunit a (cytochrome) cytochrome to cytoc	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 65.3% 65.5% 66.5% 73.2% 42.3% 51.0% 52.4% 47.3% 56.9% 46.0% 41.5% 53.3% 64.5%	HP0742 HP1630 HP1034 HP1034 HP0919 HP1237 HP0268 HP0268 HP1027 HP0061 HP1077 Salvage of r HP017 HP017 HP017 HP017 HP007 HP017 Salvage of r HP018 HP07 HP018 HP07 HP018 HP07 HP018 HP08 HP08 HP08 HP08 HP08 HP08 HP08 HP0	(prsA) purine nucleoside phosphorylase (punB) tibonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) orotate dehydrogenase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) tyrding 60-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 200-yolic-nucleotide 20-phosphoribosyltransferase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphorylase (deoD) xanthine guanine phosphorylase (deoD) xanthine guanine phosphorylase (getD) upp-lucose pyrophosphorylase (glU) UDP-glucose pyrophosphorylase (glU) UDP-lucose pyrophosphorylas (glmU) XY FUNCTIONS	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 41.5% 31.5% 41.5% 35.5% 41.5% 35.5% 50.4% 41.5% 33.9% 50.4% 41.5%
HP0898 HP0047 HP0197 Amino suga HP1632 Phosphorus HP0620 HP0698 HP1010 Polyamine I HP0042 HP0020 HP0832 Other HP0070 HP0069 HP0070 HP0073 HP0073 HP0073	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureG) urease accessory protein (ureH) urease accessory protein (ureH) urease abpha subunit (ureA) (urea midohydrolase) urease beta subunit (urea amidohydrolase) urease protein (ureC)	41.4% 47.8% 47.8% 47.8% 47.8% 58.5% 41.7% 50.0% 58.5% 41.7% 50.0% 58.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 90.0% 60.0%	HP0631 HP1538 HP1540 Entner-Dou HP1099 HP1100 Fermentatic HP0691 HP0903 HP0904 HP0905 HP0905 HP0905 HP09121 HP09121 HP1385 Glycolysis HP0154 HP0176 H	quinone-reactive Nii/Fe hydrogenase, large subunit (hydd) quinone-reactive Nii/Fe hydrogenase, small subunit (hydd) a bubunit (hydd) ubiquinol cytochrome b subunit (hed) ubiquinol cytochrome b subunit (hed) ubiquinol cytochrome c oxidoreductase, cytochrome of subunit (floch) ubiquinol cytochrome c oxidoreductase, Rieses 2Pe-2S subunit (floch) ubiquinol cytochrome c oxidoreductase, Rieses 2Pe-2S subunit (floch) description (hydrogenase 2Pe-2S subunit (floch) description (hydrogenase 2Pe-2S subunit (floch) description (hydrogenase 2Pe-2S subunit (hydrogenase 4Pe-2S subunit (hydrogenase 4Pe-2S subunit A (hydrogenase 4Pe-2S subunit	51.4% 68.5% 68.9% 639.3% 528.8% 539.2% 50.3% 65.5% 65.5% 65.5% 67.3.2% 62.9% 65.6% 68.9% 64.23% 65.6% 68.9% 69.9% 69.9% 69.9% 69.9% 69.9% 60.0%	HP0742 HP1630 HP1634 HP1084 HP0919 HP1237 HP0246 HP0266 HP0266 HP0266 HP1037 HP0011 HP1077 Salvage of r HP0104 HP0577 HP0104 HP0577 Salvage of r HP0105 HP0063 REGULATOF General HP1032	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydrocortase (pyrC) dihydrocortase (pyrC) dihydrocortase (pyrC) orotate dehydrogenase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) cortaine 50-phosphate decarboxyliase (pyrFthymidylate kinase (trink) uuridine 50-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 20-phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyl transferas (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyl transferase (principal) disputation protein (noIK) UDP-glucose pyrophosphorylase (galU) udp-glu	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 48.6% 31.5% 31.5% 41.5% 33.9% 50.4% 41.5% 50.4% 41.5% 50.4% 41.5% 41
HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0698 HP1010 Polyamine I HP0020 HP0832 Other HP0070 HP0068 HP0067 HP0073 HP0073 HP0072 HP0073 HP0072 HP0073	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) as (plucosamine fructose-6-phosphate aminotransferase (isomerizing) (glimS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidline decarboxylase (rispC) spermidline synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureG) urease accessory protein (ureH) urease accessory protein (ureH) urease accessory protein (ureA) (urea amidohydrolase) urease protein (ureC) ETABOLISM	41.4% 47.896 47.896 47.896 41.796 62.1% 41.796 50.096 38.596 33.396 45.696 26.596 97.196 94.596 96.096 96.296 98.596 100.096	HP0631 HP1639 HP1638 HP1640 Entner-Dou HP1009 HP1000 HP0692 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1385 HP0154 H	quinone-reactive Ni/Fe hydrogenase, large subunit (hydl) quinone-reactive Ni/Fe hydrogenase, small subunit (hydl) ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieses 2Pe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieses 2Pe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieses 2Pe-2S subunit (fbcH) discounties (f	51.4% 68.5% 68.9% 539.3% 528.8% 539.2% 50.3% 65.5% 65.5% 65.5% 67.3.2% 62.3% 65.0% 65.5% 67.32% 64.3% 65.4% 65.5% 66.5%	HP0742 HP1084 HP1080 Pyrimidine r. HP1084 HP0919 HP1084 HP0919 HP0237 HP0349 HP0266 HP0086 HP1087 HP0087 HP0075 HP1075 Salvage of rl HP1014 HP0175 HP0175 HP0175 HP0075 HP0083 HP0083 REGULATOF General	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) thymidylate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 20-phosphodiesterase (pdB) admine phosphoribosyltransferase (apt) phosphopentiomutaes (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (noIK) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (gluU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA) carbon starvation protein (cstA)	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 50.7% 50.7% 51.5% 55.5% 56.5% 55.5% 58.27.1% 42.8% 43.9% 44.5% 65.6% 55.5% 42.8% 44.0%
HP0898 HP0047 HP0197 Amino suge HP1532 HP1632 HP0689 HP0689 HP0680 HP0680 HP0832 Other HP0082 HP0083 HP0073 HP0073 HP0075 HP0075 HP0075	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantolinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureH) urease accessory protein (ureH) urease accessory protein (ureH) urease accessory protein (ureH) urease alpha subunit (ureA) (urea amidohydrolase) (ureB)	41.4% 47.8% 47.8% 47.8% 47.8% 58.5% 41.7% 50.0% 58.5% 41.7% 50.0% 58.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 90.0% 60.0%	HP0631 HP1539 HP1538 HP1540 Entner-Dou- HP1090 HP1100 Fermentatio HP0692 HP0903 HP0904 HP0905 HP0905 Gluconeoge HP0357 Gluconeoge HP1385 HP0121 HP0154	quinone-reactive Ni/Fe hydrogenase, large subunit (hydi) quinone-reactive Ni/Fe hydrogenase, small subunit (hydi) quinone-reactive Ni/Fe hydrogenase, small subunit (hydi) ubiquinol cytochrome to subunit (fborl) domain to the subunit (fborl) cytochrome to subunit assembly cytochrome to subunit assembly cytochrome to cytoc	51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 60.3% 60.5% 66.5% 73.2% 42.3% 51.0% 52.4% 47.3% 56.9% 46.0% 41.5% 53.3% 64.5%	HP0742 HP1084 HP0919 Ayrimidine r. HP1084 HP0919 HP1084 HP0919 HP1084 HP0811 HP1081 HP1081 HP1081 HP1081 HP1081 HP1081 HP10735 Suyas-nucle HP10735 HP0735 HP1168 HP0735 HP1168 HP1168	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) rotidine 50-monophosphate (UMP) kinase (pyrH) mucleosides and nucleotides 200-optic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphoripomoributase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferat (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (alga) nodulation protein (noliK) UDP-glucose pyrophosphorylase (gmU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA) carbon storage regulator (csrA) carbon storage regulator (csrA) carbon storage regulator (csrA) carbon storage regulator (ur)	20.7% 38.7% 48.6% 48.6% 48.6% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.5% 50.5% 50.5% 50.5% 50.5% 66.6% 88 27.1% 42.6% 66.6% 88 89 42.6% 40.0%
HP0898 HP0047 HP0197 Amino suge HP1532 HP0532 HP0532 HP0689 HP0680 HP0680 HP0832 Other HP0082 HP0832 Other HP0071 HP0073 HP0075 HP0075 ENERGY M Aerobic HP1222 HP0961	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantolinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureH) urease accessory protein (ureA) (urease accessory protein (ureA) (urea	41.4% 41.4% 47.8% 47.8% 47.8% 41.7% 41.7% 41.7% 41.7% 41.7% 41.7% 45.9% 45.9% 45.6% 45.9% 94.5% 95.0% 96.2% 96.2% 96.0% 96.0% 96.0% 40.0%	HP0631 HP1539 HP1538 HP1540 Entner-Dou- HP1090 HP1100 Fermentatio HP0691 HP0692 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP0357 Gluconeoge HP0154 HP0156	quinone-reactive Nii/Fe hydrogenase, large subunit (hydig) quinone-reactive Nii/Fe hydrogenase, small subunit (hydi), ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fborl), ubiquinol cytochrome to oxidoreductase, Reiseke 2Fe-2S subunit (fborl), acvoadipate co-4-transferase subunit A (cytip), acvoadipate co-4-transferase subunit B (cytip), acvoadipate co-4-transfe	51.4% 68.5% 68.9% 539.3% 528.8% 539.2% 50.3% 65.5% 65.5% 65.5% 67.3.2% 62.3% 65.0% 65.5% 67.32% 64.3% 65.4% 65.5% 66.5%	HP0742 HP1084 HP0919 Ayrimidine r. HP1084 HP0919 HP1084 HP0919 HP0881 HP1084 HP0881 HP1085 HP1085 HP1086 HP1087 HP0075 HP1075 HP1077 HP1078 HP078 HP078 HP078 HP078 HP078 HP078 HP078 HP088 HP088 HP088 HP088 HP1188	(prsA) purine nucleoside phosphorylase (punB) ithonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyttansferase (pyrE) orotate phosphoribosyttansferase (pyrE) orotate phosphoribosyttansferase (pyrE) rotidine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides Ø30-yolic-nucleotide 20-phosphodiesterase (pydB) adenine phosphoribosyttansferase (apt) phosphoribosyttansferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyt transferat (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (noIK) UDP-glucose pyrophosphorylase (gimU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA) carbon starvation protein (cstA) carbon storage regulator (csrA) ferric uptake regulation protein (fur) guanosine pentaphosphate phosphoryloryloriogoppa)	20.7% 38.7% 48.6% 48.6% 48.6% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.5% 50.5% 50.5% 50.5% 50.5% 66.6% 68.6% 68.6%
HP0898 HP0047 HP0197 Amino suge HP1532 HP1632 HP0689 HP0689 HP0680 HP0680 HP0832 Other HP0040 HP0081 HP0070 HP0070 HP0070 HP0075 HP0075 ENERGY M Aerobic HP1222	hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantolinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureH) urease accessory protein (ureA) (urease accessory protein (ureA) (urea	41.4% 38.5% 47.8% 47.8% 62.1% 41.7% 50.0% 41.7% 50.0% 45.6% 33.3% 45.6% 33.3% 45.6% 96.2% 98.5% 100.0% 100.0%	HP0631 HP1639 HP1638 HP1640 Entner-Doun HP1099 HP1100 Fermentatic HP0692 HP0903 HP0904 HP0905 HP0367 Gluconeoge HP1386 Glycolysis HP0161 HP0161 HP0162 HP0166 HP0166 HP0166 HP0166 HP0166 HP0166 HP0176 HP11066 HP0176 HP11066 HP0176 HP11066 HP0176 HP11066 HP0176 HP11066 HP0176 HP11066 HP0176	quinone-reactive Ni/Fe hydrogenase, large subunit (hydi) quinone-reactive Ni/Fe hydrogenase, small subunit (hydi) ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fbc4) ubiquinol cytochrome to subunit (fbc4) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbc4) ubiquinol cytochrome ci subunit (fbc4) ubiquinol cytochrome ci subunit (fbc7) developed to the cytochrome ci subunit (fbc8) developed to the cytochrome ci subunit (fbc8) developed to the cytochrome ci subunit (bc8) developed to the cytochrome ci subunit device developed to the cytochrome ci subunit developed to the cytochrome ci subunit developed to the cytochrome ci subunit developed ci subunit developed to the cytochrome ci subunit developed ci subunit discorbidate ci subunit developed ci subunit discorbidate ci subunit discorb	51.4% 68.5% 68.5% 68.9% 39.3% 528.8% 39.2% 50.3% 50.3% 65.5% 65.5% 73.2% 42.3% 51.0% 52.4% 42.3% 55.64% 52.4% 47.3% 56.9% 46.5% 46.6% 46.6% 46.7%	HP0742 HP1084 HP0919 Ayrimidine r. HP1084 HP0919 HP1084 HP0919 HP0881 HP1084 HP0881 HP1085 HP1085 HP1086 HP1087 HP0075 HP1075 HP1077 HP1078 HP078 HP078 HP078 HP078 HP078 HP078 HP078 HP088 HP088 HP088 HP088 HP1188	(prsA) purine nucleoside phosphorylase (punB) ithorucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrA) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrA) carbamoyl-phosphate synthetase (pyrA) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotale phosphoribosyltransferase (pyrE) orotale phosphoribosyltransferase (pyrE) crotiline 50-phosphate decarboxylase (pyrF) crotiline 50-phosphate (byrF) thymidylate kinase (tmk) uurdine 50-monophosphate (byrF) phosphophoribosyltransferase (pyrE) phosphophoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferas (ppt) uprine-nucleoside phosphoribosyltransferas (ppt) purine-nucleoside phosphoribosyltransferas (ppt) uprine-nucleoside phosphoribosyltransferas (ppt) purine-nucleoside phosphoribosyltransferas (ppt) purine-	20.7% 38.7% 48.6% 39.7% 48.6% 39.7% 50.7% 11.6% 31.5% 41.5% 50.3% 55.9% 56.3% 56.5% 98.27.1% 42.8% 44.3% 65.5% 98.27.1%

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	penta-phosphate guanosine-3Ö-pyrophospho	- 36.7%	HP1471	type IIS restriction enzyme R protein		HP0399	ribosomal protein S1 (rps1)	30.5%
	hydrolase (spoT) peptide methionine sulphoxide reductase	30.7%	HP1366	(BCGIB) type IIS restriction enzyme R protein		HP1320 HP1295	ribosomal protein S10 (rps10) ribosomal protein S11 (rps11)	58.2% 56.2%
		66.8%	111 1000		37.1%	HP1197	ribosomal protein S12 (rps12)	79.0%
			HP1208	ulcer associated adenine specific DNA			ribosomal protein S13 (rps13)	55.8%
HP1572 HP0703		31.9% 44.2%	HP1209			HP1306 HP1040	ribosomal protein S14 (rpS14) ribosomal protein S15 (rps15)	68.3% 57.8%
		28.7%	HP1209	ulcer-associated gene restriction endonucle (iceA)		HP1151	ribosomal protein S16 (rpS16)	46.8%
			HP1347		43.1%		ribosomal protein S17 (rps17)	55.4%
HP1365		32.4%				HP1244	ribosomal protein S18 (rps18)	55.2%
HP0166			TRANSCRIP			HP1315	ribosomal protein S19 (rps19)	61.1%
		37.1% 43.5%	Degradation	of RNA		HP1554 HP0076	ribosomal protein S2 (rps2) ribosomal protein S20 (rps20)	49.6% 41.4%
		97.7%	HP1213	polynucleotide phosphorylase (pnp) DNA-dependent RNA polymerase		HP0562	ribosomal protein S21 (rps21)	42.4%
HP0164	signal-transducing protein, histidine kinase	27.1%	HP1293	DNA-directed RNA polymerase, alpha subu	init	HP1313	ribosomal protein S3 (rps3)	56.7%
HP1364	signal-transducing protein, histidine kinase	24.9%		(rpoA)	35.3%	HP1294	ribosomal protein S4 (rps4)	51.2%
	signal-transducing protein, histidine kinase (atoS)	30.0%	HP1198	DNA-directed RNA polymerase, beta subun		HP1302 HP1246	ribosomal protein S5 (rps5) ribosomal protein S6 (rps6)	65.5% 32.1%
		34.5%				HP1196	ribosomal protein S7 (rps7)	62.2%
HP1287	transcriptional regulator (tenA)	34.7%	Transcription HP0866	n factors transcription elongation factor GreA (greA)		HP1305	ribosomal protein S8 (rps8)	45.0%
		33.3%	HP1514	transcription termination factor NusA				50.4%
REPLICATIO	N				39.1%			26.3%
Degradation			HP0001	transcription termination factor NusB (nusB)		tRNA modifi HP1141	methionyl-tRNA formyltransferase (fmt)	37.5%
		27.2%	HP1203	transcription termination factor NusG		HP1497	peptidyl-tRNA hydrolase (pth)	46.6%
		37.6%	HP0550	(nusG) transcription termination factor Rho (rho)	56.6%	HP0361	pseudouridylate synthase I (hisT)	32.2%
DNA replica	tion, restriction, modification, recombination					HP1448		29.3%
		38.2%	RNA proces			HP1062	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queA)	39.3%
	adenine specific DNA methyltransferase (dpnA)	37.4%	HP0640 HP0662		37.4% 37.3%	HP1513	selenocystein synthase (selA)	36.2%
	adenine specific DNA methyltransferase	37.470	111 0002	Tiboriuciease III (ITIC)	07.070	HP1148	tRNA (guanine-N1)-methyltransferase (trmD)	
	(HINDIIM)	33.4%	TRANSLATIO	ON			tRNA delta(2)-isopentenylpyrophosphate	00 70
	adenine specific DNA methyltransferase	00.50	General				transferase (miaA) tRNA-guanine transglycosylase (tgt)	30.7% 45.6%
	(HINFIM) adenine specific DNA methyltransferase	62.5%	HP0944	translation initiation inhibitor, putative		Translation		40.070
		33.9%	Aminoacyl t	RNA synthetases		HP0247	ATP-dependent RNA helicase, DEAD-box	
	adenine specific DNA methyltransferase		HP1241 HP0319		44.9%		family (deaD)	37.7%
		29.3%			E0.10/-		peptide chain release factor RF-1 (prfA)	52.6%
	adenine specific DNA methyltransferase (mod)	33.9%	HP0886		973%	HP0171 HP1256	peptide chain release factor RF-2 (prfB)	49.6% 43.7%
HP0593	adenine specific DNA methyltransferase	33.9%	HP0476		43.1%	HP1195	ribosome releasing factor (frr) translation elongation factor EF-G (fusA)	67.5%
		38.5%	HP0643		39.8%	HP0177	translation elongation factor EF-P (efp)	45.1%
	adenine specific DNA methyltransferase		HP0960	glycyl-tRNA synthetase, alpha subunit (glyQ)	60 104	HP1555	translation elongation factor EF-Ts (tsf)	43.1%
		42.2%	HP0972		22 606		translation elongation factor EF-Tu (tufB)	89.5%
	adenine specific DNA methyltransferase (VSPIM)	12106	HP1190	histidyl-tRNA synthetase (hisS)	32.4%	HP1298 HP1048	translation initiation factor EF-1 (infA) translation initiation factor IF-2 (infB)	65.3% 45.4%
		22106	HP1422		49.7%		translation initiation factor IF-3 (infC)	43.4%
HP0790	anti-codon nuclease masking agent (prrB)	42.9%	HP1547 HP0182		45.9%		, ,	
	chromosomal replication initiator protein	0.4.00/	HP0417		42.4%		T AND BINDING PROTEINS	
	(dnaA) cytosine specific DNA methyltransferase	34.9%	HP0403	phenylalanyl-tRNA synthetase, alpha subun	it	General	ADO torror ATD binding contrib	00.70/
	(BSP6IM)	37.0%	1100400	(pheS)	TO.7 70	HP0179 HP0613	ABC transporter, ATP-binding protein ABC transporter, ATP-binding protein	66.7% 31.1%
	cytosine specific DNA methyltransferase		HP0402	phenylalanyl-tRNA synthetase, beta subunit (pheT)			ABC transporter, ATP-binding protein	52.3%
		39.0%	HP0238		39.8%	HP1576	ABC transporter, ATP-binding protein (abc)	48.2%
	cytosine specific DNA methyltransferase (HPHIMC)	38.7%	HP1480	seryl-tRNA synthetase (serS)	48.3%	HP1465	ABC transporter, ATP-binding protein	0700
		97.4%			42.1%	HP1220	(HI1087) ABC transporter, ATP-binding protein (yhcG	37.8%
	DNA gyrase, sub B (gyrB)	46.0%	HP1253 HP0774		52.6% 54.7%		ABC transporter, ATP-binding protein (yheS)	136.3%
HP1478	DNA helicase II (uvrD)	35.3%	HP1153					43.1%
		38.8% 40.1%		of proteins, peptides and glycopeptides		HP0607	acriflavine resistance protein (acrB)	29.7%
		40.1% 32.6%		aminopeptidase a/i (pepA)		HP1432	histidine and glutamine-rich protein	50.0%
HP1470	DNA polymerase I (polA)	40.0%	HP0033	ATP-dependent C1p protease (clpA)	40.3%		histidine-rich, metal binding polypeptide (hpn)	100.0%
HP1460			HP0794	ATP-dependent clp protease proteolytic	0.4.00/		multidrug-resistance protein (hetA)	26.2%
		26.0%	HP1379			HP1082	multidrug-resistance protein (msbA)	32.4%
	DNA polymerase III delta prime subunit (holB)	48.6%	HP0223	ATP-dependent protease (sms)	44.00%	HP0600	multidrug-resistance protein (spaB)	29.7%
	DNA polymerase III epsilon subunit (dnaQ)		HP1374	ATP-dependent protease ATPase subunit		HP1181 HP0497	multidrug-efflux transporter sodium- and chloride-dependent transporte	29.1%
HP0717	DNA polymerase III gamma and tau subuni	ts	1100004			HP0498	sodium- and chloride-dependent trans-	131.770
		39.0%	HP0264	ATP-dependent protease binding subunit (clpB)	0770/		porter	30.8%
		36.6% 32.7%	HP0169		40.1%	HP0214	sodium-dependent transporter (huNaDC-1)	36.6%
		28.3%	HP0516		98.4%		s, peptides and amines	
HP0116	DNA topoisomerase I (topA)	45.1%	HP0515	heat-shock protein (hslV)	07.170	HP0940	amino acid ABC transporter, periplasmic	41.5%
HP0440			HP0470 HP0657		97.9% 24.2%	HP0939	binding protein (yckK) amino acid ABC transporter, permease	41.070
		36.6% 40.1%	HP1485		35.2%		protein (yckJ)	46.9%
		53.4%	HP1350	protease	40.6%		amino acid permease (rocE)	41.7%
HP1114	excinuclease ABC subunit B (uvrB)	53.1%	HP1012				D-alanine glycine permease (dagA) dipeptide ABC transporter, ATP-binding	44.5%
		31.5%	HP1435 HP0404	protease IV (PspA) protein kinase C inhibitor (SP:P16436)	41.7% 40.2%	111 0301	protein (dppD)	59.5%
		58.9% 48.5%	HP1019		52.9%		dipeptide ABC transporter, ATP-binding	
		32.9%	HP1584	sialoglycoprotease (gcp)	35.7%	LIDOOOO	protein (dppF)	54.8%
HP1553	helicase	33.0%	HP0382	zinc-metalloprotease (YJR117W)	36.2%	HP0298	dipeptide ABC transporter, periplasmic dipeptide-binding protein (dppA)	39.8%
HP0883 HP1059		39.0% 54.6%	Nucleoprote		44.00	HP0299	dipeptide ABC transporter, permease	00.070
	Holliday junction endodeoxyribonuclease	04.0%		histone-like DNA-binding protein HU (hup)	44.0%		protein (dppB)	49.3%
	(ruvC)	34.7%	Protein mod HP0363	nication L-isoaspartyl-protein carboxyl methyltransfel	raea	HP0300	dipeptide ABC transporter, permease protei	
		31.8%	111 0000			HP1506	(dppC) glutamate permease (gltS)	52.5% 56.9%
		27.8%				HP1171	glutamine ABC transporter, ATP-binding	00.070
	methylated-DNAÑprotein-cysteine	31.1%	HP1441	peptidyl-prolyl cis-trans isomerase B,	50.40		protein (glnQ)	51.9%
	methyltransferase (dat1)	41.0%	HP1123	cyclosporin-type rotamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-typ	58.1% ne	HP1172	glutamine ABC transporter, periplasmic	22.20
HP0387	primosomal protein replication factor (priA)	36.3%		rotamase (slyD)	40.4%	HP1169	glutamine-binding protein (glnH) glutamine ABC transporter, permease	32.2%
	recombinase (recA) recombinational DNA repair protein (recR)	99.1%	HP0793		41.8%		protein (glnP)	27.6%
HP0925 HP0911	rep helicase, single-stranded DNA-depende	00.070 nt		proteins: synthesis and modification		HP1170	glutamine ABC transporter, permease prote	
	ATPase (rep)	33.8%	HP1201		52.0%	HP0250	(glnP) oligopeptide ABC transporter, ATP-binding	30.9%
		39.4%	HP1200 HP1202		30.4% 63.8%	111 0200	protein (oppD)	39.1%
		38.1% 58.4%		ribosomal protein L11 methyltransferase	03.070	HP1252	oligopeptide ABC transporter, periplasmic	
		36.3%		(prmA)	38.4%		oligopeptide-binding protein (oppA)	28.7%
HP1245	single-strand DNA-binding protein (ssb)	32.6%	HP0084			HP1251	oligopeptide ABC transporter, permease protein (oppB)	59.6%
	single-stranded-DNA-specific exonuclease	00.00	HP1309 HP1301		65.9% 42.5%	HP0251	oligopeptide ABC transporter,	33.070
		33.6% 21.3%			62.4%		permease protein (oppC)	31.4%
		37.7%	HP1292	ribosomal protein L17 (rpl17)	48.3%	HP0819	osmoprotection protein (proV)	38.3%
HP0462	type I restriction enzyme S protein (hsdS)	37.0%	HP1303	ribosomal protein L18 (rpl18)	45.5%		osmoprotection protein (proWX) proline permease (putP)	30.4% 51.4%
	type I restriction enzyme M protein (hsdM)		HP1147 HP1316			HP0936	proline/betaine transporter (proP)	29.1%
		31.7% 48.0%	HP0126			HP0133	serine transporter (sdaC)	44.6%
HP0848		37.0%	HP0296	ribosomal protein L21 (rpl21)	46.1%	Anions		
HP0850	type I restriction enzyme M protein (hsdM)	54.4%	HP1314			HP0475	molybdenum ABC transporter, ATP-binding	00.40
HP1402	type I restriction enzyme R protein (hsdR)	26.6%	HP1317 HP1308		31.7% 52.2%		protein (modD) molybdenum ABC transporter, periplasmic	38.4%
	type I restriction enzyme M protein (hsdM) type I restriction enzyme S protein (hsdS)		HP1308 HP0297		64.7%	111:04/3	molybdate-binding protein (modA)	95.9%
	type I restriction enzyme S protein (nsdS) type II restriction enzyme M protein (hsdM)	EE ON-	HP0491	ribosomal protein L28 (rpL28)	41.7%	HP0474	molybdenum ABC transporter, permease	
HP0091	type II restriction enzyme R protein (hsdR)		HP1311	ribosomal protein L29 (rpL29)	45.6%		protein (modB)	28.7%
HP1369	type III restriction enzyme M protein (mod)	45.6%	HP1319 HP0551				nitrite extrusion protein (narK)	23.6%
HP1370 HP1371	type III restriction enzyme M protein (mod)	37.0% 26.2%	HP0200			HP1491	phosphate permease	34.8%
		30.6%	HP1204	ribosomal protein L33 (rpL33)	55.1%	HP0143	tes, organic alcohols and acids 2-oxoglutarate/malate translocator (SODiT1)	37.0%
HP1521	type III restriction enzyme R protein (res)	33.1%	HP1447	ribosomal protein L34 (rpl34)	70.5%	HP1091	alpha-ketoglutarate permease (kgtP)	45.9%
HP1472	type IIS restriction enzyme M protein (mod)	32.4%	HP0125 HP1297			HP0724	anaerobic C4-dicarboxylate transport	
	type IIS restriction enzyme M1 protein (mod	l) 59.3%	HP1297 HP1318			HP1174	protein (dcuA)	53.8%
	({Moraxella bovis} type IIS restriction enzyme M2 protein	US.370	HP1307	ribosomal protein L5 (rpl5)	53.1%	HP1174 HP0141	glucose/galactose transporter (gluP) L-lactate permease (lctP)	53.6% 55.5%
	(mod)	33.0%	HP1304	ribosomal protein L6 (rpl6)	44.4%		L-lactate permease (lctr)	58.7%
HP1517	type IIS restriction enzyme R and M protein		HP1199 HP0514		65.0% 39.6%			
	(ECO57IR)	26.7%	5517		23.070			

Cations			HP0258	conserved hypothetical integral membrane		HP0728	conserved hypothetical protein	29.3%
	cadmium-transporting ATPase, P-type (cadA)	97.5%	HP0284	protein conserved hypothetical integral membrane	32.7%	HP0734 HP0741	conserved hypothetical protein conserved hypothetical protein	31.0% 30.2%
HP0969 HP1328	cation efflux system protein (czcA) cation efflux system protein (czcA)	37.3% 28.9%	HP0362	protein conserved hypothetical integral membrane	29.2%	HP0745 HP0747	conserved hypothetical protein conserved hypothetical protein	33.7% 32.4%
HP1329	cation efflux system protein (czcA)	31.3%		protein	28.8%	HP0760	conserved hypothetical protein	36.1%
	cation-transporting ATPase, P-type (copA) copper ion binding protein (copP)	30.3% 92.4%	HP0415	conserved hypothetical integral membrane protein	44.4%	HP0810 HP0813	conserved hypothetical protein conserved hypothetical protein	31.0% 32.5%
	copper-transporting ATPase, P-type (copA) glutathione-regulated potassium-efflux system		HP0467	conserved hypothetical integral membrane protein	100.0%	HP0823 HP0860	conserved hypothetical protein conserved hypothetical protein	27.8% 52.1%
	protein (kefB)	99.3%	HP0571	conserved hypothetical integral membrane		HP0890	conserved hypothetical protein	32.2%
HP1561	iron(II) transport protein (feoB) iron(III) ABC transporter, periplasmic iron-	33.6%	HP0644	protein conserved hypothetical integral membrane	29.5%	HP0891 HP0892	conserved hypothetical protein conserved hypothetical protein	33.8% 39.1%
	binding protein (ceuE) iron(III) ABC transporter, periplasmic iron-	27.5%	HP0677	protein conserved hypothetical integral membrane	30.3%	HP0894 HP0926	conserved hypothetical protein conserved hypothetical protein	39.8% 30.7%
	binding protein (ceuE)	28.2%		protein	28.5%	HP0934	conserved hypothetical protein	33.6%
	iron(III) dicitrate ABC transporter, ATP-bindir protein (fecE)	34.4%	HP0693	conserved hypothetical integral membrane protein	46.7%	HP0956 HP0959	conserved hypothetical protein conserved hypothetical protein	36.2% 31.1%
	iron(III) dicitrate ABC transporter, permease protein (fecD)	38.3%	HP0718	conserved hypothetical integral membrane protein	33.5%	HP0966 HP0975	conserved hypothetical protein conserved hypothetical protein	29.1% 25.0%
	iron(III) dicitrate transport protein (fecA) iron(III) dicitrate transport protein (fecA)	29.7% 28.5%	HP0737	conserved hypothetical integral membrane protein		HP1020 HP1037	conserved hypothetical protein	31.5% 95.9%
HP1400	iron(III) dicitrate transport protein (fecA)	26.3%	HP0758	conserved hypothetical integral membrane		HP1046	conserved hypothetical protein conserved hypothetical protein	32.6%
	magnesium and cobalt transport protein (corA)	26.3%	HP0759	protein conserved hypothetical integral membrane	47.6%	HP1049 HP1066	conserved hypothetical protein conserved hypothetical protein	39.7% 41.3%
HP1183	NA+/H+ antiporter (napA) Na+/H+ antiporter (nhaA)	26.6% 49.2%	HP0787	protein conserved hypothetical integral membrane	31.1%	HP1149	conserved hypothetical protein	24.7%
HP1077	nickel transport protein (nixA)	98.7%		protein	25.2%	HP1160 HP1182	conserved hypothetical protein conserved hypothetical protein	34.7% 34.6%
	putative potassium channel protein, putative	25.7%	HP0851	conserved hypothetical integral membrane protein	37.3%	HP1214 HP1221	conserved hypothetical protein conserved hypothetical protein	21.5% 42.4%
Nucleosides	, purines and pyrimidines		HP0920	conserved hypothetical integral membrane	36.3%	HP1240	conserved hypothetical protein	22.5%
	nicotinamide mononucleotide transporter (pnuC)	28.0%	HP0946	protein conserved hypothetical integral membrane		HP1242 HP1259	conserved hypothetical protein conserved hypothetical protein	42.3% 44.6%
HP1180	pyrimidine nucleoside transport protein	32.9%	HP0952	protein conserved hypothetical integral membrane	35.9%	HP1284 HP1291	conserved hypothetical protein conserved hypothetical protein	36.8% 26.3%
Other	(nupC)	32.9%		protein	38.5%	HP1335	conserved hypothetical protein	33.9%
	iron-regulated outer membrane protein	2760	HP0983	conserved hypothetical integral membrane protein	32.8%	HP1337 HP1338	conserved hypothetical protein conserved hypothetical protein	27.2% 36.2%
HP0915	(frpB) iron-regulated outer membrane protein	27.6%	HP1044	conserved hypothetical integral membrane protein	30.6%	HP1394 HP1401	conserved hypothetical protein conserved hypothetical protein	33.6% 27.5%
HP0916	(frpB) iron-regulated outer membrane protein	28.1%	HP1061	conserved hypothetical integral membrane		HP1413	conserved hypothetical protein	41.6%
	(frpB)	28.8%	HP1080	protein conserved hypothetical integral membrane	35.0%	HP1414 HP1417	conserved hypothetical protein conserved hypothetical protein	27.4% 23.7%
	biopolymer transport protein (exbD) biopolymer transport protein (exbB)	29.7% 33.5%	HP1162	protein	44.0%	HP1423	conserved hypothetical protein	40.3%
HP1339	biopolymer transport protein (exbB)	46.8% 35.8%		conserved hypothetical integral membrane protein	27.6%	HP1426 HP1428	conserved hypothetical protein conserved hypothetical protein	40.0% 37.8%
HP1445	biopolymer transport protein (exbD) biopolymer transport protein (exbB)	45.5%	HP1175	conserved hypothetical integral membrane protein	40.6%	HP1443 HP1449	conserved hypothetical protein	37.9% 39.0%
	biopolymer transport protein (exbD) iron-regulated outer membrane protein	36.2%	HP1184	conserved hypothetical integral membrane		HP1453	conserved hypothetical protein conserved hypothetical protein	26.8%
	(frpB)	26.6%	HP1185	protein conserved hypothetical integral membrane	23.5%	HP1459 HP1504	conserved hypothetical protein conserved hypothetical protein	30.1% 23.9%
	nonheme iron-containing ferritin (pfr) siderophore-mediated iron transport protein	99.4%		protein	55.5%	HP1510	conserved hypothetical protein	30.6%
	(tonB)	37.2%	HP1225	conserved hypothetical integral membrane protein	31.6%	HP1533 HP1570	conserved hypothetical protein conserved hypothetical protein	25.4% 40.5%
OTHER CAT	EGORIES		HP1234	conserved hypothetical integral membrane protein	29.0%	HP1573 HP1587	conserved hypothetical protein conserved hypothetical protein	42.2% 39.0%
General HP0924	4 avalagrataneta tautamarana (dmnl)	37.7%	HP1235	conserved hypothetical integral membrane		HP1588	conserved hypothetical protein	32.0%
HP1034	4-oxalocrotonate tautomerase (dmpl) ATP-binding protein (ylxH)	36.3%	HP1330	protein conserved hypothetical integral membrane	30.9%	HP1589 HP0713	conserved hypothetical protein conserved hypothetical protein	35.1%
	PARA protein SpoOJ regulator (soj)	29.7% 47.4%	HP1331	protein	41.7%	HP0028	(plasmid pHPM180) conserved hypothetical secreted protein	41.8% 42.1%
	ss-DNA binding protein 12RNP2 precursor	46.8%		conserved hypothetical integral membrane protein	33.6%	HP0139	conserved hypothetical secreted protein	37.1%
	and atypical conditions general stress protein (ctc)	26.5%	HP1343	conserved hypothetical integral membrane protein	49.1%	HP0160 HP0190	conserved hypothetical secreted protein conserved hypothetical secreted protein	30.6% 31.4%
HP1483	gerC2 protein (gerC2)	33.3%	HP1363	conserved hypothetical integral membrane		HP0211	conserved hypothetical secreted protein	24.3%
	heat shock protein (htpX) heat shock protein B (ibpB)	32.8% 27.2%	HP1407	protein conserved hypothetical integral membrane	33.1%	HP0235 HP0257	conserved hypothetical secreted protein conserved hypothetical secreted protein	31.5% 29.2%
HP1228	invasion protein (invA)	38.2%		protein	22.4%	HP0320	conserved hypothetical secreted protein	36.4%
	nickel-cobalt-cadmium resistance protein (nccB)	21.1%	HP1466	conserved hypothetical integral membrane protein	30.9%	HP0506 HP0518	conserved hypothetical secreted protein conserved hypothetical secreted protein	29.8% 96.9%
HP1444 HP0930	small protein (smpB) stationary-phase survival protein (surE)	42.1% 37.7%	HP1484	conserved hypothetical integral membrane protein	41.2%	HP0785 HP0949	conserved hypothetical secreted protein conserved hypothetical secreted protein	26.6% 39.7%
HP0315	virulence associated protein D (vapD)	70.2%	HP1486	conserved hypothetical integral membrane	!	HP0977	conserved hypothetical secreted protein	29.4%
	virulence associated protein D (vapD) virulence associated protein homolog	28.9%	HP1487	protein conserved hypothetical integral membrane	23.8%	HP0980 HP1075	conserved hypothetical secreted protein conserved hypothetical secreted protein	57.4% 42.9%
	(vacB) virulence factor mviN protein (mviN)	36.0% 33.5%	HP1509	protein conserved hypothetical integral membrane	30.7%	HP1098 HP1117	conserved hypothetical secreted protein conserved hypothetical secreted protein	27.0% 32.3%
Colicin-relate		30.570		protein	34.3%	HP1216	conserved hypothetical secreted protein	31.9%
	colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster	25.7%	HP1548	conserved hypothetical integral membrane protein	30.6%	HP1285 HP1286	conserved hypothetical secreted protein conserved hypothetical secreted protein	38.0% 37.5%
	terY protein	25.6%	HP0138 HP1438	conserved hypothetical iron-sulfur protein conserved hypothetical lipoprotein	41.2% 32.0%	HP1464 HP1488	conserved hypothetical secreted protein	27.4% 29.8%
	nalog sensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl-		HP0151	conserved hypothetical membrane protein	21.8%	HP1551	conserved hypothetical secreted protein conserved hypothetical secreted protein	42.7%
	transferase (ksgA)	35.5%	HP0575 HP1258	conserved hypothetical membrane protein conserved hypothetical mitochondrial	38.8%	UNKNOWN		
	membrane fusion protein (mtrC) modulator of drug activity (mda66)	24.2% 62.3%		protein 4	23.2%	General		
HP1476	phenylacrylic acid decarboxylase	39.7%	HP1492 HP0032	conserved hypothetical nifU-like protein conserved hypothetical protein	48.2% 37.0%	HP0390 HP1193	adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative	38.3% 46.6%
	tetracycline resistance protein tetA(P), putative	27.0%	HP0035 HP0086	conserved hypothetical protein conserved hypothetical protein	34.1% 28.7%	HP0872	alkylphosphonate uptake protein (phnA)	61.1%
	related functions	00.00	HP0094	conserved hypothetical protein	29.8%	HP0207 HP0136	ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp)	38.9% 35.5%
	IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17	33.9% 33.9%	HP0100 HP0102	conserved hypothetical protein conserved hypothetical protein	32.0% 29.3%	HP0485 HP1104	catalase-like protein cinnamyl-alcohol dehydrogenase	30.8%
	IS605 transposase (tnpA) IS605 transposase (tnpA)	97.2% 97.2%	HP0105 HP0117	conserved hypothetical protein	39.7% 34.2%		ELI3-2 (cad)	44.0%
HP1096	IS605 transposase (tnpA)	97.2%	HP0162	conserved hypothetical protein conserved hypothetical protein	36.7%	HP0569	exonuclease VII-like protein (xseA) GTP-binding protein (gtp1)	42.5% 48.1%
	IS605 transposase (tnpA) IS605 transposase (tnpA)	97.2% 97.2%	HP0216 HP0233	conserved hypothetical protein conserved hypothetical protein	33.9% 30.5%	HP0303	GTP-binding protein (obg)	48.2%
HP0989	IS605 transposase (tnpB) IS605 transposase (tnpB)	93.4% 93.4%	HP0248	conserved hypothetical protein	30.7%	HP0480	GTP-binding protein homologue (yphC) GTP-binding protein, fusA-homolog (yihK)	36.7% 54.1%
HP1095	IS605 transposase (tnpB)	93.4%	HP0274 HP0285	conserved hypothetical protein conserved hypothetical protein	38.5% 30.8%		lipase-like protein nifS-like protein	21.7% 27.3%
HP1534 HP0438	IS605 transposase (tnpB) IS605 transposase (tnpB)	93.4% 93.4%	HP0309 HP0310	conserved hypothetical protein	31.3% 33.7%	HP0221	nifU-like protein	37.3%
HP0413	transposase-like protein, PS3IS	33.6%	HP0318	conserved hypothetical protein conserved hypothetical protein	47.2%	HP0658 HP0089	PET112-like protein pfs protein (pfs)	45.4% 34.5%
HP1007 Other	transposase-like protein, PS3IS	34.3%	HP0328 HP0334	conserved hypothetical protein conserved hypothetical protein	30.7% 30.8%	HP0322	poly E-rich protein protein E (gcpE)	28.7% 47.7%
HP0739	2-hydroxy-6-oxohepta-2,4-dienoate		HP0347	conserved hypothetical protein	31.8%	HP0431	protein phosphatase 2C homolog (ptc1)	30.7%
	hydrolase	30.1%	HP0373 HP0374	conserved hypothetical protein conserved hypothetical protein	31.4% 24.7%	HP0624	solute-binding signature and mitochondria signature protein (aspB)	1 26.4%
HYPOTHETIC	CAL		HP0388 HP0395	conserved hypothetical protein conserved hypothetical protein	39.8% 39.9%	HP0377	thiol:disulfide interchange protein (dsbC),	
General HP0831	conserved hypothetical ATP binding protein	1 32.3%	HP0396	conserved hypothetical protein	33.7%		putative	26.4%
HP0066	conserved hypothetical ATP-binding protein conserved hypothetical ATP-binding protein	1 34.7%	HP0419 HP0447	conserved hypothetical protein conserved hypothetical protein	45.6% 38.2%			
HP0312	conserved hypothetical ATP-binding protein	34.1%	HP0465 HP0466	conserved hypothetical protein	95.5% 95.7%			
HP1321 HP1430	conserved hypothetical ATP-binding protein conserved hypothetical ATP-binding protein	1 30.8% 1 38.1%	HP0468	conserved hypothetical protein conserved hypothetical protein	97.1%			
HP1507	conserved hypothetical ATP-binding protein	51.6%	HP0469 HP0496	conserved hypothetical protein conserved hypothetical protein	95.1% 99.2%			
HP1026	conserved hypothetical ATP-binding protein conserved hypothetical helicase-like protein		HP0507	conserved hypothetical protein	37.2%			
HP0022	conserved hypothetical integral membrane protein	30.8%	HP0519 HP0552	conserved hypothetical protein conserved hypothetical protein	95.3% 37.8%			
HP0189	conserved hypothetical integral membrane		HP0553 HP0639	conserved hypothetical protein conserved hypothetical protein	30.0% 41.0%			
	protein conserved hypothetical integral membrane	43.1%	HP0654	conserved hypothetical protein	32.0%			
				conserved hypothetical protein	36.0%			
	protein	27.6%	HP0656 HP0707		40.1%			
	protein conserved hypothetical integral membrane protein	27.6% 43.2%	HP0707 HP0709	conserved hypothetical protein conserved hypothetical protein	40.1% 49.6%			
HP0234	protein conserved hypothetical integral membrane		HP0707	conserved hypothetical protein	40.1%			
HP0234	protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane	43.2%	HP0707 HP0709 HP0710	conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	40.1% 49.6% 33.7%			