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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 C<sub>120</sub>

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 discovery<sup>1</sup> 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 regimens<sup>2</sup>.

Helicobacter pylori is a micro-aerophilic, Gram-negative, slowgrowing, spiral-shaped and flagellated organism. Its most characteristic enzyme is a potent multisubunit urease<sup>3</sup> 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 colonize<sup>2</sup>. H. pylori is probably the most common chronic bacterial infection of humans, present in almost half of the world population<sup>2</sup>. 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 lymphomas<sup>2</sup>. Disease outcome depends on many factors, including bacterial genotype, and host physiology, genotype and dietary habits<sup>4,5</sup>. H. pylori infection has also been associated with persistent diarrhoea and increased susceptibility to other infectious diseases<sup>6</sup>.

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
acriciai

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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#### articles

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

#### 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 pertussis<sup>10</sup>. Another region is the cag pathogenicity island (PAI), which is flanked by 31-bp direct repeats, and appears to be the product of lateral transfer<sup>11</sup>.

RNA and repeat elements. Thirty-six tRNA species were identified using tRNAscan-SE<sup>12</sup>. 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<sup>11,13</sup> 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 identified<sup>14</sup>, we arbitrarily designated basepair one at the start of a 7-mer repeat, (AGTGATT)<sub>26</sub>, 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 Riley<sup>15</sup> (Table 2). The 1,590 predicted genes had an average size of 945 bp, similar to that observed in other prokaryotes<sup>7–9</sup>, 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 complex<sup>16</sup>. 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 island<sup>11</sup> and the other is the flagellar export pathway which is assembled from orthologues of FliH, FliI, FliP, FlhA, FlhB, FliQ, FliR and FliP<sup>17</sup>. 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 structures<sup>18</sup> and assembly of surface structures involved in virulence and DNA transformation<sup>19</sup>.

#### **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 recombination<sup>20</sup>, 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: ++, Co<sup>2+</sup>, Zn<sup>2+</sup>, Cd<sup>2+</sup>; ?, 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 TopPred<sup>47</sup>.

endonuclease, *iceA1*, and its associated DNA adenine methyltransferase (M. HypI) genes<sup>21,22</sup>. 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 volcanii<sup>22</sup> and may also operate in H. pylori. Most intriguing, however, is the finding that in H. pylori the genes encoding the  $\beta$ 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).

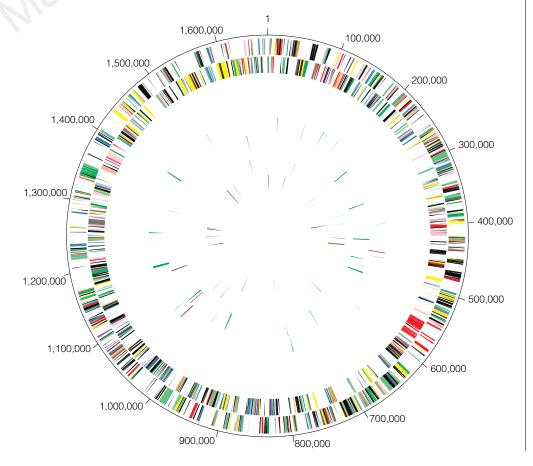
#### Adhesion and adaptive antigenic variation

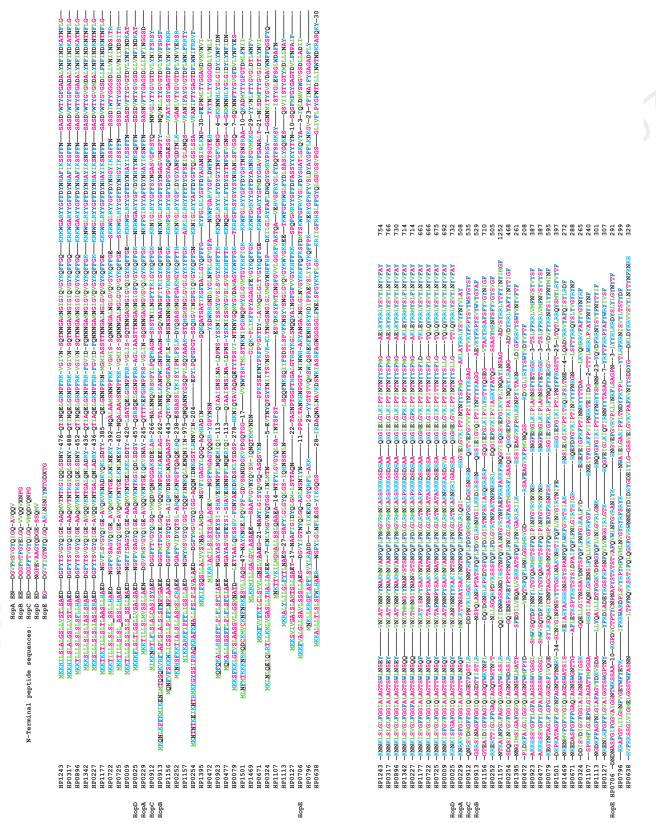
Most pathogens show tropism to specific tissues or cell types and often use several adherence mechanisms for successful attachment. *H. pylori* may use at least five different adhesins to attach to gastric epithelial cells<sup>5</sup>. One of them, HpaA (HP0797), was previously identified as a lipoprotein in the flagellar sheath and outer membrane<sup>5,23</sup>. 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<sup>24–26</sup>, one of which mediates attachment to the Lewis<sup>b</sup> 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*<sup>27</sup>.

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<sup>28,29</sup>. 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 alignment<sup>50</sup>. The most likely

candidate for HopD is HP0913, which has 15 matches to the first 20-residue N-terminal peptide sequence<sup>50</sup>. These differences may be due to strain variability. The program Signal-P<sup>48</sup> 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 hosts<sup>28</sup>. Such 'contingency' genes encode surface structures like pilins, lipoproteins or enzymes that produce lipopolysaccharide molecules<sup>28</sup>. 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 regions<sup>29</sup>. 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)<sup>5</sup>. 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<sup>11,30</sup>. Consistent with its more virulent character, *H. pylori* strain 26695 contains a single contiguous PAI region<sup>11</sup> (Fig. 4).

VacA induces the formation of acidic vacuoles in host epithelial cells, and its presence is associated epidemiologically with tissue damage and disease<sup>31</sup>. 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*<sup>5</sup>. Sequence differences at the amino terminus and central sections are noted among VacA proteins derived from Tox<sup>+</sup> and Tox<sup>-</sup> strains<sup>31</sup>. This Tox<sup>+</sup> *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

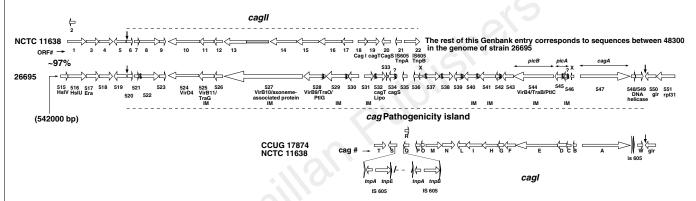
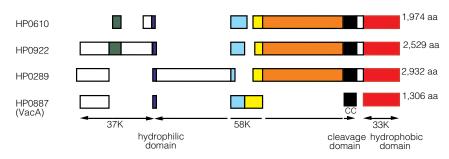


Figure 4 Comparison between the Cag pathogenicity islands of the sequenced strain, 26695 and the NCTC11638 strain. The twenty nine ORFs of the contiguous PAI in strain 26695 are represented together with the corresponding ORFs from the PAI present in NCTC11638 (AC000108 and U60176). The PAI in NCTC11638 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 suggestion<sup>11</sup>. 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)<sup>47</sup>. 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 membrane<sup>31</sup> (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* pathogenesis<sup>32</sup>. The LPS of *H. pylori* is several orders of magnitude less immunogenic than that of enteric bacteria<sup>33</sup> and the O antigen of many *H. pylori* isolates is known to mimic the human Lewis<sup>x</sup> and Lewis<sup>y</sup> blood group antigen<sup>32</sup>. 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 host<sup>5</sup>. 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. coli<sup>34</sup>, 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 bacterioferritin<sup>34</sup>, and Pfr, a non-haem cytoplasmic iron-containing ferritin used for storage of iron<sup>35</sup>. 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 colonization<sup>36</sup>. 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 regulon<sup>5</sup>.

#### 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 potential<sup>37</sup> and subsequently to modify its microenvironment through the action of urease and the release of factors that inhibit acid production by parietal cells<sup>5</sup>. A switch in membrane polarity provides an electrical barrier that prevents the entry of protons (H<sup>+</sup>). 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 cytoplasm<sup>38</sup>, 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 <b>ATG</b> 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 Ni<sup>2+</sup> supply, an essential component of urease activity<sup>39</sup>. 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 response<sup>40</sup>. 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

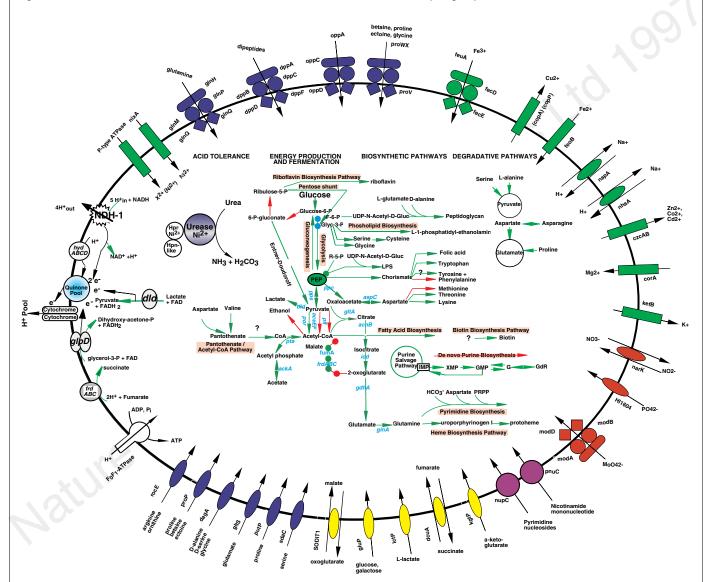


Figure 6 Solute transport and metabolic pathways of Helicobacter pylori. Transporters identified by sequence comparisons are characterists of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley<sup>15</sup>: blue, amino acids, peptides and amines; red, anions; yellow, 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 HPO<sub>4</sub><sup>2-</sup> (HI1604), NO<sub>3</sub><sup>2-</sup> (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 (Ni<sup>2+</sup> for urease activation), corA (Mg<sup>2+</sup> for phosphohydrolases, phosphotransferases, ATPases) and feoB (Fe<sup>2+</sup>

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 Ni<sup>2+</sup>-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*<sup>7</sup>. 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 organisms<sup>41</sup>. 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  $\alpha$ 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<sup>41,42</sup>.

#### 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<sup>5,21,31</sup>. The extent of molecular mimicry between *H. pylori* and its human host, an underappreciated topic, can now be fully explored<sup>43</sup>. 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*<sup>7</sup>, *Mycoplasma genitalium*<sup>8</sup>, and *Methanococcus jannaschii*<sup>9</sup>. Ninety-two per cent of the genome was covered by at least one  $\lambda$  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 GeneMark<sup>45</sup> 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 described<sup>9</sup>. ORFs were also analysed using 175 hidden Markov models constructed for a number of conserved protein families (pfam v1.0) using hmmer<sup>43</sup>. In addition, all ORFs were searched against the prosite motif database using MacPattern<sup>46</sup>. 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 TopPred<sup>47</sup> 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 bacteria<sup>48</sup>. 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 EcoCyc<sup>49</sup>.

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

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

AMINO-ACID BIOSYNTHESIS		HP0841	pantothenate metabolism flavoprotein (dfp)				41.8%
General						CMP-N-acetylneuraminic acid synthetase	
HP0695 hydantoin utilization protein A (hyuA)	28.6%	Pyridoxine	nuridoual abacabata bioquathatic arotain				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			25.7%
HP0283 3-dehydroquinate synthase (aroB)	38.1%	111 1002	(pdxl)				39.2%
HP0134 3-deoxy-D-arabino-heptulosonate	E 4.00/	Riboflavin	(1-2-2)				39.2%
7-phosphate synthase (dhs1) HP0401 3-phosphoshikimate	54.6%		GTP cyclohydrolase II (ribA)	472%	HP0044	GDP-D-mannose dehydratase (rfbD)	62.1%
1-carboxyvinyltransferase (aroA)	53.6%	HP0804	GTP cyclohydrolase II/3,4-dihydroxy-2-butar				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	(rfal) lipopolysaccharide 1,2-glucosyltransferase	28.9%
HP1280 anthranilate synthase component II (trpD)	42.5%	HP1087	riboflavin biosynthesis regulatory protein				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)	47.2%		riboflavin synthase alpha subunit (ribC) riboflavin synthase beta chain (ribE)	52.4%	0000		36.9%
HP1380 prephenate dehydrogenase (tyrA)	30.2%			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)	46.5%	HP1458	thioredoxin	38.3%		lipopolysaccharide 1,2-glucosyltransferase	
HP1278 tryptophan synthase, beta subunit (trpB)	66.1%		thioredoxin (trxA)	E1 E04			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 proteir	42.8%
HP1189 aspartate-semialdehyde dehydrogenase			thiamin biosynthesis protein (thiF)	34.6%	111 1475	(kdtB)	49.0%
(asd)	45.7%		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)				28.7%
HP0510 dihydrodipicolinate reductase (dapi)	95.3%	Pyridine nuc					28.1% 29.2%
HP1013 dihydrodipicolinate synthetase (dapA)	39.5%		NH(3)-dependent NAD+ synthetase (nadE) nicotinate-nucleotide pyrophosphorylase				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			, , , , , , , , , , , , , , , , , , , ,		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% e.	HP1450	60 kDa inner-membrane protein	40.0%			35.3%
(dapD) tetranydrodipicolinate in-succinyitransieras	e 36.1%		apolipoprotein N-acyltransferase (cute)	20.070	HP0178	spore coat polysaccharide biosynthesis protein E	36.2%
HP0098 threonine synthase (thrC)	32.9%	HP0175	cell binding factor 2	34.9%		type 1 capsular polysaccharide biosynthesis	
Glutamate family			Hypothetical protein	20.470		protein J (capJ)	29.0%
HP0380 glutamate dehydrogenase (gdhA)	59.0%		membrane protein	26.4%		UDP-3-0-(3-hydroxymyristoyl) glucosamine	_3.0 ,0
HP0512 glutamine synthetase (glnA)	48.6%		membrane-associated lipoprotein (lpp20)	98.9% 39.9%		N-acyltransferase (lpxD)	39.5%
HP1158 pyrroline-5-carboxylate reductase (proC)	28.9%		outer membrane protein (omp1)	0.0%		UDP-3-0-acyl N-acetylglcosamine deacetylas	
Pyruvate family			outer membrane protein (omp1) outer membrane protein (omp10)	0.0%			44.6%
HP0941 alanine racemase, biosynthetic (alr)	32.4%	HP0324 HP0472	outer membrane protein (omp10) outer membrane protein (omp11)	99.5%		UDP-N-acetylglucosamine acyltransferase	
HP1468 branched-chain-amino-acid	OE. 170	HP0477	outer membrane protein (omp12)	0.0%		(IpxA)	41.8%
aminotransferase (ilvE)	63.5%	HP0638	outer membrane protein (omp13)	0.0%	Surface stru	ictures	
HP0330 ketol-acid reductoisomerase (ilvC)	48.1%		outer membrane protein (omp14)	36.0%			60.2%
Serine family		HP0706	outer membrane protein (omp15)		HP0325		32.7%
HP0107 cysteine synthetase (cysK)	45.7%		outer membrane protein (omp16)				34.4%
HP0096 phosphoglycerate dehydrogenase	31.0%		outer membrane protein (omp17)				37.9%
HP0397 phosphoglycerate dehydrogenase (serA)	32.5%		outer membrane protein (omp18)				37.0%
HP0736 phosphoserine aminotransferase (serC)	30.7%		outer membrane protein (omp19)			flagellar basal-body rod protein (flgB)	31.0%
HP0652 phosphoserine phosphatase (serB)	36.5%	HP0025	outer membrane protein (omp2)	0.0%		(proximal rod protein) flagellar basal-body rod protein (flgC)	31.0%
HP1210 serine acetyltransferase (cysE)	98.2%	HP0912 HP0913	outer membrane protein (omp20) outer membrane protein (omp21)	0.0% 38.2%		(proximal rod protein)	46.0%
HP0183 serine hydroxymethyltransferase (glyA)	54.0%	HP0923	outer membrane protein (omp21)	0.0%			35.5%
BIOSYNTHESIS OF COFACTORS, PROSTHETIC GROU	ne	HP1107	outer membrane protein (omp23)				47.7%
AND CARRIERS	ro,	HP1113	outer membrane protein (omp24)				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)				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	ate 49.2%		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)	42.7%	HP1501	outer membrane protein (omp32)		HP0870 HP0908		98.9% 30.5%
HP1254 biotin synthesis protein (bioC)	32.1%	HP0127 HP0227	outer membrane protein (omp4) outer membrane protein (omp5)		HP1119	flagellar hook-associated protein 1	30.570
HP1406 biotin synthetase (bioB)	36.2%	HP0229	outer membrane protein (omp6)	38.4%		(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)	36.3%	HP0816		29.7%
pyrophosphokinase (folK)	34.6%	HP0839	outer membrane protein P1 (ompP1)	23.3%	HP0352	flagellar motor switch protein (fliG)	37.0%
HP0587 aminodeoxychorismate lyase (pabC)	32.4%	HP0955	prolipoprotein diacylglyceryl transferase (lgt		HP1031		34.4%
HP1232 dihydropteroate synthase (foIP)	34.5%	HP0655	protective surface antigen D15		HP0753		32.3%
HP1545 folylpolyglutamate synthase (folC)	35.2%		rare lipoprotein A (rlpA)			flagellar protein G (flaG)	23.3%
HP0928 GTP cyclohydrolase I (folE)	50.9%				HP0327		OO EN
HP0577 methylene-tetrahydrofolate dehydrogenase (foID)			toxin-like outer membrane protein	26.3%	HP0797	flagellar sheath adhesin hpaA	98.5%
	40.40/	HP0922	toxin-like outer membrane protein toxin-like outer membrane protein	26.3% 29.5%	HP0797 HP0584	flagellar sheath adhesin hpaA flagellar switch protein (fliN)	39.7%
, , , , , , , , , , , , , , , , , , , ,	48.4%	HP0922 HP0289	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein	26.3% 29.5% 30.6%	HP0797	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA)	
Haem and porphyrin HP0163 delta-aminolevulinic acid dehydratase	48.4% 35.1%	HP0922 HP0289 Murein sacc	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein culus and peptidoglycan	26.3% 29.5% 30.6%	HP0797 HP0584 HP0601 HP0115 HP0295	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB)	39.7% 99.8%
2100 GONG ATTITIONEVUILING ACID DETTYDTAILASE	48.4%	HP0922 HP0289 Murein saco HP0830	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein zulus and peptidoglycan amidase	26.3% 29.5% 30.6% 40.6%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flib protein (flhB)	39.7% 99.8% 99.0% 32.9% 40.5%
(hemB)	48.4% 35.1%	HP0922 HP0289 <i>Murein sacc</i> HP0830 HP0738	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein outus and peptidoglycan amidase Delanine:D-alanine:ID-alanine ligase A (ddlA)	26.3% 29.5% 30.6% 40.6% 48.5% 36.6%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flagellin B protein (flhB) fliY protein (fliN)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3%
(hemB) HP0376 ferrochelatase (hemH)	48.4%	HP0922 HP0289 Murein saco HP0830	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein zulus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyi-L-alanine amidase (amiA	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 1026.8%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flhB protein (flhB) fliY protein (fliY) Hook assembly protein, flagella (flgD)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
HP0376 ferrochelatase (hemH)	48.4% 35.1% 50.5% 33.4% e	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein anidase D-alanine:D-	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (fla) flinB protein (fliR) fliY protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagella protein (flfA)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL)	48.4% 35.1% 50.5% 33.4% e 15.3%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein sulus and peptidoglycan amidase D-alanineiD-alanine ligase A (ddlA) giutamate racemase (gir) N-acety/mruamoy/L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751	flagellar sheath adhesin hpaA flagellar switch protein (flin) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) fliry protein (flify) Hook assembly protein, flagella (flgD) paralysed flagella protein (flfA) polar flagellin (flaG)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-tRNA reductase (hemA)	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein amidase D-alanine:D-	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7% 35.0% (sor	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin (flaB) flagellin (flaG) prarlayed flagellin protein (flaB) polar flagellin (flaG) putative neureminyllactose-binding	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9%
HP0376 ferrochelatase (hemH) HP0366 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-tRNA reductase (hemA) oxygen-independent coproporphyrinogen	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein sulus and peptidoglycan amidase D-alanineiD-alanine ligase A (ddIA) glutamater accenase (gly) N-acety/muramoyi-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) peptidoglycan associated lipoprotein precu (omp18)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7% 35.0% rsor	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410	flagellar sheath adhesin hpaA flagellar witch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flhB protein (flhB) fliY protein (flhB) fliY protein (flhB) fliY protein (flhB) pralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) Oxygen-independent coproporphyrinogen oxidase (hemN)	48.4% 35.1% 50.5% 33.4% e e 51.3% 32.7% III	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddlA) giutamate racemase (gir) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (cmp18) prospho-N-acetylmuramoyl-pentapeptide	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 33.7% 35.0% 50.5% 42.6%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192	flagellar sheath adhesin hpaA flagellar witch protein (fliN) flagellin A (flaA) flagellin (flaB) fli' protein (flhB) fli' protein (flhB) pralysed flagellin protein (flgD) paralysed flagellin protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-RNA reductase (hemA) HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen	48.4% 35.1% 50.5% 33.4% 6 51.3% 32.7% III 42.4%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493	toxin-like outer membrane protein amidase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA) penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 2 (pbp2) peptidoglycan associated lipoprotein precu (omp18) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 33.7% 35.0% rsor 42.6% 44.2%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462	flagellar sheath adhesin hpaA flagellar wicht protein (fliN) flagellin A (flaA) flagellin B (flaE) flagellin B (flaE) flagellin B (flaE) flagellin B (mac) flagellin B (mac) flagellin B (mac) flagellin B (mac) flagellin B (flaE) fly Protein (fliR) fly protein (fliR) fly protein (fliR) pralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN)	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493 HP0493	toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein toxin-like outer membrane protein baulus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) gilutamate racemase (gfr) N-acety/muramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (cmp18) phospho-N-acety/muramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 33.7% 33.7% 42.6% 42.6% 42.6%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462	flagellar sheath adhesin hpaA flagellar witch protein (fliN) flagellin A (flaA) flagellin (flaB) fli' protein (flhB) fli' protein (flhB) pralysed flagellin protein (flgD) paralysed flagellin protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0209 glutamyl-tRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC)	48.4% 35.1% 50.5% 33.4% 9 51.3% 32.7% III 42.4% III 37.9% 45.7%	HP0922 HP0289 Murein sacc HP0330 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493 HP0743 HP0743 HP1373	toxin-like outer membrane protein vulus and peptidoglycan amiddase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA) penicillin-binding protein 14 (PBP-1A) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (omp18) phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 126.8% 33.7% 35.0% 42.6% 42.6% 45.2% 37.7%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232	flagellar sheath adhesin hpaA flagellar wicht protein (fliN) flagellin A (flaA) flagellin B (flaE) flagellin B (flaE) flagellin B (flaE) flagellin B (mac) flagellin B (mac) flagellin B (mac) flagellin B (mac) flagellin B (flaE) fly Protein (fliR) fly protein (fliR) fly protein (fliR) pralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0376 ferrochielatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK)	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4% III 45.7% 35.9%	HP0922 HP0289 Murein sacc HP0330 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493 HP0743 HP0743 HP1373 HP1372	toxin-like outer membrane protein bulus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) gilutamate racemase (gir) N-acety/muramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein protein protein protein (mrab) rod shape-determining protein (mrab) rod shape-determining protein (mrab)	26.3% 29.5% 40.6% 40.6% 28.6% 36.6% 33.7% 35.0% 8507 42.6% 45.2% 37.7% 45.9%	HP0797 HP0584 HP0601 HP0115 HP01295 HP1030 HP1930 HP19274 HP0751 HP0410 HP1192 HP1462 HP0232 CELLULAR	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) fliNB protein (fliNB) fliY protein (fliNB) fliY protein (fliNB) pralysed flagellin protein (flaG) 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 secreted protein involved in flagellar motility.	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0376 ferrochelatase (hemH) HP0306 glutamate-t-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyt-tRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB)	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4% III 47.7% 35.9% 46.3%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0749 HP0549 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1373 HP1373 HP0645	toxin-like outer membrane protein over an depetidoglycan amidase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyi-L-alanine amidase (amiA penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 1 (PBP-1A) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein (pppidioghon-N-acetylmuramoyl-pentapeptide-transferase (mra*) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transglycosylase (slt)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 59.6 33.7% 35.0% ssor 42.6% 37.7% 51.9% 33.6% 33.7% 37.7% 51.9% 33.7% 33.7% 35.0%	HP0797 HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232 CELLULAR General	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellar witch protein (fliN) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (fla) fliN protein (fliN) fly protein (fliN) Hook assembly protein, flagella (flgD) paralysed flagellin protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility processes	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-tRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0404 uroporphyrinogen dicarboxylase (hemE) HP1224 uroporphyrinogen lli cosynthiase (hemE)	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4% III 45.7% 35.9%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0749 HP0549 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1373 HP1373 HP0645	toxin-like outer membrane protein bulus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) gilutamate racemase (gir) N-acety/muramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein protein protein protein (mrab) rod shape-determining protein (mrab) rod shape-determining protein (mrab)	26.3% 29.5% 40.6% 28.5% 36.6% 36.6% 35.0% 35.0% 50° 42.5% 42.5% 45.2% 37.7% 42.9% 45.2% 33.7% 42.9% 45.2% 33.6% 45.2% 33.6% 45.2% 33.6% 45.2% 33.6% 45.2% 33.6%	HP0797 HP0584 HP0601 HP0115 HP01575 HP1575 HP1330 HP0907 HP1274 HP0751 HP0410 HP0410 HP1462 HP04232 CELLULAR General HP0019 HP0039	flagellar sheath adhesin hpaA flagellar switch protein (fliN) flagellin A (flaA) flagellar witch protein (fliN) flagellin A (flaA) flagellin B homologue (fla) flagellin B homologue (fla) flagellin B homologue (fla) fliN protein (fliN) fliV protein (fliN) Hook assembly protein, flagella (flgD) paralysed flagellin protein (pflA) polar flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES	39.7% 99.8% 99.8% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 272.5% 96.2% 99.2%
HP0376 ferrochelatase (hemH) HP0239 glutamate1-esemialdehyde 2,1-aminomutas (hemL) HP0269 glutamyt-18NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0264 uroporphyrinogen dearboxylase (hemE) HP1224 uroporphyrinogen (acarboxylase (hemE) Menaquinone and ubiquinone	48.4% 35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4% III 47.7% 35.9% 46.3%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0772 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645 HP1543	toxin-like outer membrane protein dasse D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gfr) N-acety/muramoyl-lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) posspho-N-acety/muramoyl-pentapepiide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) soluble lytic murein transglycosylase (slt) toxR-activated gene (tagE)	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 33.7% 35.0% rsor 42.6% 42.5% 42.5% 37.7% 51.9% 32.2% 33.6% 34.6% 3	HP0797 HP0584 HP0661 HP0115 HP0295 HP1575 HP1274 HP0390 HP0410 HP1192 HP1462 HP0423 CELLULAR General HP0019 HP0393	flagellar sheath adhesin hpaA flagellar which protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (flaB) flagellin B flagellin B (flaB) flagellin B flagellin G (flaB) flagellin G (flaB) flagellin G (flaB) potein (flaB) potein (flaB) potein flagellin (flaC) putative neuraminyllactose-binding haemagglutinin homologue (flaB) secreted protein involved in flagellar motility secreted protein involved in flagellar motility processes which is secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	39.7% 99.8% 99.0% 32.9% 40.5% 25.5% 25.5% 22.3% 21.9% 24.2% 772.5% 99.2% 26.6% 26.6% 27.2% 28.6% 29.3% 21.9% 24.2% 24.2% 24.2% 25.5% 24.2% 25.5% 24.2% 26.6% 27.2% 27.5% 2
HP0376 ferrochelatase (hemH) HP0306 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyl-RNA reductase (hemA) HP0666 xoygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen dearboyslase (hemE) HP1244 uroporphyrinogen dearboyslase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase	48.4% 35.1% 50.5% 33.4% 8 51.3% 32.7% III 42.4% III 37.9% 45.7% 45.7% 45.7% 46.3% 27.6%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0587 HP1565 HP1125 HP0493 HP0743 HP1372 HP1372 HP1372 HP1644 HP1544 HP1544 HP1544 HP1544	toxin-like outer membrane protein availus and peptidoglycan amiddase D-alaninei-D-alaninei ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyi-L-alanine amiddase (amiA penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 2 (pbp2) penicilliin-binding protein 2 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein protein (mreB) rod shape-determining p	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 126.8% 33.7% 35.0% rsor 42.6% 37.7% 51.9% 33.6% 32.2% 33.2% 45.2% 37.7% 51.9% 33.6% 22.2% 37.2% 33.2% 33.2% 23.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.3% 42.6% 33.3% 42.6% 33.3% 42.6% 33.3% 42.6% 33.3% 42.6% 33.3% 42.6% 33.3% 42.6% 43.3%	HP0797 HP0584 HP0680 HP0115 HP0115 HP0235 HP1575 HP1030 HP19274 HP0907 HP1274 HP0410 HP1462 HP1462 HP0232 CELLULAR General HP0039 HP0393 HP039 HP03	flagellar sheath adhesin hpaA flagellar witch protein (fliN) flagellin A (flaA) flagellin (flaB) protein (flhB) florein (flhP) protein (flhB) pralysed flagellia protein (flfA) polar flagellin (flaG) pratisve dragellin (flaG) putative 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)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 29.3% 25.5% 29.3% 25.5% 29.3% 26.6% 31.7% 59.2% 24.2% 79.5% 29.2% 26.6% 31.7% 27.9% 99.2%
HP0376 ferrochelatase (hemH) HP0396 (putamate1-semialdehyde 2,1-aminomutas (hemL) HP0293 (putamyte1-semialdehyde 2,1-aminomutas (hemL) HP0695 (putamyt-IRNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) oxygen-independent coproporphyrinogen oxidase (hemN) HP0207 (protoprophyrinogen decarboxylase (hemE) HP0804 (protoprophyrinogen oxidase (hemE) HP1930 (protoprophyrinogen decarboxylase (hemE) HP1930 (protoprophyrinogen decarboxylase (hemE) HP1930 (protoprophyrinogen decarboxylase (hemE) (protoprophyrinogen oxidase (hemE) (protoprophyrinogen oxidase (hemD) (protoprophyrinogen oxidase (hemD) (protoprophyrinogen oxidase (hemX) (protoprophyrinogen oxidase	48.4% 35.1% 50.5% 33.4% e e 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 26.6%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0772 HP0597 HP1565 HP1125 HP0493 HP0743 HP1372 HP0343 HP1372 HP1372 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644 HP1644	toxin-like outer membrane protein toxin-like outer periodide.  Dellanine-Dellanine ligase A (ddlA) glutamate racemase (girl) N-acetylmuramoyl-t-alanine amidase (amid penicillin-binding protein 1A (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) rod shape-determining protein (mreB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murd)  UDP-MurNac-pentapeptide presynthetase	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 33.7% 35.0% rsor 42.6% 37.7% 51.9% 37.7% 51.9% 32.2% 32.2% 32.2% 32.2% 32.2% 32.2% 32.2%	HP0797 HP0584 HP0681 HP0115 HP0295 HP1575 HP1575 HP0907 HP1274 HP0410 HP0410 HP1192 HP1462 HP0482 General HP0019 HP0383 HP0616 HP1087 HP0616 HP1067	flagellar sheath adhesin hpaA flagellar which protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (fla flagellin B flagellin B flagellin B flagellin G flagellin	39.7% 59.8% 59.0% 32.9% 40.5% 29.2% 29.2% 29.2% 29.2% 22.55% 23.9% 21.9% 24.2% 572.5% 59.2% 29.2% 24.2% 79.5% 29.2% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5
HP0376 ferrochelatase (hemH) HP0306 [Jutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyt-RNA reductase (hemA) HP0666 voxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen decarboxylase (hemD) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltransferase (ispA)	48.4% 35.1% 50.5% 33.4% 8 51.3% 32.7% III 42.4% III 42.4% III 37.9% 45.7% 45.7% 46.3% 27.6% 26.6% 39.8%	HP0922 HP0289 Murein sacc HP0830 HP0549 HP0549 HP0577 HP1565 HP0493 HP0493 HP0743 HP1372 HP0645 HP0645 HP1372 HP1644 HP1544 HP1544 HP1544 HP1544	toxin-like outer membrane protein oxin-like outer membrane protein amidase D-alaninei-D-alanine ligase A (ddlA) glutamate racemase (gir) N-acety/muramoyi-L-alanine amidase (amiA penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein 12 (pbp2) penicilliin-binding protein (ppp2) phospho-N-acety/muramoyi-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) transferase, peptidoglycon synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murG) UDP-MurNac-pentapeptide presynthetase (murF)	26.3% 29.5% 30.6% 40.6% 28.5% 40.6% 28.5% 37.7% 42.6% 45.2% 37.7% 51.9% 32.2% 37.7% 52.2% 37.7% 52.2% 37.7% 52.5% 37.7% 51.9% 32.2% 37.7% 52.5% 37.7% 37.7% 52.5% 52.5% 52.5% 52.5% 52.5% 52.5%	HP0797 HP0584 HP0601 HP0015 HP0295 HP1575 HP1030 HP0907 HP1927 HP0410 HP1192 HP0410 HP1192 HP04232 CELLULAR General HP0491 HP0491 HP0616 HP067 HP067 HP067 HP067 HP067 HP067 HP067	flagellar sheath adhesin hpaA flagellar which protein (fliN) flagellin A (flaA) flagellar witch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (flaB) protein (flhB) protein (flhB) protein (flhB) prallysed flagellia protein (flgD) paralysed flagellia protein (flgD) paralysed flagellia protein (flpA) polar flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility hamber protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (era) haemolysin	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 29.3% 25.5% 29.3% 24.2% 772.5% 99.2% 24.2% 79.5% 99.2% 99.2% 99.2% 99.2% 99.2% 99.2% 99.2%
HP0376 ferrochelatase (hemH) HP0306 (putamate1-semialdehyde 2,1-aminomutas (hemL) HP0239 glutamyt-18-nA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen oxidase (hemE) HP0804 uroporphyrinogen lid cosynthase (hemD) Menaguinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0240 octaprenyldiphosphate synthase (ispB)	48.4% 35.1% 50.5% 33.4% e e 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 26.6%	HP0982 HP0289 Murein sacx HP0830 HP0738 HP0549 HP0569 HP10697 HP1665 HP1373 HP1373 HP1373 HP1372 HP0645 HP1643 HP1543 HP1544 HP1565 HP1640 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664	toxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddiA) glutamate racemase (gfr) N-acety/muramoyi-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein (mreB) prosspho-N-acety/muramoyi-pentapepidie-transferase (mary) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxR-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murF)	26.3% 29.5% 30.6% 40.6% 40.6% 28.5% 36.6% 36.6% 36.6% 35.0% 750 42.6% 42.6% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2% 32.2% 31.2%	HP0797 HP0584 HP0801 HP0801 HP0905 HP19756 HP19756 HP1976 HP1980 HP0907 HP0907 HP0907 HP0410	flagellar sheath adhesin hpaA flagellar sheitch protein (flin) flagellin A (flaA) flagellar switch protein (flin) flagellin A (flaB) flagellin B (flaB) flagellin B flomologue (flaB) flagellin B flomologue (flaB) flagellin B flagellin G flagellin	39.7% 59.8% 59.0% 32.9% 40.5% 29.2% 29.2% 29.2% 29.2% 22.55% 23.9% 21.9% 24.2% 572.5% 59.2% 29.2% 24.2% 79.5% 29.2% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5% 29.2% 29.5
HP0376 ferrochelatase (hemH) HP0376 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-1RNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0604 uroporphyrinogen dearboxylase (hemE) HP1224 uroporphyrinogen (acarboxylase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB)	48.4% 35.1% 50.5% 33.4% 8 51.3% 32.7% III 42.4% III 42.4% III 37.9% 45.7% 45.7% 46.3% 27.6% 26.6% 39.8%	HP0922 HP0289 Murein sacc HP0830 HP0549 HP0549 HP0577 HP1565 HP0493 HP0493 HP0743 HP1372 HP0645 HP0645 HP1372 HP1644 HP1544 HP1544 HP1544 HP1544	toxin-like outer membrane protein availus and peptidoglycan amiddase D-alaninei-Dalaninei ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyi-Lalanine amiddase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (cmp18) phospho-N-acetylmuramoyi-pentapeptidertransferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreC) solubie lytic murein transglycosylase (slt) toxR-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murF) UDP-MurNac-tripeptide synthetase (murF) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide presynthetase (murE) UDP-MurNac-tripeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE)	26.3% 29.5% 30.6% 40.6% 28.5% 40.6% 28.5% 36.6% 56.6% 37.7% 51.9% 35.0% 42.6% 45.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.2%	HP0797 HP0584 HP0601 HP0015 HP0205 HP16775 HP1030 HP0907 HP0232 HP1402 HP1402 HP1402 HP1402 HP0402 HP0402 HP0403 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP0401 HP1400 H	flagellar sheath adhesin hpaA flagellar which protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) fliNB protein (fliNB) protein (fliNB) protein (fliXB) protein (fliXB) protein (fliXB) polar flagellin (flaG) pralayed flagellin protein (fliAB) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (era) haemolysin (tly) haemolysin (tly) secretion protein precursor	39.7% 99.8% 99.0% 32.9% 40.5% 24.2% 72.5% 23.9% 21.9% 23.9% 24.2% 72.5% 24.2% 72.5% 24.2% 72.5% 29.2% 26.6% 31.7% 27.9% 99.2% 95.6% 35.2% 40.2%
HP0376 ferrochelatase (hemH) HP0306 [ultamate1-semilaldehyde 2,1-aminomutas (hemL) HP0239 glutamyt-18-nA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen oxidase (hemE) HP1924 uroporphyrinogen lid cosynthase (hemD) Menaguinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis	48.4% 35.1% 50.5% 33.4% 6 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 50.6% 39.8% 31.6%	HP0982 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0597 HP1666 HP1125 HP0493 HP1373 HP1373 HP1373 HP1373 HP1374 HP1543 HP1543 HP1544 HP1545 HP1644 HP1654 HP1644 HP1654 HP1644 HP1654 HP1644 HP1664 HP16740 HP16740 HP1494 HP1494 HP1494 HP1494	toxin-like outer membrane protein amidase (amidase D-allanine-D-allanine ligase A (ddlA) glutamate racemase (gfr) N-acetylmuramoyl-Lalanine amidase (amidapenicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 1A (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) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-tripeptide synthetase (murE)	26.3% 29.5% 30.6% 40.6% 40.6% 28.5% 36.6% 36.6% 35.6% 35.0% 750r 42.6% 42.6% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2%	HP0797 HP0584 HP0601 HP0601 HP0015 HP0295 HP1575 HP10907 HP0907 HP0907 HP0907 HP0410 HP0410 HP0410 HP0410 HP0410 HP0410 HP0410 HP0410 HP0610 HP0610 HP0610 HP0610 HP0617 HP0617 HP160617	flagellar sheath adhesin hpaA flagellar which protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) floor sheath of the control of the co	39.7% 99.8% 99.0% 32.9% 99.0% 32.9% 40.5% 29.3% 225.5% 225.5% 23.9% 21.9% 23.9% 21.9% 31.7% 52.9% 99.2% 26.8% 31.7% 27.9% 96.6% 39.2% 40.2% 40.2% 45.4% 45.4%
HP0376 ferrochelatase (hemH) HP0376 glutamate-1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-1RNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1286 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphyrinogen oxidase (hemC) HP0381 profhobilinogen dearniase (hemC) HP0381 uroporphyrinogen oxidase (hemE) HP040 uroporphyrinogen dearboxylase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0229 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdopterin HP0768 protein A (moaA)	48.4% 35.1% 50.5% 32.7% 111 42.4% 111 112.4% 113.7% 114.4% 115.7% 116.3% 1	HP0982 HP0289 Murein sacx HP0830 HP0738 HP0549 HP0569 HP10697 HP1665 HP1373 HP1373 HP1373 HP1372 HP0645 HP1643 HP1543 HP1544 HP1565 HP1640 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664 HP1664	toxin-like outer membrane protein avulus and peptidoglycan amiddase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyl-Lalanine amiddase (amid penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (cmp18) 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) toxiR-activated gene (tagE) toxiR-activated gene (tagE) toxiR-activated gene (tagE) UDP-MurNac-pentapeptide presynthetase (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide propyruvyl UDP-MurSe-pentapeptide reductase (murB) UDP-N-acetylenolpyruvyl glucosamine reductase (murB)	26.3% 29.5% 40.6% 40.6% 28.5% 40.6% 28.5% 36.6% 42.6% 35.0% 42.6% 45.2% 45.2% 37.7% 51.9% 32.2% 37.2% 32.5% 32.5% 32.5% 33.6% 32.7% 33.6% 32.7% 33.6% 32.7% 33.6% 32.7% 33.6% 33.7% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7% 33.7%	HP0797 HP0584 HP0601 HP06061 HP0165 HP0205 HP1030 HP10307 HP0807 HP0807 HP0410 HP0410 HP0410 HP0410 HP192 CELLULAR General HP0333 HP0393 HP0393 HP0393 HP0393 HP10667 HP10667 HP10669 HP10869 HP10892 HP10892	flagellar sheath adhesin hpaA flagellar which protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) fliPA (flaB)	39.7% 99.8% 99.0% 32.9% 40.5% 22.39% 22.55% 22.39% 22.55% 23.9% 21.99% 24.2% (99.2% 23.9% 29.5% 29.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.4% 41.4%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-18NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0381 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0604 uroporphyrinogen oxidase (hemB) HP0404 uroporphyrinogen (acarboxylase (hemB) HP360 4-hydroxybenzoate octaprenyltransferase (ublA) geranyltranstransferase (ispA) HP0404 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0788 protein	48.4% 35.1% 50.5% 32.4% 8 51.3% 32.7% 1111 42.4% 111 42.4% 111 47.4% 111 47.6% 46.3% 26.6% 39.8% 31.6% C C 97.9%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0549 HP0747 HP0697 HP1125 HP0493 HP0743 HP1373 HP1372 HP0648 HP1543 HP1543 HP1544 HP1544 HP1544 HP1544 HP1544 HP1448 HP1448 HP0648	toxin-like outer membrane protein amidase (amidase D-allanine-D-allanine ligase A (ddlA) glutamate racemase (girl) N-acetylmuramoyl-Lalanine amidase (amidapenicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp) prospho-N-acetylmuramoyl-pentapeptide-transferase (marY) 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 (murE) uDP-MurNac-tripeptide synthetase (murE	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 36.6% 35.7% 35.6% 42.6% 37.7% 51.9% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2% 32.2% 32.2% 31.2%	HP0797 HP0584 HP0601 HP0601 HP0015 HP10295 HP10295 HP10307 HP10307 HP0907 HP0907 HP0907 HP0410 HP10410 HP	flagellar sheath adhesin hpaA flagellar which protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (fla flagellin B flagellin B flagellin B flagellin B flagellin G flagellin	39.7% 99.8% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 22.9% 22.9% 24.2% 27.25% 23.9% 24.2% 27.25% 29.2% 24.2% 26.6% 31.7% 27.9% 39.2% 39.2% 40.2% 45.4% 41.4% 41.2% 41.4% 41.2% 41.4% 41.4% 41.2% 41.4
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-18NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0381 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0604 uroporphyrinogen oxidase (hemB) HP0404 uroporphyrinogen (acarboxylase (hemB) HP360 4-hydroxybenzoate octaprenyltransferase (ublA) geranyltranstransferase (ispA) HP0404 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0788 protein	48.4% 35.1% 50.5% 32.4% 8 51.3% 32.7% 1111 42.4% 111 42.4% 111 47.4% 111 47.6% 46.3% 26.6% 39.8% 31.6% C C 97.9%	HP0982 HP0289 Murein sacc HP0830 HP0738 HP0549 HP0597 HP1666 HP1125 HP0493 HP1373 HP1373 HP1373 HP1373 HP1374 HP1543 HP1543 HP1544 HP1545 HP1644 HP1654 HP1644 HP1654 HP1644 HP1654 HP1644 HP1664 HP16740 HP16740 HP1494 HP1494 HP1494 HP1494	toxin-like outer membrane protein oxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (omp18) phospho-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-sectivated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murF) UDP-MurNac-tripeptide synthetase (murE) UDP-Nacetylenolloyruvoylglucosamine reductase (murB) UDP-Nacetylenolloyruvoylglucosamine reductase (murB) UDP-Nacetylenolloyruvoylglucosamine reductase (murZ) UDP-Nacetylmuramate-alanine ligase	26.3% 29.5% 40.6% 40.6% 28.5% 40.6% 28.5% 36.6% 42.6% 35.0% 35.0% 42.6% 45.2% 37.7% 45.5% 36.9% 32.2% 37.2% 32.5% 32.5% 32.5% 32.5% 32.7% 46.7%	HP0797 HP0584 HP0601 HP0161 HP0295 HP120295 HP12020 HP1207 HP1274 HP0275 HP1274 HP0751 HP0237 HP1462 HP0476 HP1902 CELLULAR General HP0393 HP067 HP067 HP1067 HP1067 HP1067 HP1068 HP1068 HP1068 HP1069 HP106	flagellar sheath adhesin hpaA flagellar sheith protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) fliP protein (fliY) flook assembly protein, flagella (flgD) paralysed flagellin protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) draemotysin (flaB) haemolysin (flaB) secretion protein precursor (flyIE) histoline kinase (cheA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB)	39.7% 99.8% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 22.9% 22.9% 24.2% 27.25% 23.9% 24.2% 27.25% 29.2% 24.2% 26.6% 31.7% 27.9% 39.2% 39.2% 40.2% 45.4% 41.4% 41.2% 41.4% 41.2% 41.4% 41.4% 41.2% 41.4
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-18NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0381 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemB) HP0604 uroporphyrinogen oxidase (hemB) HP0404 uroporphyrinogen (acarboxylase (hemB) HP360 4-hydroxybenzoate octaprenyltransferase (ublA) geranyltranstransferase (ispA) HP0404 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0788 protein	48.4% 35.1% 50.5% 50.5% 82.7% III 42.4% III 37.9% 45.7% 45.7% 46.3% 27.6% 46.3%	HP0922 HP02830 Murein sacc HP0830 HP0738 HP0549 HP0747 HP0587 HP0543 HP1125 HP0433 HP0743 HP1373 HP1372 HP0645 HP1543 HP1544 HP1544 HP1544 HP1544 HP1544 HP1444 HP1448 HP0648 HP0648 HP0648	toxin-like outer membrane protein amidase D-alanine-loalanine ligase A (ddlA) glutamate racemase (girl) N-acetylmuramoyl-Lalanine amidase (amid penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp) prospho-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) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murF) UDP-MurNac-tripeptide synthetase (murE) UDP-Mur	26.3% 29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 36.6% 35.7% 35.0% 42.6% 42.7% 42.9% 37.7% 51.9% 32.2% 37.2% 31.2% 28.2% 37.2% 31.2% 42.6% 32.7% 31.2% 42.6% 32.7% 31.2% 32.7% 31.2% 31.2% 31.2% 32.7% 31.2% 31.2% 31.2% 31.2%	HP0797 HP0589 HP0601 HP06061 HP0295 HP1015 HP1030 HP1030 HP0301 HP0410 HP0410 HP10232 CELLULAR General HP0032 CELLULAR General HP0039 HP0393 HP0393 HP059 HP0599 HP0599 HP10599 HP10599 HP10599 HP10599 HP10599 HP10599 HP10599 HP100392 HP100392 HP100392 HP100392 HP100392 HP100393	flagellar sheath adhesin hpaA flagellar which protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (fla flagellin B flagellin B flagellin B flagellin B flagellin G flagellin	39.7% 99.8% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 22.5% 23.9% 22.5% 23.9% 24.2% 6772.5% 99.2% 24.2% 99.2% 26.6% 33.2% 67.25% 40.2% 40.2% 41.4% 41.2% 41.4% 30.7% 67% 67% 30.7%
HP0376 ferrochelatase (hemH) HP0306 (putamate1-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0268 glutamyte1-semialdehyde 2,1-aminomutas (hemC) HP0268 (putamyte1,1-aminomyte2,1-amino	48.4% 35.1% 50.5% 33.4% 9 9 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.4% C 97.9% 36.3% 36.3% 36.2%	HP0922 HP0289 Murein sacc HP0830 HP0738 HP0738 HP0549 HP0747 HP0697 HP1125 HP0493 HP0743 HP1373 HP1372 HP0648 HP1543 HP1543 HP1544 HP1544 HP1544 HP1544 HP1544 HP1448 HP1448 HP0648	toxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) peptidoglycan associated lipoprotein precu (cmp18) phospho-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-preptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-Nacetyliucosamine enductase (murB) UDP-Nacetyliucosamine enductase (murB) UDP-Nacetyliucosamine enolopyruvyl transferase (murZ) UDP-Nacetylimuramate-alanine ligase (murC) UDP-Nacetylimuramoylalanine-D-glutamate	26.3% 29.5% 40.6% 40.6% 28.5% 40.6% 28.5% 36.6% 42.6% 35.0% 35.0% 42.6% 45.2% 37.7% 45.6% 37.2% 32.2% 37.2% 32.2% 37.2% 32.7% 46.7% 37.3%	HP0797 HP0584 HP0601 HP06061 HP0205 HP1015 HP1202 HP1207 HP1274 HP0375 HP1274 HP0470 HP0470 HP0470 HP0470 HP192 CELLULAR General HP0039 HP067 HP1067 HP1067 HP1067 HP1067 HP1068 HP1068 HP1069	flagellar sheath adhesin hpaA flagellar sheith protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flhB protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagellin protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis protein (tipA) methyl-accepting chemotaxis protein (tipB) methyl-accepting chemotaxis transducer (tipC)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 25.5% 23.9% 21.9% 24.2% //2.5% 23.9% 21.9% 24.2% //2.5% 23.9% 31.7% 31.7% 31.7% 31.7% 31.7% 31.7% 31.7% 31.2% 40.2
HP0376 ferrochelatase (hemH) HP0376 glutamate1-zemialdehyde 2,1-aminomutas (hemL) HP0269 glutamyte1-zemialdehyde 2,1-aminomutas (hemL) HP0665 glutamyte1-thNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen dearninase (hemC) HP0881 hp0604 protoporphyrinogen oxidase (hemE) HP0861 uroporphyrinogen dearnoxylase (hemE) HP1860 4-hydroxybenzoate octaprenyltransferase (hemD) Menaquinone and ubiquinone HP1860 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0292 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdenum cofactor biosynthesis proteir (moaC) HP0172 molybdopterin biosynthesis proteir (moaC) HP0172 molybdopterin biosynthesis proteir (moeA	48.4% 35.1% 50.5% 33.4% 9 9 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.4% C 97.9% 36.3% 36.3% 36.3% 36.2% 50.8%	HP0922 HP0830 Murein sacc HP0830 MUREIN SACC HP0830 HP0549 HP0549 HP0549 HP0549 HP0549 HP0493 HP0740 HP0743 HP1373 HP1372 HP0643 HP1543 HP1543 HP1544 HP1165 HP0740 HP1448 HP1448 HP0648 HP0648 HP0648 HP0648 HP0648	toxin-like outer membrane protein oxin-like outer membrane protein amidase D-alaninei-D-alanine ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyi-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppenicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppenicillin-binding protein protein (protein protein (protein daspedetermining protein (protein (protein daspedetermining protein (protein (protein daspedetermining protein (protein (protein daspedetermining protein (protein (prote	26.3% 29.5% 40.6% 40.6% 40.6% 40.6% 40.6% 40.8% 40.9%	HP0797 HP0584 HP0601 HP06061 HP0295 HP10156 HP10306 HP10306 HP10307 HP1274 HP0410 HP10410 HP10410 HP10410 HP10410 HP10410 HP1048 HP00432 CELLULAR General HP0041 HP	flagellar sheath adhesin hpaA flagellar sheith protein (filix) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B homologue (flaB) flix protein (flhB) flix protein (flhB) protein flagellar protein (flaB) polar flagellin (flaG) putative neuraminyllactose-bindin heamogglutinin homologue (hpaA) secreted protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) demotaxis protein (cheV) haemolysin ty) haemolysin secretion protein precursor (tyB) histidine kinase (cheA) mettryl-accepting chemotaxis protein (tlpB) mettryl-accepting chemotaxis protein (tlpB) metryl-accepting chemotaxis transducer (tlpC) purine-binding chemotaxis protein (cheW)	39.7% 99.8% 99.0% 32.9% 40.5% 22.9% 40.5% 22.9% 22.5% 23.9% 22.5% 23.9% 24.2% 6772.5% 99.2% 24.2% 99.2% 26.6% 33.2% 67.25% 40.2% 40.2% 41.4% 41.2% 41.4% 30.7% 67% 67% 30.7%
HP0376 ferrochelatase (hemH) HP0396 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyt-18-nA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemK) HP0804 uroporphyrinogen oxidase (hemE) HP1224 uroporphyrinogen ill cosynthase (hemE) Menaguinone and ubiquinone HP1360 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0292 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0396 molybdopterin biosynthesis protein (moeA) HP0755 molybdopterin biosynthesis protein (moeA) HP0780 molybdopterin biosynthesis protein (moeA) HP0781 molybdopterin biosynthesis protein (moeB) HP0781 molybdopterin biosynthesis protein (moeB) HP0781 molybdopterin biosynthesis protein (moeB) HP0801 molybdopterin oroverting factor, subunit 1	48.4% 35.1% 50.5% 33.4% 9 9 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.4% C 97.9% 36.3% 36.3% 36.2%	HP0922 HP0289 Murein sacc HP0738 HP0738 HP0738 HP0749 HP0772 HP0687 HP1665 HP1126 HP0493 HP0743 HP1373 HP1373 HP1373 HP1373 HP1374 HP1544 HP1644 HP1644 HP1644 HP1648 HP0648 HP0648 HP0648 HP0648 HP0648 HP0648	toxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddlA) gittamate 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 2 (pbp2) prospho-N-acetylmuramoyl-pentapeptide-transferase (mray) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-acetylead gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-M-acetylenolpyruvoylglucosamine enolpyruvyl transferase (murZ) UDP-N-acetylenolpyruvoylglucosamine enolpyruvyl transferase (murZ) UDP-N-acetylenolpyruvoylanine-D-glutamate ligase (murC) UPP-N-acetylenuramoylalanine-D-glutamate ligase (murC)	26.3% 29.5% 30.6% 40.6% 28.6% 40.6% 28.8% 35.6% 35.6% 35.0% 35.0% 35.0% 42.6% 45.2% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2% 32.2% 31.2% 32.7% 46.7% 32.7% 46.7%	HP0797 HP0584 HP0601 HP0601 HP0115 HP0235 HP1230 HP1375 HP1274 HP0751 HP1274 HP0751 HP1075 HP1274 HP0470 HP1082 CELLULAR General HP0492 CELLULAR General HP0033 HP0033 HP0067 HP057 HP0599 HP0399 HP0399 HP0399 HP0399 HP0391 Cell division	flagellar sheath adhesin hpaA flagellar sheith protein (fliN) flagellin A (flaA) flagellar switch protein (fliN) flagellin A (flaB) flagellin B (flaB) flagellin (flaB) floor secretal protein (flaB) polar flagellin (flaG) paralysed flagella protein (flaB) paralysed flagellar protein (flaB) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) demotaxis protein (flaB) haemolysin Haemolysin (fly) haemolysin secretion protein precursor (flyB) metrly-accepting chemotaxis protein (flpA) metrly-accepting chemotaxis protein (flpB) metrly-accepting chemotaxis protein (flpB) metrly-accepting chemotaxis protein (flpB) metrly-accepting chemotaxis protein (flpB) metrly-accepting chemotaxis protein (cheW)	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.9% 33.2.2% 24.2% 772.5% 23.9% 21.9% 24.2% 772.5% 26.8% 31.7% 27.9% 27.9% 27.9% 27.9% 27.9% 40.2% 40
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0665 gydramyte1NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobiniogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemE) HP0604 uroporphyrinogen decarboxylase (hemE) HP1360 (hemC) HP1360 (hemC) HP1360 (hemC) HP0929 geranytranstransferase (ispA) HP0929 geranytranstransferase (ispA) Octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdenum cofactor biosynthesis protein (moaC) HP0172 molybdenum cofactor biosynthesis protein (moaC) HP0799 molybdopterin biosynthesis protein (moeAF) HP0799 molybdopterin biosynthesis protein (moeAF) HP0799 molybdopterin biosynthesis protein (moeAF) HP0801 molybdopterin oonverting factor, subunit 2 (moaD) HP0801 molybdopterin converting factor, subunit 2	48.4% 35.1% 50.5% 33.4% 9 51.3% 51.3% 51.3% 61.379	HP0922 HP0283 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP0597 HP0597 HP0597 HP125 HP0493 HP1372 HP1645 HP1372 HP16740 HP1484 HP148 HP0648 HP0648 HP0648 HP0648 HP0649 HP0649 Surface poly	toxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane oxin-like outer membrane oxin-like outer oxin-like oxin-lik	26.3% 29.5% 30.6% 40.6% 40.6% 28.5% 40.6% 28.5% 35.0% 35.0% 35.0% 45.2% 35.9% 37.9% 31.9% 37.9% 31.9%	HP0797 HP0584 HP0601 HP06061 HP0295 HP1015 HP10295 HP10300 HP10300 HP10300 HP10301 HP0410 HP10	flagellar sheath adhesin hpaA flagellar sheith protein (fliN) flagellin A (flaA) flagellar switch protein (fliN) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla flagellin B flagellin protein (flaB) protein (flaB) protein flagellar protein flagellar protein flagellar motility bearengsqlutinin homologue (hpaA) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein flagellar motility haemolysin ty) haemolysin secretion protein protein flagellar motility-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis transducer (tlpC) purine-binding chemotaxis protein (cheW) cell division inhibitor (minD)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 22.3% 22.3% 25.5% 21.9% 24.2% 772.5% 31.7% 52.5% 31.7% 52.79% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 45.4% 41.4% 32.2% 40.2% 45.4% 41.4% 32.2% 50.2
HP0376 ferrochelatase (hemH) HP0306 (putamate1-semialdehyde 2,1-aminomutas (hemL) HP0265 (putamate1-semialdehyde 2,1-aminomutas (hemL) HP0266 (putamate1-semialdehyde 2,1-aminomutas (hemC) HP0267 (putamate1-semialdehyde) HP0268 (putamyt-HP0268) (putamyt-HP0268) (putamyt-HP0368)	48.4% 35.1% 50.5% 50.5% 51.3% 32.7% III 42.4% III 37.9% 45.7% 45.7% 45.7% 46.3% 27.6% 50.6% 31.4% C 97.9% 31.6% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4%	HP0922 HP0830 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0749 HP0749 HP0749 HP0749 HP0649 HP0743 HP1373 HP1372 HP0648 HP1643 HP1644 HP1418 HP0648 HP0648 HP0648 HP0648 HP0649 HP0649 Surface poly	toxin-like outer membrane protein amidase D-alanine-D-alanine ligase (adid) glutamate racemase (girl) N-acetylmuramoyl-lalanine amidase (amida penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp3) possible vita sascoiated protein (merB) rod shape-determining protein (merB) rod shape-determining protein (merB) rod shape-determining protein (merB) toxin-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-M-acetylenolpyruxoylglucosamine enolpyruxyl transferase (murE) UDP-M-acetylenolpyruxoylglucosamine enolpyruxyl transferase (murC) UDP-M-acetylmuramoylalanine-D-glutamate ligase (murC) UPP-M-acetylmuramoylalanine-D-glutamate ligase (murC) (sdsA)	26.3% 29.5% 30.6% 40.6% 28.6% 40.6% 28.8% 35.6% 35.6% 35.0% 35.0% 35.0% 42.6% 45.2% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2% 32.2% 31.2% 32.7% 46.7% 32.7% 46.7% 37.3% 31.1%	HP0797 HP0589 HP0601 HP06801 HP0601 HP0156 HP0295 HP12030 HP1927 HP1274 HP0761 HP0761 HP0761 HP0470 HP182 CELLULAR General HP0482 CELLULAR General HP0639 HP0333 HP067 HP0599 HP03302 HP0599 HP01302 HP0599 HP01302 HP0331 HP0391 Cell division	flagellar sheath adhesin hpaA flagellar sheith protein (fliN) flagellin A (flaA) flagellar switch protein (fliN) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) protein (fliP) hook assembly protein, flagella (flgD) paralysed flagellar protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) haemolysin haemolysin (fly) haemolysin secretion protein precursor (flyB) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) purine-binding chemotaxis protein (fleW) cell division inhibitor (minD) cell divisi	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.5% 24.2% 72.5% 23.9% 21.9% 24.2% 72.5% 29.6% 29.6% 29.6% 29.6% 29.6% 29.6% 29.6% 29.6% 31.7% 27.9%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0265 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemC) HP1267 oxidase (hemN) Oxygen-independent coproporphyrinogen Oxidase (hemN) Oxygen-independent coproporphyrinogen Oxidase (hemN) HP0231 profibobilinogen dearmoxylase (hemC) HP0681 uroporphyrinogen oxidase (hemC) HP1360 d-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltransferase (ispA) HP0929 geranyltransferase (spA) Octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (moaC) HP0712 molybdopterin biosynthesis protein (moaC) HP0739 molybdopterin biosynthesis protein (moaC) HP0801 molybdopterin biosynthesis protein (moaC) HP0802 molybdopterin biosynthesis protein (moaC) HP07039 molybdopterin onverting factor, subunit 2 (moaC) HP0802 molybdopterin converting factor, subunit 2 (moaC) HP0803 molybdopterin converting factor, subunit 2 (moaC) HP0804 molybdopterin onverting factor, subunit 2 (moaC) molybdopterin onverting factor, subunit 2 (moaC)	48.4% 35.1% 50.5% 33.4% 9 51.3% 51.3% 32.796 III 42.496 III 37.9% 45.7% 35.996 46.396 27.6% 26.6% 39.396 31.4% C C 97.996 32.2% 50.8% 31.1% 13.1% thresis	HP0922 HP09230 Murein sacc HP0830 Murein sacc HP0830 HP0830 HP0830 HP0949 HP0937 HP0937 HP0937 HP0937 HP0943 HP0943 HP0943 HP0943 HP1937 HP0943 HP1937 HP1937 HP1937 HP1937 HP1944 HP165 HP040 HP1944 HP1648 HP0648 HP0648 HP0648 HP06494 Surface poly HP09037	toxin-like outer membrane protein oxin-like outer membrane protein amidase D-alaninei-Dalanine ligase A (ddIA) glutamate racemase (gir) N-acetylmuramoyi-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp. penicillin-binding protein (ppp. penicillin-binding protein (ppp. pospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreC) solubie lytic murein transglycosylase (slt) toxR-activated gene (tagE) transferase, peptidoglycan synthesis (murG) UDP-MurNac-tripeptide presynthetase (murE) UDP-MurNac-tripeptide synthetase (murE) UDP-MurNac-tripeptide presynthetase (murE) UDP-MurSecylmuramoylalanine-D-glutamate ligase (murC) UDP-Nacetylmuramoylalanine-D-glutamate ligase (murD) saccharides, lipopolysaccharides and antig 3-deoxyd-manno-octulosonic acid transfera synthetiase (kdSA) 3-deoxyd-manno-octulosonic-acid transfera	26.3% 26.3% 30.6% 40.6% 28.8% 40.6% 28.8% 36.6% 28.8% 35.0% 35.0% 550r 42.6% 42.6% 42.7% 51.9% 51.9% 51.9% 51.9% 52.7% 51.9% 51.9% 52.7% 51.9% 52.7% 51.9% 52.7% 51.9% 52.7% 51.9% 52.7% 51.9% 52.7% 51.9% 52.7% 52.7% 52.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.4% 53.4% 53.4% 53.4%	HP0797 HP0597 HP0601 HP0601 HP0601 HP0161 HP0205 HP0007 HP10307 HP10307 HP0007 HP0407 HP041 HP0751 HP0410 HP1192 HP042 CELLULAR General HP0410 HP0593 HP0616 HP1067 HP06517 HP067 HP0680	flagellar sheath adhesin hpaA flagellar sheath protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) portein (flaB) portein (flaB) potential flagellar protein flagellar motility secreted protein involved in flagellar motility secreted protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin secretion protein protein protein flagellar motility in methy-accepting chemotaxis protein (tlpB) methy-accepting chemotaxis protein (tlpB) methy-accepting chemotaxis transducer (tlpC) purine-binding chemotaxis protein (cheW) cell division ripotein (flaS) protein (dlidsion membrane protein (flaS)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 22.3% 22.9% 40.5% 24.2% 772.5% 32.6% 21.9% 24.2% 772.5% 33.7% 25.6% 23.3% 22% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.3% 30.7% 50.2%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0283 glutamyt-1RNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP126 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0381 uroporphyrinogen oxidase (hemE) HP1224 uroporphyrinogen decarboxylase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) geranyltranstransferase (ispA) octaprenyl-tliphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein HP0788 molybdenum cofactor biosynthesis protein HP0789 molybdopterin biosynthesis protein (moaC) HP0172 molybdopterin biosynthesis protein (moaC) HP0799 molybdopterin biosynthesis protein (moaD) HP0800 molybdopterin converting factor, subunit 1 (moaD) HP0800 molybdopterin converting factor, subunit 2 (moaE) HP0769 molybdopterin-guanine dinucleotide biosyntotein dimoaD)	48.4% 35.1% 50.5% 50.5% 51.3% 32.7% III 42.4% III 37.9% 45.7% 45.7% 45.7% 46.3% 27.6% 50.6% 31.4% C 97.9% 31.6% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4% 31.4% C 97.9% 31.4%	HP0922 HP0820 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0549 HP0749 HP0697 HP0697 HP0697 HP0693 HP125 HP0493 HP0743 HP1373 HP1372 HP0648 HP1644 HP148 HP0648 HP0740 HP1494 HP1418 HP0648 HP0649 HP0649 HP06957	toxin-like outer membrane protein amidase D-alanine-D-alanine ligase (adid) glutamate racemase (girl) N-acetylmuramoyl-Lalanine amidase (amida penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein (ppp1) prospho-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-M-acetylenolpyruxoylglucosamine enolpyruxyl transferase (murE) UDP-N-acetylmuramoylalanine-D-glutamate ligase (murC) UDP-N-acetylmuramoylalanine-D-glutamate ligase (murC) UPN-N-acetylmuramoylalanine-D-glutamate ligase (murC) 3-deoxyd-manno-octulosonic acid 8-phospi synthetase (KdsA) 3-deoxyd-manno-octulosonic-acid transferase (kdtA)	26.3% 29.5% 40.6% 40.6% 28.6% 40.6% 28.8% 35.6% 35.6% 35.0% 35.0% 35.0% 42.6% 45.2% 37.7% 51.9% 32.2% 31.2% 32.2% 31.2% 32.2% 31.2% 32.7% 46.7% 32.7% 46.7% 37.3% 31.1% 46.7%	HP0797 HP0598 HP0601 HP0601 HP0601 HP0615 HP0295 HP1274 HP0761 HP0761 HP0761 HP0761 HP0761 HP0762 CELLULAR General HP0622 CELLULAR General HP0639 HP0639 HP067 HP067 HP0699 HP0699 HP0103 HP0699 HP0103 HP0039 HP0103 HP00391 Call division HP0311 Call division	flagellar sheath adhesin hpaA flagellar sheath protein (flin) flagellin A (flaA) flagellar switch protein (flin) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin G flaB) protein (fling) flow protein (fling) protein (fling) protein (fling) protein flagellar protein flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) haemolysin secretion protein proteursor (flyB) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) cell division inhibitor (minD) cell division membrane protein (fltaX) cell division protein (flsA) protein cell division protein (flsA) protein cell division protein (flsA) protein cell division protein (flsA)	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.5% 23.9% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 29.5% 21.9%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0265 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0266 glutamyte1-semialdehyde 2,1-aminomutas (hemN) HP0261 oxygen-independent coproporphyrinogen oxidase (hemN) Oxygen-independent coproporphyrinogen Oxidase (he	48.4% 35.1% 50.5% 33.4% 6 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 50.8% 31.4% C 97.9% 31.4% C 97.9% 31.1% 13.63% 31.1% 45.2% 50.8% 31.1% 46.3% 46.3% 46.	HP0922 HP0280 Murein sacc Murein sacc HP0280 HP0380 HP0038 HP0049 HP0078 HP0049 HP0078 HP0043 HP0043 HP0043 HP0043 HP0743 HP0743 HP0743 HP0743 HP1372 HP0645 HP1544 HP1155 HP0740 HP1494 HP1418 HP0648 HP0648 HP0648 HP06494  Surface poly HP00957 HP00957	toxin-like outer membrane protein oxin-like outer membrane protein available of the protein oxin-like outer membrane protein oxin-like outer membrane (girl) N-acetylmuramoyl-Lalanine amidase (amida penicillin-binding protein 12 (pbp2) prosspho-N-acetylmuramoyl-pentapeptide-transferase (mray) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-determining protein	26.3% 26.3% 29.5% 30.6% 40.6% 28.5% 40.6% 28.5% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 37.7% 51.9% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 31.2% 31.2% 31.3% 46.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 31.1% 67.7% 37.3% 37.3% 37.3% 37.3% 37.3% 37.3% 37.3% 37.3% 37.3%	HP0797 HP0597 HP05801 HP06801 HP06801 HP06801 HP01801 HP01801 HP01801 HP01801 HP10801 HP10801 HP10801 HP10801 HP10801 HP0801 HP0801 HP0801 HP0801 HP0808	flagellar sheath adhesin hpaA flagellar sheath protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flagellin B flagellin B (flaB) flagellin B homologue (flaB) flispellin B homologue (flaB) flispellin B homologue (flaB) protein (flaB) potar flagellin protein (flaB) putative neuraminyllactose-bindin heamogglutinin homologue (flaB) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin tyl) haemolysin tyl) haemolysin tyl) haemolysin secretion protein protein (flaB) methyl-accepting chemotaxis protein (flaB) methyl-accepting chemotaxis protein (flaB) methyl-accepting chemotaxis transducer (flpC) purine-binding chemotaxis protein (fleW) cell division protein (flaB) protein (dlisB) protein (flaB) protein (dlisBi) protein (flaB)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 22.3% 22.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 33.0% 40.5% 31.7% 31.7% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.3% 30.7% 50.2% 32.9% 30.7% 50.2%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyte1NNA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1266 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphybrinogen oxidase (hemC) HP0681 uroporphyrinogen oxidase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyttranstransferase (ispA) octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0798 molybdenum cofactor biosynthesis protein A (moaA) HP0799 molybdopterin biosynthesis protein (moaA) HP0799 molybdopterin biosynthesis protein (moaA) HP0799 molybdopterin biosynthesis protein (moaA) HP0800 molybdopterin biosynthesis protein (moaD) HP0800 molybdopterin converting factor, subunit 1 (moaC) HP0790 molybdopterin converting factor, subunit 2 (moaE) HP0790 molybdopterin converting factor, subunit 3 molybdopterin aconverting factor, subunit	48.4% 35.1% 50.5% 33.4% 6 6 8 13.4% 13.27% 11.2% 12.76% 12.76% 12.76% 13.5.9% 46.3% 27.6% 26.6% 31.8% 31.6% 13.4% C 97.99% 31.6% 13.4% C 97.99% 31.4% 13.4%	HP0922 HP0820 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0549 HP0749 HP0697 HP0697 HP0697 HP0693 HP125 HP0493 HP0743 HP1373 HP1372 HP0648 HP1644 HP148 HP0648 HP0740 HP1494 HP1418 HP0648 HP0649 HP0649 HP06957	toxin-like outer membrane protein amidase (amidase D-alanine-D-alanine ligase (amidase (amidase (amidase) penicillin-binding protein 2 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (ppp3) prospho-N-acetylmuramoyl-pentapeptide-transferase (mary) od shape-determining protein (mreB) toxin-activated gene (tagE) UDP-M-acetylenolpyruvoylglucosamine enolpyruvyl transferase (murE) UDP-N-acetylmuramoylalanine-D-glutamate ligase (murC) (tagA) adeoxyd-manno-octulosonic acid 8-phospi synthetase (kūsA) a-deoxyd-manno-octulosonic-acid transferase (kūtA) ADP-heptose synthase (faE) ADP-heptose synthase (faE) ADP-heptose synthase (faE)	26.3% 26.3% 28.5% 30.6% 40.6% 28.5% 40.6% 28.5% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 37.7% 51.9% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 33.2% 33.2% 33.2% 33.2% 33.3% 46.5% 33.3%	HP0797 HP0584 HP0601 HP06061 HP0295 HP0157 HP1030 HP1030 HP1030 HP1030 HP1030 HP1031 HP0410 HP1032 CELLULAR General HP0482 HP0232 CELLULAR General HP0333 HP0033 HP0067 HP1067 HP1067 HP1089 HP1088 HP	flagellar sheath adhesin hpaA flagellar sheath protein (flin) flagellin A (flaA) flagellin A (flaB) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin B homologue (flaB) flagellin G flaB) flagellin G flaB) flagellin G flaB (flaB) protein (flaB) protein (flaB) protein (flaB) protein (flaB) protein flagellin (flaG) putative neuraminyllactose-binding haemaglutinin homologue (flaB) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) flaemolysin flagelline kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) cell division inhibitor (minD) cell division membrane protein (ftaX) cell division protein (flsH) cell division protein (flsH)	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.5% 23.9% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 29.5% 21.9%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0265 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemK) Axygen-independent coproporphyrinogen oxidase (hemN) Oxygen-independent coproporphyrinogen oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemX) Oxid	48.4% 35.1% 50.5% 33.4% 6 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 50.8% 31.4% C 97.9% 31.4% C 97.9% 31.1% 13.63% 31.1% 50.8% 31.19% 31.19% 46.3% 4	HP0922 HP0280 Murein sacc HP0280 Murein sacc HP0830 HP0638 HP0649 HP0732 HP0697 HP0697 HP0697 HP0733 HP0743 HP0743 HP0743 HP0743 HP0743 HP1372 HP0645 HP1544 HP165 HP0740 HP1694 HP0646 HP164 HP0648 HP0648 HP0648 HP06494  Surface poly HP06957 HP06967 HP06967 HP06967 HP06968 HP1191	toxin-like outer membrane protein oxin-like outer membrane protein oxin-like outer membrane protein amidase D-alanine-D-alanine ligase A (ddIA) glutamate racemase (gir) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) penicillin-binding protein 2 (pbp2) prosspho-N-acetylmuramoyl-pentapeptide-transferase (mraY) rod shape-determining protein (mreB) rod shape-determining protein (mreB) rod shape-determining protein (mreB) toxin-acetylated gene (tagE) toxin-determining protein (mreB) toxin-acetylated gene (tagE) transferase, peptiloglycan synthesis (murG) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide prosynthetase (murE) UDP-MurNac-pentapeptide presynthetase (murE) UDP-MurNac-pentapeptide pres	26.3% 26.3% 28.5% 30.6% 40.6% 28.5% 40.6% 28.5% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 36.6% 37.7% 51.9% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.7% 51.9% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 33.2% 33.2% 33.2% 33.2% 33.3% 46.5% 33.3%	HP0797 HP0584 HP0601 HP06061 HP0295 HP0157 HP1030 HP1030 HP1030 HP1030 HP1030 HP1031 HP0410 HP1032 CELLULAR General HP0482 HP0232 CELLULAR General HP0333 HP0033 HP0067 HP1067 HP1067 HP1089 HP1088 HP	flagellar sheath adhesin hpaA flagellar sheath protein (flin) flagellin A (flaA) flagellin A (flaA) flagellin A (flaB) flagellin B homologue (flaB) flispellin B homologue (flaB) flispellin B (flaB) flagellin B homologue (flaB) protein (flaB) purative neuraminyllactose-bindin paemagglutinin homologue (flaB) pustative neuraminyllactose-bindin beamagglutinin homologue (flaB) secreted protein involved in flagellar motility secreted protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin secretion protein protein flaB) historiae kinase (cheA) methyl-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis transducer (tlpC) cell division protein (flsE)	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.5% 23.9% 21.9% 24.2% 72.5% 29.6 29.6 29.6 29.6 29.6 29.6 29.6 29.6
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0269 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyte1-semialdehyde 2,1-aminomutas (hemL) HP0666 glutamyte1NA reductase (hemA) oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphyrinogen oxidase (hemC) HP0681 uroporphyrinogen oxidase (hemE) HP1680 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) octaprenyl-diphosphate synthase (hemD) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0798 molybdenum cofactor biosynthesis HP0798 molybdenum cofactor biosynthesis HP0799 molybdopterin biosynthesis protein (moaA) HP0799 molybdopterin biosynthesis protein (moaA) HP0799 molybdopterin biosynthesis protein (moaB) HP0800 molybdopterin converting factor, subunit 1 (moaC) HP0799 molybdopterin converting factor, subunit 1 (moaC) HP0799 molybdopterin converting factor, subunit 2 (moaE) HP0799 molybdopterin converting factor, subunit 3	48.4% 35.1% 50.5% 35.1% 50.5% 33.4% 6 6 8 13.4% 6 142.4% 11 27.6% 27.6% 45.7% 45.7% 50.8% 31.4% C 97.9% 31.4% C 50.6% 31.5% 50.8%	HP0922 HP0283 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0549 HP0737 HP0597 HP0597 HP0597 HP0597 HP0597 HP0648 HP1544 HP165 HP0740 HP1494 HP1494 HP165 HP0648 HP0648 HP0648 HP0649 HP0603 HP0697 HP06059 HP06056 HP06068	toxin-like outer membrane protein amidase (amidase D-alanine-D-alanine ligase (amidase (amidase (amidase) penicillin-binding protein 2 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (ppp3) prospho-N-acetylmuramoyl-pentapeptide-transferase (mary) od shape-determining protein (mreB) toxin-activated gene (tagE) UDP-M-acetylenolpyruvoylglucosamine enolpyruvyl transferase (murE) UDP-N-acetylmuramoylalanine-D-glutamate ligase (murC) (tagA) adeoxyd-manno-octulosonic acid 8-phospi synthetase (kūsA) a-deoxyd-manno-octulosonic-acid transferase (kūtA) ADP-heptose synthase (faE) ADP-heptose synthase (faE) ADP-heptose synthase (faE)	26.3% 26.3% 29.5% 40.6% 40.6% 28.5% 40.6% 28.5% 40.6% 28.5% 35.0% 35.0% 42.6% 45.2% 37.7% 45.6% 45.2% 37.7% 45.6% 32.2% 37.7% 36.0% 32.7% 46.7% 33.7% 46.7% 33.5% 36.9% 32.7% 46.7% 33.5% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.3%	HP0797 HP0587 HP06801 HP06801 HP06801 HP06801 HP0181 HP0295 HP1030 HP1030 HP1030 HP1030 HP0274 HP0751 HP0470 HP0751 HP0470 HP047	flagellar sheath adhesin hpaA flagellar sheath protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaB) flagellin B homologue (fla) flab protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagellar protein (flaB) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) GTP-binding protein (cheV) GTP-binding protein (cheV) haemolysin (th) haemolysin secretion protein precursor (fylB) haemolysin secretion protein protein (flaB) methyl-accepting chemotaxis protein (flpB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsK) cell division prot	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 22.9% 40.5% 21.9% 24.2% 26.5% 23.9% 21.9% 24.2% 26.6% 31.7% 27.9% 31.7% 40.2% 40.2% 40.2% 40.5% 31.7% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.3% 31.9%
HP0376 ferrochelatase (hemH) HP0376 glutamate1-semialdehyde 2,1-aminomutas (hemL) HP0265 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemL) HP0665 glutamyt-1-semialdehyde 2,1-aminomutas (hemK) Axygen-independent coproporphyrinogen oxidase (hemN) Oxygen-independent coproporphyrinogen oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemN) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemK) Oxidase (hemX) Oxid	48.4% 35.1% 50.5% 33.4% 6 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9% 46.3% 27.6% 50.8% 31.4% C 97.9% 31.4% C 97.9% 31.1% 13.63% 31.1% 50.8% 31.19% 31.19% 46.3% 4	HP0922 HP0283 Murein sacc HP0830 Murein sacc HP0830 HP0738 HP0549 HP0737 HP0597 HP0597 HP0597 HP0597 HP0597 HP0648 HP1544 HP165 HP0740 HP1494 HP1494 HP165 HP0648 HP0648 HP0648 HP0649 HP0603 HP0697 HP06059 HP06056 HP06068	toxin-like outer membrane protein amidase (amidase D-alanine-D-alanine ligase (amidase (amidase (amidase)) amidase (amidase (amidase)) amidase (amidase) amidase (amidase (amidase) (amidase (amidase) (	26.3% 26.3% 29.5% 40.6% 40.6% 28.5% 40.6% 28.5% 40.6% 28.5% 35.0% 35.0% 42.6% 45.2% 37.7% 45.6% 45.2% 37.7% 45.6% 32.2% 37.7% 36.0% 32.7% 46.7% 33.7% 46.7% 33.5% 36.9% 32.7% 46.7% 33.5% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.1% 46.7% 37.3% 31.3%	HP0797 HP0587 HP06801 HP06801 HP06801 HP0691 HP0181 HP0295 HP1274 HP1274 HP1274 HP0751 HP1274 HP0751 HP0274 HP0751	flagellar sheath adhesin hpaA flagellar sheath protein (fliN) flagellin A (flaA) flagellin A (flaA) flagellin A (flaB) flagellin B homologue (fla) flab protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagellar protein (flaB) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) GTP-binding protein (cheV) GTP-binding protein (cheV) haemolysin (th) haemolysin secretion protein precursor (fylB) haemolysin secretion protein protein (flaB) methyl-accepting chemotaxis protein (flpB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsB) cell division protein (flsK) cell division prot	39.7% 99.8% 99.0% 32.9% 40.5% 22.3% 22.5% 23.9% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 21.9% 24.2% 79.5% 29.5% 29.5% 21.9%

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%	HP1101	glucose-6-phosphate dehydrogenase (g6pD)	36.7%
HP1159	cell filamentation protein (fic)	63.2%	HP1271	NADH-ubiquinone oxidoreductase, NQO12		HP1495	transaldolase (tal)	33.5%
Cell killing	unautalating autotoxia 04.70/		HP1272	subunit (NQO12) NADH-ubiquinone oxidoreductase, NQO13	43.2%	HP1088 HP0354	transketolase A (tktA) transketolase B (tktB)	46.7% 39.7%
HP0887 Chaperones	vacuolating cytotoxin 94.7%			subunit (NQO13)	40.2%	Sugars		
HP0010	chaperone and heat shock protein (groEL)	99.6%	HP1273	NADH-ubiquinone oxidoreductase, NQO14 subunit (NQO14)	31.2%	HP0574 HP0360	galactosidase acetyltransferase (lacA) UDP-glucose 4-epimerase	41.0% 43.1%
HP0109	chaperone and heat shock protein 70 (dnaK)	63.4%	HP1266	NADH-ubiquinone oxidoreductase, NQO3	04.00/	TCA cycle	ODI giacose 4 epimerase	40.170
HP0210	chaperone and heat shock protein C62.5 (htpG)	46.5%	HP1263	NADH-ubiquinone oxidoreductase,	31.6%	HP0779 HP0026	aconitase B (acnB) citrate synthase (gltA)	64.0% 47.8%
HP0011	co-chaperone (groES)	99.2%	HP1262	NQO4 subunit (NQO4){Triticum aestivum} NADH-ubiquinone oxidoreductase, NQO5	44.6%	HP1325	fumarase (fumC)	63.7%
HP1332	co-chaperone and heat-shock protein (dnal)	42.7%		subunit (NQO5)	-1.0%	HP0509 HP0027	glycolate oxidase subunit (glcD) isocitrate dehydrogenase (icd)	98.0% 70.7%
HP0110	co-chaperone and heat-shock protein		HP1261	NADH-ubiquinone oxidoreductase, NQO6 subunit (NQO6)	62.2%			70.770
HP1024	(grpE) co-chaperone-curved DNA-binding protein	33.0% A	HP1260	NADH-ubiquinone oxidoreductase, NQO7			AND PHOSPHOLIPID METABOLISM	
111 102 1		37.7%	HP1267	subunit (NQO7) NADH-ubiquinone oxidoreductase, NQO8	40.7%	General HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein)	
	ne-associated protein plasmid replication-partition related protein	40.4%		subunit (NQO8)	42.4%	HP1348	dehydratase (fabZ) 1-acyl-glycerol-3-phosphate acyltransferase	47.4%
Detoxification		40.470	HP1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	41.2%		(plsC) (Escherichia coli)	32.0%
HP1563	alkyl hydroperoxide reductase (tsaA)	98.5% 99.4%	Amino acid	s and amines		HP0561	3-ketoacyl-acyl carrier protein reductase (fabG)	45.7%
HP0875 HP0267	catalase chlorohydrolase	42.6%	HP1398 HP0294		39.6% 75.4%	HP0690	acetyl coenzyme A acetyltransferase	
HP0243	neutrophil activating protein (napA) (bacterioferritin)	95.8%	HP1238	aliphatic amidase (aimE)	37.2%	HP0950	(thiolase) (fadA) acetyl-CoA carboxylase beta subunit	52.0%
HP0389	superoxide dismutase (sodB)	98.6%	HP1399 HP0943		31.8% 26.2%	HP1045	(accD)	49.4% 52.3%
	thiophene and furan oxidizer (tdhF)	37.6%	HP0056	delta-1-pyrroline-5-carboxylate dehydrogenas	se 32.2%	HP0557	acetyl-CoA synthetase (acoE) acetyl-coenzyme A carboxylase (accA)	50.3%
HP0355	I peptide secretion GTP-binding membrane protein (lepA)	57.3%	HP0723	L-asparaginase II (ansB)	54.1%	HP0559 HP0962	acyl carrier protein (acpP) acyl carrier protein (acpP)	55.3% 56.3%
HP0074 HP0786	lipoprotein signal peptidase (IspA) preprotein translocase subunit (secA)	97.0% 54.0%	HP0132	L-serine deaminase (sdaA)	45.8%	HP0558	beta ketoacyl-acyl carrier protein synthase	II
HP1300	preprotein translocase subunit (secY)	41.2%	Anaerobic HP0666	anaerobic glycerol-3-phosphate dehydrogen	ase,	HP0202	(fabF) beta-ketoacyl-acyl carrier protein synthase	50.0% III
HP1255	protein translocation protein, low temperatu (secG)	ire 30.6%	HP0589	subunit C (glpC)	27.2% 42.7%		(fabH)	44.4%
HP1550	protein-export membrane protein (secD)	38.9%	HP0590	ferredoxin oxidoreductase, beta subunit	43.2%	HP0371 HP0370	biotin carboxyl carrier protein (fabE) biotin carboxylase (accC)	30.8% 52.1%
HP1549 HP0576	protein-export membrane protein (secF) signal peptidase I (lepB)	35.1% 40.3%	HP0591 HP0193	ferredoxin oxidoreductase, gamma subunit fumarate reductase, cytochrome b subunit	33.3%	HP0871	CDP-diglyceride hydrolase (cdh)	73.9% 42.4%
HP1152	signal recognition particle protein (ffh)	41.4%		(frdC)	58.8%	HP0215 HP0416	CDP-diglyceride synthetase (cdsA) cyclopropane fatty acid synthase (cfa)	39.7%
HP0795 Transforma	trigger factor (tig)	27.6%	HP0192	fumarate reductase, flavoprotein subunit (frdA)	69.4%	HP0700 HP0195	diacylglycerol kinase (dgkA) enoyl-(acyl-carrier-protein) reductase (NADI	45.8%
HP0520	cag pathogenicity island protein (cag1)	96.5%	HP0191	fumarate reductase, iron-sulfur subunit			(fabl)	45.8%
HP0530 HP0531	cag pathogenicity island protein (cag10) cag pathogenicity island protein (cag11)	98.4% 97.2%	HP1110	(frdB) pyruvate ferredoxin oxidoreductase, alpha	70.8%	HP0201	fatty acid/phospholipid synthesis protein (plsX)	37.8%
HP0532	cag pathogenicity island protein (cag12)	98.9%		subunit	41.0%	HP0808	Holo-acp synthase (acpS)	29.1%
HP0534 HP0535	cag pathogenicity island protein (cag13) cag pathogenicity island protein (cag14)	98.0% 97.6%	HP1111		43.7%	HP0090	malonyl coenzyme A-acyl carrier protein transacylase (fabD)	35.4%
HP0536	cag pathogenicity island protein (cag15)	96.4% 98.9%	HP1109	pyruvate ferredoxin oxidoreductase, delta subunit	47.0%	HP1016	phosphatidylglycerophosphate synthase	
HP0537 HP0538	cag pathogenicity island protein (cag16) cag pathogenicity island protein (cag17)	95.3%	HP1108	pyruvate ferredoxin oxidoreductase, gamma	ı	HP1357	(pgsA) phosphatidylserine decarboxylase proenzyl	35.4% me
HP0539 HP0540	cag pathogenicity island protein (cag18) cag pathogenicity island protein (cag19)	98.7% 99.5%	4 TD		37.2%		(psd)	33.2%
HP0521	cag pathogenicity island protein (cag2)	92.5%	HP0828	motive force interconversion ATP synthase FO, subunit a (atpB)	37.7%	HP1071 HP0499	phosphatidylserine synthase (pssA) phospholipase A1 precursor	99.6%
HP0541 HP0542	cag pathogenicity island protein (cag20) cag pathogenicity island protein (cag21)	97.8% 97.9%	HP1136 HP1137	ATP synthase FO, subunit b (atpF)	28.3% 32.5%		(DR-phospholipase A)	33.8%
HP0543	cag pathogenicity island protein (cag22)	95.5%	HP1212	ATP synthase FO, subunit c (atpE)	41.2%	PURINES, P	YRIMIDINES, NUCLEOSIDES AND NUCLEO	OTIDES
HP0544 HP0545	cag pathogenicity island protein (cag23) cag pathogenicity island protein (cag24)	99.0% 98.5%	HP1134 HP1132		62.7% 85.6%	General	hata alapina aunthatasa hamalagua	40.0%
HP0546 HP0547	cag pathogenicity island protein (cag25)	95.7% 92.9%	HP1135	ATP synthase F1, subunit delta (atpH)	24.6%	HP0757 2Õ-Deoxvrib	beta-alanine synthetase homologue conucleotide metabolism	40.0%
HP0522	cag pathogenicity island protein (cag26) cag pathogenicity island protein (cag3)	98.1%	HP1131 HP1133		32.7% 37.8%	HP0372	deoxycytidine triphosphate deaminase	00.00/
HP0523 HP0524	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5)	95.7% 99.1%	Electron tra	nsport		HP0865	(dcd) deoxyuridine 5Õ-triphosphate nucleotidohyd.	28.2% rolase
HP0526	cag pathogenicity island protein (cag6)	97.5%	HP0146	cbb3-type cytochrome c oxidase subunit Q (CcoQ)	44.2%		(dut)	41.4%
HP0527 HP0528	cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8)	94.6% 99.0%	HP0265	cytochrome c biogenesis protein (ccdA)	35.4%	HP0364	ribonucleoside diphosphate reductase, beta subunit (nrdB)	a 39.0%
HP0529	cag pathogenicity island protein (cag9)	98.9%	HP0378 HP0147	cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit,	37.5%	HP0680	ribonucleoside-diphosphate reductase 1 alg subunit (nrdA)	pha 28.4%
HP1378 HP1361	competence lipoprotein (comL) competence locus E (comE3)	25.5% 26.7%		membrane-bound (fixP)	33.0%	HP0825	thioredoxin reductase (trxB)	45.9%
HP1006	conjugal transfer protein (traG)	27.3%	HP0144	cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixN)	43.9%		nucleotide biosynthesis	44.8%
HP1421 HP0333	conjugative transfer regulon protein (trbB) DNA processing chain A (dprA)	30.7% 32.9%	HP0145	cytochrome c oxidase, monoheme subunit,	45.7%	HP0321 HP0618	50-guanylate kinase (gmk) adenylate kinase (adk)	33.3%
HP0042 HP0525	trbl protein virB11 homologue	31.4% 100.0%	HP1461	cytochrome c551 peroxidase	48.5%	HP1112 HP0255	adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA)	49.5% 44.6%
HP0441			HP1227		38.4%	HPU200	formyltetrahydrofolate hydrolase (purU)	49.1%
HP0017	VirB4 homologue	23.5%			52 506	HP1434		
HP0459	VirB4 homologue virB4 homologue (virB4)	23.5% 25.2%	HP0277 HP0588	ferrodoxin-like protein	52.5% 42.6%	HP1218	glycinamide ribonucleotide synthetase	
HP0459	VirB4 homologue virB4 homologue (virB4) virB4 homologue (virB4)	23.5%	HP0277 HP0588 HP1508	ferrodoxin-like protein ferrodoxin-like protein	42.6% 29.4%	HP1218 HP0854	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC)	31.8% 31.8%
CENTRAL II	VirB4 homologue virB4 homologue (virB4)	23.5% 25.2%	HP0277 HP0588 HP1508 HP1161 HP0642	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase	42.6% 29.4% 47.0% 46.1%	HP1218 HP0854 HP0409	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA)	31.8%
CENTRAL II General HP1014	VirB4 homologue virB4 yourB4 homologue (virB4) virB4 homologue (virB4) NTERMEDIARY METABOLISM 7hydroxysterold dehydrogenase (hdhA)	23.5% 25.2% 25.3% 33.2%	HP0277 HP0588 HP1508 HP1161	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase	42.6% 29.4% 47.0% 46.1% 32.7%	HP1218 HP0854 HP0409 HP0829	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-5Ö-monophosphate dehydrogenase (guaB)	31.8% 31.8% 56.1%
CENTRAL II General HP1014 HP1186	VirB4 homologue virB4 homologue (virB4) virB4 homologue (virB4) NTERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase	23.5% 25.2% 25.3% 33.2% 37.0%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% brome	HP1218 HP0854 HP0409	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-6O-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk)	31.8% 31.8% 56.1% 58.5% 67.7%
CENTRAL II General HP1014	VirB4 homologue virB4 homologue (virB4) virB4 homologue (virB4)  NTERMEDIARY METABOLISM  7-α-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (icfA) hydrogenase expression/formation protein	23.5% 25.2% 25.3% 33.2% 37.0% 33.3%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch	42.6% 29.4% 47.0% 46.1% 32.7% 54.7%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA)	31.8% 31.8% 56.1% 58.5% 67.7%
CENTRAL II General HP1014 HP1186 HP0004 HP0869	VirB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) NTERMEDIARY METABOLISM 7-α-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (cifA) hydrogenase expression/formation protein (hypA)	23.5% 25.2% 25.3% 33.2% 37.0%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634 HP0633 HP0632	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydC) subunit (hydC)	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% brome	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB)	31.8% 31.8% 56.1% 58.5% 67.7%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900	VirB4 homologue (virB4) virB4 homologue virB4 vi	23.5% 25.2% 25.3% 33.2% 37.0% 33.3%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634 HP0633 HP0632	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydB)	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% hrome 51.4%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarmoylase (pyrB)	31.8% 31.8% 56.1% 58.5% 67.7%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900 HP0899	VirB4 homologue virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4)  NTERMEDIARY METABOLISM  7-α-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (icIA) hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC)	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634 HP0633 HP0632	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flown oxidoreductase oxygen-insensitive NAD(P)H-fliroreductase oxygen-insensitive NAD(P)H-fliroreductase quinone-reactive Ni/Fe hydrogenase, (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinone-reactive Ni/Fe hydrogenase, small subunit (hydA)	42.6% 29.4% 47.0% 47.0% 46.1% 52.7% 54.7% irome 54.7% 668.5%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084 HP0919	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-60-monophosphate dehydrogenase (guaB) inosine-60-monophosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) irbonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900	VirB4 homologue virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4)  NTERMEDIARY METABOLISM  7-α-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (idA) hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) (hypC)	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634 HP0633 HP0632	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(PIH-Interodoxin-like protein flavodoxin (fldA) NAD(PIH-Introreductase oxygen-insensitive NAD(PIH-Introreductase quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoch guinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinot-tytochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinot cytochrome c oxidoreductase, vytochrome b subunit (flbcH) ubiquinot cytochrome oxidoreductase,	42.6% 29.4% 47.0% 47.0% 46.1% 53.7% 54.7% 1070 68.5% 68.9% 39.3%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084 HP0919 HP1237	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarmoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrRa)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900 HP0899	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5% 47.8%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0954 HP0634 HP0633 HP0632 HP0631 HP1539	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(PIH-Introreductase oxygen-insensitive NAD(PIH-Introreductase oxygen-insensitive NAD(PIH-Introreductase oxygen-insensitive NAD(PIH-Introreductase oxygen-insensitive NI/Fe hydrogenase, cyfoch b subunit (hydC) quinone-reactive NI/Fe hydrogenase, large subunit (hydB) quinone-reactive NI/Fe hydrogenase, large subunit (hydB) ubiquinot-tytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinot cytochrome c oxidoreductase, cytochrome c1 subunit (fbcH) ubiquinot cytochrome c3 subunit (fbcH) ubiquinot cytochrome c4 subunit (fbcH) ubiquinot cytochrome c4 subunit (fbcH) ubiquinot cytochrome c4 subunit (fbcH) ubiquinot cytochrome c5 subunit (fbcH) ubiquinot c5 s	42.6% 29.4% 47.0% 45.1% 32.7% 54.7% forome 51.4% 68.5% 68.5%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0249 HP0266	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbarmoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) CTP synthetase (pyrC)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0899 HP0899 HP0898 HP0047	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 47.8% 39.7%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0634 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe pydrogenase, oxtoci b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) ubiquinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c1 subunit (fbcH) ubiquinol cytochrome c2 oxidoreductase, Rieske 2Fe-25 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-25 subunit (fbcH)	42.6% 29.4% 47.0% 47.0% 46.1% 53.7% 54.7% 1070 68.5% 68.9% 39.3%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0349 HP0266 HP0581	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) inosine-50-monophosphate synthetase (prsA) purine nucleoside diphosphorphate synthetase (prsA) purine nucleoside phosphorylase (punB) irbonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrGa) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900 HP0899	VirB4 homologue virB4 homologue (virB4) VirB4 homologue expression/formation protein (typB4) VirB4 homologue expression/formation protein (typB6) VirB4 homologue VirB	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 47.8% 39.7%	HP0277 HP0588 HP1508 HP1161 HP0642 HP0634 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Entmer-Dou	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD[P]H-florin oxidoreductase oxygen-insensitive NAD[P]H-florin oxidoreductase quinone-reactive Ni/Fe progenase (hydD) quinone-reactive Ni/Fe Progenase, cytoch subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) ubinone-reactive Ni/Fe hydrogenase, snall subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, rytochrome c oxidoreductase, rytochrome c oxidoreductase, Rieske 2-Fe-28 subunit (fbcF) doroff	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 608.5% 68.5% 68.5% 68.9% 39.3%	HP1218 HP0854 HP0409 HP0854 HP0198 HP0742 HP1530 Pyrimidine I HP1084 HP0919 HP1237 HP0349 HP0266 HP0681 HP1051	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) irbonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrC)	31.8% 31.8% 56.1% 56.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 41.5%
CENTRAL II  General HP1014 HP1186 HP0004 HP0869 HP0900 HP0899 HP0899 HP0898 HP0047 HP0197	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 41.4% 38.5% 47.8% 39.7% 62.1%	HP0277 HP0588 HP1608 HP1618 HP1618 HP0642 HP0954 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Entmer-Dou HP1099	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD[P]H-florin oxidoreductase oxygen-insensitive NAD[P]H-florin oxidoreductase quinone-reactive Ni/Fe progenase (hydD) quinone-reactive Ni/Fe Progenase, cytoch subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2-Fe-2S subunit (fbcH) duriquinol cytochrome c oxidoreductase, Rieske 2-Fe-2S subunit (fbcH) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda)	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 608.5% 68.5% 68.5% 68.9% 39.3% 92.8% 93.3%	HP1218 HP0854 HP0409 HP0829 HP0198 HP0742 HP1530 Pyrimidine r HP1084 HP0919 HP0266 HP0349 HP0266 HP0581 HP1011 HP1051 HP1011 HP1051 HP1011 HP1051 HP1011 HP1051 HP10055	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ribonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrD) orotate phosphoribosyltransferase (pyrC)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 39.0%
CENTRAL II  General HP1014 HP1186 HP0004 HP0869 HP0899 HP0898 HP0047 HP0197 Amino suge	Virfl4 homologue virfl4) virfl4 homologue (virfl4) virfl4 homologue extreosion/homologue extreosion/homologue expression/formation protein (hypd) hydrogenase expression/formation protein (hypd) hydrogenase expression/formation protein (hypd) hydrogenase expression/formation protein (hypd) hydrogenase expression/formation protein (hypd) sadenosylmethionine synthetase 2 (metX) are glucosamine fructose-6-phosphate aminotransferase (isomerzing) (glmS)	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5% 47.8% 39.7%	HP0277 HP0588 HP1608 HP1161 HP0642 HP06954 HP0633 HP0633 HP0631 HP1539 HP1538 HP1540 Entner-Dou HP1099	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-florodoxin (fldA) nad(	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 10.70m 65.5% 68.5% 68.5% 68.8% 39.3%	HP1218 HP0854 HP0409 HP0854 HP0198 HP0742 HP1530 Pyrimidine I HP1084 HP0919 HP1237 HP0349 HP0266 HP0681 HP1051	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis asparatae transcariamoylase (purB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) rotdine 50-hosphate dearboxylase (pyrF) tymidylate kinase (trik) uridine 50-monophosphate (UMP) kinase	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% 41.0% 31.5% 41.5% 41.5% 35.5% (33.9%
CENTRAL II General HP1014 HP1186 HP0004 HP0869 HP0900 HP0899 HP0898 HP0047 HP0197 Amino suga Phosphorus HP0620	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 32.2% 37.0% 33.3% 28.1% 33.3% 33.3% 38.5% 41.4% 38.5% 47.8% 62.1% 50.0% 50.0% 50.0% 50.0% 50.0% 50.0%	HP0277 HP0588 HP1608 HP1618 HP1618 HP0642 HP0954 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Entmer-Dou HP1099	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) nad(P)H-florodoxin (fldA) nad(P)H-florodoxin (fldA) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (flydB) quinone-reactive Ni/Fe hydrogenase, large subunit (flydB) subunit (flydB) subunit (flydB) ubiquinol-qtochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (flbcH) ubiquinol cytochrome c oxidoreductase, relacion (floF) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (flbcH) ubiquinol cytochrome c oxidoreductase, fleske 2Fe-2S subunit (flbcF) 2-keto-3-deoxy-6-phosphogluconate aldolase (edd) -5-hosphogluconate dehydratase	42.6% 42.6% 42.0% 47.0% 45.1% 52.7% 54.7% 67.7% 68.5% 68.5% 68.9% 39.3% 39.3% 50.3% 50.3% 50.7%	HP1218 HP0864 HP0409 HP0829 HP0188 HP0742 HP1530 HP1034 HP1034 HP0919 HP1237 HP0236 HP0381 HP0266 HP0581 HP1017 HP	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) uridine 50-pnosphate decarboxylase (pyrE) uridine 50-monophosphate (UMP) kinase (pyrH)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 39.0%
CENTRAL II  General  HP1014  HP1018  HP1089  HP0089  HP0899  HP0898  HP0047  HP0197  Amino suga  HP1532  Phosphorus	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.3% 33.2% 37.0% 33.9% 34.4% 36.3% 41.4% 38.5% 47.8% 41.7% 41.7%	HP0277 HP0588 HP1608 HP1608 HP1601 HP0642 HP0634 HP0633 HP0632 HP0631 HP1539 HP1539 HP1540 Entner-Dou HP1099 HP1100 Fermentatic HP0681	ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (hydB) quinone-reactive Ni/Fe hydrogenase, sarge subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (hydA) lubiquinol cytochrome is subunit (hydA) lubiquinol cytochrome is subunit (hyd-) ubiquinol cytochrome is subunit (floF) display of the subunit (hydF) display	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 608.5% 68.5% 68.5% 68.9% 39.3% 92.8% 93.3%	HP1218 HP0864 HP0409 HP0829 HP0188 HP0742 HP1530 HP1034 HP1034 HP0919 HP1237 HP0236 HP0381 HP0266 HP0581 HP1017 HP	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate 50-monophosphate (UMP) kinase (pyrH) urdine 50-monophosphate (UMP) kinase (pyrH) 20-20-yclichoucleotides 20-20-yclichoucleotides 20-20-yclichoucleotides	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 48.6% 39.7% 50.7% 41.5% 41.5% 41.5% 35.5% (39.0% 33.9% 50.4%
CENTRAL II General HP1014 HP1016 HP1086 HP00004 HP0899 HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0680 HP0680 HP0680 HP0680 HP0690 P0lyamine II	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 34.4% 36.5% 47.8% 39.7% 62.1% 50.0% 52.9% 39.7% 62.1% 50.0% 52.9% 38.5% 50.0%	HP0277 HP0588 HP1508 HP1508 HP16181 HP0642 HP0634 HP0633 HP0631 HP0631 HP1539 HP1538 HP1548 HP1549 HP1549 HP1099 HP1099 HP10091 HP100891 HP100891	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe pydrogenase (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydG) quinone-reactive Ni/Fe Pydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (hydA) lubiquinol cytochrome is subunit (hydH) ubiquinol cytochrome is subunit (floF) lubiquinol cytochrome is subunit (floF) doroff 2-keto-3-deoxy-6-phosphogluconate aidolase (eda) 6-phosphogluconate dehydratae Ni 3-axxadipate coA-transferase subunit A (ryiD) 3-axxadipate coA-transferase subunit B (ryiD)	42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 68.5% 68.9% 39.3% 68.9% 39.2% 66.5% 70.3%	HP1218 HP0869 HP0829 HP0198 HP0742 HP0198 HP0742 HP1080 Pyrimidine I HP1081 HP0349 HP0349 HP0266 HP1081 HP1011 HP1081 HP10777 Salvage of I	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylprophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrBa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) vordiale 50-phosphate dearboxylase (pyrE) orotale phosphoribosyltransferase (pyrE) vordiale 50-phosphate dearboxylase (pyrF) tymindylate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pdB)	31.8% 31.8% 56.1% 56.1% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% -33.9% 50.4%
CENTRAL II General HP1014 HP1014 HP1016 HP0004 HP0889 HP0900 HP0899 HP0898 HP0047 HP0197 HP0197 HP0152 Phosphorus HP0620 HP1010 Polyamine I	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 34.4% 38.5% 47.89 49.7% 41.7% 50.0% 62.1%	HP0277 HP0588 HP1508 HP1508 HP1608 HP1618 HP0634 HP0633 HP0633 HP0631 HP1539 HP1539 HP1538 HP1540 Entmer-Dou HP1100 Fermentatic HP0692 HP0692 HP0693	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (flydB) quinone-reactive Ni/Fe hydrogenase, large subunit (flydB) ubiquinone-reactive Ni/Fe hydrogenase, small subunit (flydB) ubiquinol-cytochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (flbcH) ubiquinol cytochrome c oxidoreductase, fleske 2Fe-2S subunit (flbcF) ubiquinol cytochrome c oxidoreductase, fleske 2Fe-2S subunit (flbcF) 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase Nacoadipate coA-transferase subunit A (yxiD) 3-oxoadipate coA-transferase subunit B (yxiE) (yxiE) acetate kinase (ackA) (Escherichia coli)	42.6% 42.6% 42.0% 47.0% 45.1% 52.7% 54.7% 67.7% 68.5% 68.5% 68.9% 39.3% 39.3% 59.3% 59.3% 65.5% 65.5%	HP1218 HP0849 HP0849 HP0849 HP0829 HP0188 HP0187 HP0184 HP0184 HP0184 HP0184 HP0187 HP0286 HP0381 HP0286 HP0381 HP0286 HP0381 HP0286 HP0381 HP0286 HP0381 HP10184 HP0187	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcrabamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) orotale orotale ded-pyrbase (pyrB) orotale phosphoribosyltransferase (pyrE) vordine 50-phosphate decarboxylase (pyrF) tudine 50-monophosphate (UMP) kinase undlesoides and nucleotides 030-yolic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (de6B)	31.8% 31.8% 56.1% 56.5% 67.7% 56.5% 20.7% 38.7% 48.6% 39.7% 50.7% 41.5% 35.5% 33.9% 50.4%
CENTRAL II General HP1014 HP1014 HP1016 HP0004 HP0899 HP0899 HP0899 HP0898 HP0017 Amino suge HP0197 Amino suge HP0620 HP0620 HP0696 HP1010 Polyamine I	VirB4 homologue (virB4) virB4	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 33.3% 41.4% 38.5% 47.8% 52.1% 50.0% 52.1% 50.0% 52.1% 50.0% 52.1% 41.7% 50.0% 38.5% 33.3% 45.6% 33.3% 45.6%	HP0277 HP0588 HP1508 HP1508 HP1608 HP1618 HP0634 HP0634 HP0635 HP0631 HP1539 HP1538 HP1540 Entmer-Dou HP1009 HP1009 HP1009 HP0692 HP0692 HP0903 HP0903 HP09094 HP09094	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cyfoch o subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydB) ubiquinol cyfochrome c oxidoreductase, cyfochrome b subunit (fbcH) ubiquinol cyfochrome c oxidoreductase, cyfochrome c sudoreductase, fieske 2Fe-2S subunit (fbcH) ubiquinol cyfochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase Nacoadipate coA-transferase subunit A (xxiD) 3-oxoadipate coA-transferase subunit B (xxiE) acetate kinase (ackA) [Escherichia coli) phosphate acetylsransferase (pta)	42.6% 42.6% 42.0% 47.0% 45.1% 52.7% 51.7% 51.4% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 6 65.5% 65.5% 65.5% 65.5% 65.5%	HP1218 HP0864 HP0409 HP0829 HP0188 HP0742 HP1530 Pyrimidine r HP1081 HP1237 HP0349 HP0266 HP0581 HP1026 HP1474 HP0174 HP0775 Salvage of r HP0104 HP0104 HP01672	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-phosphodiesterase (cpdB) addenine phosphoribosyltransferase (apt)	31.8% 56.1% 58.5% 67.7% 38.7% 48.6% 56.5% 60.7% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5%
CENTRAL II  General HP1014 HP1014 HP1016 HP0000 HP0089 HP0089 HP0089 HP0087 HP0197 Amino suga HP1032 Phosphorus HP0620 HP0620 HP0620 HP0620 HP0620 HP0630 HP1040 HP0410 HP	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 34.4% 36.5% 41.4% 36.5% 62.1% 50.0% 62.1% 50.0% 62.1% 33.3% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5% 33.5%	HP0277 HP0588 HP1508 HP1608 HP16181 HP0642 HP0634 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 HP1100 Fermentatic HP0691 HP0691 HP0692 HP0904 HP0904 HP0904 HP0904 HP0904 HP09057	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (fldA) NAD(P)H-florodoxin (flydD) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (flydB) su	42.6% 42.6% 42.6% 47.0% 46.1% 52.7% 54.7% 51.4% 68.5% 68.9% 39.3% 68.5% 68.5% 67.3% 66.5% 73.2% 65.5%	HP1218 HP0849 HP0849 HP0829 HP0188 HP0189 HP0187 HP1530 Pyrimidine r HP1094 HP037 HP0349 HP0268 HP0581 HP1237 HP0349 HP00681 HP1267 HP0104 HP1017 HP1017 HP1017 HP1017 HP0075 HP1017 HP0075	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ribonucleotide biosynthesis aspartate transcarbamoylase (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) nucleosides and nucleotides D;00-yclic-nucleotide 20-phosphodiesterase (cpdB) phosphopentomutase (deoB) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (apt)	31.8% 31.8% 56.1% 58.5% 67.7% 56.5% 50.7% 38.7% 56.9% 50.7% -1.0% 31.5% 41.5% 33.9% 50.4% 33.9% 50.4%
CENTRAL II  General HP1014 HP1014 HP1016 HP0000 HP0089 HP0089 HP0089 HP0089 HP0097 Amino suga HP1532 Phosphorus HP0620 HP0689 HP1602 HP0680 HP0620 HP0680 HP0620 HP0680 HP0620 HP0680 HP0620 HP0680 HP0620 HP0680	Virf84 homologue (virf84) hydrogenase expression/formation protein (hypR) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypE) hydrogenase expression/formation protein (hypE) hydrogenase expression/formation protein (hypE) hydrogenase expression/formation protein (hypE) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate arminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) h-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE)	23.5% 25.2% 25.3% 33.2% 33.3% 33.3% 33.3% 33.3% 33.5% 33.5% 33.3% 33.5% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.5% 33.3% 33.3% 47.8% 39.7% 62.1% 50.0% 26.5% 33.3% 47.6% 26.5% 97.1% 97.1%	HP0277 HP0588 HP1508 HP1508 HP16181 HP0642 HP0634 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 HP1100 Fermentatic HP0691 HP0691 HP0691 HP0904 HP0904 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0906 HP0905 HP0906 HP0905 HP0906 HP0	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-firrodoxin-fldA protein flavodoxin (fldA) NAD(P)H-firrodoxin-fldA protein flavodoxin (fldA) NAD(P)H-firrodoxin-flox oxygen-insensitive NAD(P)H-firrodoxidase oxygen-insensitive NAD(P)H-firrodoxidase oxygen-insensitive NAD(P)H-firrodoxidase, cylochrome-flox flox flox flox flox oxygen-flox flox oxygen-flox flox flox oxygen-flox flox flox oxygen-flox flox flox flox flox flox flox flox	42.6% 42.6% 42.0% 47.0% 45.1% 32.7% 54.7% 67.7% 68.5% 68.5% 68.5% 68.9% 39.3% 50.3% 50.7% 66.5% 66.5% 73.2% 66.5% 66.5% 66.5% 73.2% 66.5% 66.5% 73.2% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5% 66.5%	HP1218 HP0864 HP0409 HP0829 HP0188 HP0742 HP1081 HP1530 Pyrimidine r HP1084 HP0374 HP0374 HP0374 HP0375 HP0386 HP0581 HP1237 HP0376 HP0576 HP0577 Salvage of r HP0177 HP0077 HP0077 Salvage of r HP0187 HP0178 HP0775 Sulvage of sulvag	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) vordate phosphoribosyltransferase (pyrE) orotidine 50-phosphate decarboxylase (pyrE) virdine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-00-qiclin-culeotide 20-phosphodiesterase (cpdB) purine-nucleoside phosphoribosyltransferase (apt) phosphorpentomutase (deoB) purine-nucleoside phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (apt)	31.8% 56.1% 58.5% 67.7% 38.7% 48.6% 56.5% 60.7% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5% 56.5%
CENTRAL II General HP1014 HP1186 HP0009 HP0899 HP0898 HP0047 HP0197 Amino suge HP0620 HP0520 HP0620 HP0680 HP1010 Polyamine I HP0422 HP0022 Other HP0082 Other	VirB4 homologue virB4 homologue (virB4) virB4 homologue expression/formation protein (vppB) virB4 homologue expression/formation protein (vppB) virB4 homologue expression/formation protein (vppC) virB4 homologue expression/formation protein (vppB) virB4 homologue virB4 homologu	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 34.4% 38.5% 47.8% 52.5% 39.7% 52.5% 39.7% 52.5%	HP0277 HP0588 HP1508 HP1508 HP1508 HP1618 HP0642 HP0633 HP0633 HP0631 HP1539 HP1539 HP1540 Entner-Dou HP1099 HP1509 HP1099 HP1099 HP1099 HP1099 HP0091 HP0091 HP0091 HP0091 HP0091 HP0090 HP0093 HP0093 HP0093 HP0096 HP1365 HP1365 HP1365 HP1365 HP1365 HP1365 HP1365	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD[P]H-florodoxin (fldA) NAD[P]H-florodoxin (fldA) NAD[P]H-florodoxin (fldA) NAD[P]H-florodoxin (fldA) NAD[P]H-florodoxin (fldA) NAD[P]H-florodoxin (fldA) national florodoxin (fldA) national fldA) national fldA national fldA) national fldA national fldA) national fldA national fldA)	42.6% 42.6% 42.6% 47.0% 46.1% 52.7% 54.7% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 67.3% 65.7% 65.5% 66.5% 77.2% 66.5% 77.2% 66.5% 77.2% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3%	HP1218 HP0849 HP0849 HP0829 HP0182 HP0184 HP0742 HP1530 Pytimidine t HP1084 HP0891 HP1287 HP0391 HP1287 HP0391 HP1287 HP0091 HP1287 HP0091 HP1287 HP0091 HP1287 HP0095 HP1287 HP0095 HP1287 HP0095 HP1287 HP0095 HP1287 HP0095 HP1178 HP0777  Salvage of t HP0104 HP0572 HP1178 HP0785 Sugar-nucle HP0043	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransterase (pyrE) orotatine 50-phosphate decarboxylase (pyrE) virdien 50-phosphate (glutamine 50-phosphoribosyltransterase (pyrC) audice 50-phosphoribosyltransterase (pyrE) purlie-nucleosides and nucleotides 20-30-qcilic-nucleotides 20-phosphodiesterase (cpdB) phosphorpentomutase (deoB) ynthesis and conversions mannose-6-phosphate isomerase (pmI) or (algA)	31.896 31.896 56.196 56.596 67.796 56.596 20.796 38.796 48.696 39.796 41.696 33.996 50.796 31.596 41.696 33.996 50.796 41.696 33.996 50.796 41.696 33.996 50.796 41.696 33.996 50.796 41.696 41
CENTRAL II General HP1014 HP1186 HP1030 HP0899 HP0898 HP0047 HP0197 Amino suge HP0620 HP0589 HP1532 Phosphorus HP0620 HP0680 HP1010 P0/smine I HP0622 Other HP0042 Other HP0042 HP0042 Other HP0042 HP00481	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 33.3% 26.1% 34.4% 38.5% 47.8% 59.6 47.8% 59.6 59.6 59.6 59.6 59.6 59.6 59.6 59.6	HP0277 HP0588 HP1508 HP1508 HP1508 HP1618 HP0642 HP0634 HP0633 HP0631 HP1539 HP1538 HP1538 HP1549 HP1549 HP1099 HP1090 HP1090 HP0901 HP0901 HP0901 HP0904 HP0905 HP1386 HP	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe Pydrogenase (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydD) quinone-reactive Ni/Fe Pydrogenase, large subunit (hydB) quinone-reactive Ni/Fe Pydrogenase, small subunit (hydA) ubiquinol cytochrome of subunit (fbcH) control oxygen cytochrome oxidoreductase, Rieske 2Pe-2S subunit (fbcH) control oxygen cytochrome oxidoreductase (eda) 6-phosphogluconate dehydratase oxygen control oxygen cytochrome oxidoreductase (eda) 3-oxoadipate oxidoreductase subunit A (vxiD) 3-oxoadipate oxidoreductase subunit B (vxiD) 3-oxoadipate oxidoreductase (pal) phosphotransacelylase (pal) phosphot	42.6% 42.6% 42.6% 42.0% 47.0% 46.1% 52.7% 54.7% 68.5% 68.5% 68.5% 68.9% 39.3% 50.3% 50.7% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 66.5% 67.3% 67.3% 67.6%	HP1218 HP0849 HP0849 HP0829 HP0189 HP0182 HP1530 Pytimidine t HP1084 HP0881 HP1084 HP0881 HP1081 HP1287 HP0085 HP1287 HP0005 HP1287 HP0077 Salvage of t HP0104 HP0572 HP1178 HP0105 Sugar-nucle HP0073 Sugar-nucle HP0074 HP0074 HP0074 HP0075 HP0074 HP0075 HP0074 HP0075	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (praB) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis asparate transcarbarnoylase (pyrB) carbamoyl-phosphate synthese (glutamine-hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) rotidine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pydB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferase (gpt)	31.8% 56.1% 58.5% 59% 55.5% 58
CENTRAL II General HP1014 HP1018 HP1080 HP0089 HP0089 HP0089 HP0087 HP0197 Amino suge HP1532 HP0620 HP0689 HP0620 HP0680 HP0620 HP0680 HP0620 HP0681 HP0620 HP0681 HP0620 HP0681 HP0620 HP0681 HP0620 HP0681 HP0620 HP0681	VirfB4 homologue virfB4) virfB4 homologue (virfB4) hydrogenase expression/formation protein (hypB4) s-adenosylmethionine synthetase 2 (metX) arising single fructions expression/formation protein (hypB4) s-adenosylmethionine synthetase 2 (metX) someonate (isomerizing) (glmS) sompounds inorganic pyrophosphatase (ppa) hymothythydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (speA) earboxynorspermidine decarboxylase (speA) sypermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureH) urease accessory protein (ureH) urease accessory protein (ureB) urease ac	23.5% 25.2% 25.3% 33.2% 33.3% 28.1% 33.3%	HP0277 HP0588 HP1508 HP1508 HP1508 HP1618 HP0634 HP0633 HP0633 HP0631 HP1539 HP1538 HP1540 HP1509 HP1100 Fermentatic HP0692 HP0903 HP0903 HP0904 HP0904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10905 HP10905 HP10905 HP10905 HP10905 HP10906 HP1090	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe hydrogenase, cyfoch 5 subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doraff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 73 axoxadipate coA-transferase subunit A (xxiD) 3-axoxadipate coA-transferase subunit B (xxiE) accetate kinase (ackA) (Escherichia coli) phosphate acetyltransferase (pla) short-chain alcohol dehydrogenase 3-mesis fructose-1,6-bisphosphatase phosphoenolpyruvate synthase (ppsA) phosphofrase (eno)	42.6% 42.6% 42.6% 47.0% 45.1% 52.7% 51.7%	HP1218 HP0849 HP0849 HP0829 HP0188 HP0189 HP0189 HP1530 Pyrimidine r HP1091 HP1237 HP0349 HP0268 HP0581 HP1257 HP0349 HP1010 HP1267 HP0104 HP1077 Salvage of r HP0104 HP0572 HP1178 HP0178 HP0773 Sugar-nucle HP0784 HP0785 Sugar-nucle	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis asparatae transcariamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) protidine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (ppt) orotate biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-slucose pyrophosphorylase (galU) UDP-lucose pyrophosphorylase (galU) UDP-lucose pyrophosphorylase	31.8% 56.1% 56.5% 59% 50.2% 50.5% 59% 52.7% 44.8% 44.3% 65.5% 55.5% 58.271% 56.5% 56
CENTRAL II  General HP1014 HP1014 HP1018 HP1080 HP0089 HP0089 HP0089 HP0087 HP0197 Amino suge HP0629 HP0639 HP0639 HP0630	Virf84 homologue (virf84) virf84	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 33.3% 26.1% 34.4% 38.5% 47.8% 59.6 47.8% 59.6 59.6 59.6 59.6 59.6 59.6 59.6 59.6	HP0277 HP0588 HP1508 HP1508 HP16081 HP16181 HP0634 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 HP1100 Fermentatic HP0991 HP0992 HP0903 HP0903 HP0904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10904 HP10906 HP10907 HP1	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-firrodoxin-fldE protein flavodoxin (fldA) NAD(P)H-firrodoxin-fldE protein flavodoxin (fldA) NAD(P)H-firrodoxin-floxin	42.6% 42.6% 42.6% 47.0% 45.1% 52.7% 51.7% 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 6 65.5% 65.5% 65.5% 65.5% 65.5% 42.3% 51.0% 62.9% 42.3% 51.0% 65.6% 66.9% 44.3%	HP1218 HP0864 HP0869 HP0829 HP0188 HP0189 HP0189 HP1530 Pyrimidine r HP1037 HP0349 HP0266 HP0581 HP1237 HP0349 HP00581 HP1267 HP037 HP127 HP0389 HP178 HP0077 Salvage of r HP0104 HP0572 HP0178 HP0178 HP0178 HP078 Sugar-nucle HP0646 HP0645 HP0645 HP0645 HP0645 HP0646	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphoribase (purB) ribonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transfera (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (noIK) UDP-glucose pyrophosphorylase (galU) UDP-lucose pyrophosphorylase (glmU)	31.89b 31.89b 56.19b 56.59b 67.79c 56.59b 20.79b 38.79b 48.69b 50.79b 35.59b 35.59b 35.59b 50.39b 50.39b 55.59b 89c 27.19b
CENTRAL II  General HP1014 HP1014 HP1018 HP1080 HP0089 HP0089 HP0089 HP0089 HP0197 Amino suge HP1532 HP0620 HP0689 HP0620 HP0689 HP0620 HP0680 HP0047 HP0070 HP0080 HP0070 HP0080 HP0070 HP0071 HP0071 HP0073 HP0072	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 33.3% 26.1% 34.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.5% 596 39.7% 69.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5% 99.5%	HP0277 HP0588 HP1508 HP1508 HP16181 HP0642 HP0634 HP0633 HP0631 HP0631 HP1539 HP1539 HP1539 HP1540 HP1540 HP1540 HP1540 HP1099 HP1100 Fermentatic HP0691 HP0903 HP0903 HP0903 HP0904 HP0905 HP1035 HP0176 Gluconeoge HP1385 HP0176 HP1036	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (hydG) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome of oxidoreductase, cytochrome be subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome of subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Pe-2S subunit (fbcH) cytochrome of subunit (fbcH) cytochrome of subunit (fbcH) down of the cytochrome of subunit (fbcH) and cytochrome of s	42.6% 29.4% 42.6% 29.4% 47.0% 461.9% 32.7% 54.7% 54.7% 51.4% 68.5% 69.5%	HP1218 HP0849 HP0849 HP0849 HP0829 HP0188 HP0187 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0349 HP0268 HP0581 HP1257 HP0349 HP1257 HP0349 HP1267 HP1010 HP127 HP1010 HP1011 HP1011 HP1077 Salvage of r HP0773 Sugar-nucle HP0043 HP0044 HP00643 HP00643 HP00648	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaA) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis asparatae transcariamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) protidine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 200-yolic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (ppt) orotate biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-slucose pyrophosphorylase (galU) UDP-lucose pyrophosphorylase (galU) UDP-lucose pyrophosphorylase	31.8% 56.1% 56.5% 59% 50.2% 50.5% 59% 52.7% 44.8% 44.3% 65.5% 55.5% 58.271% 56.5% 56
CENTRAL II  General HP1014 HP1014 HP1018 HP1080 HP0089 HP0089 HP0089 HP0087 HP0197 Amino suge HP0629 HP0639 HP0639 HP0630	VirB4 homologue virB4) virB4 homologue (virB4) virB4 v	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 33.3% 26.1% 34.4% 36.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.5% 596 39.7% 69.5% 99	HP0277 HP0588 HP1508 HP1508 HP16181 HP0642 HP0634 HP0633 HP0631 HP1539 HP1539 HP1539 HP1540 HP1554 H	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H nitroreductase coxygen-insensitive NAD(P)H nitroreductase coxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe Pydrogenase (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydD) quinone-reactive Ni/Fe Pydrogenase, sarge subunit (hydD) quinone-reactive Ni/Fe Pydrogenase, small subunit (hydA) ubiquinol cytochrome is outdoreductase, cytochrome is subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Pe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Pe-2S subunit (fbcH) cotoril 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase Ni/Sichal (hydE) acetate kinase (ackA) (Escherichia coli) phosphotransacelylase (pla) short-chain alcohol dehydrogenase anesis fructose-1,6-bisphosphate subunollyruxate synthase (ppsA) phosphoglycerate kinase enolase (eno) fructose-bisphosphate aldolase (tsr) glucose-6-phosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) glyceraldehyde-3-phosphate dehydrogenase (ggp)	42.6% 42.6% 42.6% 42.6% 47.0% 46.1% 52.7% 54.7% 51.4% 68.5% 68.5% 68.9% 63.3% 50.3% 50.3% 65.5% 73.2% 65.5% 73.2% 65.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 73.2% 66.5% 73.3% 66.5%	HP1218 HP0869 HP0869 HP0829 HP0188 HP0188 HP0188 HP0189 HP1530 Pyrimidine r HP1091 HP1237 HP0349 HP0236 HP0381 HP0266 HP0381 HP027 HP0349 HP127 HP0349 HP127 HP0349 HP177 Salvage of r HP0104 HP0672 HP177 HP0178 HP077 Sugar-nucle HP0045 HP0043 HP0045 HP0046 HP0047 REGULATOR	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbarnoylase (pyrB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) dihydrorottase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) uridine 50-monophosphate (UMP) kinase (pytH) phosphopentomutase (deaB) purine-nucleoside 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deaD) xanthine guanine phosphoribosyl transfera: (ppt) uridita 50-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylas (gliU) UDP-glucose pyrophosphorylas (glimU) RY FUNCTIONS	31.8% 31.8% 56.5% 67.7% 56.5% 58.5% 59.50.7% 38.7% 38.7% 39.7% 39.7% 31.5% 35.5% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.5% 56.
CENTRAL II  General HP1014 HP1014 HP1018 HP1080 HP0089 HP0089 HP0089 HP0090 HP0197 Amino suge HP0197 Amino suge HP0520 HP0620 HP0620 HP0620 HP0620 HP0620 HP0070 HP0070 HP0070 HP0071 HP0073 HP0075 HP0075	VirfB4 homologue virfB4 homologue (virfB4) virfB4 homologue expression/formation protein (vppB) virfB4 expression/formation protein (vppB) virfB4 expression/formation protein (vppB) virfB4 expression/formation protein virfB4 expression/formation virfB4 expression/formation virfB4 expression/form	23.5% 25.2% 25.3% 33.2% 33.3% 28.1% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 35.5% 37.5% 52.1% 52.5% 59.5%	HP0277 HP0588 HP1508 HP1508 HP16181 HP0642 HP0634 HP0633 HP0631 HP0631 HP1539 HP1539 HP1539 HP1540 HP1540 HP1540 HP1540 HP1099 HP1100 Fermentatic HP0691 HP0903 HP0903 HP0903 HP0904 HP0905 HP1035 HP0176 Gluconeoge HP1385 HP0176 HP1036	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H-firrordoxin-like protein flavodoxin (fldA) NAD(P)H-firrordoxin-like protein flavodoxin (fldA) NAD(P)H-firrordoxin-like protein flavodoxin (fldA) NAD(P)H-firrordoxin-like protein flavodoxin flavodoxin-like protein flavodo	42.6% 29.4% 42.6% 29.4% 47.0% 46.1% 32.7% 54.7% 54.7% 54.7% 54.7% 58.5% 68.5%	HP1218 HP0849 HP0849 HP0849 HP0829 HP0188 HP0189 HP0189 HP1530 Pyrimidine r HP1084 HP1084 HP1084 HP1084 HP0381 HP0286 HP0381 HP0286 HP0381 HP0481 HP0572 HP0735 Sugar-nucle HP0045 HP0673 HP0045 HP0683 REGULATOR General HP1032	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-50-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthese (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) vordiale 50-phosphate dearboxylase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) urdine 50-monophosphate (UMP) kinase (pyrH) phosphopentomucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferase (ppf) ordide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (glimU) UDP-glucose pyrophosphorylase (glimU) UDP-glucose pyrophosphorylase (dili) atternative transcription initiation factor, sign (fiiA)	31.8% 31.8% 56.1% 56.5%
CENTRAL II General General HP1014 HP1014 HP1014 HP1016 HP0000 HP0089 HP0089 HP0089 HP0090 HP017 Amino suge HP0197 Amino suge HP0620 HP0620 HP0620 HP0620 HP0630 HP0000 HP0007	VirB4 homologue virB4 homologue (virB4) virB4 homologue expression/formation protein (vppB) virB4 homologue expression/formation protein (vppC) virB4 homologue expression/formation protein (virB4 homologue expression/formation (vppC) virB4 homologue expres	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 26.1% 33.3% 26.1% 33.3% 26.1% 34.7% 33.3% 26.1% 34.7% 50.0% 52.1% 39.7% 62.1% 39.7% 62.1% 39.7% 62.1% 39.7% 62.1% 50.0%	HP0277 HP0588 HP1508 HP1508 HP1508 HP1608 HP1618 HP0631 HP0633 HP0632 HP0633 HP0631 HP1639 HP1539 HP1539 HP1539 HP1540 Entmer-Dou HP1009 HP1000 Fermentatic HP0691 HP0692 HP0903 HP0904 HP0904 HP0904 HP1346 HP0176 HP0176 HP1106 HP1074	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe phydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydFe) subunit (hydFe) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) oxidipinol cytochrome c oxidoreductase, Rieske 2F	42.6% 42.6% 42.6% 47.0% 46.1% 32.7% 54.7% 68.5% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 39.2% 65.5% 65.5% 65.5% 65.5% 65.6% 42.3% 51.0% 65.5% 56.6% 66.6% 66.9% 66.6% 66.9% 66.6% 66.9% 66.6%	HP1218 HP0849 HP0849 HP0849 HP0829 HP0188 HP0187 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0349 HP0286 HP0581 HP1257 HP0349 HP1257 HP0349 HP1257 HP0777 Salvage of r HP0077 HP0104 HP0572 HP1178 HP0777 HP0045 HP0646 HP0648 HP10683 HP1068	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoritosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) voridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20:00-yciic-nucleotide 20-phosphodiesterase (cpdB) purine-nucleoside phosphorylase (deoD) yanthine guanine phosphoribosyl transfera (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (gaIU) UDP-glucose pyrophosphorylase (gmU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA)	31.89b 31.89b 56.19b 56.19b 56.59b 56.59b 50.55.59b 80 62.719b 34.89b 44.39b 65.69b 44.39b 45.69b 44.39b 45.69b 44.39b 45.69b 45.60b 45
CENTRAL II General HP1014 HP1014 HP1016 HP1080 HP0089 HP0898 HP0089 HP0990 HP09	Virf84 homologue (virf84) hydrogenase expression/formation protein (typA) hydrogenase expression/formation protein (typB) hydrogenase expression/formation protein (typD) hydrogenase expression/formation protein (typD) hydrogenase expression/formation protein (typD) hydrogenase expression/formation protein (typD) hydrogenase expression/formation protein (typB) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-mettyhydratroinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidline decarboxylase (nspC) spermidline synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureH) urease applies subunit (ureA) (urea amidohydrolase) (ureB) urease epitein (ureC)	23.5% 25.2% 25.3% 33.2% 33.3% 28.1% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 35.5% 37.5% 52.1% 52.5% 59.5%	HP0277 HP0588 HP1508 HP1681 HP1681 HP06842 HP0633 HP0633 HP0631 HP1539 HP1539 HP1538 HP1540 HP1690 HP1009 HP1000 Fermentatic HP0691 HP0892 HP0903 HP0904 HP0905 HP0905 HP1090 HP1	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase coxygen-insensitive NAD(P)H- nitroreductase curson-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe Pydrogenase (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydG) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydA) quinone-reactive Ni/Fe Pydrogenase, small subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (fbcF) display of the cytochrome is subunit as properties of the cytochrome is subunit as subunit as subunit as considered as a subunit as cytochrome is subunit as phosphogluconate and phosphogluconate and phosphogluconate and phosphogluconate (phosphogluconate) phosphogluconate (phosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) phosphogluconate mutase (pgm) phosphoglycerate mutase (pgm) phosphoglycerate mutase (pgm) phosphogluconate isomerase (pgi)	42.6% 42.6% 42.6% 42.6% 47.0% 46.1% 52.7% 54.7% 51.4% 68.5% 68.9% 68.9% 65.3% 50.3% 50.3% 50.4% 65.9% 66.9% 66.9% 66.9% 66.9% 66.9% 66.9% 66.9% 66.9% 66.9%	HP1218 HP0849 HP0849 HP0829 HP0189 HP0189 HP0189 HP0180 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1257 HP0369 HP0581 HP1257 HP0104 HP0107 HP0107 HP0107 HP0107 HP0107 HP0107 HP0107 HP0108 HP108 HP108 HP108 HP1188 HP1188	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbamoylase (pyrB) 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) ryntiquiate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20:00-yclic-nucleotide 20-phosphodiesterase (pydB) purine-nucleoside phosphorylase (deoD) yanthine guanine phosphoribosyl transferas (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (nolK) UDP-glucose pyrophosphorylase (gmU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA) carbon storage regulator (csrA) ferric uptake regulation protein (tur)	31.89b 31.89b 56.19b 56.19b 56.59b 50.55.59b 80 42.89b 44.39b 45.39b 45.30b 45.
CENTRAL II General HP1014 HP1014 HP1018 HP1080 HP0089 HP0898 HP0089 HP0898 HP0047 HP0197 Amino suge HP1522 Phosphorus HP0620 HP0689 HP1632 Other HP0040 HP0070 HP0083 HP0071 HP0071 HP0072 HP0075 HP0075 HP0075 HP0075 HP0075	Virf84 homologue (virf84) hydrogenase expression/formation protein (typ8A) hydrogenase expression/formation protein (typ8B) hydrogenase expression/formation protein (typ8B) hydrogenase expression/formation protein (typ9B) s-adenosylmethionine synthetase 2 (metX) arg glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) hydrogenase polyphosphate kinase (ppx) hydrogenase inorganic pyrophosphatase (ppa) hydrogenase accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureB) urease accessory protein (ureB) urease accessory protein (ureB) urease accessory protein (ureB) urease ac	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 34.1% 34.5% 34.5% 39.7% 62.1% 50.0% 52.9% 33.3% 45.6% 50.0%	HP0277 HP0588 HP1508 HP1681 HP1681 HP06842 HP0633 HP0633 HP0633 HP0632 HP1539 HP1538 HP1540 HP1538 HP1540 HP1099 HP1100 Fermentatic HP0691 HP0892 HP0904 HP0904 HP0905 HP0905 HP10907 HP10904 HP0904 HP0905 HP10904 HP0904 HP0904 HP0904 HP109	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe Pydrogenase (hydD) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydG) quinone-reactive Ni/Fe Pydrogenase, cytoch subunit (hydA) quinone-reactive Ni/Fe Pydrogenase, small subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (hydA) ubiquinol cytochrome is subunit (fbcF) display of the cytochrome of cytochrome of subunit (fbcF) display of the cytochrome of	42.6% 42.6% 42.6% 47.0% 46.1% 32.7% 54.7% 68.5% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 39.2% 65.5% 65.5% 65.5% 65.5% 65.6% 42.3% 51.0% 65.5% 56.6% 66.6% 66.9% 66.6% 66.9% 66.6% 66.9% 66.6%	HP1218 HP0849 HP0849 HP0829 HP0189 HP0189 HP0189 HP0180 HP1530 Pyrimidine r HP1084 HP0193 HP1237 HP0349 HP0268 HP0581 HP1257 HP0268 HP0581 HP1267 HP0104 HP0172 HP1077 HP0179 HP0179 HP0179 HP0179 HP0179 HP0179 HP0045 HP0646 HP0646 HP0648 HP0649 HP1679 HP178 HP0777 HP0777 HP0777 HP0777 HP0778	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotidine 50-phosphate dearboxylase (pyrE) rotidine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 2/c0-yclic-nucleotide 2/c-phosphodiesterase (pdB) phosphopentomutase (deoB) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (gpt) cotide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (nolK) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (glmU) RY FUNCTIONS alternative transcription initiation factor, sign (fliA) carbon starvation protein (cstA) carbon storage regulator (csrA) ferric uptake regulation protein (furl) guanosine pentaphosphate phosphoryloryloryloppid	31.8% 31.8% 56.1% 56.5% 56.5% 50.5% 65.5%
CENTRAL II  General HP1014 HP1014 HP1018 HP1080 HP0089 HP0898 HP0089 HP0898 HP0097 HP0197 Amino suga HP1522 Phosphorus HP0620 HP0689 HP0620 HP0689 HP0620 HP0681 HP0071 HP0071 HP0073 HP0072 HP0075 HP0075 HP0075 HP0075 HP0075 HP0075 HP0077	Virf84 homologue (virf84) hydrogenase expression/formation protein (typ8A) hydrogenase expression/formation protein (typ8B) hydrogenase expression/formation protein (typ8B) hydrogenase expression/formation protein (typ9B) s-adenosylmethionine synthetase 2 (metX) arg glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) hydrogenase polyphosphate kinase (ppx) hydrogenase inorganic pyrophosphatase (ppa) hydrogenase accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureB) urease accessory protein (ureB) urease accessory protein (ureB) urease accessory protein (ureB) urease ac	23.5% 25.2% 25.3% 33.2% 37.0% 33.3% 28.1% 33.3% 28.1% 33.3% 28.1% 33.3% 28.1% 33.3% 41.4% 33.5%	HP0277 HP0287 HP0588 HP1508 HP1508 HP1508 HP1608 HP16081 HP0632 HP0631 HP1639 HP1538 HP1540  Entiner-Dou HP109 HP1009 HP1	ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fldA) NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase oxygen-insensitive NAD(P)H- nitroreductase quinone-reactive Ni/Fe Pydrogenase, cytoch b subunit (PydC) quinone-reactive Ni/Fe Pydrogenase, cytoch oxygen-reactive Ni/Fe Pydrogenase, large subunit (PydB) quinone-reactive Ni/Fe Pydrogenase, large subunit (PydB) quinone-reactive Ni/Fe Pydrogenase, small subunit (PydB) quinone-reactive Ni/Fe Pydrogenase, cytochrome c oxidoreductase, cytochrome c 1 subunit (PbcH) quinquinol qytochrome c oxidoreductase, Rieske 2Fe-2S subunit (PbcH) quinquinol qytochrome c oxidoreductase, Rieske 2Fe-2S subunit (PbcH) quinquinol qytochrome c oxidoreductase, Rieske 2Fe-2S subunit (PbcH) quinquinol qytochrome c oxidoreductase, (Pcda) 6-phosphogluconate dehydratase (Ph) 3-αxoxadipate co-A-transferase subunit A ((γχI)) 3-αxoxadipate co-A-transferase subunit B ((γχI)) 3-αxoxadipate co-A-transferase subunit B ((γχI)) 3-αxoxadipate co-A-transferase subunit B ((γχI)) 3-αxoxadipate co-A-transferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphatese-phosphate aldolase (tsr) glucokinase (glk) glucose-6-phosphate dehydrogenase (pp) glyceraldehyde-3-phosphate dehydrogenase (pp) phosphoglycerate mutase (pgm) trosephosphate isomerase (tpi) soxphate apthway	42.6% 42.6%	HP1218 HP0849 HP0849 HP0829 HP0189 HP0189 HP0189 HP0180 HP1530 Pyrimidine r HP1084 HP0919 HP1237 HP0349 HP0256 HP0581 HP1257 HP0369 HP0581 HP1257 HP0104 HP0107 HP0179 HP0179 HP0179 HP0179 HP0179 HP0045 HP0646 HP0684 HP0685 HP1474 HP00955 HP1474 HP00955 HP1474 HP0197 HP0197 HP0197 HP0198 HP0198 HP0198 HP0198 HP0198 HP0198 HP0198 HP0198 HP1188 HP1188 HP1188	glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine-60-monophosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesia aspartate transcratamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrBa) carbamoyl-phosphate synthase (pyrBa) CTP synthetase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) dihydrocrotase (pyrC) trynidylate kinase (trink) uridine 50-monophosphate (UMP) kinase (pyrH) purine-phosphoribosyltransferase (pyrE) sadenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (apt) uride biosynthesis and conversions mannose-6-phosphate isomerase (pml) or (algA) nodulation protein (nolK) UDP-Rivacetylglucosamine pyrophosphoryla (glmU) UDP-Rivacetylglucosamine pyrophosphoryla (glmU) UPR-Nacetylglucosamine pyrophosphoryla (glmU) xarbon storage regulator (csrA) ferric uptake regulation protein (furl) guanosine pethasphosphate phosphohydrol	31.896 31.896 51.896 67.796 56.596 67.796 56.596 50.796 38.796 48.696 39.796 31.696 31.696 33.596 50.396 50.396 40.396 44.396 44.396 44.396 44.396 44.396 44.396 44.396 44.396 44.398

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	penta-phosphate guanosine-3Ö-pyrophospho	- 36.7%	HP1471	type IIS restriction enzyme R protein	00.00/	HP0399	ribosomal protein S1 (rps1)	30.5%
	hydrolase (spoT) peptide methionine sulphoxide reductase	30.7%	HP1366	(BCGIB) type IIS restriction enzyme R protein	28.2%	HP1320 HP1295	ribosomal protein S10 (rps10) ribosomal protein S11 (rps11)	58.2% 56.2%
		66.8%			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		93.4%	HP1306 HP1040	ribosomal protein S14 (rpS14) ribosomal protein S15 (rps15)	68.3% 57.8%
		28.7%	HP1209	ulcer-associated gene restriction endonucle (iceA)	95.5%	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	n of RNA	00.004	HP1554 HP0076	ribosomal protein S2 (rps2) ribosomal protein S20 (rps20)	49.6% 41.4%
		97.7%	HP1213	polynucleotide phosphorylase (pnp) DNA-dependent RNA polymerase	38.9%	HP0562	ribosomal protein S21 (rps21)	42.4%
HP0164	signal-transducing protein, histidine kinase	27.1%	HP1293	DNA-directed RNA polymerase, alpha subu	ınit	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%			47.8%	HP1196	ribosomal protein S7 (rps7)	62.2%
HP1287	transcriptional regulator (tenA)	34.7%	Transcriptio HP0866	n factors transcription elongation factor GreA (greA)	EO 20%	HP1305	ribosomal protein S8 (rps8)	45.0%
		33.3%	HP1514	transcription termination factor NusA	50.5%			50.4%
REPLICATION	N		111 1014		39.1%			26.3%
Degradation			HP0001	transcription termination factor NusB (nusB)	)30.2%	tRNA modifi HP1141	ication methionyl-tRNA formyltransferase (fmt)	37.5%
		27.2%	HP1203	transcription termination factor NusG	41.0%	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)	37.370	HP1148	tRNA (guanine-N1)-methyltransferase (trmD)	
	(HINDIIM)	33.4%	TRANSLATI	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	45.6%	Translation		40.070
		33.9%	Aminoacyl t	RNA synthetases		HP0247	ATP-dependent RNA helicase, DEAD-box	
	adenine specific DNA methyltransferase		HP1241 HP0319		44.9% 35.8%		family (deaD)	37.7%
		29.3%	HP0617		50.1%		peptide chain release factor RF-1 (prfA)	52.6%
	adenine specific DNA methyltransferase		HP0886		97.3%		peptide chain release factor RF-2 (prfB)	49.6%
HP0593	(mod) adenine specific DNA methyltransferase	33.9%	HP0476		43.1%	HP1256 HP1195	ribosome releasing factor (frr) translation elongation factor EF-G (fusA)	43.7% 67.5%
		38.5%	HP0643		39.8%		translation elongation factor EF-P (efp)	45.1%
	adenine specific DNA methyltransferase		HP0960	glycyl-tRNA synthetase, alpha subunit (glyQ)	60.1%	HP1555	translation elongation factor EF-Ts (tsf)	43.1%
		42.2%	HP0972		33.6%		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		42.9%	HP1547		45.9% 58.6%		, ,	
	chromosomal replication initiator protein		HP0182 HP0417		42.4%	TRANSPOR	T AND BINDING PROTEINS	
		34.9%	HP0403	phenylalanyl-tRNA synthetase, alpha subun		General		
HP1121	cytosine specific DNA methyltransferase (BSP6IM)	37.0%		(pheS)	48.7%	HP0179 HP0613	ABC transporter, ATP-binding protein ABC transporter, ATP-binding protein	66.7% 31.1%
	cytosine specific DNA methyltransferase	01.010	HP0402	phenylalanyl-tRNA synthetase, beta subunit			ABC transporter, ATP-binding protein	52.3%
	(DDEM)	39.0%	HP0238		30.0% 39.8%	HP1576		48.2%
	cytosine specific DNA methyltransferase	38.7%	HP1480		48.3%		ABC transporter, ATP-binding protein	
		97.4%	HP0123	threonyl-tRNA synthetase (thrS)	42.1%	LIDAGGG	(HI1087)	37.8%
	DNA gyrase, sub B (gyrB)	46.0%	HP1253	tryptophanyl-tRNA synthetase (trpS)	52.6%	HP1220 HP0853	ABC transporter, ATP-binding protein (yhcG ABC transporter, ATP-binding protein (yhcS)	1363%
HP1478	DNA helicase II (uvrD)	35.3%	HP0774 HP1153		54.7% 43.7%			43.1%
		38.8%		of proteins, peptides and glycopeptides	43.770	HP0607	acriflavine resistance protein (acrB)	29.7%
		40.1% 32.6%	HP0570	aminopeptidase a/i (pepA)	38.5%	HP1432	histidine and glutamine-rich protein	50.0%
		40.0%	HP0033		40.3%		histidine-rich, metal binding polypeptide	100.0%
		42.0%	HP0794	ATP-dependent clp protease proteolytic			(hpn) multidrug-resistance protein (hetA)	26.2%
HP0500	DNA polymerase III beta-subunit (dnaN)	26.0%	LID4070		64.6%	HP1082	multidrug-resistance protein (msbA)	32.4%
	DNA polymerase III delta prime subunit	40.00	HP1379 HP0223		43.9% 41.0%	HP0600	multidrug-resistance protein (spaB)	29.7%
	(holB) DNA polymerase III epsilon subunit (dnaQ)	48.6% 35.1%	HP1374	ATP-dependent protease ATPase subunit	71.070	HP1181	multidrug-efflux transporter	29.1%
HP0717	DNA polymerase III gamma and tau subuni			(clpX)	56.3%	HP0497 HP0498	sodium- and chloride-dependent transporte sodium- and chloride-dependent trans-	r31.7%
	(dnaX)	39.0%	HP0264	ATP-dependent protease binding subunit	0770	111 0430	porter	30.8%
		36.6%	HP0169		97.7% 40.1%	HP0214		36.6%
		32.7% 28.3%	HP0516		98.4%	Amino acids	s, peptides and amines	
HP0116		45.1%	HP0515	heat-shock protein (hslV)	57.1%	HP0940	amino acid ABC transporter, periplasmic	
HP0440	DNA topoisomerase I (topA)	31.7%	HP0470		97.9%	LIDOOOO	binding protein (yckK) amino acid ABC transporter, permease	41.5%
HP0602	endonuclease III	36.6%	HP0657		24.2%	HP0939	protein (yckl)	46.9%
		40.1% 53.4%	HP1485 HP1350		35.2% 40.6%	HP1017	amino acid permease (rocE)	41.7%
		53.1%	HP1012		29.6%	HP0942	D-alanine glycine permease (dagA)	44.5%
HP0821		31.5%	HP1435		41.7%	HP0301	dipeptide ABC transporter, ATP-binding	EO E0/
		58.9%	HP0404 HP1019	protein kinase C inhibitor (SP:P16436)	40.2% 52.9%	HP0302	protein (dppD) dipeptide ABC transporter, ATP-binding	59.5%
		48.5% 32.9%	HP1019 HP1584		35.7%		protein (dppF)	54.8%
		33.0%	HP0382	zinc-metalloprotease (YJR117W)	36.2%	HP0298	dipeptide ABC transporter, periplasmic	
HP0883	Holliday junction DNA helicase (ruvA)	39.0%	Nucleoprote			LIDOOOO	dipeptide-binding protein (dppA)	39.8%
		54.6%		histone-like DNA-binding protein HU (hup)	44.6%	HP0299	dipeptide ABC transporter, permease protein (dppB)	49.3%
	Holliday junction endodeoxyribonuclease	34.7%	Protein mod			HP0300	dipeptide ABC transporter, permease protei	
		31.8%	HP0363	L-isoaspartyl-protein carboxyl methyltransfer			(dppC)	52.5%
HP0995	integrase/recombinase (xerD)	27.8%	HP1299		43.0% 43.0%	HP1506 HP1171	glutamate permease (gltS) glutamine ABC transporter, ATP-binding	56.9%
		31.1%	HP1441	peptidyl-prolyl cis-trans isomerase B,	10.0 10	nr II/I	protein (glnQ)	51.9%
	methylated-DNAÑprotein-cysteine methyltransferase (dat1)	41.0%		cyclosporin-type rotamase (ppi)	58.1%	HP1172	glutamine ABC transporter, periplasmic	
	primosomal protein replication factor (priA)		HP1123	peptidyl-prolyl cis-trans isomerase, FKBP-typ rotamase (slyD)	pe 40.4%	LIDAAOS	glutamine-binding protein (glnH)	32.2%
HP0153	recombinase (recA)	99.1%	HP0793		41.8%	HP1169	glutamine ABC transporter, permease protein (glnP)	27.6%
	recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende	36.5%		proteins: synthesis and modification		HP1170	glutamine ABC transporter, permease prote	
		nt 33.8%	HP1201		52.0%		(glnP)	30.9%
		39.4%	HP1200		30.4%	HP0250	oligopeptide ABC transporter, ATP-binding	00.40/
		38.1%	HP1202		63.8%	HP1252	protein (oppD) oligopeptide ABC transporter, periplasmic	39.1%
		58.4%	HP1068	ribosomal protein L11 methyltransferase (prmA)	38.4%	III ILUL	oligopeptide-binding protein (oppA)	28.7%
		36.3% 32.6%	HP0084		50.0%	HP1251	oligopeptide ABC transporter, permease	
	single-stranded-DNA-specific exonuclease	02.070	HP1309	ribosomal protein L14 (rpl14)	65.9%		protein (oppB)	59.6%
	(recJ)	33.6%	HP1301		42.5%	HP0251	oligopeptide ABC transporter, permease protein (oppC)	31.4%
		21.3% 37.7%	HP1312 HP1292		62.4% 48.3%	HP0819	osmoprotection protein (proV)	38.3%
		370%	HP1303	ribosomal protein L18 (rpl18)	45.5%	HP0818	osmoprotection protein (proWX)	30.4%
HP0463	type I restriction enzyme M protein (hsdM)	29.4%	HP1147	ribosomal protein L19 (rpl19)	50.9%	HP0055 HP0936	proline permease (putP)	51.4% 29.1%
HP0464	type I restriction enzyme R protein (hsdR)	31.7%	HP1316 HP0126		58.9% 54.8%	HP0936 HP0133	proline/betaine transporter (proP) serine transporter (sdaC)	44.6%
HP0846 HP0848		48.0% 37.0%	HP0126 HP0296		46.1%	Anions		
	type I restriction enzyme S protein (nsdS) type I restriction enzyme M protein (hsdM)		HP1314	ribosomal protein L22 (rpl22)	44.9%	HP0475	molybdenum ABC transporter, ATP-binding	
HP1402	type I restriction enzyme R protein (hsdR)	26.6%	HP1317	ribosomal protein L23 (rpl23)	31.7%		protein (modD)	38.4%
HP1403	type I restriction enzyme M protein (hsdM)	37.1%	HP1308 HP0297		52.2% 64.7%	HP0473	molybdenum ABC transporter, periplasmic	QE 00/-
	type I restriction enzyme S protein (hsdS)	EE ON-	HP0491		64.7% 41.7%	HP0474	molybdate-binding protein (modA) molybdenum ABC transporter, permease	95.9%
	type II restriction enzyme M protein (hsdM) 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	ribosomal protein L3 (rpl3)	41.8%		nitrite extrusion protein (narK)	23.6%
HP1370	type III restriction enzyme M protein (mod)	37.0%	HP0551		49.3%	HP1491	phosphate permease	34.8%
	type III restriction enzyme R protein	26.2%	HP0200 HP1204		41.7% 55.1%		tes, organic alcohols and acids	0700
HP1371		30.6%			70.5%	HP0143 HP1091	2-oxoglutarate/malate translocator (SODiT1) alpha-ketoglutarate permease (kgtP)	37.0% 45.9%
HP1371 HP0592		33.1%	HP1447					
HP1371 HP0592 HP1521	type III restriction enzyme R protein (res)	33.1% 32.4%	HP0125	ribosomal protein L35 (rpl35)	50.8%			
HP1371 HP0592 HP1521 HP1472 HP1367	type III restriction enzyme R protein (res) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M1 protein (mod)	32.4% I)	HP0125 HP1297	ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36)	81.6%	HP0724	anaerobic C4-dicarboxylate transport protein (dcuA)	53.8%
HP1371 HP0592 HP1521 HP1472 HP1367	type III restriction enzyme R protein (res) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M1 protein (mod ([Moraxella bovis]	32.4%	HP0125 HP1297 HP1318	ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L4 (rpl4)	81.6% 40.6%	HP0724 HP1174	anaerobic C4-dicarboxylate transport protein (dcuA) glucose/galactose transporter (gluP)	53.8% 53.6%
HP1371 HP0592 HP1521 HP1472 HP1367	type III restriction enzyme R protein (res) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M1 protein (mod ([Moraxella bovis) type IIS restriction enzyme M2 protein	32.4% I) 59.3%	HP0125 HP1297	ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L4 (rpl4) ribosomal protein L5 (rpl5) ribosomal protein L6 (rpl6)	81.6%	HP0724 HP1174 HP0141	anaerobic C4-dicarboxylate transport protein (dcuA) glucose/galactose transporter (gluP) L-lactate permease (lctP)	53.8% 53.6% 55.5%
HP1371 HP0592 HP1521 HP1472 HP1367 HP1368	Type III restriction enzyme R protein (res) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M1 protein (mod (Moraxella bowls) type IIS restriction enzyme M2 protein (mod) type IIS restriction enzyme R and M protein (mod)	32.4% I) 59.3% 33.0%	HP0125 HP1297 HP1318 HP1307 HP1304 HP1199	ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L4 (rpl4) ribosomal protein L5 (rpl5) ribosomal protein L6 (rpl6) ribosomal protein L7/L12 (rpl7/112)	81.6% 40.6% 53.1% 44.4% 65.0%	HP0724 HP1174 HP0141	anaerobic C4-dicarboxylate transport protein (dcuA) glucose/galactose transporter (gluP)	53.8% 53.6%
HP1371 HP0592 HP1521 HP1472 HP1367 HP1368	Type III restriction enzyme R protein (res) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M protein (mod) type IIS restriction enzyme M1 protein (mod (Moraxella bowls) type IIS restriction enzyme M2 protein (mod) type IIS restriction enzyme R and M protein (mod)	32.4%  ) 59.3% 33.0%	HP0125 HP1297 HP1318 HP1307 HP1304	ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L4 (rpl4) ribosomal protein L5 (rpl5) ribosomal protein L6 (rpl6) ribosomal protein L7/L12 (rpl7/112)	81.6% 40.6% 53.1% 44.4%	HP0724 HP1174 HP0141	anaerobic C4-dicarboxylate transport protein (dcuA) glucose/galactose transporter (gluP) L-lactate permease (lctP)	53.8% 53.6% 55.5%

Cations			HP0258	conserved hypothetical integral membrane		HP0728	conserved hypothetical protein	29.3%
HP0791	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%
HP1503 HP1073	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%
HP1072 HP0471	copper-transporting ATPase, P-type (copA) glutathione-regulated potassium-efflux syst		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%
HP0687 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%
HP1562	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%
HP0888	binding protein (ceuE)	28.2%		protein	28.5%	HP0934	conserved hypothetical protein	33.6%
	iron(III) dicitrate ABC transporter, ATP-bindi protein (fecE)	34.4%	HP0693	conserved hypothetical integral membrane protein	46.7%	HP0956 HP0959	conserved hypothetical protein conserved hypothetical protein	36.2% 31.1%
HP0889	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%
HP0686 HP0807	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%
HP1344	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 HP1552	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%
HP0490	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%
	es, purines and pyrimidines		HP0920	conserved hypothetical integral membrane	36.3%	HP1240	conserved hypothetical protein	22.5%
HP1290	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%
HP0876	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%
HP1129 HP1130	biopolymer transport protein (exbD) biopolymer transport protein (exbB)	29.7% 33.5%	HP1162	protein	44.0%	HP1423	conserved hypothetical protein	40.3%
HP1339 HP1340	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%
HP1446 HP1512	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%
HP0653 HP1341	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 CA	ATEGORIES		HP1234	conserved hypothetical integral membrane protein	29.0%	HP1573 HP1587	conserved hypothetical protein conserved hypothetical protein	42.2% 39.0%
General HP0924	A avalagratagets to temperage (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%
HP1000 HP1139	PARA protein SpoOJ regulator (soj)	29.7% 47.4%	HP1331	protein	41.7%	HP0028	(plasmid pHPM180) conserved hypothetical secreted protein	41.8% 42.1%
HP0827	ss-DNA binding protein 12RNP2 precursor	46.8%		conserved hypothetical integral membrane protein	33.6%	HP0139	conserved hypothetical secreted protein	37.1%
Adaptation HP1496	ns 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%
HP0927 HP0280	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%
HP0970	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%
HP0967 HP1248	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%
HP0885	(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%
	ated functions	55.576		protein	34.3%	HP1216	conserved hypothetical secreted protein	31.9%
HP1126 HP0428	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%
111 0420	terY protein	25.6%	HP0138 HP1438	conserved hypothetical iron-sulfur protein	41.2% 32.0%	HP1464 HP1488	conserved hypothetical secreted protein	27.4% 29.8%
Drug and HP1431	analog sensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl-		HP0151	conserved hypothetical lipoprotein 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		
HP0606 HP0630	membrane fusion protein (mtrC) modulator of drug activity (mda66)	24.2% 62.3%		protein 4	23.2%	General		
HP1476 HP1165	phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P),	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%
HF 1100	putative	27.0%	HP0035 HP0086	conserved hypothetical protein conserved hypothetical protein	34.1% 28.7%	HP0872	alkylphosphonate uptake protein (phnA)	61.1%
	on-related functions	00.00	HP0094	conserved hypothetical protein	29.8%	HP0207 HP0136	ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp)	38.9% 35.5%
HP1008 HP0414	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%
HP0988 HP0998	IS605 transposase (tnpA) IS605 transposase (tnpA)	97.2% 97.2%	HP0105 HP0117	conserved hypothetical protein conserved hypothetical protein	39.7% 34.2%		ELI3-2 (cad)	44.0%
HP1096	IS605 transposase (tnpA)	97.2%	HP0162	conserved hypothetical protein	36.7%	HP0981 HP0569	exonuclease VII-like protein (xseA) GTP-binding protein (gtp1)	42.5% 48.1%
HP1535 HP0437	IS605 transposase (tnpA) IS605 transposase (tnpA)	97.2% 97.2%	HP0216 HP0233	conserved hypothetical protein conserved hypothetical protein	33.9% 30.5%	HP0303 HP0834	GTP-binding protein (obg) GTP-binding protein homologue (yphC)	48.2% 36.7%
HP0989 HP0997	IS605 transposase (tnpB) IS605 transposase (tnpB)	93.4% 93.4%	HP0248	conserved hypothetical protein	30.7%	HP0480	GTP-binding protein, fusA-homolog (yihK)	54.1%
HP1095	IS605 transposase (tnpB)	93.4%	HP0274 HP0285	conserved hypothetical protein conserved hypothetical protein	38.5% 30.8%	HP1489 HP0405	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 conserved hypothetical protein	31.3% 33.7%	HP0221	nifU-like protein	37.3%
HP0413	transposase-like protein, PS3IS	33.6%	HP0318	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 HP0625	poly E-rich protein protein E (gcpE)	28.7% 47.7%
HP0739	2-hydroxy-6-oxohepta-2,4-dienoate	00.40/	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 mitochondrial signature protein (aspB)	26.4%
HYPOTHE	TICAL		HP0388 HP0395	conserved hypothetical protein conserved hypothetical protein	39.8% 39.9%	HP0377	thiol:disulfide interchange protein (dsbC),	26.4%
General HP0831	conserved hypothetical ATP binding protein		HP0396	conserved hypothetical protein	33.7%		putative	۷۵.4%
HP0066 HP0269	conserved hypothetical ATP-binding protein conserved hypothetical ATP-binding protein	n 34.7%	HP0419 HP0447	conserved hypothetical protein conserved hypothetical protein	45.6% 38.2%			
HP0312	conserved hypothetical ATP-binding protein	n 34.1%	HP0465 HP0466	conserved hypothetical protein conserved hypothetical protein	95.5% 95.7%			
HP1321 HP1430	conserved hypothetical ATP-binding protein conserved hypothetical ATP-binding protein	า 30.8% า 38.1%	HP0468	conserved hypothetical protein	97.1%			
HP1507 HP1567	conserved hypothetical ATP-binding protein conserved hypothetical ATP-binding protein	า 51.6%	HP0469 HP0496	conserved hypothetical protein conserved hypothetical protein	95.1% 99.2%			
HP1026	conserved hypothetical helicase-like protein	n 35.2%	HP0507 HP0519	conserved hypothetical protein conserved hypothetical protein	37.2% 95.3%			
HP0022	conserved hypothetical integral membrane protein	30.8%	HP0552	conserved hypothetical protein	37.8%			
HP0189	conserved hypothetical integral membrane		HP0553 HP0639	conserved hypothetical protein conserved hypothetical protein	30.0% 41.0%			
HP0226	protein conserved hypothetical integral membrane		HP0654	conserved hypothetical protein	32.0%			
HP0228	protein conserved hypothetical integral membrane	27.6%	HP0656 HP0707	conserved hypothetical protein conserved hypothetical protein	36.0% 40.1%			
	protein	43.2%	HP0709 HP0710	conserved hypothetical protein conserved hypothetical protein	49.6% 33.7%			
HP0234	conserved hypothetical integral membrane		HP0716	conserved hypothetical protein	30.2%			
	protein	32.4%	HFU/16	concerved hypotholical protein				