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errata

The yeast genome directory

Nature 387 (suppl.) (1997)

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

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

Michael I. Bergman

Nature 389, 60-63 (1997)

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

cAMP-induced switching in turning direction of nerve growth cones

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

Nature 388, 275-279 (1997)

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

corrections

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

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

Nature **387**, 583–586 (1997)

In this Letter, we overlooked a citation of G. Oszlanyi *et al.*, *Phys. Rev. B* **54**, 11849 (1996), who reported the observation of covalently bound $(C_{60})_2^{2-}$ dianions from the X-ray powder diffraction patterns of the metastable phases of KC₆₀ and RbC₆₀.

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. KarpI, Hamilton O. Smith¶, Claire M. Fraser* & J. Craig Venter*

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

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

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

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

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Table 1 Genome features	
General	
Coding regions (91.0%) Stable RNA (0.7%) Non-coding repeats (2.3%) Intergenic sequence (6.0%)	
RNA	
Ribosomal RNA 23S-5S 23S-5S 16S 16S 5S	Coordinates 445,306-448,642 bp 1,473,557-1,473,919 bp 1,209,082-1,207,584 bp 1,511,138-1,512,635 bp 448,041-448,618 bp
Transfer RNA 36 species (7 clusters, 12 single genes)	
Structural RNA 1 species (ssrD)	629,845-630,124 bp
DNA	
Insertion sequences IS605 13 copies (5 full-length, 8 partial) IS606 4 copies (2 full-length, 2 partial)	
Distinct G + C regions region 1 (33% G + C) 452-479 kb region 2 (35% G + C) 539-579 kb region 3 (33% G + C) 1,049-1,071 kb region 4 (43% G + C) 1,264-1,276 kb region 5 (33% G + C) 1,590-1,602 kb	Associated genes IS605, 5SRNA and repeat 7; <i>virB4</i> 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 499 no database match	

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

General features of the genome

Genome analysis. The genome of *H. pylori* strain 26695 consists of a circular chromosome with a size of 1,667,867 base pairs (bp) and average G + C content of 39% (Figs 1 and 2). Five regions within the genome have a significantly different G + C composition (Table 1 and Fig. 1). Two of them contain one or more copies of the insertion sequence IS605 (see below) and are flanked by a 5S ribosomal RNA sequence at one end and a 521 bp repeat (repeat 7) near the other. These two regions are also notable because they contain genes involved in DNA processing and one contains 2 orthologues of the *virB4/ptl* gene, the product of which is required for the transfer of oncogenic T-DNA of *Agrobacterium* and the secretion of the *pertussis* toxin by *Bordetella pertussis*¹⁰. Another region is the *cag* pathogenicity island (PAI), which is flanked by 31-bp direct repeats, and appears to be the product of lateral transfer¹¹.

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

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

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

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

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

Paralagous families. Ninety-five paralogous gene families comprising 266 gene products (16% of the total) were identified (www.tigr.org/tdb/mdb/hpdb/hpdb.html). Of these, 67 (173 proteins) have an assigned role. Sixty-four have only 2 members, while the porin/adhesin-like outer membrane protein family (Fig. 2) is the largest with 32 members. The largest number of paralogues with assigned roles fall into the functional categories of cell envelope, transport and binding proteins, and proteins involved in replication. The large number of cell envelope proteins might reflect either a reduced biosynthetic capacity or a need to adapt to the challenging gastric environment.

Cell division and protein secretion

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

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

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

Recombination, repair and restriction systems

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

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

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

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

Transcription and translation

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

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

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

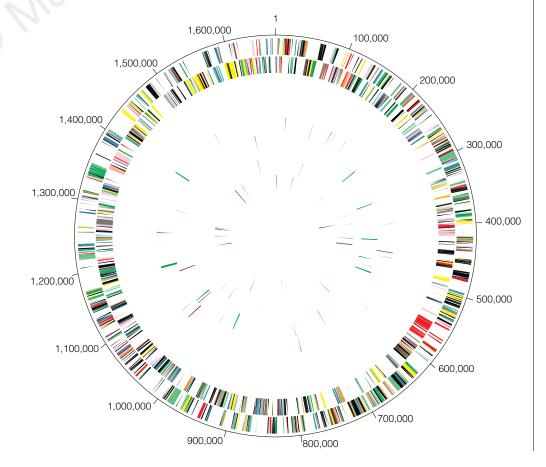
Adhesion and adaptive antigenic variation

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

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

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

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



H-Ferminal peptide sequences: Repair Science - 00000000000000000000000000000000000		- KRWW -	 The American Structure Structure	YUFRAX 754 YUFRAX 754 YUFRAX 730 YUFRAX 734 YUFRAX 734 YUFRAX 661 YUFRAX 665 YUFRAX 665 YUFRAX 665 YUFRAX 665 YUFRAX 663 YUFRAX 508 YUFRAX 508	HINK KATTE TE TE
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F р 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 amino-

terminal sequences, represented at the top of the alignment⁵⁰. The most likely

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

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

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

Virulence

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

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

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

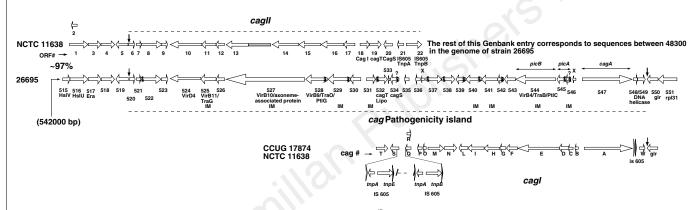


Figure 4 Comparison between the Cag pathogenicity islands of the sequenced strain, 26695 and the NCTC11638 strain. The twenty nine ORFs of the contiguous PAI in strain 26695 are represented together with the corresponding ORFs from the PAI present in NCTC11638 (AC000108 and U60176). The PAI in NCTC11638 is divided by the IS 605 elements into two regions, cag/ and cag/l. The PAI in NCTC11638 is flanked by a 31-bp (TTACAATTTGAGCCCATTCTTTAGCTTGTTTT) direct repeat (vertical arrows) as described¹¹. Some of the genes encode proteins with similarity to proteins involved either in DNA transfer (Vir and Tra proteins) or in export of a toxin (Ptl protein)¹⁰. However, these genes do not have the conserved contiguous arrangement found in the VirB, Tra and Ptl operons, suggesting that this PAI is not derived from these systems. Most genes of the PAI have no database match, contrary to a previous suggestion¹¹. Thirteen of the proteins have a signal peptide (squiggle line), three of them with a weaker probability (squiggled line+?). The average length of the signal peptides is 25 amino acids, suggesting that this PAI is of Gram-negative origin. Eight proteins are predicted to have at least two membrane-spanning domains and to be integral membrane proteins (IM)⁴⁷. Although the two PAI are ~97% identical at the nucleotide level, there are several notable and perhaps biologically relevant differences between the two sequences. Four of the genes differ in size. In the PAI of strain 26695, HP 520 and 521 are shorter, whereas HP523 is longer, and HP 527 actually spans both ORF13 and 14. In addition, the N-terminal part of HP527 is 129 amino acids longer than the corresponding region in ORF14. HP548/549 contains a frameshift and is therefore probably inactive in strain 26695. The stippled box preceding ORF13 represents an N-terminal extension not annotated in the Genbank entry for the PAI of NCTC11638. The 'x' indicates ORFs that are neither GeneMark-positive nor GeneSmith-positive, so were not included in our gene list. However, these ORFs may be biologically significant. We do not represent cagR as an ORF, because it is completely contained within ORFQ, and is GeneMark-negative.

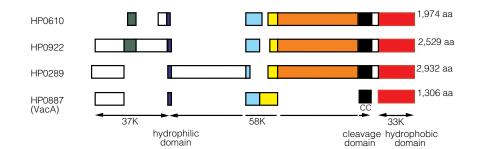


Figure 5 Conserved domains of VacA and related proteins. HP887 is the vacuolating cytotoxin (vacA) gene from *H. pylori* 26695 strain. HP610, HP922 and HP289 are related proteins. Blocks of aligned sequence and the length of each protein are shown. Arrows designate the extents of each VacA domain. The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

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

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

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

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

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

Acidity, pH and acid tolerance

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

HP no.	ID	No. of repeats	Gene status	Poly(A) or Poly(F) tracts in 5' interg	jenic region
9	OMP	11 CT	Off		Poly(A)	
208	glycos. transf.	11 AG	Truncated		Poly(A)	
538	OMP	6 CT	On		No	
722	OMP	8 CT	Off		Poly(T)	
725	OMP	6 CT	Off		Poly(T)	
44	Нуро	9 AG	Truncated		No	
96	OMP	11 CT	On		Poly(A)	
417	Cons. Hypo	9 AG	Truncated		No	
(h) Homonoly	meric $poly(C)$ and $poly(G)$ tracts with	nin codina sequence				
	meric poly(C) and poly(G) tracts wit	nin coding sequence ID	Tract len	qth		Gene status
IP no.		0 1	Tract len C15	gth		Gene status Off
IP no. 8		ID		gth		
IP no. 8 17 79		ID Hypo Hypo Tucosyl transf.	C15 G12 C13	gth		Off On On
HP no. 18 117 179 164		ID Hypo Hypo ucosyl transf. Typel R	C15 G12 C13 C15	gth		Off On On On
HP no. 58 217 379 464 319		ID Hypo Hypo iucosyl transf. Typel R glycos. transf.	C15 G12 C13 C15 C15	gth		Off On On On Truncated
HP no. 58 217 379 464 519 551		ID Hypo Hypo iucosyl transf. Typel R Jlycos. transf. Hypo	C15 G12 C13 C15 C13 C13 C13	gth		Off On On On Truncated On
HP no. 58 217 379 464 619 651 1353		ID Hypo Hypo ucosyl transf. Typel R glycos. transf. Hypo Hypo	C15 G12 C13 C15 C13 C13 C13 C13	gth		Off On On Truncated On Truncated
IP no. 8 17 79 64 19 51 353 471		ID Hypo Hypo Licosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R	C15 G12 C13 C15 C15 C13 C13 C13 C15 G14	gth		Off On On Truncated On Truncated On
1P no. 18 117 179 164 119 151 353 471 522		ID Hypo Hypo Ucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase	C15 G12 C13 C15 C13 C13 C13 C13 C15 G14 G12	gth		Off On On Truncated On Truncated
9 fp no. 18 17 17 164 19 151 152 Genes possib		ID Hypo Hypo Ucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase	C15 G12 C13 C15 C13 C13 C13 C13 C15 G14 G12	gth HP no.	ID	Off On On Truncated On Truncated On
1P no. 8 117 79 64 19 51 353 471 522 Senes possib 1P no.	ly regulated by homopolymeric pol ID Tract	ID Hypo Hypo Ucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase ((A) or poly(T) tracts in 5' intergen HP no.	C15 G12 C13 C15 C13 C13 C15 G14 G12 ic regions ID Tract	HP no.		Off On On Truncated On Truncated On Truncated
1P no. 8 117 79 64 19 551 353 471 522 Genes possib 1P no.	ly regulated by homopolymeric poly ID Tract OMP A14	ID -ypo -ypo ucosyl transf. Typel R -ypo -ypo -ypo TypelIS-R Vethyl ase ((A) or poly(T) tracts in 5' intergen HP no. 25	C15 G12 C13 C15 C13 C15 G14 G12 ic regions ID Tract OMP T15	HP no. 208	rfaJ	Off On On Truncated On Truncated On Truncated Tract A11
1P no. 18 17 179 164 19 151 353 471 522 Genes possib 1P no. 127	ly regulated by homopolymeric poly ID Tract OMP A14 OMP T14	ID Hypo Hypo Licosyl transf. Typel R Jlycos. transf. Hypo TypelIS-R Methyl ase ((A) or poly(T) tracts in 5' intergen HP no. 25 228	C15 G12 C13 C15 C13 C15 C13 C13 C15 G14 G12 ic regions ID Tract OMP T15 IMP A14	HP no. 208 349	rfaJ pyrG	Off On On Truncated On Truncated On Truncated Tract A11 T15
HP no. 18 217 379 464 351 1353 1471 1522 Genes possib HP no. 3 227 350	ly regulated by homopolymeric poly ID Tract OMP A14 OMP T14 IMP A15	ID -ypo -ypo -ypo -ypol R glycos. transf. -ypo	C15 G12 C13 C15 C13 C15 C13 C15 G14 G14 G12 ic regions ID Tract OMP T15 IMP A14 cagA A14	HP no. 208 349 629	<i>rfaJ pyrG</i> Hypo	Off On On Truncated On Truncated On Truncated Tract A11 T15 T15
HP no. 58 217 379 464 619 651 1353 1471 1522	ly regulated by homopolymeric poly ID Tract OMP A14 OMP T14	ID Hypo Hypo Hypo Jypel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase r(A) or poly(T) tracts in 5' intergen HP no. 25 228 547 725	C15 G12 C13 C15 C13 C15 C13 C13 C15 G14 G12 ic regions ID Tract OMP T15 IMP A14	HP no. 208 349	rfaJ pyrG	Off On On Truncated On Truncated On Truncated Tract A11 T15

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^{2+} supply, an essential component of urease activity³⁹. The others may be involved in the elimination of toxic metals from the cytoplasm and not in pH regulation.

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

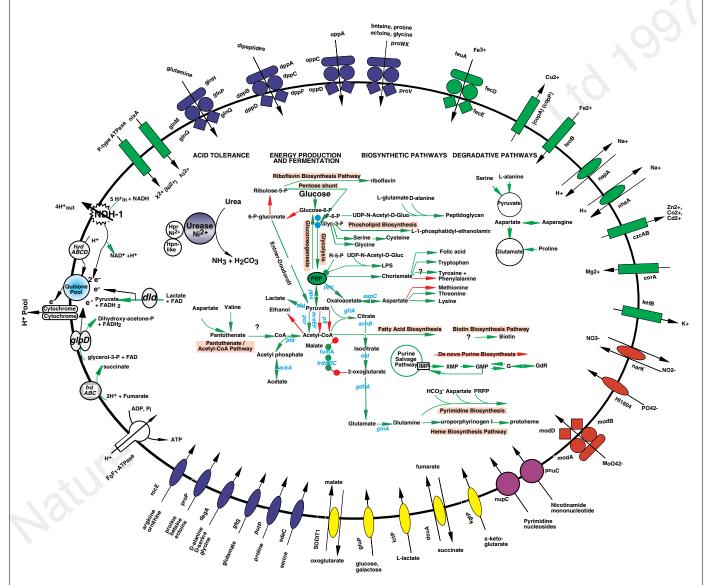


Figure 6 Solute transport and metabolic pathways of Helicobacter pylori. Transporters identified by sequence comparisons are characteristc of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley¹⁵: blue, amino acids, peptides and amines; red, anions; yellow, carbohydrates,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

import under anaerobic conditions for cytochromes, catalase). An integrated view of the main components of the central metabolism of H. pylori strain 26695 is presented. The use of glucose as the sole carbohydrate source is emphasized. Urease, a multisubunit Ni2+-binding enzyme, is crucial for colonization and for survival of H. pylori at acid pH, and is indicated as a complex (purple circle) with Hpn, a Ni²⁺-binding cofactor, and a newly identified Hpn-like protein (HP1432). A question mark is attached to pathways that could not be completely elucidated. Pathways or steps for which no enzymes were identified are represented by a red arrow. Pathways for macromolecular biosynthesis (RNA, DNA and fatty acids) have been omitted. ackA, acetate kinase; acnB, aconitase B; aspC, aspartate aminotransferase; dld, D-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.

proteins, sensor-regulator pairs and other proteins may be acid-induced.

Regulation of gene expression

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

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

Metabolism

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

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

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

Evolutionary relationships of H. pylori

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

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

Conclusion

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

Methods

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

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



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

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

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

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

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

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

General	D BIOSYNTHESIS	
HP0695 Aromatic a	hydantoin utilization protein A (hyuA) amino-acid family	28.6%
HP1038 HP0283	3-dehydroquinase type II (aroQ) 3-dehydroquinate synthase (aroB)	99.4% 38.1%
HP0134 HP0401	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (dhs1) 3-phosphoshikimate	54.6%
HP1279	1-carboxyvinyltransferase (aroA)	53.6% 47.0%
HP1282		47.9%
HP1280 HP1281	anthranilate synthase component II (trpD) anthranilate synthase component II (trpD)	42.5% 40.2%
HP0663	chorismate synthase (aroC)	47.2%
HP1380 HP1249	prephenate dehydrogenase (tyrA) shikimate 5-dehydrogenase (aroE)	30.2% 36.6%
HP0157 HP1277	shikimic acid kinase I (aroK) tryptophan synthase, alpha subunit (trpA)	36.1% 46.5%
HP1278	tryptophan synthase, alpha subunit (trpA) tryptophan synthase, beta subunit (trpB)	66.1%
Aspartate HP0649	aspartate ammonia-lyase (aspA)	55.5%
HP1189	aspartate-semialdehyde dehydrogenase (asd)	45.7%
HP1229 HP0106	aspartokinase (lysC) 48.0% cystathionine gamma-synthase (metB)	47.7%
HP0290	diaminopimelate decarboxylase (dap decarboxylase) (lysA)	42.7%
HP0566	diaminopimelate epimerase (dapF)	30.0%
HP0510 HP1013	dihydrodipicolinate reductase (dapB) dihydrodipicolinate synthetase (dapA)	95.3% 39.5%
HP0822 HP1050	homoserine dehydrogenase (metL) homoserine kinase (thrB)	37.7% 27.7%
HP0672	solute-binding signature and mitochondrial	
HP0212	signature protein (aspB) succinyl-diaminopimelate desuccinylase	47.3%
HP0626	(dapE) tetrahydrodipicolinate N-succinyltransferase	42.3%
	(dapD)	36.1% 32.9%
HP0098 Glutamate	threonine synthase (thrC) family	32.9%
HP0380 HP0512	glutamate dehydrogenase (gdhA) glutamine synthetase (glnA)	59.0% 48.6%
HP1158	pyrroline-5-carboxylate reductase (proC)	28.9%
Pyruvate fa HP0941	amily alanine racemase, biosynthetic (alr)	32.4%
HP1468	branched-chain-amino-acid aminotransferase (ilvE)	63.5%
HP0330	ketol-acid reductoisomerase (ilvC)	48.1%
Serine farr HP0107	illy cysteine synthetase (cysK)	45.7%
HP0096	phosphoglycerate dehydrogenase	31.0%
HP0397 HP0736	phosphoglycerate dehydrogenase (serA) phosphoserine aminotransferase (serC)	32.5% 30.7%
HP0652 HP1210	phosphoserine phosphatase (serB)	36.5% 98.2%
HP0183	serine acetyltransferase (cysE) serine hydroxymethyltransferase (glyA)	98.2% 54.0%
	IESIS OF COFACTORS, PROSTHETIC GROUP	PS,
AND CARI General	RIERS	
HP0220	synthesis of [Fe-S] cluster (nifS)	48.0%
<i>Biotin</i> HP0598	8-amino-7-oxononanoate synthase (bioF)	34.9%
Biotin	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA)	34.9% te 49.2%
<i>Biotin</i> HP0598	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz	34.9% te 49.2% yme
Biotin HP0598 HP0976 HP1140 HP0407	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bisC)	34.9% te 49.2% yme 36.9% 42.7%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bioE) biotin synthesis protein (bioC) biotin synthesise (bioB)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/bioin acetyl coenz A carboxylase synthetase (birA) biotin sufboxide reductase (bisC) biotin synthesis protein (bioC)	34.9% te 49.2% yme 36.9% 42.7% 32.1%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bisC) biotin synthesis protein (bioC) biotin synthesis (bioD) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin-	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.2% 36.0%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP1036 HP0587	8-amino-7-oxononanoste synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bisC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dilhydro-6-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismatel yase (pabC)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0% 34.6% 32.4%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP1036 HP0587	P-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/foldin acetyl coenz A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC)	34.9% te 49.2% yme 36.9% 42.7% 36.2% 36.0% 34.6% 32.4% 32.4%
Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP1036 HP0587 HP1232 HP1545 HP0528	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotranetrase (bioA) biotin operion repressor/biotin acetyl coenz A catboyitase synthesiae (bioC) biotin synthesiae proteini (bioC) biotin synthesiae (bioB) dethiobiotin synthesiae (bioD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (foIA) aminodeoxychorismate lyase (pabC) dihydropfere synthase (foIP) folyfop/gultamate synthase (foIC) GTP cyclopfydiase (foIE)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0% 34.6% 32.4%
Biotin HP0598 HP0976 HP1140 HP1407 HP1254 HP1406 HP1029 Folic acid HP1036 HP10587 HP1545 HP1945 HP0928 HP0577	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotranetrase (bioA) biotin operion repressor/biotin acetyl coenz A catboyitase synthesiae (bioC) biotin synthesis protein (bioC) biotin synthesise protein (bioC) biotin synthesise (bioB) dethiobiotin synthesea (bioD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paBC) dihydropteret synthase (foIP) folyfoplylutamete synthase (foIP) folyfoplylutamete synthase (foIP) methylene-tetrahydrolate dehydrogenase (foID)	34.9% te 49.2% yme 36.9% 32.1% 36.2% 36.0% 34.6% 32.4% 34.5% 50.9% 48.4%
Biotin HP0598 HP0976 HP140 HP1407 HP1254 HP1029 <i>Folic</i> acid HP1036 HP0293 HP1545 HP0293	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bisC) biotin synthesis protein (bioC) biotin synthesis (bioD) dethibiotin synthetase (bioD) dethibiotin synthetase (bioD) 7.8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (foIK) aminodeoxychorismate lyase (pabC) dihydropteroate synthase (foIC) GTP cyclohydrofase (foIC) GTP cyclohydrofase (foIC) GTP cyclohydrofase (foIC) gara-aminobenzoate synthetase (pabB)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0% 34.6% 32.4% 34.5% 35.2% 50.9%
Biotin HP0598 HP0976 HP1140 HP1407 HP1254 HP1406 HP1029 Folic acid HP1036 HP10587 HP1545 HP1945 HP0928 HP0577	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bicA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bicC) biotin synthesis protein (bicC) biotin synthesis (bicD) dethiotionin synthetase (bicD) dethiotionin synthetase (bicD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (folR) aminodeoxychorismate Ivase (paBC) dihydro-6-hydroxymethylpterin- pyrophosphokinase (folR) aminodeoxychorismate Ivase (paBC) dihydro-fordase (folP) foly/polydutamete synthase (folP) foly/polydutamete synthase (folP) methylene-tetrahydrololate dehydrogenase (folD) porphyrin delta-aminolevulinic acid dehydratase	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0% 34.6% 32.4% 34.5% 35.2% 50.9% 48.4% 35.1%
Biotin HP0596 HP0476 HP1400 HP1400 HP1400 HP1402 F0ico acid HP1224 HP1029 F0ico acid HP1232 HP1524 HP0577 HP0523 Haem and HP1053 HP0576	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin suffoxide reductase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioD) dethiobiotin synthetase (bioD) dethiobiotin synthetase (bioD) 7. 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (pabC) dihydro-fo-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (pabC) dihydro-fo-tarate synthase (foIC) GTP cyclohydrolase 1 (foIE) methylene-tetrahydrololate dehydrogenase (foID) para-aminolevulnic acid dehydratase (hemB) ferrochelatase (hemH)	34.9% te 49.2% yme 36.9% 32.1% 36.2% 36.2% 36.0% 34.6% 32.4% 35.2% 50.9% 48.4% 35.1% 50.5% 50.5%
Biotin HP0598 HP0976 HP140 HP140 HP1254 HP1406 HP1029 Folic acid HP1036 HP0587 HP1545 HP0528 HP0577 HP0528 HP0573 Haem and HP053	9-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioE) dihydropteroate synthese (bioC) GTP cyclohydrolase (loE) GTP cyclohydrolase (loE) para-aminobenzoate synthetase (pabB) porphyrin delta-aminobenzoate synthetase (pabB) procheitase (hemH) glutamati-1-semialdehyde 2,1-aminomutase	34.9% te 49.2% yme 36.9% 32.1% 36.2% 36.2% 36.0% 34.6% 32.4% 35.2% 50.9% 48.4% 35.1% 50.5% 50.5%
Biotin HP0598 HP0498 HP1400 HP140 HP140 HP140 HP0497 HP1264 HP0029 Folic acid HP1036 HP0587 HP1532 HP1646 HP0528 HP0577 HP0531 HP0536 HP0376 HP0239 HP0239	9-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenz A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioC) dihydropteroate synthese (bioC) GTP cyclohydrolase (bioF) tolyipolydjutarets ynthese (bioC) para-aminobenzoate synthetase (pabB) para-aminobenzoate synthetase (pabB) porphyrin della-aminolevulinic acid dehydratase (hemB) ferrocheitase (hemH) glutamyt-1-semialdehyde 2,1-aminomutase (hemL).	34.9% te 49.2% yme 36.9% 42.7% 32.2% 36.0% 34.6% 32.4% 32.4% 32.4% 35.2% 50.9% 50.9% 50.9% 51.3% 51.3% 51.3%
Biotin HP0598 HP0498 HP1400 HP1400 HP1400 HP1400 HP1406 HP0293 HP1638 HP0283 HP0376 HP0336 HP0336 HP0336 HP0336 HP0336 HP0336 HP0386 HP0386	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carbox/lase synthetase (birA) biotin suffoxide reductase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (bioD) dihydropteroate synthase (bioD) dihydropteroate synthase (bioD) dihydropteroate synthase (biOC) dihydropteroate synthese (biOC) dihydropteroate synthese (biOC) dihydropteroate synthese (biOC) dihydropteroate synthese (biOC) dihydropteroate synthetase (biOC) dihydropteroate synthetase (biOC) dihydropteroate synthetase (biOC) dihydropteroate synthetase (biOC) dihydropteroate synthetase (biOC) detha-aminobenzoate synthetase (pabB) porphyrin delta-aminolevulinic acid dehydratase (hemB) ferrochelatase (hemH) gutamytel-1-semiaidehyde 2,1-aminomutase (hemIL) gutamytel/NA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.2% 36.2% 36.2% 34.5% 35.2% 50.9% 48.4% 35.1% 50.5% 51.3% 51.3% 52.7% 42.4%
Biotin HP0598 HP0479 HP1400 HP1400 HP1400 HP1406 HP0407 HP1406 HP0029 Folic acid HP1036 HP0283 Ham and HP0376 HP0386 HP0283 HP0366 HP0239 HP0366 HP0239	8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carbox/lase synthetase (birA) biotin suffoxide reductase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lysas (pabC) dihydropteroate synthase (folC) folf cyclohydrolase (folC) dihydropteroate synthase (folC) GTP cyclohydrolase (folC) gtra cyclohydrolase (folC) gtra cyclohydrolase (folC) gtra cyclohydrolase (folC) gtra cyclohydrolase (folC) gtra cyclohydrolase (folC) gtra cyclohydrolase (folC) gurapyrin delta-aminobenzoate synthetase (pabB) porphyrin delta-aminolevulinic acid dehydratase (hemB) ferrochelatase (hemH) gutamytel-1-semiaidehyde 2,1-aminomutase (hemI), gutamytelTNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN)	34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.2% 36.2% 36.2% 35.2% 50.9% 48.4% 35.1% 50.5% 51.3% 51.3% 52.7% 42.4% 37.9%
Biotin HP0598 HP0140 HP0407 HP140 HP140 HP0407 HP1264 HP1036 HP0587 HP1036 HP0587 HP0233 Haem and HP0163 HP0376 HP0336 HP0336 HP0239 HP0239 HP0239 HP0239 HP0239 HP0239 HP02376 HP0237	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/botin acetyl coenz A carboxylase synthetise (birA) biotin suffodde reductase (bicC) biotin synthesis protein (bioC) biotin synthesis (bicC) biotin synthesis (bicC) dethiobiotin synthetase (bicC) adminodeoxychorismate (bicC) aminodeoxychorismate (bicC) (biC) para-aminobenzoate synthase (bicC) para-aminobenzoate synthese (bicC) para-aminobenzoate synthase (bicC) adita-aminolevulinic acid dehydratase (hemL) glutamate-1-semialdehyde 21-aminomutase (hemL) glutamyt-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxyboline adenome deaminase (hemC)	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 36.2% 36.2% 35.2% 50.3% 35.2% 50.5% 33.4% 51.3% 32.7% 42.4% 37.9%
Biotin HP0598 HP0140 HP0407 HP140 HP140 HP0407 HP140 HP0407 HP140 HP0376 HP0376 HP038 HP0587 HP0381 HP0577 HP0233 H20376 HP0376 HP0239 HP02376 HP0239 HP0239 HP0239 HP02376 HP02376 HP02376 HP0237	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotranetrase (bioA) biotin operon repressor/biotin acetyl coenz A carboyitase synthases (bicC) biotin synthesise protein (bicC) biotin synthesise protein (bicC) biotin synthesise protein (biCC) biotin synthesise (bicB) dethiobiotin synthetase (bicD) 7. 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (paBC) dihydropteretarshydrolaite dehydrogenase (folD) para-aminobenzoate synthase (folC) GTP cyclorydroilaite (tolE) methylene-terrahydrololaite dehydrogenase (folD) para-aminobenzoate synthase (paBB) porphyrin delta-aminolevulinic acid dehydratase (hemB) glutamyl-IRNA reductase (hemA) oxydase.(hemN) oxydase.(hemN) porphobilinogen deaminase (hemC) protoporphyrinogen villase (hemR)	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 36.2% 36.2% 35.2% 50.9% 35.5% 50.9% 50.5% 50.5% 50.5% 50.5% 51.3% 32.7% 42.4% 37.9% 42.4%
Biotin HP0958 HP0140 HP0479 HP1400 HP140 HP0407 HP140 HP0407 HP140 HP035 HP036 HP037 HP0597 HP0577 HP0578 HP0376 HP0376 HP0376 HP0386 HP0329 HP0386 HP0381 HP0381 HP0381 HP0381	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetise (biA) biotin sulfodel reductase (biAC) biotin synthesis protein (biAC) biotin synthesis protein (biAC) biotin synthesis (biAC) biotin synthesis (biAC) dethiobiotin synthetase (biAC) aminodeoxychorismate (vase (paCC) dihydro-6-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate (vase (paCC) dihydro-6-hydroxymethylpterin- gyrophosphokinase (foIR) aminodeoxychorismate (vase (paCC) dihydro-feter synthase (foIC) GTP cyclohydroisse (foIE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate syntheste (paBB) porphyrin delta-aminolevulinic acid dehydratase (hemL) glutamate-1-semialdehyde 2,1-aminomutase (hemL) glutamate-1-semialdehyde 2,1-aminomutase (hemL) glutamate-1-semialdehyde 2,1-aminomutase (hemL) glutamate-1-semialdehyde 2,1-aminomutase (hemL) grotpoorphyrinogen deaminase (hemC) protpoolingen deaminase (hemC) protpoolingen deaminase (hemC)	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 36.2% 36.2% 35.2% 50.3% 35.2% 50.5% 33.4% 51.3% 32.7% 42.4% 37.9%
Biotin HP0958 HP0140 HP0479 HP1400 HP140 HP0407 HP140 HP0407 HP140 HP035 HP036 HP037 HP0597 HP0577 HP0578 HP0376 HP0376 HP0376 HP0386 HP0329 HP0386 HP0381 HP0381 HP0381 HP0381	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (biA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (biA) biotin suffoxide reductase (biAC) biotin synthesis protein (biAC) biotin synthesis protein (biAC) biotin synthesis (biAC) biotin synthesis (biAC) dethiobiotin synthetase (biAC) aminodeoxychorismate (vase (paBC)) aminodeoxychorismate (vase (paBC)) dithiodro-8-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate (vase (paBC)) dithiodrodeoxychorismate (vase (paBC)) dithiodrodeoxychorismate (vase (paBC)) dithiodrodeoxychorismate (vase (paBC)) aminodeoxychorismate (vase (paBC)) dithiodrodeoxychorismate (vase (paBC)) dithiodrodeoxychorismate (vase (paBC)) gorphyrin delta-aminolexulinic acid dehydratase (hemL) glutamate-1-semialdehyde 2,1-aminomutase (hemL) guygen-independent coproporphyrinogen III oxidase (hemH) porphobilinogen deaminase (hemC) porphyrinogen deaminase (hemE) uroporphyrinogen deaminase (hemE) uroporphyrinogen III cosyrthase (hemE)	34.9% te 49.2% 36.9% 42.7% 36.9% 32.1% 36.2% 36.2% 36.2% 35.2% 50.9% 35.1% 50.5% 35.1% 50.5% 32.4% 50.5% 32.7% 42.4% 33.4% 51.3% 52.7% 42.4%
Biotin HP0598 HP07976 HP07976 HP1400 HP0407 HP1400 HP1400 HP1406 HP0598 HP1036 HP0597 HP0593 HP0577 HP0293 HP0577 HP0336 HP0336 HP0336 HP0336 HP03376 HP03381 HP06391 HP0237 HP0381 HP0424 Menaquint HP1226 HP0391 HP0392	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (biA) biotin operon repressor/biotin acetyl coenz A carboxylase synthetase (biA) biotin suffoxide reductase (biAC) biotin synthesis protein (biAC) biotin synthesis protein (biAC) biotin synthesis (biAC) biotin synthesis (biAC) dethiobiotin synthetase (biAC) aminodeoxychorismate (vasc (paBC)) aminodeoxychorismate (vasc (paBC)) dithiodro-8-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate (vasc (paBC)) dithiodrodeoxychorismate (vasc (paBC)) dithiodrodeoxychorismate (vasc (paBC)) aminodeoxychorismate (vasc (paBC)) dithiodrodeoxychorismate (vasc (paBC)) aminodeoxychorismate (vasc (paBC)) dithiodrodeoxychorismate (vasc (paBC)) dithiodrodeoxychorismate (vasc (paBC)) gorphyrin delta-aminoberuzoate synthase (foIC) gorphyrin delta-aminoberuzoate synthase (paBB) porphyrin delta-aminoberuzoate synthase (paBB) gorphyrin delta-aminoberuzoate synthase (paBB) gorphyrin gutamate-1-semialdehyde 21-aminomutase (hemL) gygen-independent coproporphyrinogen III oxidase (hemK) gorphobilinogen deaminase (hemC) protoporphyrinogen deaminase (hemE) uropophyrinogen deaminase (hemE) uropophyrinogen deaminase (hemE) uropophyrinogen deaminase (hemE) uropophyrinogen III cosynthase (hemE) uropophyrinogen IIII cosynthase (hemE)	34.9% te 49.2% yme 36.9% 42.7% 36.9% 32.1% 36.2% 36.2% 35.2% 50.9% 35.2% 50.5% 35.2% 50.5% 35.4% 51.3% 51.3% 51.3% 52.5%
Biotin HP0598 HP0140 HP01407 HP1408 HP1406 HP1406 HP10587 HP10368 HP0237 HP0237 HP0376 HP0385 HP0237 HP0237 HP0237 HP0237 HP0237 HP0237 HP0237 HP0304 HP1286 HP0237 HP0384 HP0384 HP0385 HP1226 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP0384 HP1380	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboxylase synthasiae (bicC) biotin synthesiae pythetaise (bicC) biotin synthesiae (bicD) dethiobiotin synthetase (bicD) 7. 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-terativativate synthase (folF) foly/polyglutamate synthase (folF) foly/polyglutamate synthase (folF) foly/polyglutamate synthase (folF) glutamyl-ter-atrahydrololate dehydrogenase (folD) para-aminobenzoate synthase (folF) delta-aminolexulinic acid dehydratase (hemB) ferrochelatase (hemH) glutamyl-tRNA reductase (hemA) oxydase (hemN) porphobilinogen deaminase (hemC) protoporphyrinogen lit oxidase (hemN) porphobilinogen (dearboxylase (hemE)) uroporphyrinogen lit oxyntase (hemD) more and ubiquinone 4-hydroxybenzoate octaprenyltransferase (ibiA) geranyltranstransferase (ispA) octaprenyltransferase (ispA) octaprenyltranstransferase (ispA)	34,9% te 49,2% 42,7% 32,1% 32,1% 32,2% 36,2% 32,4% 34,6% 32,4% 34,6% 32,4% 35,2% 50,9% 48,4% 35,1% 50,5% 33,4% 51,3%
Biotin HPO598 HP0140 HP0407 HP140 HP140 HP140 HP1254 HP0376 HP132 HP1406 HP0577 HP0577 HP0538 HP0538 HP0538 HP0386 HP0237 HP03376 HP0237 HP03376 HP03376 HP03376 HP03376 HP03376 HP03376 HP03376 HP03376 HP0341 HP0329 HP0341 HP0327 HP0341 HP0341 HP0341 HP0341 HP1224 HP0341 HP12321	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboxylase synthasiae (bicC) biotin synthesiae pythetaise (bicC) biotin synthesiae pythetaise (bicC) biotin synthesiae (bicD) 7. 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-8-hydroxymethylpterin- gyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-tertarihydrololate dehydrogenase (folD) para-aminobenzoate synthase (folF) ferrochelatase (hermk) glutamyl-1RNA reductase (hermA) oxydase (hermN) oxydase (hermN) oxydase (hermN) portphobilinogen dearboxylase (hermE) uroporthyrinogen lid cosynthase (hermE)	34.9% te 49.2% yme 36.9% 42.7% 36.9% 32.1% 36.2% 36.2% 35.2% 50.9% 35.2% 50.5% 35.2% 50.5% 35.4% 51.3% 51.3% 51.3% 52.5%
Biotin HP0598 HP0140 HP0470 HP1400 HP140 HP0407 HP140 HP0407 HP140 HP0407 HP1264 HP0376 HP0587 HP0293 HP0577 HP0293 HP0376 HP0376 HP0336 HP03376 HP0239 HP0336 HP03376 HP03381 HP04293 HP0381 HP0394 HP0394 HP0394 HP0394 HP0394	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboyidse synthasise (bicF) biotin synthesise protein (bicC) biotin synthesise protein (bicC) biotin synthesise protein (bicC) biotin synthesise (bicD) 7. 8-dihydro-8-hydroxymethylperin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-8-hydroxymethylperin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-teransity (folF) tolyipolyglutamete synthase (tolC) GTP cyclohydrolase (tolC) methylene-teranydrololate dehydrogenase (folD) para-aminobenzoate synthase (tolC) glutamyl-tene-indehydrolase (tolE) methylene-teranydrololate dehydratase (hemB) ferrochelatase (hemH) glutamyl-tRNA reductase (hemA) oxydase (hemN) porphoblinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen lid coxynthase (tolF) oxidase (hemN) porphoblinogen ele coxyntase (hemE) uroporphyrinogen lid coxynthase (telF) oxidase (hemN) oxydase (hemA) oxydase (hemA) oxidase (hemA) oxydase (hemA) oxidase (hemA)	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 36.2% 35.2% 50.3% 50.5% 50.5% 50.5% 50.5% 51.3% 52.7% 51.3% 52.7% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.9% 37.9% 42.9% 37.9% 33.9% 42.9% 33.9% 33.9% 33.9%
Biotin HPO598 HPO407 HP140 HP4254 HP140 HP426 HP246 HP057 HP1036 HP0577 HP0231 HP0536 HP0537 HP0537 HP0538 HP0538 HP05376 HP03376 HP03376 HP03376 HP03376 HP03376 HP0329 HP0329 HP0328 HP0329 HP0328 HP0329 HP0329 HP0320 Menaquint HP0329 HP0329	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboy/ises eynthetase (bicC) biotin synthetase (bicC) biotin synthetase (bicD) dethiobiotin synthetase (bicD) 7. 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (paDC) dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (paDC) dihydro-teransity lyase (folF) tolyipolyglutamete synthase (folF) tolyipolyglutamete synthase (folF) tolyipolyglutamete synthase (folF) tolyipolyglutamete synthase (folF) tolyipolyglutamete synthase (folF) tolyipolyglutamete synthase (folF) glutamyl-ter-etra'hydrofolate dehydrogenase (fhoT) glutamyl-ter-etra'hydrofolate dehydratase (hemB) terrochelatase (hemH) glutamyl-ten-etra'hydrolyde 2,1-aminomutase (hemR) porphoblinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen lid coxynthase (hemE) molyddeunum cofactor biosynthesis protein A (moaA) molyddeunum cofactor biosynthesis protein (moaC)	34,9% te 49,2% 36,9% 32,7% 32,7% 32,7% 32,4% 34,6% 32,4% 34,6% 32,4% 35,2% 50,9% 50,5% 50,9% 50,5% 33,4% 51,3% 51,4%
Biotin HPO598 HPO407 HP140 HP4254 HP140 HP246 HP254 HP1036 HP0587 HP1284 HP0587 HP0283 HP0577 HP0336 HP0376 HP03376 HP03376 HP03376 HP0329 HP0328 HP0328 HP0328 HP0328 HP0328 HP0386 HP0380 HP0380	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboy/ises eynthetase (bicC) biotin synthesise protein (bicC) biotin synthesise protein (bicC) biotin synthesise protein (bicC) biotin synthesise (bicD) 7. 8-dihydro-8-hydroxymethylperin- pyrophosphokinase (folK) aminodeoxychorismate lyase (paDC) dihydro-8-hydroxymethylperin- pyrophosphokinase (folK) aminodeoxychorismate lyase (paDC) dihydro-teransity lyase (folF) tolyhoolyglutamete synthase (tolC) GTP cyclohydrolase (tolC) methylene-teransydrolotiate dehydrogenase (folD) para-aminobenzoate synthase (tolC) glutamyl-tene-indicate dehydrogenase (hemB) ferrochelatase (hemH) glutamyl-tRNA reductase (hemA) oxydase (hemN) porphobilinogen dearboxylase (hemE) uroporphyrinogen dicarboxylase (hemE) uroporphyrinogen dicarboxylase (hemE) uroporphyrinogen dicarboxylase (hemE) uroporphyrinogen dicarboxylase (hemE) uroporphyrinogen dicarboxylase (hemE) uroporphyrinogen lit.coxynthase (tspB) parto-aminogen lit.coxynthase (tspB) protoporphyrinogen lit.coxynthase (tspB) protoporphyrinogen lit.coxynthase (tspB) actarerer/biohyschate synthase (tspB) erim molyddopterin biosynthesis protein (mocA) molyddopterin biosynthesis protein (mocB)	34,9% te 49,2% 36,9% 32,7% 32,7% 32,7% 32,4% 34,6% 32,4% 34,6% 32,4% 35,2% 50,9% 50,5% 50,9% 50,5% 33,4% 51,3% 51,4%
Biotin HP0598 HP0140 HP0407 HP140 HP140 HP0407 HP140 HP0407 HP140 HP0407 HP1406 HP0376 HP0581 HP0381 HP0376 HP0336 HP0336 HP03376 HP0239 HP0336 HP0239 HP03381 HP0381 HP0392 HP0629 HP0629 HP0376 HP0381 HP0381 HP0394 HP0376 HP0381 HP0394 HP0395 HP0788 HP0798 HP0758	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferse (bioA) biotin operion repressor/biotin acetyl coenz A carboy/ises eynthetase (bicC) biotin synthetase (bicD) biotin synthetase (bicD) dethiobiotin synthetase (bicD) 7. 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-8-hydroxymethylpterin- pyrophosphokinase (folK) aminodeoxychorismate lyase (pabC) dihydro-terating synthase (folF) foly/polydiutamete synthase (folF) foly/polydiutamete synthase (folF) foly/polydiutamete synthase (folF) foly/polydiutamete synthase (folF) growphyrin delta-aminolexulinic acid dehydratase (hemB) ferrochelatase (hemH) glutamyl-IRNA reductase (hemA) oxydase (hemN) oxydase (hemN) porphobilinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen lidoxylase (hemE) uroporphyrinogen lidoxynthesis protein (modD) molyddopterin bioxynthesis protein (moeA) molyddopterin bioxynthesis protein (moeA) molyddopterin bioxynthesis protein (moeA) molyddopterin bioxynthesis protein (moeA)	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 35.2% 50.9% 35.2% 50.9% 33.4% 51.3% 51.3% 52.7% 51.3% 52.7% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.
Biotin HPO598 HPO407 HP140 HP4254 HP140 HP246 HP254 HP1036 HP0587 HP1284 HP0587 HP0283 HP0577 HP0336 HP0376 HP03376 HP03376 HP03376 HP0329 HP0328 HP0328 HP0328 HP0328 HP0328 HP0386 HP0380 HP0380	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (biA) biotin operon repressor/biofin acetyl coenz A carboxylase synthesise (biA) biotin synthesis protein (biC) biotin synthesis protein (biC) biotin synthesis protein (biC) biotin synthesis (biA) dethiobiotin synthetase (biA) aminodeoxychorismate lyase (paC) ditrydory6-hydroxymethylperin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paC) ditrydory6-hydroxymethylperin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paC) ditrydory6rolase (foIP) folyfoolyglutamete synthase (foIC) GTP cyclohydrolase (foIE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthase (foIC) delta-aminolevulinic acid dehydratase (hemL) glutamyl-RINA reductase (hemA) gurganyl-RINA reductase (hemA) gurganyl-RINA reductase (hemA) oxygen-independent coproportyrinogen III oxidase (hemN) oxygen-independent corpoorphyrinogen III oxidase (hemN) porphobilinogen deaminase (hemC) protoporphyrinogen axidase (hemE) uroporphyrinogen axidase (hemE) uroporphyrinogen axidase (hemE) octaprenyl-diphosphate synthase (spB) <i>erin</i> motybdopterin biosynthesis protein (moeA) motybdopterin biosynthesis protein (moeA) motybdopterin converting factor, subunit 2	34.9% te 49.2% 36.9% 32.1% 36.2% 36.2% 36.2% 35.2% 50.9% 35.2% 50.9% 33.4% 51.3% 51.3% 51.3% 52.7% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 43.5% 37.9% 42.9% 37.9% 42.9% 37.9% 43.5% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 42.9% 37.9% 37.9% 42.9% 37.
Biotin HPO598 HPO140 HPO407 HP140 HP0407 HP1254 HP058 HP1030 HP0587 HP1254 HP0577 HP0587 HP0587 HP0330 HP05376 HP03376 HP03376 HP03376 HP03376 HP03376 HP03376 HP0329 HP0328 HP0328 HP0328 HP0329 HP0328 HP0329 HP0329 HP0329 HP0329 HP0329 HP0380 HP0380 HP0381	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (biA) biotin operion repressor/biofin acetyl coenz A carboxylase synthetiae (biA) biotin synthesis protein (biC) biotin synthesis protein (biC) biotin synthesis protein (biC) biotin synthesis (biA) dethiobiotin synthetase (biA) aminodeoxychorismate (biA) aprahyrin porphyrinodease (biA) gutamytRNA reductase (hertA) gutamytRNA reductase (hertA) axygen-independent coproporphyrinogen III axidase (hertN) ayagen-independent coproporphyrinogen III axidase	34.9% te 49.2% 42.7% 36.3% 36.2% 36.2% 36.2% 36.2% 35.2% 50.5% 35.2% 50.5% 33.4% 50.5% 33.4% 50.5% 33.4% 51.3% 32.7% 42.4% 42.4% 42.4% 42.4% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 43.5% 31.4% C C 7.9% 36.3% 31.4% 50.5% 33.1% 33.1% 33.1% 50.5% 50.5% 33.1% 33.1% 50.5% 50.5% 33.1% 33.1% 50.5% 50.5% 33.1% 33.1% 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% 35.5%
Biotin HPO598 HPO140 HPO376 HP1400 HP140 HP140 HP140 HP140 HP140 HP140 HP140 HP0581 HP1036 HP0233 Haem and HP0636 HP0236 HP0237 HP0237 HP02381 HP0237 HP0381 HP0587 HP0298 HP0297 HP0298 HP0298 HP0298 HP0376 HP0376	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa sminotransferse (bicA) biotin operion represso/biotin acetyl coenz A catboxylase synthesise (bicA) biotin synthesise proteins (bicA) biotin synthesise proteins (bicA) biotin synthesise (bicB) biotin synthesise (bicB) dethiobiotin synthesise (bicC) biotin synthesise (bicB) dethiobiotin synthesise (bicC) aminodeoxychorismate lyase (paBC) dihydro-6-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paBC) dihydro-fordase (foIP) folylpolydutamete synthase (foIC) GTP cyclohydrolase (foIE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthase (foIC) growphrin delta-aminolevulinic acid dehydratase (hemB) growphrin A reductase (hemA) oxygen-independent coproportyrinogen III oxidase (hemN) oxygen-independent coproportyrinogen III oxidase (hemN) oxygen-independent coproportyrinogen III oxidase (hemN) oxygen-independent coproportyrinogen III oxidase (hemN) oportpyrinogen dearminase (hemC) protoportpyrinogen dearminase (hemC) protoportpyrinogen dearminase (hemC) protoportpyrinogen dearbydse (hemE) uroporphyrinogen doxidase (hemD) once and ubiquinone 4-hydroxyberzoate octaprenytransferase (ubiA) geranytranstransferase (ispA) octaprenyl-diphosphate synthasis protein (moeA) molybdopterin biosynthesis protein (moeB) molybdopterin biosynthesis protein (moeA) molybdopterin biosynthesis protein (moeB) molybdopterin biosynthesis protein (moeA) molybdopterin biosynthesis p	34,9% te 49,2% 42,7% 32,1% 32,2% 36,2% 32,4% 34,6% 32,4% 34,6% 32,4% 35,2% 50,9% 48,4% 35,1% 50,5% 33,4% 50,5% 33,4% 51,3%
Biotin HP0598 HP0140 HP0376 HP1400 HP0407 HP1400 HP1400 HP1406 HP0587 HP1036 HP0587 HP0293 HP0320 HP0336 HP0336 HP0336 HP0336 HP0336 HP0336 HP0336 HP0336 HP03376 HP03381 HP0682 HP0340 HP1226 HP0368 HP0376 HP0381 HP0381 HP0381 HP0381 HP0386 HP0788 HP0788 HP0788 HP0788 HP0788 HP0780 HP0780 HP0800 HP0769	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa sminotranetrase (biA) biotin operion represso/biotin acetyl coenz A catboxylase synthesise (biA) biotin synthesis protein (biOC) biotin synthesis protein (biOC) biotin synthesis (biA) dethiobiotin synthesise (biA) dethiobiotin synthesise (biA) adihydro-6-hydroxymethylperin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paC) dihydro-6-hydroxymethylperin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paC) dihydro-fordase (foIP) folyipolyglutamete synthase (foIC) GTP cyclorydrolase (foIE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthase (foIC) graphyrin delta-aminolevulinic acid dehydratase (hem3) glutamate-1-semialdehyde 2,1-aminomutase (hem3) glutamate-1-semialdehyde 2,1-aminomutase (hem3) glutamate-1-semialdehyde 2,1-aminomutase (hem3) glutamate-1-semialdehyde 2,1-aminomutase (hem3) glutamate-1-semialdehyde 2,1-aminomutase (hem1) gurappryrinogen deatroxyclase (hemE) uroporphyrinogen deatroxyclase (hemE) proteoprityrinogen axidase (hemE) uroporphyrinogen deatroxyclase (hemE) uroporphyrinogen deatroxyclase (hemE) uroporphyrinogen deatroxyclase (hemB) molydodpterin biosynthesis protein (moeA) molydodpterin converting factor, subunit 1 (mosD) molydodpterin converting factor, subunit 2 (mosA) a-methy-2-oxobutanoate hydroxymethyltran (panB)	34,9% te 49,2% 42,7% 32,1% 32,2% 36,2% 32,4% 34,6% 32,4% 34,6% 32,4% 35,2% 50,9% 48,4% 35,1% 50,5% 33,4% 50,5% 33,4% 51,3%
Biotin HPO598 HPO140 HPO376 HP1400 HP140 HP140 HP140 HP140 HP140 HP140 HP140 HP0581 HP1036 HP0233 Haem and HP0636 HP0236 HP0237 HP0237 HP02381 HP0237 HP0381 HP0587 HP0298 HP0297 HP0298 HP0298 HP0298 HP0376 HP0376	8-amino-7-oxononanoate synthase (bicF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/bolin acetyl coenz A carboxylase synthetise (biA) biotin suffoder reductase (biAC) biotin synthesis protein (biOC) biotin synthesis protein (biOC) biotin synthesis (biOC) dethiobiotin synthetase (biOC) dethiobiotin synthetase (biOC) aminodeoxychorismate lyase (paCC) diflydro-6-hydroxymethylpterin- pyrophosphokinase (foIR) aminodeoxychorismate lyase (paCC) diflydro-6-hydroxymethylpterin- gyrophosphotyloridase (foIC) detha-aminobenzoate synthase (foIC) detha-aminobenzoate synthase (foIC) detha-aminobenzoate synthase (foIC) detha-aminobenzoate synthase (foIC) detha-aminobenzoate synthase (foIC) gara-aminobenzoate synthase (foIC) detha-aminobenzoate synthase (foIC) gara-aminobenzoate synthase (foIC) guroporphyrinogen deaminase (hernC) protoporphyrinogen deaminase (hernC) protoporphyrinogen deaminase (hernC) protoporphyrinogen deaminase (hernC) protein A (moaA) motybdopterin biosynthesis protein (moaA) motybdopterin biosynthesis protein (moaA) motybdopterin biosynthesis protein (moaA) motybdopterin converting factor, subunit 1 (moaC) motybdopterin converting factor, subunit 1 (moaA) motybdopterin converting factor, subunit 1 (moaA) amethyl-2-oxobutanoate hydroxymethyltran (panB) asperate 1-decarboxylase (panD)	34.9% te 49.2% 49.2% 36.9% 32.1% 36.2% 36.2% 35.2% 50.5% 35.2% 50.5% 35.4% 50.5% 33.4% 50.5% 32.4% 33.4% 50.5% 32.7% 42.4% 37.9% 42.8% 37.9% 42.8% 37.9% 42.8% 37.9% 37.9% 42.8% 37.9% 37.

	uentitues.	
HP0841	pantothenate metabolism flavoprotein (dfp)	31.3%
Pyridoxine HP1583	pyridoxal phosphate biosynthetic protein A (pdxA)	34.2%
HP1582	pyridoxal phosphate biosynthetic protein J (pdxJ)	42.6%
Riboflavin	0770	17.00
HP0802 HP0804	GTP cyclohydrolase II (ribA) GTP cyclohydrolase II/3,4-dihydroxy-2-butar	47.2%
	4-phosphate synthase (ribA, ribB)	44.0%
HP1505 HP1087	riboflavin biosynthesis protein (ribG) riboflavin biosynthesis regulatory protein	33.1%
	(ribC)	28.9%
HP1574 HP0002	riboflavin synthase alpha subunit (ribC) riboflavin synthase beta chain (ribE)	32.8% 52.4%
	, glutaredoxin and glutathione	0L.+ /0
HP1118	gamma-glutamyltranspeptidase (ggt)	53.2%
HP1458 HP0824	thioredoxin thioredoxin (trxA)	38.3% 51.5%
HP1164	thioredoxin reductase (trxB)	28.5%
Thiamine HP0814	thiamin biosynthesis protein (thiF)	34.6%
HP0843	thiamin phosphate pyrophosphorylase/	
HP0845	hyroxyethylthiazole kinase (thiB) thiamin phosphate pyrophosphorylase/	35.7%
HP0844	hyroxyethylthiazole kinase (thiM) thiamine biosynthesis protein (thi)	37.9% 41.0%
Pyridine nuc	cleotides	
HP0329 HP1355	NH(3)-dependent NAD+ synthetase (nadE) nicotinate-nucleotide pyrophosphorylase	37.5%
	(nadC)	36.3%
HP1356	quinolinate synthetase A (nadA)	34.2%
CELL ENVE		
HP1450	, <i>lipoproteins and porins</i> 60 kDa inner-membrane protein	40.0%
	apolipoprotein N-acyltransferase (cute)	28.0% 34.9%
	cell binding factor 2 Hypothetical protein	28.4%
LIDOE67	mombrana protain	26.4% 98.9%
HP 1004	membrane-associated lipoprotein (lpp20) outer membrane protein	39.9%
HP0009	outer membrane protein (omp1)	0.0%
HP0472	outer membrane protein (omp11)	99.5%
HP04//	outer membrane protein (omp12)	0.0%
HP0671	outer membrane protein (omp14)	36.0%
HP0706 HP0722		33.5% 43.3%
HP0725	outer membrane protein (omp17)	43.3%
HP0796 HP0896 HP0025		0.0% 36.6%
		0.0%
HP0913	outer membrane protein (omp21)	0.0% 38.2%
HP0923	outer membrane protein (omp22)	0.0%
HP1107 HP1113		0.0% 36.0%
HP1156	outer membrane protein (omp25)	0.0%
HP1177		23.0% 37.0%
HP1243	outer membrane protein (omp28)	0.0%
HP0079	outer membrane protein (omp3)	0.0%
HP1395 HP1469	outer membrane protein (omp30) outer membrane protein (omp31)	0.0%
HP1501	outer membrane protein (omp32)	0.0%
HP0227	outer membrane protein (omp4) outer membrane protein (omp5)	0.0% 36.8%
HP0229 HP0252	outer membrane protein (omp6) outer membrane protein (omp7)	38.4% 30.6%
HP0254	outer membrane protein (omp7)	37.6%
HP0317 HP0839	outer membrane protein (omp9) outer membrane protein P1 (ompP1)	36.3% 23.3%
HP0955	prolipoprotein diacylglyceryl transferase (lgt)34.4%
HP0655 HP1571	prolipoprotein diacylglyceryl transferase (Igt protective surface antigen D15 rare lipoprotein A (rIpA)	27.5% 37.6%
HP0610	toxin-like outer membrane protein	26.3%
HP0922 HP0289	toxin-like outer membrane protein toxin-like outer membrane protein	29.5% 30.6%
	culus and peptidoglycan	
HP0830 HP0738	amidase D-alanine:D-alanine ligase A (ddlA)	40.6% 28.5%
HP0549	glutamate racemase (glr)	36.6%
HP0597	N-acetylmuramoyl-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A)	33.7%
HP1565 HP1125	penicillin-binding protein 2 (pbp2)	35.0%
111 1120		42.6%
HP0493	phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)	45.2%
	rod shape-determining protein (mreB)	37.7%
HP1373 HP1372	rod shape-determining protein (mreB) rod shape-determining protein (mreC)	51.9% 33.6%
HP0645	soluble lytic murein transglycosylase (slt)	32.2%
HP1543 HP1544	toxR-activated gene (tagE) toxR-activated gene (tagE)	37.2% 31.2%
HP1155	transferase, peptidoglycan synthesis	28.2%
HP0740	(murG) UDP-MurNac-pentapeptide presynthetase	
HP1494	(murF) UDP-MurNac-tripeptide synthetase (murE)	25.7% 36.0%
HP1418	UDP-N-acetylenolpyruvoylglucosamine	32.7%
HP0648	reductase (murB) UDP-N-acetylglucosamine enolpyruvyl	
HP0623	transferase (murZ) UDP-N-acetylmuramate-alanine ligase	46.7%
HP0494	(murC) UDP-N-acetylmuramoylalanine-D-glutamate	37.3%
Surface not	ligase (murD) ysaccharides, lipopolysaccharides and antig	31.1% ens
HP0003	3-deoxy-d-manno-octulosonic acid 8-phospl synthetase (kdsA)	hate 53.4%
HP0957	3-deoxy-d-manno-octulosonic-acid transfera (kdtA)	
HP0858 HP1191	ADP-heptose synthase (rfaE) ADP-heptose-lps heptosyltransferase II	40.6%
	(rfaF)	33.2%
HP0859	ADP-L-glycero-D-mannoheptose-6-epimeras (rfaD)	ie 32.7%

1100055		44.000
HP0855 HP0326	alginate O-acetylation protein (algl) CMP-N-acetylneuraminic acid synthetase	41.8% 31.9%
HP0230	(neuA) CTP:CMP-3-deoxy-D-manno-octulosonate-	31.9%
	cytidylyl-transferase (kdsB)	36.2%
HP1392 HP0379	fibronectin/fibrinogen-binding protein fucosyltransferase	25.7% 39.2%
HP0651	fucosyltransferase	39.2%
HP0044 HP0867	GDP-D-mannose dehydratase (rfbD) lipid A disaccharide synthetase (lpxB)	62.1% 32.0%
HP0159	lipopolysaccharide 1,2-glucosyltransferase	
HP0208	(rfaJ)	28.9%
	lipopolysaccharide 1,2-glucosyltransferase (rfaJ)	26.7%
HP0805	lipooligosaccharide 5G8 epitope biosynthes associated protein (lex2B)	36.9%
HP0826	lipooligosaccharide 5G8 epitope biosynthes associated protein (lex2B)	sis- 39.2%
HP1416	lipopolysaccharide 1,2-glucosyltransferase	
HP0679	(rfaJ) lipopolysaccharide biosynthesis protein	29.2%
HP1475	(wbpB)	42.8%
	lipopolysaccharide core biosynthesis protei (kdtB)	n 49.0%
HP0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	31.7%
HP0619	lipopolysacharide biosynthesis glycosyl	
HP1105	transferase (lic2B) LPS biosynthesis protein	37.2% 28.7%
HP1578	LPS biosynthesis protein	28.1%
HP1581 HP0857	methicillin resistance protein (IIm) phosphoheptose isomerase (gmhA)	29.2% 44.5%
HP1275	phosphonepiose isomerase (grink)	44.0%
	{Pseudomonas aeruginosa}	39.6%
HP1429	polysialic acid capsule expression protein (kpsF)	46.0%
HP0366	spore coat polysaccharide biosynthesis	
HP0178	protein C spore coat polysaccharide biosynthesis	35.3%
	protein E	36.2%
HP0421	type 1 capsular polysaccharide biosynthesi protein J (capJ)	is 29.0%
HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine	
UD1050	N-acyltransferase (lpxD)	39.5%
HP1052	UDP-3-0-acyl N-acetylgicosamine deacetyla (envA)	se 44.6%
HP1375	UDP-N-acetylglucosamine acyltransferase (IpxA)	41.8%
Surface stru		41.0%
HP0840	flaA1 protein	60.2%
HP0325 HP0351	flagellar basal-body L-ring protein (flgH) flagellar basal-body M-ring protein (fliF)	32.7% 34.4%
HP0246	flagellar basal-body P-ring protein (flgl)	37.9%
HP1557 HP1559	flagellar basal-body protein (fliE) flagellar basal-body rod protein (flgB)	37.0%
	(proximal rod protein)	31.0%
HP1558	flagellar basal-body rod protein (flgC) (proximal rod protein)	46.0%
HP1092	flagellar basal-body rod protein (flgG)	35.5%
HP1585 HP1041	flagellar basal-body rod protein (flgG) flagellar biosynthesis protein (flhA)	47.7%
HP1041 HP1035	flagellar biosynthesis protein (flhF)	43.1% 35.5%
HP0684	flagellar biosynthesis protein (fliP)	43.4% 38.7%
HP0770 HP0685	flagellar biosynthetic protein (flhB) flagellar biosynthetic protein (fliP)	38.7% 55.6%
HP1419	flagellar biosynthetic protein (fliQ)	52.3%
HP0173 HP0353	flagellar biosynthetic protein (fliR) flagellar export protein (fliH)	26.4% 29.1%
HP1420	flagellar export protein ATP synthase (flil)	47.6%
HP0870 HP0908	flagellar hook (flgE) flagellar hook (flgE)	98.9% 30.5%
HP1119	flagellar hook-associated protein 1	
HP0752	(HAP1) (flgK) flagellar hook-associated protein 2 (fliD)	27.6% 28.9%
HP0815	flagellar motor rotation protein (motA)	32.9%
HP0816 HP0352	flagellar motor rotation protein (motB) flagellar motor switch protein (fliG)	29.7% 37.0%
HP1031	flagellar motor switch protein (fliM)	34.4%
HP0753 HP0327	flagellar protein (fliS)	32.3% 23.3%
HP0797	flagellar protein G (flaG) flagellar sheath adhesin hpaA	98.5%
HP0584	flagellar switch protein (fliN)	39.7%
HP0115	flagellin A (flaA) flagellin B (flaB)	99.8% 99.0%
HP0295	flagellin B homologue (fla)	32.9%
HP1575 HP1030	flhB protein (flhB) fliY protein (fliY)	40.5% 29.3%
HP0907	Hook assembly protein, flagella (flgD)	25.5%
HP1274 HP0751	paralysed flagella protein (pfIA) polar flagellin (flaG)	23.9% 21.9%
HP0410	putative neuraminyllactose-binding	
HP1192	haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility	24.2%
HP1462	secreted protein involved in flagellar motility	y96.2%
HP0232	secreted protein involved in flagellar motility	/99.2%
CELLULAR	PROCESSES	
General HP0019	abamatavia protain (aba)/)	26.004
	chemotaxis protein (cheV) chemotaxis protein (cheV)	26.8% 31.7%
HP0616	chemotaxis protein (cheV)	27.9%
HP0517	chemotaxis protein (cheY) GTP-binding protein (era)	99.2% 95.6%
HP1490	haemolysin	39.2%
	Haemolysin (tly) haemolysin secretion protein precursor	40.2%
	(hylB)	45.4%
HP0392 HP0099	histidine kinase (cheA) methyl-accepting chemotaxis protein (tlpA)	41.4%
HP0103	methyl-accepting chemotaxis protein (tlpB)	
HP0082	methyl-accepting chemotaxis transducer (tlpC)	28.2%
HP0391	purine-binding chemotaxis protein (cheW)	
	1	
Cell divisior		50.2%
Cell division HP0331 HP0749	cell division inhibitor (minD) cell division membrane protein (ftsX)	25.7%
Cell division HP0331 HP0749 HP0978	cell division membrane protein (ftsX) cell division protein (ftsA) protein	25.7% 31.9%
Cell division HP0331 HP0749 HP0978 HP0748	cell division membrane protein (ftsX) cell division protein (ftsA) protein cell division protein (ftsE)	31.9% 37.6%
Cell division HP0331 HP0749 HP0978 HP0748 HP0286 HP1069	cell division membrane protein (ftsX) cell division protein (ftsA) protein	31.9% 37.6% 41.2% 98.6%
Cell division HP0331 HP0749 HP0978 HP0748 HP0286 HP1069 HP1556	cell division membrane protein (ftsX) cell division protein (ftsA) protein cell division protein (ftsE) cell division protein (ftsH) cell division protein (ftsH) cell division protein (ftsI)	31.9% 37.6% 41.2% 98.6% 30.6%
Cell division HP0331 HP0749 HP0978 HP0748 HP0286 HP1069 HP1556 HP1090	cell division membrane protein (ftsX) cell division protein (ftsA) protein cell division protein (ftsF) cell division protein (ftsH) cell division protein (ftsH) cell division protein (ftsI) cell division protein (ftsK)	31.9% 37.6% 41.2% 98.6% 30.6% 39.8%
Cell division HP0331 HP0749 HP0978 HP0748 HP0286 HP1069 HP1556 HP1090 HP1560	cell division membrane protein (ftsX) cell division protein (ftsA) protein cell division protein (ftsE) cell division protein (ftsH) cell division protein (ftsH) cell division protein (ftsI)	31.9% 37.6% 41.2% 98.6% 30.6% 39.8%

P0331	cell division inhibitor (minD)	50.2%
P0749	cell division membrane protein (ftsX)	25.7%
P0978	cell division protein (ftsA) protein	31.9%
P0748	cell division protein (ftsE)	37.6%
P0286	cell division protein (ftsH)	41.2%
P1069	cell division protein (ftsH)	98.6%
P1556	cell division protein (ftsl)	30.6%
P1090	cell division protein (ftsK)	39.8%
P1560	cell division protein (ftsW) Escherichia coli	32.7%
P0763	cell division protein (ftsY)	46.6%

HP0332	cell division topological specificity factor	22.00
HP0979 HP1159	(minE) cell divison protein (ftsZ) cell filomontation protein (fic)	33.8% 43.3% 63.2%
Cell killing	cell filamentation protein (fic)	03.270
Chaperones		
HP0109	chaperone and heat shock protein (groEL) chaperone and heat shock protein 70	
HP0210	(dnaK) chaperone and heat shock protein C62.5	63.4%
HP0011	(htpG) co-chaperone (groES)	46.5% 99.2%
HP1332 HP0110	co-chaperone and heat-shock protein (dnaJ) co-chaperone and heat-shock protein	42.7%
HP1024	(grpE) co-chaperone-curved DNA-binding protein	33.0% 4
	(CbpA)	37.7%
HP1138	ne-associated protein plasmid replication-partition related protein	40.4%
	alkyl hydroperoxide reductase (tsaA)	98.5%
HP0267	catalase chlorohydrolase neutrophil activating protein (napA)	99.4% 42.6%
HP0389	(bacterioferritin) superoxide dismutase (sodB)	95.8% 98.6%
HP1452	thiophene and furan oxidizer (tdhF)	37.6%
HP0355		57.3% 97.0%
HP0786	preprotein translocase subunit (secA)	54.0% 41.2%
HP1255	protein translocation protein, low temperatu (secG)	
HP1550 HP1549	protein-export membrane protein (secD) protein-export membrane protein (secF)	38.9% 35.1%
HP0576 HP1152	signal peptidase I (lepB) signal recognition particle protein (ffh)	40.3% 41.4%
HP0795 Transforma	trigger factor (tig)	27.6%
HP0520	cag pathogenicity island protein (cag1)	96.5% 98.4%
HP0531 HP0532	cag pathogenicity island protein (cag11) cag pathogenicity island protein (cag12)	97.2% 98.9%
HP0534 HP0535	cag pathogenicity island protein (cag13) cag pathogenicity island protein (cag14)	98.0% 97.6%
HP0536 HP0537	cag pathogenicity island protein (cag14) cag pathogenicity island protein (cag15) cag pathogenicity island protein (cag16)	96.4% 98.9%
HP0538 HP0539	cag pathogenicity island protein (cag16) cag pathogenicity island protein (cag17) cag pathogenicity island protein (cag18)	95.3% 98.7%
HP0540 HP0521	cag pathogenicity island protein (cag2)	99.5% 92.5%
HP0541 HP0542	cag patriogenicity island protein (cag21)	97.8% 97.9%
HP0543 HP0544	cag pathogenicity island protein (cag22) cag pathogenicity island protein (cag23)	95.5% 99.0%
HP0545 HP0546	cag pathogenicity island protein (cag25)	98.5% 95.7%
HP0547 HP0522 HP0523	cag pathogenicity island protein (cag3)	92.9% 98.1% 95.7%
111 0020	cay pathogenicity island protein (cay+)	
HP0524	cag pathogenicity island protein (cag5)	99.1%
HP0524 HP0526 HP0527 HP0528	cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8)	99.1% 97.5% 94.6% 99.0%
HP0524 HP0526 HP0527 HP0528 HP0529 HP1378	cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence lipoprotein (comL)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5%
HP0526 HP0527 HP0528 HP0529 HP1378 HP1361	cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence lipoprotein (comL) competence locus E (comE3)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7%
HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421	cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence lipoprotein (comL)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5%
HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0333 HP0042 HP0525	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lipoprotein (comL) completance locus E (comE3) conjugal transfer protein (traG) DNA processing chain A (dprA) tribl protein wiR11 homologue	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0%
HP0527 HP0528 HP0528 HP1378 HP1361 HP106 HP1421 HP0333 HP0042 HP04255 HP0441 HP0017	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lipoprotein (comL) comjugati transfer protein (traG) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein virB1 homologue virB4 homologue (virB4)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2%
HP0526 HP0527 HP0528 HP0529 HP1378 HP1378 HP1378 HP1421 HP0333 HP0042 HP0425 HP0441 HP0017 HP0459	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comE3) conjugal transfer eputon protein (trB) DNA processing chain A (dprA) trbl protein virB1 homologue (virB4) virB4 homologue (virB4)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5%
HP0527 HP0528 HP0528 HP1378 HP1378 HP1361 HP1006 HP1421 HP0333 HP0042 HP0424 HP0525 HP0441 HP0017 HP0459 CENTRAL II <i>General</i>	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lipoprotein (comL) completance locus E (comE3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2% 25.2%
HP0527 HP0528 HP0528 HP1378 HP1378 HP1361 HP1421 HP0333 HP0042 HP0525 HP0441 HP0047 HP0459 CENTRAL II General HP1014 HP1014 HP1186	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comEs) conjugati transfer eguton protein (trB) DNA processing chain A (dprA) trb) protein virB4 homologue (virB4) virB4 homologue (virB4)	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 32.9% 25.2% 25.5% 25.3% 33.4% 33.2% 37.0%
HP0527 HP0528 HP0529 HP1378 HP1361 HP106 HP1421 HP0333 HP0042 HP0423 HP0042 HP0441 HP0017 HP0459 CENTRAL II <i>General</i> HP114	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comEs) conjugati transfer eguton protein (trB) DNA processing chain A (dprA) trb protein VirB4 homologue (virB4) virB4 homologue (virB4)	99.1% 97.5% 97.5% 99.0% 98.9% 25.5% 26.7% 27.3% 27.3% 30.7% 32.9% 31.4% 25.2% 25.2% 25.2% 25.2% 25.3% 33.2% 33.2% 37.0% 33.3%
HP0527 HP0528 HP0528 HP1378 HP1378 HP1361 HP1006 HP1421 HP0042 HP0525 HP0441 HP0017 HP0459 CENTRAL II General HP1014 HP1014 HP1064	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) completence lioporotein (comL) conjugati transfer eguton protein (trB) DNA processing chain A (dprA) trb protein VirB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VTERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase	99.1% 97.5% 99.0% 99.0% 99.0% 25.5% 26.7% 26.7% 21.3% 30.7% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2%
HP0527 HP0527 HP0528 HP1378 HP1361 HP1361 HP1361 HP1361 HP1361 HP0423 HP0423 HP04251 HP0453 HP04251 HP0454 HP0454 HP0454 HP0459 General HP1186 HP1014 HP1186 HP1014 HP10869	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag3) cag pathogenicity island protein (cag4) competence lioporotein (comL) competence locus E (comE3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) VirB4 homologue (VirB4) VirB4 homologue (VirB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 10.0% 23.5% 25.2% 25.3% 33.2% 33.2% 33.3% 28.1%
HP0527 HP0527 HP0528 HP1378 HP1381 HP1054 HP1381 HP1047 HP0042 HP0042 HP0045 HP0441 HP0055 HP0441 HP0055 HP0441 HP0059 HP0044 HP1016 HP1052 HP10528 HP10538	cag pathogenicity island protein (cagb) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (comL) competence locus E (comE3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) VirB4 homologue (VirB4) VirB4 homologue (VirB4) VITERMEDIARY METABOLISM 7-c-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC)	99.1% 97.5% 99.0% 99.0% 99.0% 25.5% 26.7% 26.7% 21.3% 30.7% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2%
HP0527 HP0527 HP0528 HP1378 HP1529 HP1378 HP1052 HP1381 HP1036 HP1421 HP00333 HP0421 HP0042 HP0525 HP041 HP007 HP041 HP007 HP041 HP1086 HP0004 HP0090 HP0899	cag pathogenicity island protein (cagb) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (comL) competence locus E (comE3) conjugati transfer eguton protein (trB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (vi	99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 33.3% 33.5% 28.1% 33.5% 35.5%
HP0620 HP0520 HP0528 HP0529 HP1378 HP1529 HP1361 HP1064 HP1062 HP1361 HP1042 HP0629 CENTRAL II General HP0045 HP104 HP104 HP104 HP1069 HP0090 HP0899 HP0898 HP0047 HP0197	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag3) cag pathogenicity island protein (cag4) competence lioporotein (comL) competence locus E (comE3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trbl protein VirB4 homologue (VirB4) virB4 homologue (vi	99.1% 97.5% 94.6% 99.0% 25.5% 26.7% 22.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 33.3% 33.2%
HP0520 HP0520 HP0528 HP0529 HP1378 HP1529 HP1381 HP1006 HP1421 HP0459 HP0459 HP0459 General HP1041 HP0459 HP0459 HP0459 HP0459 HP0899 HP0899 HP0898 HP0047 HP0197 Amino sugg	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag3) cag pathogenicity island protein (cag4) competence lioporotein (comE) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trb] protein VirB4 homologue (VirB4) virB4 homologue (virB	99.1% 97.5% 94.6% 99.0% 25.5% 26.7% 22.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3% 33.2% 33.3% 33.2%
HP052b HP052b HP052b HP052b HP1378 HP152b HP1378 HP1052b HP1378 HP1042 HP052b HP0047 HP0451 HP1014 HP1014 HP10869 HP0899 HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comE3) conjugati transfer epution (traG) conjugati transfer epution protein (trbB) DNA processing chain A (dprA) trib protein wirB4 homologue (wirB4) wirB4 homo	99.1% 97.5% 94.6% 95.0% 98.9% 98.9% 26.7% 27.5% 30.7% 22.5% 23.2% 31.4% 23.5% 23.5% 23.3% 23.3% 23.3% 24.1% 41.4%
HP052b HP052b HP052b HP052b HP1378 HP1052b HP1378 HP1052b HP1381 HP1006 HP1421 HP0333 HP1042 HP052b HP0047 HP017 HP0089 HP0898 HP0047 HP0189 HP0898 HP0047 HP0189 Amino suge HP1532 Phosphorus HP0620	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comE3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) virB4 homologue (VirB4	99.1% 97.5% 94.6% 94.6% 98.9% 25.5% 26.7% 26.7% 27.3% 30.7% 22.5% 23.2% 31.4% 31.4% 23.5% 41.4% 38.5% 41.4% 38.5% 41.7% 62.1%
HP0520 HP0520 HP0528 HP0529 HP1378 HP1529 HP1381 HP1062 HP1381 HP1042 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0899 HP0899 HP0898 HP0047 HP01532 Phosphorus HP0620 HP06	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) competence lipoprotein (comL) competence locus E (comEs) conjugati transfer egution protein (trB) DNA processing chain A (dprA) trD protein VirB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VTERMEDIARY METABOLISM VirB4 homologue (virB4) virB4 homologue (virB4) vir	99.1% 99.1% 94.6% 98.9% 98.9% 26.7% 26.7% 26.7% 27.3% 30.7% 22.5% 23.3%23.3% 23.3% 23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3% 23.3%23.3% 23.3%23.3%
HP0520 HP0520 HP0528 HP0529 HP1378 HP1529 HP1381 HP1062 HP1381 HP1042 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0899 HP0899 HP0898 HP0047 HP01532 Phosphorus HP0620 HP06	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag3) cag pathogenicity island protein (cag4) competence lioporotein (comE) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (virB4) virB4 homologue (virB4	99.1% 97.5% 94.6% 94.6% 98.9% 25.5% 26.7% 26.7% 27.3% 30.7% 22.5% 23.2% 31.4% 31.4% 23.5% 41.4% 38.5% 41.4% 38.5% 41.7% 62.1%
HP0520 HP0520 HP0528 HP0529 HP1378 HP1529 HP1361 HP1062 HP0361 HP1042 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP014 HP1186 HP0004 HP0149 HP1045 HP0049 HP0149 HP014 HP0149 HP01	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagb) cag pathogenicity island protein (cagb) competence lioporotein (comL) competence locus E (comEs) conjugati transfer eguton protein (trB) DNA processing chain A (dprA) trD protein VirB4 homologue (virB4) virB4 homologue (vi	99.1% 99.1% 94.6% 98.9% 98.9% 26.7% 26.7% 26.7% 27.3% 30.7% 22.5% 23.3% 23.3% 23.3% 23.3% 41.4% 33.5% 41.4% 33.5%
HP0620 HP0520 HP0521 HP0528 HP0529 HP0529 HP1361 HP1378 HP1378 HP1378 HP1378 HP1378 HP1361 HP037 HP0459 HP0469 HP047 HP186 HP0049 HP0889 HP0890 HP0891 HP0892 HP0893 HP0894 HP0890 HP0802 HP0820 HP082	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) competence lioporotein (comL) completence lioporotein (comL) completence lioporotein (comL) completence lioporotein (comL) completence lioporotein (comL) DNA processing chain A (dprA) trbl protein virB4 hormologue (virB4) virB4 hormologue (virB4)	98.1% 97.5% 94.6% 94.6% 25.5% 26.7% 26.7% 27.3% 30.7% 22.5% 22.5% 22.3% 31.4% 22.5% 22.5% 23.3% 41.4% 33.5% 41.4% 33.5% 41.4% 33.5% 41.4% 33.5% 41.7% 52.5% 33.5% 41.7% 52.5% 33.5% 41.5% 41.5% 33.5% 41.5% 45.5%
HP0520 HP0520 HP0529 HP0529 HP1378 HP1529 HP1378 HP1052 HP1361 HP1042 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0164 HP0164 HP0164 HP0164 HP0164 HP0164 HP0164 HP0064 HP0169 HP0888 HP0047 HP0189 HP0888 HP0047 HP0189 HP0888 HP0047 HP0189 HP0888 HP0047 HP0189 HP0889 HP0889 HP0889 HP0889 HP0889 HP0889 HP0889 HP0889 HP0889 HP0890 HP0800 HP	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (caga) cag pathogenicity island protein (caga) competence lioporotein (comL) competence locus E (comEa) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase (crA) virD4 protein canhydrase carbonic anhydrase (crA) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) S-adenosylmethionine synthetase 2 (metX) rc glucosamine fructose-6-phosphate aminotransferase (losmerizing) (glmS) campounds inorganic pyrophosphatase (ppk) hydroyenase (ppk) hydroyenas	981% 975% 946% 946% 989% 989% 989% 989% 989% 989% 267% 267% 225% 227% 232% 232% 232% 232% 232% 233% 232% 232% 233% 232% 233% 232% 233% 232% 233% 232% 233% 232% 233%23% 233% 23
HP0520 HP0520 HP0529 HP0529 HP1378 HP1529 HP1381 HP1062 HP0361 HP1062 HP0361 HP0062 HP0383 HP0041 HP0459 HP0452 HP0451 HP004 HP1089 HP0899 HP0899 HP0898 HP0047 HP0197 Amino suge HP0620	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (caga) cag pathogenicity island protein (caga) competence lioporotein (comL) competence locus E (comEa) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) S-adenosylmethionine synthetase 2 (metX) rs glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) compounds inorganic pyrophosphatase (ppk) hydroyenase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF)	99.1% 99.1% 94.6% 94.6% 95.7% 25.7% 25.7% 22.7% 30.7% 22.5% 23.2% 23.2% 31.4% 23.5% 23.3% 23.5% 23.3% 41.7% 62.1% 41.7% 62.1% 41.7% 62.1% 41.7% 62.1% 33.3% 43.5%
HP0620 HP0529 HP0529 HP0529 HP1378 HP1529 HP1378 HP1052 HP1361 HP1006 HP1421 HP0352 HP0047 HP0459 HP0047 HP0052 HP0090 HP0899 HP0899 HP0899 HP0899 HP0898 HP0047 HP017 Amino suge HP0520 HP0899 HP0899 HP0890 HP0800 HP0890 HP080	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comEa) conjugati transfer egulon protein (trbB) DNA processing chain A (dprA) trb protein wir81 homologue (wir84) wir84 homologue (wir84) wir84 homologue (wir84) VTERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hypA) hydrogenase expression/formation pr	99.1% 99.1% 94.6% 94.6% 95.7% 25.7% 25.7% 22.7% 30.7% 22.5% 22.5% 23.2% 31.4% 31.4% 23.5% 33.3% 24.1% 41.4% 41.4% 41.7% 50.0% 62.1% 41.7% 50.0% 50.7% 33.3% 41.7% 50.0% 50.7%
HP0620 HP0520 HP0521 HP0528 HP0529 HP0529 HP1361 HP1378 HP1381 HP1381 HP0529 HP1378 HP1361 HP037 HP0421 HP0452 HP041 HP041 HP041 HP041 HP041 HP0452 HP0441 HP0452 HP0452 HP0461 HP0052 HP0459 HP0052 HP0890 HP0893 HP0620 HP0620 HP0620 HP0620 HP0620 HP0622 HP0020 HP0832 Other HP0073 HP0073	cag pathogenicity island protein (cagh) cag pathogenicity island protein (cagh) cag pathogenicity island protein (caga) cag pathogenicity island protein (caga) competence lioporotein (comL) competence locus E (comEa) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic arhydrase carbonic arhydrase (crA) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic arhydrase carbonic arhydrase (crA) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) rs glucosamine fructose-6-phosphate arminotransferase (isomerizing) (glmS) compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyhosphatek kinase (ppk) hydroytesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF)	99.1% 99.1% 94.6% 94.6% 98.9% 98.9% 98.9% 25.5% 25.5% 25.5% 25.5% 22.7% 22.5% 22.5% 23.2% 23.3% 22.5% 23.3% 22.1% 41.4% 41.7% 62.1% 41.7% 62.1% 41.7% 62.1% 41.7% 62.1% 41.7% 62.5% 33.3% 44.6% 62.5% 55.5%
HP0620 HP0520 HP0521 HP0528 HP0529 HP0529 HP1361 HP1378 HP1381 HP1381 HP0529 General HP0421 HP0452 General HP0464 HP047 HP1089 HP0089 HP0890 HP0890 HP0891 HP0892 HP0893 HP0894 HP0895 HP0892 HP0893 HP0894 HP0895 HP0892 Other HP0071 HP0073 HP0073 HP0073 HP0073 HP0074	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence lioporotein (comL) completione locus E (comEa) conjugati transfer egulon protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue	981% 975% 946% 946% 989% 989% 989% 989% 989% 989% 225% 227% 227% 30.7% 225% 22.5% 22.5% 23.2% 23.3% 23.2% 41.4% 33.2% 41.4% 33.5% 41.4% 50.0% 52.6% 52.6% 52.6% 53.3% 45.6% 50.0% 52.6% 50.0% 52.6% 50.0% 52.6% 50.0% 50
HP052b HP052b HP052b HP052b HP052b HP1378 HP152b HP1381 HP1052b HP0381 HP1042 HP052b HP0333 HP042b HP044b HP045b H	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) completence lioporotein (comL) completence lioporotein (comC) conjugati transfer egulon protein (trbB) DNA processing chain A (dprA) trb protein wirB4 homologue (wirB4) wirB4 homologue (wirB4) hydrogenase expression/formation protein (hypA) hydrogenase	981% 975% 946% 946% 989% 989% 989% 989% 989% 989% 225% 227% 227% 30.7% 225% 22.5% 22.5% 23.2% 23.3% 23.2% 41.4% 33.2% 41.4% 33.5% 41.4% 50.0% 52.6% 52.6% 52.6% 53.3% 45.6% 50.0% 52.6% 50.0% 52.6% 50.0% 52.6% 50.0% 50
HP0620 HP0527 HP0528 HP0529 HP0529 HP0529 HP1361 HP1378 HP1381 HP1378 HP1381 HP0529 CENTRAL II HP041 HP045 CENTRAL II General HP1041 HP1089 HP0049 HP0047 HP0089 HP0047 HP0089 HP0047 HP0089 HP0089 HP0089 HP0089 HP0080 HP0081 HP00820 HP00820 HP00832 Other HP00071 HP00072	cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) cag pathogenicity island protein (cag) competence lioporotein (comL) competence locus E (comEa) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein wirB4 homologue (wirB4) wirB4 homologue (wirB4	99.1% 99.1% 94.6% 94.6% 95.0% 95.0% 95.0% 95.7% 93.7% 25.2% 25.2% 25.2% 25.3% 33.3% 33.3% 41.4% 38.5% 33.3% 41.4% 38.5% 33.3% 41.4% 38.5% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.4% 33.3% 41.5%

HP1270	subunit (NQO10) NADH-ubiquinone oxidoreductase, NQO11	-1.0%
	subunit (NQO11) ({Paracoccus denitrificans	42.6%
HP1271	NADH-ubiquinone oxidoreductase, NQO12 subunit (NQO12)	43.2%
HP1272	NADH-ubiquinone oxidoreductase, NQO13 subunit (NQO13)	40.2%
HP1273	NADH-ubiquinone oxidoreductase, NQO14 subunit (NQO14)	31.2%
HP1266	NADH-ubiquinone oxidoreductase, NQO3 subunit (NQO3)	31.6%
HP1263	NADH-ubiquinone oxidoreductase, NQO4 subunit (NQO4){Triticum aestivum}	44.6%
HP1262	NADH-ubiquinone oxidoreductase, NQO5	-1.0%
HP1261	subunit (NQO5) NADH-ubiquinone oxidoreductase, NQO6	
HP1260	subunit (NQO6) NADH-ubiquinone oxidoreductase, NQO7	62.2%
HP1267	subunit (NQO7) NADH-ubiquinone oxidoreductase, NQO8	40.7%
HP1268	subunit (NQO8) NADH-ubiquinone oxidoreductase, NQO9	42.4%
	subunit (NQO9)	41.2%
HP1398	ds and amines alanine dehydrogenase (ald)	39.6%
HP0294 HP1238	aliphatic amidase (aimE) aliphatic amidase (aimE)	75.4% 37.2%
HP1399 HP0943	arginase (rocF) D-amino acid dehydrogenase (dadA)	31.8% 26.2%
HP0056	delta-1-pyrroline-5-carboxylate dehydrogena	
HP0723	(Synechocystis sp.) L-asparaginase II (ansB)	54.1%
HP0132 Anaerobic	L-serine deaminase (sdaA)	45.8%
HP0666	anaerobic glycerol-3-phosphate dehydroger subunit C (glpC)	nase, 27.2%
HP0589 HP0590	ferredoxin oxidoreductase, alpha subunit	42.7%
HP0591	ferredoxin oxidoreductase, beta subunit ferredoxin oxidoreductase, gamma subunit	
HP0193	fumarate reductase, cytochrome b subunit (frdC)	58.8%
HP0192	fumarate reductase, flavoprotein subunit (frdA)	69.4%
HP0191	fumarate reductase, iron-sulfur subunit (frdB)	70.8%
HP1110	pyruvate ferredoxin oxidoreductase, alpha subunit	41.0%
HP1111	subunit pyruvate ferredoxin oxidoreductase, beta subunit	41.0%
HP1109	pyruvate ferredoxin oxidoreductase, delta	
HP1108	subunit pyruvate ferredoxin oxidoreductase, gamma	47.0% a
ATD proto	subunit	37.2%
HP0828	ATP synthase FO, subunit a (atpB)	37.7%
HP1136 HP1137	ATP synthase FO, subunit b (atpF) ATP synthase FO, subunit bÕ (atpFÕ)	28.3% 32.5%
HP1212	ATP synthase FO, subunit c (atpE)	41.2% 62.7%
HP113/		
HP1134 HP1132	ATP synthase F1, subunit alpha (atpA) ATP synthase F1, subunit beta (atpD)	85.6%
HP1135	ATP synthase FO, subunit c (atpE) ATP synthase F1, subunit alpha (atpA) ATP synthase F1, subunit beta (atpD) ATP synthase F1, subunit deta (atpH) ATD synthase F1, subunit deta (atpH)	85.6% 24.6%
HP1135 HP1131	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC)	85.6% 24.6% 32.7%
HP1135 HP1131 HP1133 Electron tr	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC) ATP synthase F1, subunit gamma (atpG) ansport	85.6% 24.6% 32.7% 37.8%
HP1135 HP1131 HP1133 Electron tr HP0146	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ)	85.6% 24.6% 32.7% 37.8%
HP1136 HP1131 HP1133 Electron tr. HP0146 HP0265 HP0378	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycdF)	85.6% 24.6% 32.7% 37.8%
HP1135 HP1131 HP1133 Electron tr HP0146 HP0265	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit opsilon (atpC) ATP synthase F1, subunit gamma (atpG) ansport (CcoG) c(CcoG) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (vcfb) cytochrome c oxidase, dimem subunit,	85.6% 24.6% 32.7% 37.8% 44.2% 35.4%
HP1136 HP1131 HP1133 Electron tr. HP0146 HP0265 HP0378	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit,	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1136 HP1131 HP1133 <i>Electron tri</i> HP0146 HP0265 HP0378 HP0147	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (vcfb) cytochrome c oxidase, dimem subunit, membrane-bound (ftkP) cytochrome c oxidase, dimem subunit, membrane-bound (ftkP) cytochrome c oxidase, neme b and copper binding subunit, membrane-bound (fixN) cytochrome c oxidase, dimensionelme subunit,	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1135 HP1131 HP1133 <i>Electron tr</i> HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbt3-type cytochrome c oxidase subunit G (ccoQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dineme subunit, memtrane-bound (ftAP) cytochrome c oxidase, dineme subunit, memtrane-bound (ftAP) cytochrome c oxidase, dineme subunit memtrane-bound (ftAQ) cytochrome c oxidase, dineme subunit memtrane-bound (ftAQ)	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% - 43.9% 45.7% 48.5%
HP1135 HP1131 HP1133 Electron tr. HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport (Coc0) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dimeme subunit, membrane-bound (fixP) cytochrome c oxidase, dimeme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c 6583	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% - 43.9% 45.7% 48.5% 38.4%
HP1135 HP1133 Electron tr. HP0146 HP0265 HP0277 HP0144 HP0144 HP0145 HP1461 HP1227 HP0277 HP0277 HP0288	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport (cbb3-type cytochrome c oxidase subunit Q (coc0) cytochrome c biogenesis protein (vcfb) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fixQ) cytochrome c oxidase, dimensionale and cytochrome c oxidase, dimonoheme subunit membrane-bound (fixQ) cytochrome c 553 ferredoxin-like protein	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 45.7% 48.5% 38.4% 52.5%
HP1135 HP1131 HP1133 <i>Electron</i> tr HP0146 HP0265 HP0147 HP0144 HP0145 HP1461 HP1461 HP1227 HP0277 HP0588 HP1508	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CcoQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dineme subunit, memtrane-bound (ftkP) cytochrome c oxidase, dineme subunit, memtrane-bound (ftkP) cytochrome c oxidase, dineme subunit, memtrane-bound (ftkP) cytochrome c oxidase, dineme subunit, memtrane-bound (ftkO) cytochrome c553 ferredoxin-like protein ferredoxin-like protein	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 33.0% - - 43.9% 45.7% 48.5% 52.5% 42.6%
HP1135 HP1133 Electron tr. HP0146 HP0265 HP0277 HP0144 HP0144 HP0145 HP1461 HP1227 HP0277 HP0277 HP0288	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dineme subunit, memtrane-bound (ftkP) cytochrome c 653 percotiase cytochrome c553 ferredoxin- flexodoxin-flike protein flexodoxin-flike protein flexodoxin (ftdA) NAD(P)H-Harin oxidoreductase	85.6% 24.6% 32.7% 37.5% 44.2% 33.0% 43.9% 43.9% 43.9% 45.7% 48.5% 42.6% 29.4% 42.6% 29.4% 47.0%
HP1135 HP1131 HP1133 Electron tr HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP12277 HP0588 HP1508 HP1160 HP1161	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport (bb3type cytochrome c oxidase subunit Q (coc0) cytochrome c biogenesis protein (vcfb) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c 651 peroxidase cytochrome c553 ferredoxin-like protein ferrodoxin-like protein	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1135 HP1131 HP1133 Electron tr. HP0146 HP0285 HP0378 HP0147 HP0144 HP1045 HP1461 HP1461 HP1461 HP1227 HP0588 HP1508	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (vcf) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkQ) cytochrome c 651 peroxidase cytochrome c653 ferredoxin- ferradoxin-like protein ferradoxin-like protei	85.8% 24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% - - 33.0% - 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 29.4% 42.6% 29.4% 42.6% 29.4% 42.6% 32.7% 54.7% 54.7%
HP1135 HP1131 HP1133 Electron tr. HP0146 HP0265 HP0378 HP0144 HP0144 HP0144 HP1461 HP145 HP1461 HP1227 HP0277 HP0277 HP0588 HP1161 HP1604 HP16042 HP0954 HP0642	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit membrane-bound (fkA) cytochrome c653 peroxidase cytochrome c653 ferradoxin ferradoxin-like protein ferradoxin-like NJFE hydrogenase, (tryoD quinone-reactive NJFE hydrogenase, (tryoD quinone-reactive NJFe hydrogenase, large	85.6% 24.6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 33.0% 43.3% 43.3% 45.7% 48.5% 38.4% 52.5% 42.6% 42.6% 42.6% 42.6% 42.6% 52.4% 52.5% 42.6% 52.5% 42.6% 52.4% 52.5% 42.6% 52.5%
HP1135 HP1131 HP1133 Electron tr. HP0146 HP0285 HP0378 HP0147 HP0144 HP0144 HP1461 HP1461 HP1461 HP1461 HP1608 HP1608 HP16084 HP0642 HP0653	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkR) cytochrome c653 peroxidase cytochrome c653 ferredoxin ferredoxin-like protein flavdoxin (IdA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, (hydD quinone-reactive Ni/Fe hydrogenase, large subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-ractive Ni/Fe hydrogenase, small	85.6% 224.6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 43.9% 43.9% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 48.5% 42.6% 32.7% 51.4% 68.5%
HP1135 HP1133 Electron tr. HP0146 HP0285 HP0378 HP0147 HP0144 HP0144 HP0144 HP1461 HP1481 HP1638 HP1608 HP16082 HP0632 HP0632	APP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (ocd) cytochrome c biogenesis protein (ocd) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit membrane-bound (fkP) cytochrome c oxidase protechrome c oxidase protechrome c oxidase protechrome consective subunit (MA) MAD(P)H-Hatke protein flavddoxin (ftdA) MAD(P)H-Hatke protein flavddoxin (ftdA) MAD(P)H-Hatke protein flavddoxin (ftdA) MAD(P)H-Hatke protein flavddoxin (ftdA) MAD(P)H-Hatke protein subunit (MdC) quinone-reactive Ni/Fe hydrogenase, sytoc subunit (MdB) quinone-reactive Ni/Fe hydrogenase, small subunit (MdA)	85.8% 24.6% 32.7% 37.8% 44.2% 35.4% 35.4% 33.0%
HP1131 HP1131 HP1133 HP1146 HP0146 HP0285 HP0147 HP0144 HP0147 HP0144 HP0145 HP1481 HP1277 HP0582 HP0642 HP0654 HP0654 HP0653 HP0632 HP0631 HP1539	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CccQ) cytochrome c biogenesis protein (cdG) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit membrane-bound (fixP) cytochrome c 553 ferredoxin- flexpodxin-like protein flexpodxin-like protein flexpodxin-like protein flexpodxin-like protein flexpodxin-like protein flexpodxin-like protein guinone-reactive Ni/Fe hydrogenase, cytoc b subunit (hydF) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (hydA)	85.6% 224.6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 43.9% 43.9% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 48.5% 42.6% 32.7% 51.4% 68.5%
HP1131 HP1131 HP1133 HP1133 Electron tr HP0146 HP0285 HP0147 HP0144 HP0147 HP0145 HP1481 HP1481 HP1277 HP0508 HP1608 HP16084 HP1633 HP0632 HP0631 HP1539 HP1538	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Ccco) cytochrome c biogenesis protein (cdG) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, memb and coppe binding subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit membrane-bound (fixP) cytochrome c oxidase, monoheme subunit membrane-bound (fixP) cytochrome c553 ferredoxin- flevodoxin-like protein flevodoxin-like protein flevodoxin-like protein flevodoxin-like protein guinone-reactive Ni/Fe hydrogenase, (stroc b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (bC+1)	85.6% 224.6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 43.9% 43.9% 43.9% 43.9% 43.5% 52.5% 43.6% 38.4% 52.5% 42.6% 38.4% 52.5% 68.5% 68.5% 68.9%
HP1131 HP1131 HP1133 HP1146 HP0146 HP0285 HP0147 HP0144 HP0147 HP0144 HP0145 HP1481 HP1277 HP0582 HP0642 HP0654 HP0654 HP0653 HP0632 HP0631 HP1539	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CccQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dimeme subunit, memtrane-bound (fkP) cytochrome c oxidase, dimeme subunit, memtrane-bound (fkP) cytochrome c oxidase, dimeme subunit membrane-bound (fkO) cytochrome c oxidase, dimeme subunit membrane-bound (fkO) cytochrome c653 ferredoxin-like protein flavdoxin-like protein flavdoxin (fidA) MAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) guinone-reactive Ni/Fe hydrogenase, small subunit (hydG) ubiquiol cytochrome c oxidoreductase, cytochrome coxidoreductase, cytochrome octive Ni/Fe hydrogenase, small subunit (hydG)	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 33.0% 43.3% 43.3% 43.3% 45.7% 48.5% 48.5% 52.5% 42.6% 52.5% 42.6% 52.5% 42.6% 52.5% 46.1% 52.7% 68.5% 68.5% 68.9% 33.3%
HP1131 HP1131 HP1133 HP1133 Electron tr HP0146 HP0146 HP0147 HP0145 HP1461 HP14461 HP14461 HP14461 HP1450 HP1461 HP1450 HP1461 HP1633 HP0633 HP0633 HP0633 HP0631 HP1539 HP1538 HP1540 Entner-Dot	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c oxidase, diheme subunit, memtrane-bound (fkD) cytochrome c oxidase, diheme subunit, memtrane-bound (fkD) cytochrome c553 ferredoxin- flevdoxin-fike protein flevdoxin-fike protein flevdoxin (fldA) NAD(P)H-flex protein flevdoxin (fldA) NAD(P)H-flex protein flevdoxin (fldA) NAD(P)H-flex protein flevdoxin (fldA) NAD(P)H-flex protein flevdoxin (fldA) subunit (flvdB) quinone-reactive Ni/Fe hydrogenase, cytoc b subunit (flvd) quinone-reactive Ni/Fe hydrogenase, small subunit (flvd) quinone-reactive Ni/Fe hydrogenase, small subunit (flvdA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH)	85.6% 224.6% 32.7% 37.8% 33.0% 44.2% 35.4% 33.0% 43.9% 43.9% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 29.4% 42.6% 51.4% 68.5% 51.4% 68.5% 68.5% 68.5% 68.5% 68.5% 39.3%
HP1135 HP1137 HP1133 HP1133 HP0146 HP0146 HP0147 HP0144 HP0145 HP1461 HP1461 HP147 HP0688 HP1461 HP1277 HP05688 HP1161 HP0632 HP0633 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Dot HP1599	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CocQ) cytochrome c biogenesis protein (ocG) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c553 ferredoxin-like protein flavdoxin-fike protein flavdoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, large subunit (hydE) quinone-reactive Ni/Fe hydrogenase, small subunit (flvA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, hisquinole systerinome c subiquinoles cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Risske ZFe-23 subunit (fbcH) 2-keto-3-deoxy-6-phosphogluconate aldolas (eda)	85.6% 224.6% 32.7% 37.8% 37.8% 33.0% 44.2% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 42.9% 52.5% 42.6% 52.5% 42.6% 52.5% 42.6% 52.5% 42.9% 52.5% 43.9% 52.5% 43.9% 52.5% 43.9% 52.5% 51.4% 56.8% 68.5% 68.5% 68.5% 68.9% 39.2% 51.4%
НР1131 НР1131 НР1131 НР1133 Екейтоп т. НР0146 НР0285 НР0147 НР0144 НР0145 НР141 НР0145 НР145 НР145 НР1637 НР0632 НР0632 НР0633 НР0632 НР1638 НР1638 НР1539 НР1539 НР1508 НР1539 НР1509 НР1509 НР1509 НР1509 НР1509	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (coG) cytochrome c biogenesis protein (coG) cytochrome c oxidase, diherme subunit, membrane-bound (fixP) cytochrome c oxidase, diherme subunit, membrane-bound fixP) cytochrome c oxidase, beme b and coppe binding subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound fixP) cytochrome c oxidase, monoheme subunit, membrane-bound fixP) cytochrome c 653 ferredoxin-like protein ferrodoxin-like protei	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 35.4% 33.0% 45.7% 43.9% 45.7% 48.5% 38.4% 45.5% 42.6% 29.4% 42.6% 29.4% 48.5% 38.4% 52.5% 42.6% 29.4% 48.1% 52.5% 48.5% 68.5% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 68.5% 68.9% 39.2% 68.5%
HP1135 HP1137 HP1133 HP1133 HP0146 HP0146 HP0147 HP0144 HP0145 HP1461 HP1461 HP147 HP0688 HP1461 HP1277 HP05688 HP1161 HP0632 HP0633 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Dot HP1599	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (codA) cytochrome c oxidase, diherme subunit, membrane-bound fikA) cytochrome c oxidase, diherme subunit, membrane-bound fikA) cytochrome c oxidase, monoheme subunit, membrane-bound fikA) cytochrome c oxidase, monoheme subunit, membrane-bound fikA) cytochrome c oxidase cytochrome c 653 ferredoxin-like protein ferrodoxin-like protein subunit (flyCh) ubiquinol (cynchrome c oxidoreductase, cynchrome c subunit (flocF) doroff 2-keto-3-deoxy-6-phosphogluconate alcolas ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-ferrodoxin-f	85.6% 22.4% 32.7% 32.7% 33.7% 33.0% 44.2% 33.0% 43.9% 45.7% 48.5% 29.4% 42.6% 42.6% 42.6% 42.6% 42.6% 48.5% 52.5% 42.6% 48.5% 68.5% 68.9% 39.3% 28.8% 39.2% 68.5% 68.9% 39.2% 68.5% 68.9%
HP1131 HP1131 HP1131 HP1131 HP1133 Electron tr HP0146 HP0285 HP0378 HP0147 HP0145 HP1481 HP1481 HP0277 HP0588 HP1630 HP06533 HP0653 HP0584 HP0633 HP0632 HP0538 HP1538 HP1508 HP1508 HP1508 HP1509 HP1509 HP1009	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbt3-type cytochrome c oxidase subunit G (coc0) cytochrome c biogenesis protein (ocdA) cytochrome c oxidase, dineme subunit, membrane-bound (fkP) cytochrome c oxidase, dineme subunit, membrane-bound (fkP) cytochrome c oxidase, dineme subunit membrane-bound (fkP) cytochrome c oxidase, dineme subunit membrane-bound (fkP) cytochrome c 653 ferredoxin-like protein flavdoxin-like protein flavdoxin-like protein flavdoxin-like protein flavdoxin (fidA) MAD(P)H-flavin oxidoreductase cytochrome c653 ferredoxin-like protein flavdoxin (fidA) MAD(P)H-flavin oxidoreductase cytopen-reactive Ni/Fe hydrogenase, lydD quinone-reactive Ni/Fe hydrogenase, cytoc b subunit (hydG) quinone-reactive Ni/Fe hydrogenase, cytoc b subunit (hydG) ubiquiol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquiol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquiol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquiol cytochrome c oxidoreductase, flavdoreductase, cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquiol cytochrome c oxidoreductase, flavdoreductase, flavdoreductase, cytochrome c subunit (fbcH) ubiquiol cytochrome c oxidoreductase, flav	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 43.9% 45.7% 48.5% 29.4% 42.6% 42.6% 42.6% 42.6% 42.6% 48.5% 52.5% 42.6% 48.5% 52.5% 48.5% 68.5% 68.9% 39.3% 28.8% 39.2% 65.5%
HP1135 HP1131 HP1131 HP1133 Electron tr HP0146 HP047 HP0145 HP1481 HP0147 HP0145 HP1481 HP1227 HP0588 HP16058 HP16058 HP1633 HP0633 HP0633 HP1639 HP1538 HP1538 HP1540 Entner-Doc HP1059 HP1508	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (ocd) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, fkP, MAD(P)-Halke protein flavddoxin-fike protein flavddoxin (ftA) NAD(P)-Halke protein flavddoxin (ftA) NAD(P)-Halke protein tavddoxin (ftA) NAD(P)-Halke protein subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) quinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, fileske 2Fe-2S subunit (fbcF) doroff 2-keto3-deoxy-6-phosphogluconate aldolas (cda) 6-phosphogluconate dehydratase on 3-oxoadipate coA-transferase subunit A (yyE)	85.6% 22.4% 32.7% 32.7% 33.7% 33.0% 44.2% 33.0% 43.9% 45.7% 48.5% 29.4% 42.6% 42.6% 42.6% 42.6% 42.6% 48.5% 52.5% 42.6% 48.5% 68.5% 68.9% 39.3% 28.8% 39.2% 68.5% 68.9% 39.2% 68.5% 68.9%
НР135 НР131 НР133 Ексито пт. НР0146 НР0285 НР0378 НР044 НР0145 НР1427 НР0146 НР1427 НР0145 НР1421 НР0277 НР0588 НР1626 НР0633 НР0633 НР0633 НР0633 НР0633 НР0633 НР0633 НР0633 НР0631 HP1508 HP1509 HP1509 HP1509 HP1508 HP1509 HP1509 HP1509 HP1509 HP1509 HP1099 HP1099 HP0991 HP0992 HP0904	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (codA) cytochrome c biogenesis protein (codA) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c553 ferredoxin-like protein flavodoxin-like protein flavodoxin-like protein flavodoxin-like protein flavodoxin (fitA) NAD(P)+Hain oxidoreductase oxygen-hisensitive NAD(P)H nitroreductase, cytochrome b subunit (hcf-1) quinone-reactive Ni/Fe hydrogenase, sufg subunit (hydA) quinone-reactive Ni/Fe hydrogenase, sufg subunit (hydA) quinol cytochrome c oxidoreductase, cytochrome c osubunit (bcC+1) ubiquinol cytochrome c oxidoreductase, felseke 2Fe-2 subunit (bcF) 2-keto-3-deoxy-6-phosphogluconate aldolas (cytoChrome c oxidoreductase, for 3-oxoadipate coA-transferase subunit A (yx)D acateta kinase (acA) (Escherioka coli) phosphate acetyttensferase (pta)	85.6% 224.6% 32.7% 37.8% 33.7% 33.0% 43.9% 45.7% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 62.5% 68.9% 39.3% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 65.5% 73.2% 65.5%
HP1131 HP1131 HP1133 Electron tr HP0146 HP0285 HP0147 HP0144 HP0145 HP144 HP0145 HP147 HP0277 HP0588 HP1160 HP0632 HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Dot HP100 Fermentall HP0692 HP0692 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0094 HP0095 HP0095	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Ccc0) cytochrome c biogenesis protein (cdG) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, diherme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c551 peroxidase cytochrome c552 peroxidase cytochrome c oxidoreductase aubunit (hydC) quinone-reactive Ni/Fe hydrogenase, Iarge subunit (hydA) quinone-reactive Ni/Fe hydrogenase, amali subunit (hydA) quinone-reactive Ni/Fe hydrogenase subunit A (xyAD) 3-oxoadipate coA-transferase subunit A (xyAD) shor-chain alcohd dehydrogenase	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 43.9% 45.7% 48.5% 48.5% 29.4% 42.6% 52.5% 42.6% 52.5% 48.5% 68.5% 68.9% 39.3% 28.8% 39.2% 68.5% 66.5% 65.5%
HP1133 HP1131 HP1133 HP1133 HP0146 HP0146 HP0146 HP0147 HP0148 HP0144 HP0145 HP1461 HP1461 HP1277 HP0588 HP1058 HP10583 HP0632 HP0583 HP1538 HP1538 HP1540 Entner-Dool HP0692 HP0937 HP0938 HP1509 HP1508 HP1538 HP1509 HP1609 HP0632 HP0891 HP0892 HP09034 HP09054 HP09054 HP09054 HP0892 HP0892 HP08034 HP08054 HP08054 HP08054 HP08054 HP08054 HP08054 </td <td>ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CocQ) cytochrome c biogenesis protein (ocG) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c553 ferredoxin-like protein flavdoxin-fike protein flavdoxin (fidA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, tytoc subunit (hydG) quinone-reactive Ni/Fe hydrogenase, smalt subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c cutores cotochrome cotochrom</td> <td>85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 43.9% 45.7% 48.5% 29.4% 42.6% 48.5% 29.4% 42.6% 48.5% 52.5% 42.6% 68.5% 68.9% 39.3% 28.8% 39.2% e 50.3% 50.3% 50.7% 65.5%</td>	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CocQ) cytochrome c biogenesis protein (ocG) cytochrome c oxidase, diheme subunit, memtrane-bound (fkP) cytochrome c553 ferredoxin-like protein flavdoxin-fike protein flavdoxin (fidA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, tytoc subunit (hydG) quinone-reactive Ni/Fe hydrogenase, smalt subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c cutores cotochrome cotochrom	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 43.9% 45.7% 48.5% 29.4% 42.6% 48.5% 29.4% 42.6% 48.5% 52.5% 42.6% 68.5% 68.9% 39.3% 28.8% 39.2% e 50.3% 50.3% 50.7% 65.5%
HP1133 HP1131 HP1133 HP1133 HP0146 HP0146 HP0147 HP0146 HP1481 HP1481 HP1481 HP1481 HP1481 HP1481 HP047 HP048 HP0578 HP1618 HP1508 HP1638 HP0533 HP1538 HP1508 HP1508 HP1508 HP1508 HP1533 HP1508 HP1508 HP1509 HP1508 HP1508 HP1509 HP1538 HP16091 HP0692 HP0931 HP0692 HP09357 Gluconeog HP0121	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CocQ) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, dineme subunit, membrane-bound (fbP) cytochrome c oxidase, dineme subunit, membrane-bound (fbP) cytochrome c oxidase, dineme subunit, membrane-bound (fbQ) cytochrome c oxidase, dineme subunit, membrane-bound (fbQ) cytochrome c oxidase, dineme subunit, membrane-bound (fbQ) cytochrome c oxidase, cytochrome c oxidase, subunit, membrane-bound (fbQ) cytochrome c553 ferredoxin-like protein flavdoxin-fike protein flavdoxin (fIdA) NAD(P)-Halwin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, large subunit (fhydE) quinone-reactive Ni/Fe hydrogenase, small subunit (fhydF) quinone-reactive Ni/Fe hydrogenase, small subunit (fhod-) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c d subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.3% 45.4% 43.3% 45.7% 43.3% 45.7% 48.5% 48.5% 52.5% 42.6% 52.5% 42.6% 68.5% 68.9% 39.3% 28.8% 39.2% 65.5%
HP1135 HP1135 HP1131 HP1133 Electron tr HP0146 HP0147 HP0148 HP0147 HP0147 HP0146 HP147 HP0147 HP0146 HP0147 HP0148 HP0277 HP0681 HP1608 HP10633 HP0632 HP0633 HP0633 HP1538 HP1538 HP1509 Entner-Doit HP0692 HP0903 HP0904 HP09057 Gluconeog HP1385	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, dineme subunit, membrane-bound (fkP) cytochrome c553 ferredoxin- file protein flavdoxin-file protein flavdoxin-file protein flavdoxin (ftA) NAD(P)-Halwin oxidoreductase oxygen-insensitive NAD(P)H nitrorequase, subunit quinone-reactive Ni/Fe hydrogenase, cytoc b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, sull subunit (hydC) quinone-reactive Ni/Fe hydrogenase, sull subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c osubunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, fileske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, fileske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, fileske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, fileske 2Fe-2S subunit (fbcH) soctate kinase (fackA) (Escherichia coli) phosphate acetlytransfirase subunit A (ypiE) soctate kinase (fackA) (Escherichia coli) phosphate acetlytran	85.6% 224.6% 32.7% 37.8% 44.2% 35.4% 33.0% 45.7% 43.9% 45.7% 48.5% 38.4% 45.5% 42.6% 48.5% 29.4% 48.5% 38.4% 52.5% 48.5% 39.4% 52.5% 48.5% 53.7% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 65.5% 73.2% 50.7% 50.7% 50.7% 50.5% 51.0% 52.6% 52.6%
HP1133 HP1131 HP1131 HP1133 HP0146 HP0146 HP0147 HP0148 HP0144 HP0145 HP141 HP0145 HP141 HP0145 HP1637 HP0145 HP1641 HP0277 HP0277 HP0583 HP1631 HP0632 HP0633 HP0633 HP1538 HP1540 Entre-Doi HP1540 HP0557 Gluconocol HP0385 HP0387 <	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coc0) cytochrome c biogenesis protein (cod1) cytochrome c biogenesis protein (cod3) cytochrome c oxidase, diherne subunit, membrane-bound fik/0) cytochrome c oxidase, diherne subunit, membrane-bound fik/0) cytochrome c oxidase, monoheme subunit, membrane-bound fik/0) cytochrome c oxidase, monoheme subunit, membrane-bound fik/0) cytochrome c oxidase, monoheme subunit, membrane-bound fik/0) cytochrome c fis/1 perioxidase cytochrome cfis/1 eriodoxin-like protein feridoxin-like hydrogenase, large subunit (hydC) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol c	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 33.0% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 48.5% 38.4% 52.5% 42.6% 48.5% 39.4% 48.1% 52.5% 48.5% 39.4% 48.5% 39.3% 68.5% 68.5% 65.5% 73.2% 50.7% 50.7% 51.0% 52.6% 51.0% 52.6% 55.5%
HP1135 HP1135 HP1131 HP1133 Electron tr HP0146 HP0146 HP0147 HP0148 HP0147 HP0146 HP1421 HP0145 HP1421 HP0145 HP1508 HP1621 HP0588 HP1638 HP0633 HP0633 HP0633 HP0633 HP0634 HP0635 HP1508 HP1508 HP1509 HP1508 HP0631 HP0635 HP06361 HP0637 Gluconeoc HP0357 Gluconeoc HP0357 Gluconeoc HP0357	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (ocd) cytochrome c oxidase, dineme subunit, membrane-bound (fkP) cytochrome c oxidase, heme b and coppe binding subunit, membrane-bound (fixN) cytochrome c oxidase, heme b and coppe binding subunit, membrane-bound (fixN) cytochrome c oxidase, heme b and coppe binding subunit, membrane-bound (fixN) cytochrome c oxidase, heme b and coppe binding subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and coppe binding subunit, membrane-bound (fixP) cytochrome c553 ferredoxin- fike protein flavdoxin-fike protein flavdoxin-fike protein flavdoxin-fike protein flavdoxin (fitA) NAD(P)-Halte protein flavdoxin (fitA) NAD(P)-Halte protein flavdoxin (fitA) NAD(P)-Halte protein flavdoxin (fitA) aubinet (hydC) quinone-reactive Ni/Fe hydrogenase, sufal subunit (hydA) quinone-reactive Ni/Fe hydrogenase, subunit (hydA)	85.6% 224.6% 32.7% 37.8% 33.3% 44.2% 35.4% 33.0% 45.7% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 62.9% 52.5% 42.9% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 65.5% 73.2% 65.5% 73.2% 51.0%
HP1135 HP1131 HP1131 HP1133 Electron tr HP0146 HP0146 HP0147 HP0148 HP0147 HP0146 HP1427 HP0145 HP142 HP0285 HP0277 HP0682 HP0683 HP1638 HP1638 HP1508 HP1583 HP1583 HP1509 HP1583 HP1509 HP1508 HP1509 HP1509 HP1509 HP1508 HP1509 HP1509 HP1509 HP1509 HP037 Gloconeog HP0357 Glyconby61 HP0351 HP0154 HP0154 HP0176 HP0170 HP1163 HP0164 HP0176	APP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, membrane-bound (fixN) cytochrome c553 ferredoxin- file protein flavdoxin-file protein flavdoxin (ffA) NAD(P)-Harlin oxidoreductase oxygen-insensitive NAD(P)H nitrorequase, subunit (hydC) quinone-reactive Ni/Fe hydrogenase, subunit subunit (hydC) quinone-reactive Ni/Fe hydrogenase, subunit (hydD) quinone-reactive Ni/Fe hydrogenase, subunit (hydD) quinone-reactive Ni/Fe hydrogenase, subunit (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/Fe hydrogenase (hydE) quinone-reactive Ni/F	85.6% 22.4% 32.7% 37.8% 33.7% 35.4% 33.0% 43.9% 45.7% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 48.1% 52.5% 42.6% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 65.5% 73.2% 65.5% 73.2% 50.7% 50.3% 50.7% 51.0% 56.5% 73.2% 42.3% 50.0% 56.9%
HP1135 HP1131 HP1131 HP1133 Electron tr HP0146 HP0285 HP0378 HP0147 HP0444 HP0145 HP1481 HP1227 HP0285 HP1481 HP1227 HP0288 HP1481 HP0277 HP0588 HP1630 HP1633 HP0633 HP0633 HP0633 HP0633 HP1639 HP1538 HP1540 Entrer-Dox HP1639 HP1538 HP1540 Entrer-Dox HP1039 HP1538 HP1540 Entrer-Dox HP0391 HP0393 HP0395	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) arport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (ocd) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, dimeme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fkP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c553 ferredoxin- file protein flavdoxin-file protein flavdoxin-file protein flavdoxin-file protein flavdoxin-file protein flavdoxin (ftA) NAD(P)-Halm oxidoreductase oxygen-insensitive NAD(P)H nitroreductase ayunone-reactive Ni/Fe hydrogenase, sufd subunit (hydC) quinone-reactive Ni/Fe hydrogenase, suff subunit (hydA) quinone-reactive Ni/Fe hydrogenase, suff subunit (hydA) quinoter e oxidoreductase, endase (con f fuctose-biosphosphatase finatose-biosphosphatase finatose (glk) glucose-6-phosphatase (gla) glucose-6-phosphosphatase finatose (glk) glucose-6-phosphosphatase finatose (glk) glucose-6-phosphosphatase finatose (glk) glucose-6-phosphosphatase finatose-biosphosphatase finatose-biosphosphatase (glk) g	85.6% 22.4% 32.7% 37.5% 33.0% 44.2% 35.4% 43.3% 45.7% 43.9% 45.7% 48.5% 52.5% 42.0% 52.5% 42.0% 52.5% 42.0% 52.5% 68.9% 68.9% 68.9% 68.9% 65.5%
HP1135 HP1131 HP1131 HP1133 Electron tr HP0146 HP0285 HP0147 HP0144 HP0145 HP1481 HP1227 HP0268 HP1161 HP1227 HP0268 HP1161 HP10277 HP0588 HP1163 HP1633 HP0632 HP0633 HP1633 HP1538 HP1538 HP1540 Entrer-Doc HP1099 HP1538 HP1540 Entrer-Doc HP1099 HP1538 HP1540 HP0992 HP0305 HP0305 HP0305 HP0305 HP0305 HP0321 HP1345 Glycoolysis HP0154 HP0321 HP1346	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (cdG) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, monoherne subunit membrane-bound (fixP) cytochrome c oxidase, monoherne subunit membrane-bound (fixP) cytochrome c oxidase, monoherne subunit membrane-bound (fixP) cytochrome c dsf3 ferredoxin-like protein flavodoxin-fike protein flavodoxin-fike protein flavodoxin-fike protein flavodoxin-fike protein flavodoxin-fike protein subunit (hydC) quinone-reactive Ni/Fe hydrogenase, synD subunit (hydC) quinone-reactive Ni/Fe hydrogenase, sufJ quinone-reactive Ni/Fe hydrogenase, synD subunit (hydC) quinone-reactive Ni/Fe hydrogenase, sufJ subunit (hydC) quinone-reactive Ni/Fe hydrogenase, synD subunit (hydC) quinone-reactive Ni/Fe hydrogenase, sufJ subunit (hydC) quinone-reactive Ni/Fe hydrogenase, synD subunit (hydC) quinone-reactive Ni/Fe hydrogenase subunit (hydC) quinone-reactive Ni/Fe hydrogenase (synD g1)cereate hydrogenase (synD g1)cereate hydrogenase (synD g1)cereate hydrogenase (synD g1)cerate kinase enolase (g1) g1)cerate kinase enolase (g1) g1)cerate kinase enolase (g1) g1)cerate kinase enolase (g1) g1)cerate kinase enolase (g1) g1)cerate kinase enolase (g2) g1)cerate kinase enolase (g2) g1)cerate kinase enolase (g2)	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 35.4% 35.4% 33.0% 45.7% 43.9% 45.7% 48.5% 38.4% 42.6% 29.4% 42.6% 29.4% 42.6% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 65.5% 73.2% 42.3% 50.7% 50.3% 50.7% 50.5% 66.9% 56
HP1131 HP1131 HP1131 HP1133 Electron tr HP0146 HP0147 HP0148 HP0147 HP0144 HP0145 HP141 HP0145 HP141 HP0145 HP1637 HP0145 HP1641 HP0145 HP1631 HP0632 HP0633 HP0633 HP0633 HP0633 HP0633 HP0634 HP0635 HP0636 HP0637 HP0588 HP1509 HP1509 HP1509 HP1500 HP05057 Gluconecol HP076 HP0125 HP0166 HP0267 HP0166 HP0274	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Cocq) cytochrome c biogenesis protein (coff) cytochrome c biogenesis protein (coff) cytochrome c oxidase, diherme subunit, membrane-bound (fixP) cytochrome c oxidase, diherme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c 653 ferredoxin-like protein ferrodoxin-like protein fixodoxin (flcA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flcH) ubiquinol cytochrome c oxidoreductase, cytochrome b c subunit (flcH) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flc	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 45.7% 43.9% 45.7% 48.5% 29.4% 42.6% 29.4% 42.6% 29.4% 42.6% 29.4% 48.5% 38.4% 52.5% 42.6% 68.5% 68.9% 39.3% 28.8% 68.5% 65.5% 73.2% 50.7% 65.5% 73.2% 50.7% 50
HP1133 HP1131 HP1131 HP1133 HP0146 HP0146 HP047 HP0146 HP1481 HP1481 HP1481 HP1277 HP0588 HP1638 HP1638 HP0642 HP0653 HP0632 HP0632 HP1508 HP1508 HP160954 HP0632 HP0632 HP0631 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1509 HP1538 HP0591 HP0821 HP0821 HP0351 H	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit G (CocQ) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, dineme subunit, membrane-bound (fkP) cytochrome c oxidase, cytochrome c oxidase, and context context context context context membrane-bound (fkP) cytochrome c oxidase, cytochrome c oxidase, cytochrome c oxidase, cytochrome c oxidase, cytochrome c cist automatic protein flavdoxin (fldA) ADCIPI-Halte protein flavdoxin (fldA) ADCIPI-Halte protein flavdoxin (fldA) ADCIPI-Halte protein flavdoxin (fldA) aubinetre NJ/Fe hydrogenase, cytoc b subunit (hydC) quinone-reactive NJ/Fe hydrogenase, cytoc b subunit (hydF) quinone-reactive NJ/Fe hydrogenase, cytoc b subunit (hydA) quinone-reactive NJ/Fe hydrogenase, cytoc b subunit (hydA) quinotex-sphosphosphosphosphosphosphose flaves e2Fe-2S subunit (fbC-f) ducokinase (ablA) (fbC-h) glucokinase (ablA) (fbC-h) glucokinase (ablA) (fbC-h) glucokinase (glA) glucose-6-phosphata elohydrogenase (geD) phosphosphate subunerase (p)) glucose-6-phosphata elohydrogenase (geD) phosphosphate subunerase (p)) glucose-6-phosphate elohydrogenase (geD) phosphos	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 45.7% 43.9% 45.7% 48.5% 29.4% 47.0% 48.5% 29.4% 47.0% 48.6% 68.9% 39.3% 28.8% 39.3% 28.8% 39.2% 65.5% 65
HP1133 HP1131 HP1133 HP1133 HP0146 HP0146 HP0147 HP0148 HP0147 HP0144 HP0145 HP1427 HP0144 HP0145 HP1508 HP1608 HP1638 HP0632 HP0633 HP0632 HP0632 HP0633 HP1508 HP1538 HP1609 HP1609 HP1638 HP1509 HP1609 HP100 Fermentatil HP0892 HP0934 HP0357 Glyconycsis HP0175 HP0305 HP0176 HP0325 HP0176 HP0326 HP0176 HP0327 HP0178 HP0178 HP0178 HP0178	ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit detta (atpH) ATP synthase F1, subunit gamma (atpG) ansport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (cdG) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, diherne subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit membrane-bound (fixP) cytochrome c oxidase, monoheme subunit membrane-bound (fixP) cytochrome c 553 ferredoxin- flexodoxin-like protein flexodoxin-like protein subunit (hydC) quinone-reactive Ni/Fe hydrogenase, enrol subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydC) quinone-reactive Ni/Fe hydrogenase (str) fuctosehosphogluconate dehydragenase enolase (eno) fructose-flosiphosphatae phosphotenopyruvate synthase (pa) phosphoglycerate kinase enolase (eno) fructose-flosiphosphatae (pa) phosphoglycerate kinase enolase (eno) fructose-flosiphosphatae (pa) gluceare-thosphate isomerase (pa) gluceare-thosphate isomerase (pa) gluceare-thosphate isomerase (pa) gluceare-thosphate isomerase (pa) gluceare-th	85.6% 22.4% 32.7% 37.8% 44.2% 35.4% 43.9% 43.9% 45.7% 43.9% 45.7% 48.5% 29.4% 47.0% 48.5% 29.4% 47.0% 48.6% 68.9% 39.3% 28.8% 39.3% 28.8% 39.2% 65.5% 65

HP1101	(devB) glucose-6-phosphate dehydrogenase	29.2%
HP1495	(g6pD) transaldolase (tal)	36.7% 33.5%
HP1088	transketolase A (tktA)	46.7%
HP0354 Sugars	transketolase B (tktB)	39.7%
HP0574	galactosidase acetyltransferase (lacA)	41.0%
HP0360 TCA cycle	UDP-glucose 4-epimerase	43.1%
HP0779 HP0026	aconitase B (acnB)	64.0% 47.8%
HP1325	citrate synthase (gltA) fumarase (fumC)	63.7%
HP0509 HP0027	glycolate oxidase subunit (glcD) isocitrate dehydrogenase (icd)	98.0% 70.7%
FATTY ACI	D AND PHOSPHOLIPID METABOLISM	
General		
HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (fabZ)	47.4%
HP1348	1-acyl-glycerol-3-phosphate acyltransferase (plsC) (Escherichia coli)	32.0%
HP0561	3-ketoacyl-acyl carrier protein reductase	
HP0690	(fabG) acetyl coenzyme A acetyltransferase	45.7%
HP0950	(thiolase) (fadA) acetyl-CoA carboxylase beta subunit	52.0%
HP1045	(accD) acetyl-CoA synthetase (acoE)	49.4% 52.3%
HP0557	acetyl-coenzyme A carboxylase (accA)	50.3%
HP0559 HP0962	acyl carrier protein (acpP) acyl carrier protein (acpP)	55.3% 56.3%
HP0558	beta ketoacyl-acyl carrier protein synthase (fabF)	II 50.0%
HP0202	beta-ketoacyl-acyl carrier protein synthase (fabH)	III 44.4%
HP0371	biotin carboxyl carrier protein (fabE)	30.8%
HP0370 HP0871	biotin carboxylase (accC) CDP-diglyceride hydrolase (cdh)	52.1% 73.9%
HP0215 HP0416	CDP-diglyceride synthetase (cdsA) cyclopropane fatty acid synthase (cfa)	42.4% 39.7%
HP0700	diacylglycerol kinase (dgkA)	45.8%
HP0195	enoyl-(acyl-carrier-protein) reductase (NADI (fabl)	H) 45.8%
HP0201	fatty acid/phospholipid synthesis protein (plsX)	37.8%
HP0808 HP0090	Holo-acp synthase (acpS)	29.1%
	malonyl coenzyme A-acyl carrier protein transacylase (fabD)	35.4%
HP1016	phosphatidylglycerophosphate synthase (pgsA)	35.4%
HP1357	phosphatidylserine decarboxylase proenzy (psd)	me 33.2%
HP1071	phosphatidylserine synthase (pssA)	99.6%
HP0499	phospholipase A1 precursor (DR-phospholipase A)	33.8%
PURINES,	PYRIMIDINES, NUCLEOSIDES AND NUCLEO	DTIDES
General		
HP0757 2Õ-Deoxvn	beta-alanine synthetase homologue ibonucleotide metabolism	40.0%
HP0372	deoxycytidine triphosphate deaminase (dcd)	28.2%
HP0865	deoxyuridine 50-triphosphate nucleotidohyd	rolase
HP0865 HP0364	deoxyuridine 5Ö-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet	rolase 41.4% a
HP0364	deoxyuridine 50-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdB)	rolase 41.4% a 39.0%
HP0364 HP0680	deoxyuridine 5Ö-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdB) ribonucleoside-diphosphate reductase 1 al subunit (nrdA)	rolase 41.4% a 39.0% pha 28.4%
HP0364 HP0680 HP0825 Purine ribo	deoxyuridine 50-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdB) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) mucleotide biosynthesis	rolase 41.4% a 39.0% oha
HP0364 HP0680 HP0825 <i>Purine ribc</i> HP0321	deoxyuridine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet suburit (nrdA) suburit (nrdA) suburit (nrdA) nucleotide biosynthesis SQ-gurylate kinase (mk)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8%
HP0364 HP0680 HP0825 Purine ribo HP0321 HP0618 HP1112	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis BQuarylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (purB)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0618 HP1112 HP0255 HP1434	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis EQuarylate kinase (gmk) adenylate kinase (dak) adenylate kinase (gurB) adenylosuccinate lysate (purA) form/tetrahydrolotate hydrolase (purU)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3%
HP0364 HP0680 HP0825 Purine ribo HP0321 HP0618 HP1112 HP0255	deoxyurdine 5C-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) thioredoxin reductase (trxB) nucleotide biosynthesis 5Gyaryntae kinase (gmk) adenyfate kinase (ak) adenyfate kinase (gurB) adenyfosuccinate lyase (purB) adenyfosuccinate lyase (purB) adenyfosuccinate synthetase (purA) form/tertarphytofolate hydroiase (purD) glycinamide ribonucleotide synthetase (purD)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0618 HP1112 HP0255 HP1434 HP1218 HP0854	deoxyuridine 50-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrd8) inbonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (txB) nucleotide biosynthesis 50-garnylate kinase (gmk) adenylosuccinate synthesise (purB) adenylosuccinate synthesise (purB) adenylosuccinate synthesise (purB) formylterahydrofolate hydrolase (purU) glycinamide ribonucleotide synthesise (purD) GMP reductase (guaC)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8%
HP0364 HP0680 HP0825 Purine ribo HP0321 HP0251 HP1112 HP0255 HP1434 HP1218	deoxyuridine 5C-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrd3) subunit (nrd3) hioracleoside-diphosphate reductase 1 al subunit (nrd4) biografiae kinase (txB) nucleotide biosynthesis 50-ganylate kinase (ark) adenylate kinase (ark) GMP reductase (guaC) GMP synthase (guaA) inosine-5C-monophosphate dehydrogenase	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 31.8% 56.1%
HP0364 HP0680 HP0825 Purine riboc HP0821 HP0618 HP1112 HP0255 HP1434 HP1218 HP0854 HP0854 HP0859 HP0198	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdA) subunit (nrdA) hucleotide biosynthesis 50-gunylate kinase (ark) adenylate kinase (ark) adenylate kinase (ark) adenylate kinase (ark) adenylate kinase (ark) adenylosuccinate synthetase (purB) adenylosuccinate synthetase (purD) glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP synthase (guaA) inosine-50-monphosphate dehydrogenase (guaB) nucleotide diphosphate kinase (ndk)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8%
HP0364 HP0880 HP0825 Purine ribc HP0321 HP0318 HP0451 HP1434 HP0255 HP1434 HP0409 HP0854 HP0409 HP0859 HP0198 HP0198	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdA) subunit (nrdA) hucleotide biosynthesis 50-gunylate kinase (trxB) nucleotide biosynthesis 50-gunylate kinase (trxB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) downloe inbonucleotide synthetase (purD) glycinamide ribonucleotide synthetase (purD) GMP reductase (guaC) GMP reductase (guaC) GMP synthase (guAA) inosine-50-monphosphate dehydrogenase (guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA)	rolase 41.4% 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.5% 56.1% 56.1% 56.1% 56.5%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0321 HP0325 HP0325 HP1218 HP0434 HP1218 HP0454 HP0409 HP0854 HP0409 HP0742 HP01530	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdB) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis Gogunylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gurA) denylate kinase (gurA) denylate kinase (gurA) glycinamide nbonucleotide synthetase (purD) GMP synthase (guaA) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) punceloside diphosphate kinase (ndk) pune nucleoside phosphate (punB)	rolase 41.4% a 39.0% bha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 31.8% 56.1% 58.5% 67.7%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0321 HP0321 HP0325 HP0325 HP0325 HP0325 HP0325 HP0329 HP0329 HP0742 HP1530 Pyrimidine HP1034	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdB) ribonucleoside-diphosphate reductase 1 ali subunit (mdA) thioredoxin reductase (trxB) subunit (mdA) tadenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gurB) adenylosuccinate synthetase (purD) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) andersyntase (guaC) functionsylpyrophosphate kinase (ndk) nucleoside diphosphate kinase (ndk) purine nucleoside phosphotylase (purB) ribonucleotide biosynthesis aspartate transcarbamoylase (pyrB)	rolase 41.4% 39.0% oha 28.4% 45.9% 44.8% 33.3% 49.5% 44.6% 49.5% 56.1% 56.1% 56.1% 56.5%
HP0364 HP0680 HP0825 Purine r0021 HP0618 HP112 HP0255 HP018 HP1218 HP0354 HP0409 HP0742 HP1530 Pyrimidine HP1084 HP1084 HP1089 HP1084 HP1089	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdB) ribonucleoside-diphosphate reductase 1 ali subunit (mdA) thioredoxin reductase (trxB) subunit (mdA) tadenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gurB) adenylosuccinate synthetase (purD) GMP synthase (guaA) GMP synthase (guaA) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) nucleoside diphosphate kinase (ndk) nucleoside diphosphate kinase (ndk) nucleoside diphosphate kinase (ndk) nicoincetotide biosynthesis aspartate transcarbamoylase (purB) carbamoyl-phosphate synthase (gutaM) carbamoyl-phosphate synthase (gutaM) carbamoyl-phosphate synthase (gutaM)	rolase 41.4% 39.0% oha 28.4% 45.9% 44.8% 43.3% 49.5% 44.6% 49.1% 31.8% 56.1% 56.5% 56.5% 20.7% 38.7% 48.6%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0325 HP1434 HP128 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP0459 HP1530 Pyrimidine HP1684 HP069 HP1237	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdb) thioredoxin reductase (trxB) nucleotide biosynthesis BÖguarylate kinase (gmk) adenylosuccinate lyase (purB) adenylosuccinate (guaC) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) phosphoritosylprophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) nichonucleotide biosynthesis aspartate transcarbarnoylase (gyrB) carbarout/phosphate synthetase (gyrB) carbarout/phosphate synthetase (gyrB)	rolase 4.14% 39.0% 58.4% 45.9% 44.8% 33.3% 44.8% 33.3% 49.5% 44.6% 49.1% 31.8% 31.8% 58.5% 67.7% 56.5% 20.7% 38.7% 48.6%
HP0364 HP0825 Purine ribc HP0825 HP0321 HP0321 HP0321 HP0321 HP0321 HP0321 HP0321 HP0329 HP0329 HP0329 HP0329 HP0329 HP0349 HP0349 HP0349 HP0349 HP0349 HP0349 HP0349	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdb) thioredoxin reductase (trxB) nucleotide biosynthesis EÖquarylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylosuccinate systhetase (purA) form/tetrahydrolate hydrolase (purU) glycinamide ribonucleotides (purU) glycinamide ribonucleotides (purU) GMP reductase (guaC) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) phosphoribosphate kinase (purB) nucleoside diphosphate kinase (purB) nucleoside biosynthesis aspartate transcarbamoylase (purB) nibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphates synthetase (pyrB) CTP synthetase (pyrG)	rolase 4,14% 3,30% 0ha 28,4% 44,5% 44,8% 33,3% 44,5% 44,6% 33,3% 49,5% 44,6% 33,3% 56,1% 58,5% 67,7% 56,5% 20,7% 50,
HP0364 HP0825 Purine ribc HP0325 HP0321 HP0321 HP0255 HP1334 HP0255 HP1345 HP0255 HP1434 HP0409 HP0289 HP0198 HP0198 HP0198 HP0198 HP0198 HP0198 HP0349 HP0286 HP0284 HP0285 HP0285 HP0286 HP0285 HP02	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdb) thioredoxin reductase (trxB) nucleotide biosynthesis EÖguarylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylate kinase (gmk) adenylosuccinate sysnthetase (purA) form/tetrahydrolotate hydrolase (purU) glycinamide ribonucleotides (purU) glycinamide ribonucleotides (purU) GMP reductase (guaC) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) phosphoribosphate kinase (prB) carbemychposphate synthetase (praA) purine nucleoside biosynthesis aspartate transcarbemoylase (pyrB) carbemychposphates (pyrB) carbemychposphates (pyrB) CTP synthetase (pyrG) dihydroorotase (pyrC) dihydroorotase (pyrC)	rolase 41.4% 39.0% 59.0% 44.8% 45.9% 44.8% 433.3% 49.5% 44.6% 49.5% 56.1% 56.5% 20.7% 56.5% 20.7% 58.5% 67.7% 58.5% 67.7% 58.5% 67.7% 58.5% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7% 50.7%
HP0364 HP0680 HP0625 Purine ribc HP0615 HP121 HP0255 HP1324 HP0255 HP1324 HP0255 HP1324 HP0329 HP0329 HP0329 HP0329 HP1530 HP1034 HP1084 HP10919 HP10266 HP1057 HP1057	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdB) ribonucleoside-diphosphate reductase 1 ali subunit (mdA) thioredoxin reductase (trxB) mucleotide biosynthesis SQgarylate kinase (gmk) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate synthetase (purD) GMP synthase (guaA) GMP synthase (guaA) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) purine nucleoside phosphate kinase (ndk) nucleoside diphosphate kinase (ndk) nucleoside diphosphate synthetase (praA) nucleoside diphosphate synthetase (praA) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrA) carbamoy-phosphate synthetase (pyrA) carbamoy-phosphate synthetase (pyrA) carbamoy-phosphate synthetase (pyrA) carbamoy-phosphate synthetase (pyrA) dihydroorase (pyrC) dihydroorase (pyrC) dihydroorase (pyrC)	rolase 41.4% 33.0% 41.4% 44.8% 45.9% 44.8% 433.3% 49.5% 44.6% 49.5% 56.1% 56.5% 56.5% 56.5% 50.7% 56.5% 20.7% 56.5% 20.7% 56.5% 20.7% 50.7
HP0364 HP0680 HP0625 Purine riboc HP0615 HP1018 HP0255 HP1434 HP0625 HP1434 HP0629 HP1218 HP0742 HP1084 HP0742 HP1084 HP0919 HP1027 HP1027 HP00266 HP1037 HP1027 HP107 H	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdB) ribonucleoside-diphosphate reductase 1 ali subunit (mdA) thioredoxin reductase (trxB) mucleotide biosynthesis 50garnylate kinase (arkI) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purA) form/letrariyirofolate hydrolase (purA) form/letrariyirofolate hydrolase (purA) dimmiler inbonucleotide synthetase (purD) GMP synthase (guaA) GMP synthase (guaA) nucleoside diphosphate kinase (ndk) purine nucleoside phosphate kinase (ndk) nucleoside diphosphate kinase (ndk) purine nucleoside phosphate synthetase (prsA) nucleoside diphosphate synthetase (prsB) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrB) carbamoy-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosylfransferase (pyrC) orotate phosphoribosphorosylfanses (pyrC) orotate phosphoribosphorase (pyrC) orotate phosphoribosphate decarboxylase (pyrE) orotatine 50-phosphate decarboxylase (pyrB)	rolase 41.4% 33.0% 41.4% 44.8% 45.9% 44.8% 433.3% 49.5% 44.6% 49.5% 56.1% 56.5% 56.5% 56.5% 50.7% 56.5% 20.7% 56.5% 20.7% 56.5% 20.7% 50.7
HP0364 HP0680 HP0625 Purine ribc HP0618 HP112 HP0255 HP1434 HP0255 HP1434 HP0409 HP0829 HP0829 HP0742 HP1518 HP0742 HP1684 HP0919 HP084 HP0919 HP084 HP0919 HP084 HP0919 HP0851 HP1084 HP0919 HP0257 HP084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1094 HP0919 HP0851 HP1094 HP0919 HP	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdb) ribonucleoside-diphosphate reductase 1 ali subunit (mdb) ribonucleoside-diphosphate reductase 1 ali subunit (mdb) Digger (mdb) adenylosuccinate (synthesis SÖ-guarylate kinase (mk) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) denylosuccinate synthetase (purA) form/tertaryloroloite hydroise (purC) GMP synthase (guaB) inosine-SO-monophosphate dehydrogenase (guaB) punie olide diphosphate kinase (ndk) phosphoritosylpyrophosphate synthetase (prsA) punie nucleoside phosphorylase (purB) ribonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrA) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphorbosyltar sectosylase (pyrE) orotate 5O-monophosphate (UMP) kinase (pyrH)	rolase 41.4% a 39.0% oha 28.4% 44.8% 43.33% 49.5% 44.6% 49.5% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 56.5% 20.7% 48.6% 39.7% 50.7% 50.7% 50.3% 20.7%
HP0364 HP0680 HP0625 Purine ribc HP0618 HP112 HP0255 HP1434 HP0255 HP1434 HP0409 HP0829 HP0829 HP0742 HP1518 HP0742 HP1684 HP0919 HP084 HP0919 HP084 HP0919 HP084 HP0919 HP0851 HP1084 HP0919 HP0257 HP084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1084 HP0919 HP0851 HP1094 HP0919 HP0851 HP1094 HP0919 HP	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdb) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis Göguarylate kinase (gmk) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) adenylosuccinate lyase (purB) denylosuccinate lyase (purB) denylosuccinate lyase (purB) denylosuccinate lyase (purB) denylosuccinate lyase (purB) denylosuccinate lyase (purB) diphosphoritose (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaB) nucleoside diphosphate kinase (ndk) phosphoritosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis aspartate transcarbarroglase (pyrB) carbarnoyi-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorciase (pyrC) dihydroorciase (pyrC) arotdine 50-phosphortose (pyrD) arotdine tophosphortosylrans (farse (pyrE) arotdine tophosphate (carboxylrase (pyrE) arotdine tophosphate (carboxylrase (pyrE) arotdine tophosphate (pyrE) arotdine tophosphate (UNP) kinase (pyrH) nucleoside and nucleotides	rolase 41.4% a 39.0% oha 28.4% 45.9% 44.8% 45.9% 44.8% 49.5% 44.6% 49.5% 31.8% 56.1% 58.5% 67.7% 56.5% 20.7% 56.5%
HP0364 HP0680 HP0825 Purine ribc HP0321 HP0318 HP112 HP0255 HP1434 HP0255 HP1434 HP0289 HP0829 HP0829 HP0829 HP0829 HP0742 HP1530 Pyrimidine HP1084 HP0919 HP1237 HP0349 HP0286 HP1034 HP0777 Salvage of HP014	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdB) ribonucleoside-diphosphate reductase 1 ali subunit (nrdA) thioredoxin reductase (trxB) nucleotide biosynthesis SQ-garylate kinase (atk) adenylate kinase (gmk) adenylosuccinate syste (purA) form/tetrahydrofolate hydroilse (purU) glycinamide ribonucleotides (purU) glycinamide ribonucleotide synthetase (purD) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) inosine5O-monphosphate dehydrogenase (graB) nucleoside diphosphate kinase (ndk) phosphoritosylprophosphate synthetase (praA) purine nucleoside phosphorylase (purB) ribonucleotide biosynthesis aspartate transcarbarroylase (pyrB) carbarroy-phosphate synthetase (pyrC) dihydrooratae (pyrC) dihydrooratae (pyrC) dihydrooratae (pyrC) dihydrooratae (prC) dihydrooratae (prC) dihydrooratae (prC) dihydrooratae (phosphate (UMP) kinase (pyrH) orotate phosphoripospitae (UMP) kinase (pyrH) nucleosides and nucleotides &3Q-opic-nucleotide 2O-phosphotiestrase &3Q-opic-nucleotide 2O-phosphotiestrase &3Q-opic-nucleotide 2O-phosphotiestrase &3Q-opic-nucleotide 2O-phosphotiestrase &3Q-opic-nucleotide 2O-phosphotiestrase &3Q-opic-nucleotide 2O-phosphotiestrase	rolase 41.4% a 39.0% 41.4% 45.9% 44.8% 45.9% 44.8% 49.5% 44.6% 49.5% 58.5% 67.7% 58.5% 67.7% 56.5% 20.7% 20.
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HP0384 HP0384 HP0825 Purine ribc HP0821 HP0825 Purine ribc HP0825 HP128 HP0825 HP128 HP0829 HP128 HP0829 HP1728 HP099 HP1237 HP0829 HP10286 HP0819 HP0286 HP1084 HP0077 Salvage of HP072 HP178 HP0043 HP0454 HP0453 Sugar-nucl HP0453 HP0454 HP0451 HP0451 HP0452 HP0453 HP0453 HP0454 HP032 HP1083 HP0451 HP032 HP1083 HP0454 HP032 HP1083 HP1492	deoxyurdine SQ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdf) ribonucleoside-diphosphate reductase 1 ali subunit (nrdf) ribonucleoside-diphosphate reductase 1 ali subunit (nrdf) nucleoside biosynthesis Gguarylate kinase (grkf) adenylosuccinate syste (purB) adenylosuccinate syste (purB) adenylosuccinate syste (purB) adenylosuccinate systemes (purB) inonucleoside phosphate synthese (purB) ribonucleoside biosynthesis asparate transcarbarnoylase (purB) carbarnoyl-phosphate synthetase (purB) asparate transcarbarnoylase (purB) carbarnoyl-phosphate synthetase (purC) dihydroorates (purC) dihydroorates (purC) dihydroorates (purC) adhydroorates (purC) adhydroorates (purC) and phosphoribosyltransferase (pyrC) arbarnoyl-phosphate (DMP) kinase (pyrH) nucleoside and nucleotides £3Q-qclic-nucleotide 20-phosphoribasyltransferase (purC) adhydroorates (purC) adhydroorates (purD) orotate phosphoribosyltransferase (purD) phosphopenhate isomerase (purD) and the guntine phosphoribasyltransferase (purC) dipulation protein (ciK) uDP-N-acetylglucosamine pyrophosphorylas (giRU) DP-N-acetylglucosamine pyrophosphorylas (giRU)	rolase rolase 41.4% a 39.0% 41.4% 41.4% 41.4% 43.9% 44.8% 433.3% 44.8% 435.3% 44.8% 435.5% 67.7% 58.5% 67.7% 56.5% 20.7% 56.5% 20.7% 56.5% 31.5% 55.5% 55.5% 55.5% 55.5% 27.1% 42.8% 43.3% 55.5% 55.5% 27.1% 42.8% 43.3% 55.5% 5
HP0384 HP0384 HP0825 Purine ribc HP0821 HP0821 HP0821 HP0821 HP0821 HP0821 HP0825 HP1216 HP0829 HP0829 HP0829 HP0829 HP0742 HP1084 HP0851 HP0861 HP0861 HP0349 HP0349 HP0349 HP0349 HP0351 HP0349 HP0372 HP137 HP037 Salvage of HP178 HP072 HP178 HP0735 Sugarnucl HP0663 REGULATC General HP168	deoxyurdine SÖ-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (nrdf) ribonucleoside-diphosphate reductase 1 ali subunit (nrdf) ribonucleoside-diphosphate reductase 1 ali subunit (nrdf) nucleoside biosynthesis SÖ_gurylate kinase (grk) adenylate kinase (grk) adenylate kinase (grk) adenylosuccinate systel (grrf) adenylosuccinate systel (grrf) adenylosuccinate systel (grrf) adenylosuccinate systel (grrf) adenylosuccinate systel (grrf) diphosphotbase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) GMP synthase (guaC) aphosphotbosyltare kinase (nrk) punien nucleoside phosphate synthetase (graA) nucleoside diphosphate kinase (grrfR) carbarnoyi-phosphate synthetase (grrfB) carbarnoyi-phosphate synthetase (grrfB) carbarnoyi-phosphate synthetase (grrfC) dihydrooratae (grrfC) dihydrooratae (grrfC) dihydrooratae (grrfC) dihydrooratae (grrfC) orotate nbosphoribosyltranes(grrfE) orotate nbosphoribosyltranes(grrfE) orotatine phosphoribosyltranes(grrfE) punine-nucleoside phosphorylase (galD) punine-nucleoside nbosphorylase (galD) punine-nucleoside nbosphorylase (galD) orotate nbosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphoribosyltranes(grrfE) punine-nucleoside phosphorylase (galD) DP-duccae grrfE) adenine phosphoribosyltranes(grrfE) adenine phosphorib	rolase rolase 41.4% a 39.0% 41.4% 41.4% 41.4% 43.9% 44.8% 433.3% 44.8% 435.3% 44.8% 44.8% 435.3% 67.7% 58.5% 67.7% 58.5% 67.7% 58.5% 56.5% 20.7% 31.5% 55.5% 31.5% 55.5% 55.5% 55.5% 55.5% 27.1% 42.8% 43.3% 55.5% 5
HP0384 HP0384 HP0825 Purine ribc HP0818 HP0818 HP0818 HP0825 Purine ribc HP0818 HP0821 HP0825 HP1218 HP0829 HP0829 HP0742 HP1039 HP084 HP0919 HP084 HP0919 HP084 HP0919 HP0319 HP0827 HP0319 HP0827 HP0319 HP0777 Salvage of HP072 HP0735 Sugarnuc HP0451 HP0452 HP0453 HP0464 HP0454 HP0466 HP0466 HP04672 HP168 HP1468	deoxyurdine 50-triphosphate nucleotidohyd (dut) ribonucleoside diphosphate reductase, bet subunit (mdB) ribonucleoside-diphosphate reductase 1 ali subunit (mdA) thioredoxin reductase (trxB) mucleotide biosynthesis 50-gusrylate kinase (trxB) adenylate kinase (trxB) rucleoside diphosphate kinase (trxB) rucleoside diphosphate kinase (trxB) rucleoside diphosphate synthetase (trxB) rucleoside biosynthesis aspartate transcarbarolyalse (tryB) carbarnoy-phosphate synthetase (trxB) carbarnoy-phosphate synthetase (trxB) carbarnoy-phosphate synthetase (tryCB) carbarnoy-phosphate synthetase (tryCB) carbarnoy-phosphate synthetase (tryCB) carbarnoy-phosphate synthetase (tryCB) carbarnoy-phosphate (synCB) carbarnoy-phosphate (synCB) carbarnoy-phosphate (tryCB) carbar bioxynthesis and conversions mannose-0-phosphate isomerase (tryCB) andthine guanine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-ucleoside phosphorylase (deuD) anthine guanine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-ucleoside phosphorylase (deuD) anthine guanine phosphoribosyltransferase (apt) phosphopentomutase (deuB) phosphopentomutase (deuB) purine-ucleoside phosphorylase (geIU) UDP-A acetylglucosamine prophosphorylase (geIU) UDP-A acetylglucosamine prophosphorylase (fitA) carbon storage regulator protein ((tr)A) carbon storage regulator protein (tryCh)	rolase rolase 41.4% 33.0% 45.9% 44.8% 33.3% 49.5% 44.8% 31.8% 31.8% 31.8% 56.1% 20.7% 56.5% 20.7% 56.5% 20.7% 56.5% 38.7% 48.6% 39.7% 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% 50.7% 50.7% 50.3% 55.5% 33.9% 55.5% 33.9% 55.5% 55.5% 33.9% 55.5%

HP0775	penta-phosphate guanosine-3Õ-pyrophospho)-
HP0224	hydrolase (spoT) peptide methionine sulphoxide reductase	36.7%
	(msrA)	66.8%
HP1025 HP1572	putative heat shock protein (hspR) regulatory protein DniR	46.2% 31.9%
HP0703 HP1021	response regulator response regulator	44.2% 28.7%
HP1043	response regulator	26.8%
HP1365 HP0166	response regulator response regulator (ompR)	32.4% 51.0%
HP0714	RNA polymerase sigma-54 factor (rpoN)	37.1%
HP0088 HP0792	RNA polymerase sigma-70 factor (rpoD) sigma-54 interacting protein	43.5% 97.7%
HP0164 HP1364	signal-transducing protein, histidine kinase	27.1% 24.9%
HP1364 HP0244	signal-transducing protein, histidine kinase signal-transducing protein, histidine kinase	
HP0048	(atoS) transcriptional regulator (hypF)	30.0% 34.5%
HP1287 HP0727	transcriptional regulator (tenA)	34.7%
	transcriptional regulator, putative	33.3%
REPLICATIO		
Degradation HP0275	ATP-dependent nuclease (addB)	27.2%
HP0259	exonuclease VII, large subunit (xseA)	37.6%
HP0142	ation, restriction, modification, recombination A/G-specific adenine glycosylase (mutY)	38.2%
HP0050	adenine specific DNA methyltransferase (dpnA)	37.4%
HP0910	adenine specific DNA methyltransferase	
HP1352	(HINDIIM) adenine specific DNA methyltransferase	33.4%
HP0263	(HINFIM) adenine specific DNA methyltransferase	62.5%
	(hpaim)	33.9%
HP0481	adenine specific DNA methyltransferase (MFOKI)	29.3%
HP0260	adenine specific DNA methyltransferase	
HP0593	(mod) adenine specific DNA methyltransferase	33.9%
HP1522	(mod)	38.5%
	adenine specific DNA methyltransferase (mod)	42.2%
HP0478	adenine specific DNA methyltransferase (VSPIM)	42.1%
HP0054	adenine/cytosine DNA methyltransferase	32.1%
HP0790 HP1529	anti-codon nuclease masking agent (prrB) chromosomal replication initiator protein	42.9%
HP1121	(dnaA)	34.9%
	cytosine specific DNA methyltransferase (BSP6IM)	37.0%
HP0051	cytosine specific DNA methyltransferase (DDEM)	39.0%
HP0483	cytosine specific DNA methyltransferase	38.7%
HP0701	(HPHIMC) DNA gyrase, sub A (gyrA)	38.7% 97.4%
HP0501 HP1478	DNA gyrase, sub B (gyrB) DNA helicase II (uvrD)	46.0% 35.3%
HP0548	DNA helicase, putative	38.8%
HP0615 HP0621	DNA ligase (lig) DNA mismatch repair protein (MutS)	40.1% 32.6%
HP1470 HP1460	DNA polymerase I (polA)	40.0% 42.0%
HP 1460	DNA polymerase III alpha-subunit (dnaE)	42.0%
HP0500		26.0%
HP0500 HP1231	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit	26.0%
HP1231 HP1387	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB) DNA polymerase III epsilon subunit (dnaQ)	26.0% 48.6% 35.1%
HP1231	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III gamma and tau subun	26.0% 48.6% 35.1% its
HP1231 HP1387 HP0717 HP0012	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG)	26.0% 48.6% 35.1% its 39.0% 36.6%
HP1231 HP1387 HP0717 HP0012 HP1523 HP1393	DNA polymerase III beta-subunit (dnAN) DNA polymerase III delta prime subunit (holB) DNA polymerase III egailon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA recombinase (recG) DNA recomprotein (recN)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3%
HP1231 HP1387 HP0717 HP0012 HP1523	DNA polymerase III beta-subunit (dnAN) DNA polymerase III delta prime subunit (holB) DNA polymerase III genilon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA promase (dnaG) DNA repair protein (recN) DNA topoisomerase I (topA)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1%
HP1231 HP1387 HP0717 HP0012 HP1523 HP1393 HP0116 HP0440 HP0602	DNA polymerase III beta-subunit (dnAN) DNA polymerase III detla prime subunit (holB) DNA polymerase III apailon subunit (dnAO) DNA polymerase III gamma and tau subun (dnAX) DNA primase (dnAG) DNA recombinase (recG) DNA repointinase (recG) DNA topoisomerase I (topA) DNA topoisomerase I (topA)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6%
HP1231 HP0717 HP0012 HP1523 HP1393 HP0116 HP0440 HP0602 HP0585 HP0705	DNA polymerase III beta-subunit (dnAN) DNA polymerase III delta prime subunit (holB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III epsilon subunit (dnaQ) DNA primase (dnaG) DNA recombinase (recG) DNA recombinase (recG) DNA ropoisomerase I (topA) endonuclease III endonuclease III endonuclease III (th) exclusionate ABC subunit A (uvrA)	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 40.1% 53.4%
HP1231 HP0717 HP0717 HP1523 HP1393 HP0116 HP0440 HP0602 HP0585 HP0705 HP1114	DNA polymerase III beta-subunit (dnAN) DNA polymerase III detta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA proimase (dnaG) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) endonuclease III endonuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 40.1% 53.4% 53.4%
HP1231 HP1387 HP0717 HP012 HP1523 HP016 HP0440 HP0602 HP0585 HP114 HP0705 HP114 HP0821 HP1526	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (hoIB) DNA polymerase III apailon subunit (dnAO) DNA polymerase III gamma and tau subun (dnAC) DNA repair protein (recN) DNA repair protein (recN) DNA topoisomerase I (topA) endonuclease III endonuclease III (topA) endonuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrC) excidence ABC subunit B (uvrC) excidence ABC subunit B (uvrC)	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 45.1% 31.7% 53.6% 40.1% 53.4% 53.1% 53.1% 53.1% 53.9%
HP1231 HP1387 HP0717 HP0012 HP1523 HP0116 HP0440 HP0602 HP0585 HP0705 HP1114 HP0821 HP0526 HP0713	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III apailon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) endonuclease III endonuclease III (topA) excinuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease (fexA) glucose inhibited division protein (gidA)	26.0% 48.6% 35.1% its 39.0% 36.6% 22.7% 28.3% 45.1% 31.7% 53.6% 40.1% 53.4% 53.1% 31.5%
HP1231 HP1387 HP0717 HP0012 HP1523 HP0116 HP0440 HP0685 HP0705 HP0705 HP0705 HP0114 HP114 HP1526 HP0213 HP1063 HP1063 HP1553	DNA polymerase III beta-subunit (dnAn) DNA polymerase III deta prime subunit (holB) DNA polymerase III again subunit (dnAO) DNA polymerase III again and tau subun (dnaX) DNA repair protein (recG) DNA repair protein (recN) DNA topoisomerase I (topA) endonuclease III (topA) endonuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit C (uvrC) exoladoxyribonuclease (lexA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA)	26.0% 48.6% 35.1% 18 39.0% 36.6% 32.7% 22.3% 45.1% 31.7% 36.6% 40.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 48.5% 32.9%
HP1231 HP1387 HP0717 HP1012 HP1523 HP0116 HP0400 HP0602 HP0705 HP1114 HP0821 HP0705 HP1114 HP08213 HP1523 HP1553 HP1653 HP1653	DNA polymerase III beta-subunit (dnAn) DNA polymerase III deta prime subunit (holB) DNA polymerase III agains subunit (dnAO) DNA polymerase III gamma and tau subun (dnaX) DNA repair protein (recG) DNA repair protein (recN) DNA topoisomerase I (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease (ruVA) Holiiday junction DNA helicase (ruvA)	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 53.4% 53.1% 53.4% 53.1% 53.9% 48.5% 53.9%
HP1231 HP1387 HP0717 HP0012 HP1523 HP016 HP0602 HP0602 HP0602 HP0602 HP0705 HP1114 HP0826 HP07213 HP1526 HP1525 HP1653 HP1653 HP1653 HP1653 HP10883	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnaX) DNA recombinase (recG) DNA recombinase (recG) DNA repoisonerase I (topA) DNA tropoisonerase I (topA) DNA tropoisonerase I (topA) endonuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (urB) excinuclease (hBC) glucose-inhibited division protein (gldB) helicase Holiday junction DNA helicase (ruvA) Holiday junction endocexyribonuclease	26.0% 48.6% 35.1% 35.1% 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 53.4% 53.4% 53.9% 48.5% 32.9% 33.0% 53.30% 54.6%
HP1231 HP1387 HP0717 HP0717 HP0622 HP1523 HP0186 HP0705 HP0400 HP06821 HP0585 HP0705 HP114 HP06821 HP06821 HP0683 HP0675	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holC) DNA polymerase III gamma and tau subun (dnaX) DNA recombinase (rec0) DNA recombinase (rec0) DNA repoisonerase I (topA) DNA tropoisonerase I (topA) endonuclease III endonuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (urB) excinuclease (hold division protein (gldB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC)	26.0% 48.6% 35.1% 15 39.0% 36.6% 22.7% 28.3% 45.1% 37.7% 36.6% 45.1% 53.4% 53.4% 53.4% 31.7% 36.6% 48.5% 32.9% 33.0% 54.6% 33.0% 54.6% 31.8%
HP1231 HP1387 HP0717 HP0717 HP1523 HP0182 HP0393 HP0116 HP0440 HP0686 HP0706 HP114 HP0686 HP0705 HP1623 HP1653 HP1653 HP1653 HP1653 HP1659 HP0877	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holC) DNA polymerase III gamma and tau subun (dnaX) DNA ropoimerase II (gnA) DNA ropoisomerase I (gnA) DNA topoisomerase I (gnA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (urB) excinuclease ABC subunit B (urB) excinuclease ABC subunit B (urC) glucose-inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC)	26.0% 48.6% 35.1% 35.1% 33.0% 32.7% 28.3% 45.1% 32.7% 53.4% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.4\% 53.4\%
HP1231 HP1387 HP0712 HP1523 HP1393 HP1393 HP239 HP076 HP0685 HP0706 HP0682 HP0706 HP0706 HP1526 HP0706 HP1583 HP1653 HP1653 HP1653 HP1659 HP0877 HP0675 HP0975	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (haX) DNA polymerase III gamma and tau subun (dnaX) DNA repair protein (recG) DNA repair protein (recG) DNA tropoisomerase I (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) excinuclease ABC subunit B (uvrA) excinuclease ABC subunit B (uvrA) excinuclease ABC subunit B (uvrC) excinuclease ABC subunit B (uvrC) excinuclease ABC subunit B (uvrC) excidences inhibited division protein (gidA) glucose-inhibited division protein (gidA) relicase Holliday junction DNA helicase (ruvB) Holliday junction DNA helicase (ruvB) Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) membrane bound endonuclease (nuc)	26.0% 48.6% 35.1% 18 33.0% 32.7% 22.3% 45.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 48.5% 32.9% 53.9% 33.0% 34.7% 31.8%
HP1231 HP1387 HP0717 HP0717 HP1523 HP1393 HP0116 HP0440 HP0440 HP0486 HP0705 HP1121 HP1526 HP0705 HP1526 HP077 HP1526 HP0877 HP0877 HP0875 HP0875 HP0877 HP0756 HP0875 HP0877	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA projemerase II (goA) DNA repair protein (reCN) DNA tropoisomerase I (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) endonuclease III (topA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrC) exodeoxyribonuclease (texA) glucose-inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruxB) Holliday junction DNA helicase (ruxB)	26.0% 48.6% 33.0% 33.0% 33.0% 33.0% 32.7% 28.3% 45.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 48.5% 32.9% 54.6% 34.7% 54.6% 34.7% 54.6% 34.7% 54.6% 34.7% 54.6%
HP1231 HP1387 HP0717 HP0712 HP1523 HP1393 HP0393 HP0393 HP0400 HP0400 HP0400 HP0706 HP0400 HP0706 HP140 HP0628 HP063 HP063 HP0675 HP0675 HP0676	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnAX) DNA projemerase II gamma and tau subun (dnAX) DNA tropiosonerase I (topA) DNA tropiosonerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidA) Holiday junction DNA helicase (ruvA) Holiday junction enddecoxynbouclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (reC) methylate-DNARprotein-cysteine methyltransferse (dat1) primosomal protein replication factor (priA) recombinase (recA)	26.0% 48.6% 35.1% 139.0% 36.6% 32.7% 52.3% 45.1% 53.4% 53.4% 53.1% 53.4% 53.4% 53.1% 53.3% 53.3% 53.3% 53.3% 54.6% 32.9% 33.0% 54.6% 31.9% 54.6% 31.9% 51.5% 54.6% 54.7% 51.9% 51.5% 54.6% 54.7% 55.3%
HP1231 HP1387 HP0717 HP0717 HP1523 HP1523 HP1393 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0877 HP0675 HP0877 HP0875 HP0877 HP0876 HP0383 HP0676 HP0387 HP0678	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnAX) DNA projmase (dnaG) DNA reportinase (recG) DNA repointinase (recG) DNA repointinase (recG) DNA tropiosomerase I (topA) DNA tropiosomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease (III (topA) diucse-inhibited division protein (gidB) helicase helidiasy junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction endodeoxynbonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNARprotein-cysteline methyltransferase (dat1) primosomal protein replication factor (priA) recombinasi (recA) recombinasi DNA repair protein (recR) rep helicase, single-stranded DNA-depende	26.0% 43.6% 43.6% 53.0% 53.0% 53.0% 53.0% 53.0% 53.1% 53.5% 53.1% 53.5% 53.1%
HP1231 HP1387 HP0717 HP0717 HP1523 HP1523 HP1539 HP0716 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0707 HP0683 HP0687 HP0687 HP0687 HP06976 HP0387 HP0768 HP09186 HP09387 HP0768	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnAX) DNA projmerase III gamma and tau subun (dnAX) DNA tropiosonerase I (topA) DNA tropiosonerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) glucose inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction endodeoxynbonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) methyfate-DNARprotein-cysteine methyfuransferse (tat1) primosomal protein replication factor (priA) recombinasional DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep)	26.0% 48.6% 36.1% 10 33.0% 33.0% 32.7% 22.3% 45.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 34.7% 31.5% 54.6% 34.7% 31.1%
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HP1231 HP1387 HP0717 HP0717 HP1012 HP1823 HP1393 HP1393 HP016 HP016 HP016 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0706 HP0707 HP0827 HP0823 HP0877 HP0823 HP0877 HP0823 HP0926 HP0323 HP0926 HP0326 HP0321 HP0326 HP0327 HP0326 HP0327 HP0326 HP0327 HP0326 HP0326 HP0327 HP0326 HP0327 HP0326 HP0327 HP0326 HP0327 HP037 HP	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnAX) DNA projemerase III gamma and tau subun (dnAX) DNA tropoisomerase I (topA) DNA tropoisomerase I (topA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit B (uvrB) exclunclease ABC subunit C (uvrC) excluces inhibited division protein (gidB) helicase heliday (unction DNA helicase (truA) Holiday (unction DNA helicase (truA) Holiday (unction DNA helicase (truA) Holiday (unction DNA helicase (truA) Holiday (unction endodecwythonuclease (truC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteline methyltransferse (dat1) primosomal protein replication factor (priA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende AIPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribbonuclease I (mA)	26.0% 43.6% 43.6% 43.6% 15 39.0% 36.6% 32.7% 45.1% 32.7% 46.1% 53.4% 53.1% 53.1% 53.1% 53.1% 53.4% 53.1% 53.4% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.5% 11.0% 53.6% 11 53.8% 53.4% 53.1%
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HP1231 HP1387 HP0717 HP0717 HP1717 HP1523 HP0145 HP0440 HP0685 HP0705 HP0705 HP0705 HP0705 HP114 HP0685 HP0705 HP1683 HP1683 HP1683 HP1687 HP0695 HP0697 HP0697 HP0687 HP0687 HP0387 HP0	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnaX) DNA repombinase (rec0) DNA repositionase (topA) DNA topolisomerase I (topA) DNA topolisomerase I (topA) DNA topolisomerase I (topA) endonuclease III (nh) excinuclease III (nh) excinuclease ABC subunit B (urR) excinuclease (ABC subunit B (urR) excinuclease (IntA) glucose-inhibited division protein (gidB) helicase (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteine methyltranterse (rec1) recombinase (rec3) replicative DNA helicase (nuc) methylated-DNAsperise (sonuclease (nuc) replicative DNA helicase (anB) restriction modification system S subunit ribonuclease H (mNA) ribonuclease H (mNA) ribonuclease H (mNA) ribonuclease H (mNA) ribonuclease H (mNA) ribonuclease H (mNA) ribonuclease III (nhB) single-strandeDNA-sing protein (ssb) single-strandeDNA-sing protein (scb) single-strandeDNA-sing protein (scb) single-strandeDNA-sing protein (scb) single-strandeDNA-single factor (torC) type I restriction enzyme S protein (nsCR)	26.0% 48.6% 39.0% 36.6% 10 39.0% 36.6% 32.7% 32.7% 32.2% 45.1% 32.2% 45.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.6% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 33.3% 33.0% 33.3% 33.4% 53.4% 33.4% 53.4% 33.4% 53.4% 33.6% 33.6% 33.6%
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HP1231 HP1387 HP0717 HP0717 HP1923 HP1393 HP1393 HP1393 HP0622 HP0626 HP0705 HP0705 HP0705 HP0705 HP0877 HP0675 HP0877 HP0675 HP0877 HP0675 HP09911 HP1362 HP09911 HP1362 HP09911 HP1362 HP09911 HP1362 HP0937 HP0676 HP0937 HP0675 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP0937 HP0676 HP067	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnaX) DNA ropombinase (racG) DNA repair portein (recN) DNA ropoisomerase I (topA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) endonuclease III (nh) excinuclease III (nh) excinuclease ABC subunit B (urR) excinuclease ABC subunit B (urR) excinuclease ABC subunit B (urR) excinuclease ABC subunit B (urR) excinuclease ABC subunit B (urR) glucose-inhibited division protein (gidB) felicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction ANA helicase (ruvB) Holiday junction ANA helicase (ruvB) Holiday junction ANA helicase (ruvB) Holidad Jonda (DNA helicase (ruvB) Holidad JONA helicase (ruvB) Holidad Jonda (DNA helicase (ruvB) Holidad Jonda (DNA helicase (ruvB) Holidad JONA helicase (ruvB) Holi	26.0% 48.6% 39.0% 36.6% 10 39.0% 36.6% 32.7% 32.7% 32.7% 32.7% 32.7% 53.4% 53.4% 53.4% 53.4% 53.4% 53.6% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 33.0% 33.3% 33.0% 33.3% 33.3% 33.4% 33.4% 33.4% 33.4% 33.4% 33.6% 33.6% 33.6% 33.6%
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HP1231 HP1387 HP0717 HP0717 HP19837 HP0112 HP1983 HP018 HP0823 HP0602 HP0705 HP0705 HP0705 HP0705 HP0877 HP0633 HP0633 HP0633 HP0633 HP0633 HP0877 HP0755 HP09911 HP1053 HP0675 HP09911 HP1053 HP0661 HP19243 HP0661 HP1245 HP0948 HP07484 HP07462 HP07484 HP074664 HP074664 HP074664 HP074664 HP074664 HP074664 HP074664 HP074664 HP074664 HP	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA projmase (dnAG) DNA recombinase (recG) DNA repair protein (recN) DNA tropoisomerase I (topA) DNA tropoisomerase I (topA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit B (uvrB) exclunclease ABC subunit D (uvrC) exodeoxyribonuclease (terA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) heliciase Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated DNAAPinclein-cysteine methyltrasifect (chA) protein terB) single-stranded DNA-specific exonuclease (recD) site-specific recombinase (terA) resorbination DNA helicase (dnB) restriction modification system S subunit ribonuclease HI (mhB) single-stranded-DNA-specific exonuclease (recD) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme R protein (fisAB) type I restriction enzyme R protein (fisAB)	26.0% 43.6% 43.6% 53.1% 15 39.0% 36.6% 32.7% 45.1% 53.9% 45.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.3% 53.2%% 53.3% 53
HP1231 HP1387 HP0717 HP0717 HP171387 HP0718 HP1393 HP0116 HP0440 HP0685 HP0705	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III deta prime subunit (holA) DNA polymerase III gamma and tau subun (dnAX) DNA recombinase (recG) DNA recombinase (recG) DNA repointinase (recG) excludease ABC subunit B (urR) excludease ABC subunit B (urR) excludease ABC subunit B (urR) glucose-inhibited division protein (gldB) helicase (ruxG) Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction DNA helicase (ruvB) Holliday junction DNA helicase (ruvB) Holliday junction DNA helicase (ruvC) methylated-DNANprotein-cysteline methyltransferse (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) resortibinational DNA repair protein (recR) rep helicase (fmAB) restriction modification system S subunit ribonuclease H (mhA) single strand DNA-binding protein (ssB) single strand CDNA-binding protein (ssB) ype I restriction enzyme K protein (hsdM) ype I restriction enzyme K protein (hsdM)	26.0% 48.6% 43.6% 43.6% 43.0% 36.6% 32.7% 45.1% 33.6% 22.3% 40.1% 53.4% 53.4% 53.4% 53.4% 53.6% 41.0% 53.4% 54.6% 33.0% 54.6% 34.7% 33.8% 33.9% 54.6% 33.9% 53.9% 54.6% 33.9% 53.9% 54.6% 33.9% 53.9% 54.6% 33.9% 54.7% 55.3%
HP1231 HP1387 HP0717 HP0717 HP1717 HP1717 HP012 HP1393 HP0116 HP0440 HP0685 HP0705 HP0705 HP0705 HP114 HP0821 HP1526 HP0705 HP07	DNA polymerase III beta-subunit (dnAn) DNA polymerase III deta prime subunit (noIB) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA propionerase II (topA) DNA tropoisomerase I (topA) ducces inhibited division protein (gidA) glucose inhibited division protein (gidB) Holliday junction DNA helicase (truA) Holliday junction endodeoxynbonuclease (truC) Integrase/recombinase (xerC) Integrase/recombinase (xerC) Integrase/recombina	26.0% 43.6% 43.6% 43.6% 53.0% 53.0% 53.9% 53.9% 53.9% 53.4% 53.1% 53.4% 53.4% 53.1% 53.4% 53.0% 53.0% 54.6% 33.0% 54.6% 33.0% 54.6% 33.0% 54.5% 54.5% 53.4% 53.0% 54.5% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.7% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.7% 53.7% 53.0% 53.6% 53.7% 53.7% 53.6% 53.7% 53.7% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.6% 53.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.7% 53.6% 53.7%
HP1231 HP1387 HP0717 HP0717 HP171387 HP0717 HP17139 HP0112 HP1723 HP0116 HP0440 HP0685 HP0705 HP0705 HP0705 HP114 HP0821 HP1526 HP0705	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III aprime subunit (holA) DNA polymerase III aprime subunit (hax) DNA projemerase II (aprime) DNA recombinase (rec0) DNA recombinase (rec0) excludease ABC subunit A (uvrA) excludease ABC subunit B (urB) excludease ABC subunit C (uvC) glucose-inhibited division protein (gdB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction DNA helicase (ruvB) Holiday junction DNA helicase (ruvC) methylate-DNANprotein-cysteline methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) resorbinational DNA repair protein (recR) rep helicase (dnaB) restriction modification system S subunit ribonuclease HII (rhB) single-stranded-DNA-specific exonuclease (rec) ype I restriction enzyme K protein (hsdM) ype I restriction enzyme M protein (hsdM)	26.0% 48.6% 43.6% 43.1% 53.0% 53.9% 53.9% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 54.6% 34.7% 54.6% 34.7% 54.6% 34.7% 54.6% 35.9% 54.6% 33.9% 54.6% 33.9% 54.6% 33.9% 54.6% 33.9% 54.6% 53.9% 54.6% 53.9% 54.6% 55.3% 54.4% 55.3% 54.4% 55.3% 54.4% 55.3%
HP1231 HP1387 HP0717 HP0717 HP1717 HP1717 HP1723 HP1393 HP0116 HP0420 HP0420 HP0420 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077 HP077 HP077 HP077 HP077 HP077 HP075 HP0877 HP075 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP0877 HP075 HP08777 HP08777 HP08777 HP07777 HP07777 HP07777 HP0777777 HP07777777777	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnAX) DNA polymerase III gamma and tau subun (dnAX) DNA projmerase III gamma and tau subun (dnAX) DNA projmase (taG) DNA recombinase (taG) DNA tropoisomerase I (topA) DNA tropoisomerase I (topA) DNA topoisomerase I (topA) exclunclease ABC subunit A (uvrA) exclunclease ABC subunit B (uvrB) exclunclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) Holiiday junction DNA helicase (truA) Holiiday junction DNA helicase (truA) Holiiday junction DNA helicase (truA) Holiiday junction Endodeoxyribonuclease (truC) Integrase/recombinase (xerC) Integrase/recombinase (xerC) Integrase/recombinase (terC)) methylated DNA/protein-cysteine methyltransferase (datI) primosomal protein replication factor (prIA) recombinase (terA) recombinase (terA) resortion modification system S subunit ribonuclease HI (thAB) single-strandeDNA-specific exonuclease (reC) site-specific recombinase (treA) restriction enzyme K protein (tsAB) type I restriction enzyme K protein (tsAB) t	26.0% 43.6% 43.6% 43.6% 53.1% is 33.0% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.3% 53.1% 53.3% 53.
HP1231 HP1387 HP0717 HP0717 HP1717 HP1717 HP1723 HP1393 HP0116 HP1723 HP0162 HP0705 HP0705 HP1121 HP1723 HP1723 HP1723 HP1723 HP1723 HP1723 HP1723 HP1723 HP0777 HP077 HP0777 HP0777 HP0777 HP0777 HP0777 HP0777 HP0777 HP07777 HP07777 HP0777 HP0777	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnAX) DNA polymerase III gamma and tau subun (dnAX) DNA polymerase III gamma and tau subun (dnAX) DNA proteinase (teG) DNA repair potein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) exclinuclease ABC subunit B (uvrB) exclinuclease ABC subunit B (uvrB) exclinuclease ABC subunit B (uvrB) exclinuclease ABC subunit G (uvrC) exotdexyribonuclease (teVA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) heliciase Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction endodecxyribonuclease (truC) rintegrase/recombinase (xerC) methylated DNA/bindein-ostein methylates/DNA/grotein-ostein endtylatasferase (dat1) primosomal protein replication factor (priA) recombinase (teCA) recombinase (teCA) recombinase (teCA) resolitation a DNA-binding protein (tsD) single-strand-DNA-specific exonuclease (teC) site-specific recombinase (trasscription-repair coupling factor (trCF) type I restriction enzyme K protein (tsdS) type I restriction enzyme K protei	26.0% 48.6% 43.6% 53.0% 53.0% 53.0% 53.0% 53.9% 53.7% 53.4% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.4% 53.1% 53.3% 53.0% 54.5% 53.0% 54.5% 53.0% 54.5% 53.0% 53.2% 53.0% 53.2% 53.2% 53.2% 53.2% 53.2% 53.2% 53.2% 53.2% 53.3%
HP1231 HP1387 HP0717 HP0717 HP171387 HP0718 HP17182 HP0718 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP1714 HP0821 HP1728 HP1728 HP1728 HP1728 HP1728 HP0787	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (holB) DNA polymerase III agamma and tau subun (harX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA projemerase II (topA) DNA tropoisonerase I (topA) DNA tropoisonerase I (topA) endonuclease III (th) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (urB) excinuclease (ABC subunit B (urB) helicase (incon DNA helicase (nuA) Holliday junction DNA helicase (nuC) methylated-DNANprotein-cysteline methyltransferse (dat1) primosomal protein replication factor (prIA) recombinase (recA) recombinase (recA) recombinase (recA) restriction enzyme K protein (fsdK) type I restriction enzyme K protein (fsdK)	26.0% 48.6% 43.6% 43.1% 53.0% 53.4% 53.0% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 34.7% 54.6% 34.7% 54.6% 34.7% 54.6% 33.4% 53.3% 33.4% 53.3% 33.4% 53.3% 53.4% 55.3% 51.7% 55.3%
HP1231 HP1337 HP0717 HP0717 HP17393 HP0118 HP1393 HP0116 HP0420 HP0686 HP0706 HP114 HP0687 HP1523 HP1621 HP1526 HP0705 HP1523 HP1627 HP0683 HP1624 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III agamma and tau subun (harX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III (agamma and tau subun (dnAX) DNA tropiosomerase I (topA) DNA tropiosomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) glucose inhibited division protein (gidB) helicase Holiiday junction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvB) Holiiday junction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvA) Holiiday junction Ava helicase (ruvA) Holiiday junction DNA helicase (ruvA) Holiiday junction DNA helicase (ruvB) Holiiday junction Ava helicase (ruvC) methylate-DNANprotein-cysteine methyltransferse (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) restriction enzyme K protein (hsdK) ype I restriction enzyme K protein (hsdK) ype II restricti	26.0% 48.6% 43.6% 43.1% 53.0% 53.4% 53.0% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 34.7% 54.6% 34.7% 54.6% 34.7% 54.6% 33.4% 53.3% 33.4% 53.3% 33.4% 53.3% 53.4% 55.3% 51.7% 55.3%
HP1231 HP1337 HP0717 HP0717 HP17393 HP0118 HP1393 HP0116 HP0440 HP0686 HP0706 HP114 HP0687 HP1523 HP1621 HP1526 HP0705 HP1523 HP1627 HP0687 HP	DNA polymerase III beta-subunit (dnAh) DNA polymerase III deta prime subunit (holB) DNA polymerase III agamma and tau subun (harX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III agamma and tau subun (dnAX) DNA polymerase III (agamma and tau subun (dnAX) DNA tropiosonerase I (topA) DNA tropiosonerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) glucose inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) helicase (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylate-DNAApprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) resorbinational DNA-repair protein (recR) rep helicase, (dnaB) restriction enzyme K protein (hsdB) yea I restriction enzyme K protein (hsdB) yea II restriction enzyme K prote	26.0% 48.6% 43.6% 53.0% 53.0% 53.0% 53.0% 53.0% 53.0% 54.6% 54.6% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 55.3% 52.2% 53.0% 55.3%
HP1231 HP1337 HP0717 HP0717 HP17393 HP0118 HP1393 HP0116 HP0420 HP0686 HP0706 HP114 HP0687 HP1523 HP1621 HP1526 HP0705 HP1523 HP1627 HP0683 HP1624 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP0687 HP0768 HP	DNA polymerase III beta-subunit (dnAN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnAX) DNA polymerase III gamma and tau subun (dnAX) DNA polymerase III gamma and tau subun (dnAX) DNA proteinase (teG) DNA repair potein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) exclinuclease ABC subunit A (uvrA) exclinuclease ABC subunit B (uvrB) exclinuclease ABC subunit G (uvrC) exotdexyribonuclease (teVA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) reliciase Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) Holliday junction endodecxyribonuclease (truC) methylate/DNA/gprotein-cystein methylate/DNA/gprotein-cystein methylate/DNA/gprotein-cystein primosomal protein replication factor (priA) recombinase (teCA) recombinase (teCA) recombinase (teCA) recombinase (teCA) resolution modification system S subunit ribonuclease H (mNA) ribonuclease H (mNA) single-strande/DNA-specific exonuclease (teC) site-specific recombinase transcription-repair coupling factor (trCF) type I restriction enzyme K protein (tsdS) type II restricti	26.0% 48.6% 43.6% 53.0% 53.0% 53.0% 53.0% 53.0% 53.0% 54.6% 54.6% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 54.6% 53.0% 55.3% 52.2% 53.0% 55.3%

HP1471	type IIS restriction enzyme R protein (BCGIB)	28.2%		
HP1366	type IIS restriction enzyme R protein	37.1%		
HP1208	ulcer associated adenine specific DNA	93.4%		
HP1209	ulcer-associated gene restriction endonucle	ase		
HP1347	(iceA) uracil-DNA glycosylase (ung)	95.5% 43.1%		
TRANSCRIPTION				
Degradatior HP1213		38.9%		
	DNA-dependent RNA polymerase			
HP1293	DNA-directed RNA polymerase, alpha subu (rpoA)	35.3%		
HP1198	DNA-directed RNA polymerase, beta subun (rpoB)	it 47.8%		
Transcriptio HP0866	n factors transcription elongation factor GreA (greA)	50 3%		
HP1514	transcription termination factor NusA			
HP0001	transcription termination factor NusB (nusB)	39.1% 30.2%		
HP1203	transcription termination factor NusG (nusG)	41.0%		
HP0550	transcription termination factor Rho (rho)	56.6%		
RNA proces HP0640	sing poly(A) polymerase (papS)	37.4%		
HP0662	ribonuclease III (rnc)	37.3%		
TRANSLATI	DN			
<i>General</i> HP0944	translation initiation inhibitor, putative	45.6%		
Aminoacyl t	RNA synthetases			
HP0319	arginyl-tRNA synthetase (argS)	44.9% 35.8%		
HP0617 HP0886		50.1% 97.3%		
HP0476 HP0643	glutamyl-tRNA synthetase (gltX)	43.1% 39.8%		
HP0960	glycyl-tRNA synthetase, alpha subunit			
HP0972	glycyl-tRNA synthetase, beta subunit (glyS)	60.1% 33.6%		
HP1190 HP1422	histidyl-tRNA synthetase (hisS) isoleucyl-tRNA synthetase (ileS)	32.4% 49.7%		
HP1547 HP0182		45.9% 58.6%		
HP0417 HP0403	methionyl-tRNA synthetase (metS)	42.4%		
		48.7%		
HP0402		30.0%		
HP0238 HP1480		39.8% 48.3%		
HP0123	threonyl-tRNA synthetase (thrS)	42.1% 52.6%		
	tyrosyl-tRNA synthetase (tyrS)	54.7% 43.7%		
	of proteins, peptides and glycopeptides			
HP0570	aminopeptidase a/i (pepA)	38.5% 40.3%		
HP0794	ATP-dependent clp protease proteolytic	64.6%		
HP1379	ATP-dependent protease (Ion)	43.9%		
HP0223 HP1374	ATP-dependent protease ATPase subunit	41.0%		
HP0264	ATP-dependent protease binding subunit	56.3%		
HP0169	(clpB)	97.7% 40.1%		
HP0516 HP0515	heat-shock protein (hslU) ORF1	98.4% 57.1%		
HP0470	oligoendopeptidase F (pepF)	97.9% 24.2%		
HP0657 HP1485	processing protease (ymxG) proline dipeptidase (pepQ)			
HP1350		35.2%		
HP1012	protease protease (pggE)	35.2% 40.6% 29.6%		
HP1435	protease protease (pqqE) protease IV (PspA)	35.2% 40.6% 29.6% 41.7%		
HP1435 HP0404 HP1019	protease protease (pqqE) protease IV (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htrA)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9%		
HP1435 HP0404 HP1019 HP1584 HP0382	protease protease (paqE) protease IV (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YR117W)	35.2% 40.6% 29.6% 41.7% 40.2%		
HP1435 HP0404 HP1019 HP1584 HP0382 Nucleoprote	protease protease (paqE) protease IV (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YR117W)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2%		
HP1435 HP0404 HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein mod	protease protease (pqcE) protease (V (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htrA) sialoglycoprotease (gcp) zinc-metalloprotease (YJR117W) sins histone-like DNA-binding protein HU (hup) <i>filifaction</i>	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6%		
HP1435 HP0404 HP1019 HP1584 HP0382 <i>Nucleoprote</i> HP0835 <i>Protein mod</i> HP0363	protease protease (pqcE) protease (V (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htA) sialoglycoprotease (gcp) zinc-metalloprotease (Y/R117W) <i>ins</i> histon-elike DNA-binding protein HU (hup) <i>lification</i> L-isoaspartyl-protein carboxyl methyltransfe (pcm)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% rase 43.0%		
HP1435 HP0404 HP1019 HP1584 HP0382 <i>Nucleoprote</i> HP0835 <i>Protein moc</i> HP0363 HP1299	protease (pqqE) protease (pqqE) protease (V (PspA) protein kinase C inhibitor (SP:P16436) serine protease (htrA) sialoglycoprotease (pqP117W) zinc-mtetalloprotease (YP117W) ins histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidyl-protyl <i>cis-trans</i> isomerse B,	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% rase 43.0% 43.0%		
HP1435 HP0404 HP1019 HP1584 HP0382 <i>Nucleoprote</i> HP0835 <i>Protein moc</i> HP0363 HP1299	protease protease (pqcE) protease (V (PspA) protease IV (PspA) protein kinase C inhibitor (SP:P16436) serine protease (N174) sialoglycoprotease (pp) zinc-metalloprotease (Y/R17W) ins histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cis-trans isomerase, FKBP-typ	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% ase 43.0% 43.0% 58.1% pe		
HP1435 HP0404 HP1019 HP1584 HP0382 Nucleoprote HP0835 Protein moc HP0363 HP1299 HP1299	protease (paqE) protease (paqE) protease (V (PspA) protein kinase (inhibitor (SP:P16436) protein kinase (inhibitor (SP:P16436) serine protease (triA) sialogivcoprotease (qcp) zinc-metalloprotease (qcp) ins histone-like DNA-binding protein HU (hup) <i>ification</i> Lisoaspartyl-protein carboxyl methyltransfet (pcm) methionine amino peptidase (map) peptidyl-prolyl <i>cis-trans</i> isomerase B, cyclosporin-type rotamase (ppi) peptidyl-prolyl <i>cis-trans</i> isomerase, FKBP-tyr rotamase (styD)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% 43.0% 43.0% 58.1%		
HP1435 HP0404 HP1019 HP1584 HP0382 Nucleoprote HP0355 Protein moc HP0363 HP1299 HP1441 HP1123 HP0793 <i>Ribosomal J</i>	protease protease (pqcE) protease (V (PspA) protease (V (PspA) protein kinase C inhibitor (SP:P16436) protein kinase C inhibitor (SP:P16436) serine protease (trtA) silody-coprotease (gcp) zinc-metalloprotease (YJR117W) <i>ins</i> histone-like DNA-binding protein HU (hup) <i>lification</i> Lisoasparty-tp-rotein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidy-protyl <i>cis-trans</i> isomerase, B, cyclosporin-type rotamase (bpi) peptidy-protyl <i>cis-trans</i> isomerase, FKBP-typ rotamase (styD) polypeptide deformylase (def) <i>proteins: synthesis and modification</i>	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% 7ase 43.0% 43.0% 58.1% be 40.4% 41.8%		
HP1435 HP0404 HP0404 HP0382 HP0382 Protein moc HP0385 Protein moc HP0383 HP1299 HP1441 HP1123 HP0793 <i>Ribosomal µ</i> HP1201 HP1201	protease protease (pqcE) protease (V (PspA) protease (V (PspA) protein kinase C inhibitor (SP:P16436) serine protease (NtA) sinos protein kaloprotease (Y/R117W) ins histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cis-trans isomerase F, FKBP-tyr rotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (rpt1) ribosomal protein L10 (rpt10)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% rase 43.0% 43.0% 58.1% pe 40.4% 40.4% 41.8% 52.0% 30.4%		
HP1435 HP0404 HP0404 HP0404 HP0382 Nucleoprote HP0835 Protein moc HP0835 HP1299 HP1441 HP123 HP0793 <i>Ribosomal (</i> HP1200 HP1200 HP1200 HP1202 HP1202	protease (paqE) protease (paqE) protease (V (PspA) protease (V (PspA) protein kinase C inhibitor (SP:P16436) serine protease (NrA) sins metalloprotease (Y/R117W) ins histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporn-type rotamase (ppi) peptidyl-protyl cis-trans isomerase B, cyclosporn-type rotamase (ppi) peptidyl-protyl cis-trans isomerase, FKBP-typ rotamase (slyD) proteins: synthesis and modification ribosomal protein L11 (prl11) ribosomal protein L11 (prl10)	35.2% 40.6% 40.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% rase 43.0% 43.0% 58.1% re 40.4% 41.8% 52.0%		
HP1435 HP0404 HP1019 HP1584 HP0382 <i>Nucleoprote</i> HP0385 <i>Protein</i> m002 HP1299 HP1441 HP1123 HP0793 <i>Ribosomal</i> HP1200 HP1200 HP1202 HP1208	protease (paqE) protease (paqE) protease (V (PspA) protease (V (PspA) protein kinase (Inibitor (SP:P16436) serine protease (Inibitor (SP:P16436) sindoy/coprotease (qcp) zinc-metalloprotease (Qcp) zinc-metalloprotease (Qcp) sindoy histone-like DNA-binding protein HU (hup) histone-like DNA-binding protein KU (pcm) methionine amino peptidase (map) peptidy-prolyl <i>cis-trans</i> isomerase B, cyclosporin-type rotamase (qc)) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (pt11) ribosomal protein L1 (pt11) ribosomal protein L11 methyltransferase (prmA)	35.2% 40.6% 29.6% 41.7% 40.2% 52.9% 35.7% 36.2% 44.6% rase 43.0% 43.0% 58.1% pe 40.4% 40.4% 41.8% 52.0% 30.4%		
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HP0399	ribosomal protein S1 (rps1)	30.5%
HP1320	ribosomal protein S10 (rps10)	58.2%
LID1107	ribosomal protein S11 (rps11) ribosomal protein S12 (rps12)	56.2% 79.0%
HP1296	ribosomal protein S12 (rps12) ribosomal protein S13 (rps13) ribosomal protein S14 (rpS14)	55.8% 68.3%
HP1040	ribosomal protein S15 (rps15)	57.8%
	ribosomal protein S16 (rpS16) ribosomal protein S17 (rps17)	46.8% 55.4%
HP1244	ribosomal protein S18 (rps18)	55.2%
HP1315 HP1554	ribosomal protein S19 (rps19) ribosomal protein S2 (rps2)	61.1% 49.6%
HP0076	ribosomal protein S20 (rps20)	41.4%
HP1313	ribosomal protein S3 (rps3)	42.4% 56.7%
HP1294 HP1302	ribosomal protein S4 (rps4) ribosomal protein S5 (rps5)	51.2% 65.5%
HP1246	ribosomal protein S6 (rps6)	32.1%
	ribosomal protein S7 (rps7) ribosomal protein S8 (rps8)	62.2% 45.0%
HP0083	ribosomal protein S9 (rps9)	50.4%
tRNA modifi		26.3%
HP1141	methionyl-tRNA formyltransferase (fmt)	37.5%
	peptidyl-tRNA hydrolase (pth) pseudouridylate synthase I (hisT)	46.6% 32.2%
	ribonuclease P, protein component (rnpA) S-adenosylmethionine:tRNA	29.3%
	ribosyltransferase-isomerase (queA)	39.3%
HP1513 HP1148	selenocystein synthase (selA) tRNA (guanine-N1)-methyltransferase (trmD)	36.2% 39.1%
HP1415	tRNA delta(2)-isopentenylpyrophosphate	
HP0281	transferase (miaA) tRNA-guanine transglycosylase (tgt)	30.7% 45.6%
Translation	factors	
HP0247	ATP-dependent RNA helicase, DEAD-box family (deaD)	37.7%
HP0077	nentide chain release factor RE-1 (nrfA)	52.6%
HF 1200	ribosome releasing factor (frr)	49.6% 43.7%
	translation elongation factor EF-G (fusA) translation elongation factor EF-P (efp)	67.5% 45.1%
HP1555	translation elongation factor EF-Ts (tsf)	43.1%
LD1200		89.5% 65.3%
HP1048	translation initiation factor IF-2 (infB)	45.4%
HP0124	translation initiation factor IF-3 (infC)	43.4%
	T AND BINDING PROTEINS	
General HP0179	ABC transporter, ATP-binding protein	66.7%
HP0613 HP0715	ABC transporter, ATP-binding protein ABC transporter, ATP-binding protein	31.1% 52.3%
HP1576	ABC transporter, ATP-binding protein (abc)	48.2%
HP1465	ABC transporter, ATP-binding protein (HI1087)	37.8%
HP1220	ABC transporter, ATP-binding protein (yhcG) ABC transporter, ATP-binding protein (yhcG)	
HP0853 HP1577	ABC transporter, AIP-binding protein (ynes) ABC transporter, permease protein (yaeE)	43.1%
	acriflavine resistance protein (acrB) histidine and glutamine-rich protein	29.7% 50.0%
HP 1432 HP 1427	histidine-rich, metal binding polypeptide	
HP1206	(hpn) multidrug-resistance protein (hetA)	100.0% 26.2%
HP1082	multidrug-resistance protein (msbA)	32.4%
HP0600 HP1181	multidrug-resistance protein (spaB) multidrug-efflux transporter	29.7% 29.1%
HP0497 HP0498	sodium- and chloride-dependent transporter	r31.7%
	sodium- and chloride-dependent trans- porter	30.8%
HP0214	sodium-dependent transporter (huNaDC-1)	36.6%
	s, peptides and amines amino acid ABC transporter, periplasmic	
HP0939	binding protein (yckK) amino acid ABC transporter, permease	41.5%
	protein (yckJ)	46.9%
HP1017 HP0942	amino acid permease (rocE) D-alanine glycine permease (dagA)	41.7% 44.5%
HP0301	dipeptide ABC transporter, ATP-binding protein (dppD)	59.5%
HP0302	dipeptide ABC transporter, ATP-binding	
HP0298	protein (dppF) dipeptide ABC transporter, periplasmic	54.8%
	dipeptide-binding protein (dppA)	39.8%
HP0299	dipeptide ABC transporter, permease protein (dppB)	49.3%
HP0300	dipeptide ABC transporter, permease protei (dppC)	n 52.5%
HP1506	glutamate permease (gltS)	56.9%
HP1171	glutamine ABC transporter, ATP-binding protein (glnQ)	51.9%
HP1172	glutamine ABC transporter, periplasmic	
HP1169	glutamine-binding protein (glnH) glutamine ABC transporter, permease	32.2%
HP1170	protein (glnP) glutamine ABC transporter, permease protei	27.6% in
	(gInP)	30.9%
HP0250	oligopeptide ABC transporter, ATP-binding protein (oppD)	39.1%
HP1252	oligopeptide ABC transporter, periplasmic	28.7%
HP1251	oligopeptide-binding protein (oppA) oligopeptide ABC transporter, permease	
HP0251	protein (oppB) oligopeptide ABC transporter,	59.6%
	permease protein (oppC)	31.4%
HP0819 HP0818	osmoprotection protein (proV) osmoprotection protein (proWX)	38.3% 30.4%
HP0055 HP0936	proline permease (putP) proline/betaine transporter (proP)	51.4% 29.1%
HP0936 HP0133	serine transporter (sdaC)	44.6%
Anions HP0475	molybdenum ABC transporter, ATP-binding	
	protein (modD)	38.4%
HP0473	molybdenum ABC transporter, periplasmic molybdate-binding protein (modA)	95.9%
HP0474	molybdenum ABC transporter, permease	
HP0313	protein (modB) nitrite extrusion protein (narK)	28.7% 23.6%
HP1491	phosphate permease	34.8%
HP0143	tes, organic alcohols and acids 2-oxoglutarate/malate translocator (SODiT1)	
HP1091	alpha-ketoglutarate permease (kgtP) anaerobic C4-dicarboxylate transport	45.9%
	protein (dcuA)	53.8%
HP1174 HP0141	glucose/galactose transporter (gluP) L-lactate permease (lctP)	53.6% 55.5%
HP0140	L-lactate permease (IctP)	58.7%

Cationa		
Cations HP0791	cadmium-transporting ATPase, P-type	97.5%
HP0969	(cadA) cation efflux system protein (czcA)	37.3% 28.9%
HP1328 HP1329	cation efflux system protein (czcA) cation efflux system protein (czcA)	31.3%
HP1503 HP1073	cation-transporting ATPase, P-type (copA) copper ion binding protein (copP)	30.3% 92.4%
HP1072 HP0471	copper-transporting ATPase, P-type (copA) glutathione-regulated potassium-efflux syste	m
HP0687	protein (kefB) iron(II) transport protein (feoB)	99.3% 33.6%
HP1561	iron(III) ABC transporter, periplasmic iron- binding protein (ceuE)	27.5%
HP1562	iron(III) ABC transporter, periplasmic iron- binding protein (ceuE)	28.2%
	iron(III) dicitrate ABC transporter, ATP-bindir protein (fecE)	34.4%
HP0889	iron(III) dicitrate ABC transporter, permease protein (fecD)	38.3%
HP0686 HP0807	iron(III) dicitrate transport protein (fecA) iron(III) dicitrate transport protein (fecA)	29.7% 28.5%
HP1400 HP1344	iron(III) dicitrate transport protein (fecA) magnesium and cobalt transport protein	26.3%
HP 1183	(corA) NA+/H+ antiporter (napA)	26.3% 26.6%
HP1552 HP1077	Na+/H+ antiporter (nhaA) nickel transport protein (nixA)	49.2% 98.7%
HP0490	putative potassium channel protein, putative	25.7%
<i>Nucleosides</i> HP1290	s, purines and pyrimidines nicotinamide mononucleotide transporter	
HP1180	(pnuC) pyrimidine nucleoside transport protein	28.0%
Other	(nupC)	32.9%
HP0876	iron-regulated outer membrane protein (frpB)	27.6%
HP0915	iron-regulated outer membrane protein (frpB)	28.1%
HP0916	(rpp) iron-regulated outer membrane protein (frpB)	28.8%
HP1129 HP1130	biopolymer transport protein (exbD) biopolymer transport protein (exbB)	29.7% 33.5%
HP1339 HP1340	biopolymer transport protein (exbB) biopolymer transport protein (exbD)	46.8% 35.8%
HP1445 HP1446	biopolymer transport protein (exbB) biopolymer transport protein (exbD)	45.5% 36.2%
HP1512	iron-regulated outer membrane protein (frpB)	26.6%
HP0653 HP1341		99.4%
	(tonB)	37.2%
OTHER CAT	EGORIES	
<i>General</i> HP0924 HP1034	4-oxalocrotonate tautomerase (dmpl)	37.7%
HP1000 HP1139	ATP-binding protein (ylxH) PARA protein	36.3% 29.7% 47.4%
HP0827	SpoOJ regulator (soj) ss-DNA binding protein 12RNP2 precursor	
Adaptations	and atypical conditions	
HP1496	general stress protein (ctc)	26.5%
HP1483 HP0927	gerC2 protein (gerC2) heat shock protein (htpX)	33.3% 32.8%
HP1483 HP0927 HP0280 HP1228	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA)	33.3%
HP1483 HP0927 HP0280 HP1228 HP0970	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB)	33.3% 32.8% 27.2% 38.2% 21.1%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0930	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967	gerC2 protein (gerC2) heat shock protein (hpX) heat shock protein (hpX) invasion protein (nrA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein (vapD)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (bpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 Colicin-relati	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) invasion protein (invA) invasion protein (invA) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein bomolog (vacB) virulence factor mviN protein (mviN) <i>et functions</i>	33.3% 32.8% 27.2% 38.2% 21.1% 37.7% 28.9% 36.0% 33.5%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP09305 HP0315 HP0967 HP1248 HP0885	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) invasion protein (htpA) nickel-cobalt-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein b (vapD) virulence associated protein b (vapD) virulence associated protein (mviN) ed functions collicin tolerance-like protein (tolB) phage/collicin/ellurit resistance cluster	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0330 HP0315 HP0967 HP1248 HP0885 <i>Colicin-relate</i> HP1126 HP0428	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) ed functions colicin tolerance-like protein (toIB) phage/colicin/tellurtf resistance cluster terY protein	33.3% 32.8% 27.2% 38.2% 21.1% 37.7% 28.9% 36.0% 33.5%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP1248 HP12885 <i>Colicin-relat</i> HP128 HP0428 <i>Drug and ai</i> HP1431	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ad functions colicin tolerance-like protein (toIB) phage/colicin/tellurite resistance cluster terY protein nalog sensitivity 16S (RNA (adenosine-N5.N6-)-dimethyl- transferase (ksgA)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7%
HP1483 HP0927 HP0280 HP1228 HP0280 HP0380 HP0315 HP0987 HP0987 HP1248 HP0885 <i>Colicin-relat</i> HP1248 HP0428 <i>Drug and a</i> HP0428 <i>Drug and a</i> HP0430 HP0606 HP0630	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (fuPA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) ad functions collicin toferance-like protein (toIB) phage/collicin/tellurtle resistance cluster terY protein T6S (rRNA (adenosine-N6.N6-)-dimethyl- transferase (ksgA) membrane tusion protein (mrC)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 35.5% 24.2% 62.3%
HP1483 HP0927 HP0280 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0367 HP1248 HP0885 <i>Colicin-relat</i> HP126 HP0428 <i>Drug and a</i> HP1431 HP0606	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (fupA) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ad functions collicin toferance-like protein (toIB) phage/collicin/tellurtle resistance cluster terY protein SG rRNA (adenosine-N6.N6-)-dimethyl- transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 24.2%
HP1483 HP0927 HP0280 HP0280 HP1228 HP0370 HP1444 HP0395 HP0315 HP0315 HP0357 HP1248 HP0357 HP1248 HP0428 Drug and al HP1430 HP0428 Drug and al HP0430 HP1476 HP0450	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) invasion protein (linvA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase sunival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (brD) dividence factor mviN protein (mviN) ad functions colicin tolerance-like protein (toIB) phage/colicin/tellurite resistance cluster terY protein madg sensitivity 165 rRNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda66)	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 35.5% 24.2% 62.3%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0370 HP1444 HP0370 HP0376 HP0376 HP0376 HP0376 HP0385 <i>Colicin-relat</i> HP1481 HP04885 <i>Colicin-relat</i> HP1426 HP0428 <i>Drug and a</i> HP1431 HP0620 HP1476 HP1477 HP147	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (fupA) invasion protein (furA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mvN protein (mvN) <i>ad functions</i> colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein terY protein (mtrC) membrane tusion protein (mtrC) medulator of drug activity (mde66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions	33.3% 32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 36.0% 33.5% 25.7% 25.6% 25.6% 25.6% 24.2% 62.3% 39.7%
HP1483 HP0927 HP0280 HP1228 HP0970 HP1444 HP0385 HP0316 HP0385 <i>Colicin-relat</i> HP128 HP128 HP128 HP1431 HP1431 HP0428 <i>Drug and a</i> HP1431 HP0428 <i>Drug and a</i> HP1431 HP0620 HP1476 HP0428 HP0476 HP1476 HP1088 HP0474 HP1008 HP0474 HP0089	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (fupA) invasion protein (furA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mvN protein (mvN) ad functions colicin tolerance-like protein (toIB) phage/colicin/rtellurite resistance cluster terY protein trY protein (mtrC) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15200 insertion sequence from SARA17 15200 finsertion sequence from SARA17 15200 finsertion sequence from SARA17	33.3% 32.8% 32.8% 32.8% 21.1% 42.1% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 42.2% 62.3% 33.9% 33.9% 33.9%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP09370 HP0350 HP0315 HP0947 HP1248 HP0885 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP1426 HP1428 <i>Drug and a</i> HP1431 HP1455 <i>Transposon</i> HP1495 HP0418 HP14988 HP0498 HP1098	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) virulence factor mviN protein (mvIN) virulence factor mviN protein (toIB) phage/colicin/tellurite resistance cluster terY protein resonantivity transferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA(P), putative -stated functions (s200 insertion sequence from SARA17 (S200 insertion sequence from SARA17 (S200 fmsPinosase (tnpA) (S806 fmanposase (tnpA) (S806 fmanposase (tnpA)	33.3% 32.8% 32.8% 32.8% 33.2% 21.1% 42.1% 37.7% 37.7% 37.7% 37.7% 32.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 22.3% 33.7% 27.0% 33.9%
HP1483 HP0927 HP0280 HP1928 HP0970 HP1228 HP0930 HP1444 HP0315 HP0930 HP1930 HP0930 HP1930 HP0930 HP097 HP0985 Colicin-relat HP126 HP0428 Drug and at HP1426 HP0428 Drug and at HP1086 HP1435 HP0086 HP1097 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097 H	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence factor mviN protein (mvIN) ef functions colicin tolerance-like protein (toIB) phage/colicin/tellurtle resistance cluster terY protein nalog sensitivity transferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacytica cid decarboxylase tetracycline resistance protein tetA(P), putative realized functions 15200 insertion sequence from SARA17 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA)	33.3% 22.8% 22.8% 22.8% 232.2% 21.1% 42.1% 70.2% 28.9% 28.9% 28.9% 28.9% 28.9% 28.9% 28.9% 28.9% 25.7% 25.7% 25.5% 24.2% 24.2% 24.2% 24.2% 25.5% 24.2% 25.5% 27.0% 27.0% 23.3% 27.0%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP09370 HP1248 HP0885 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP1426 HP0428 <i>Drug and a</i> HP1431 HP1451 <i>Transposon</i> HP1465 <i>Transposon</i> HP1088 HP0988 HP0987 HP0987 HP0987 HP0987	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein L (vapD) virulence associated protein homolog (wacB) virulence factor mviN protein (mvIN) <i>ed functions</i> collicin tolerance-like protein (toIB) phage/collicin/tellurtle resistance cluster terY protein nalog sensitivity 1553 (rRNA (adenosine-N6,N6+)-dimethyl- transferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mde66) phenylacvylica cid decarboxylase tetracycline resistance from SARA17 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15305 transposase (tnpA) 15305 transposase (tnpA)	33.3% 22.9% 27.2% 38.2% 21.1% 37.7% 37.7% 37.7% 36.0% 33.5% 25.7% 25.5% 24.2% 62.3% 62.3% 24.2% 33.9% 33.9% 33.9% 33.9% 27.2%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP09305 HP0315 HP0350 HP0315 HP0355 Colicin-relat HP0428 Drug and ai HP1426 HP0428 Drug and ai HP1430 HP1476 HP16050 HP1476 HP10988 HP0938 HP0375 HP0385 HP1636 HP0375 HP0385 HP1636 HP16375 HP0386 HP16375 HP0387 H	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) phage/colicin/telluurite resistance cluster terY protein ralog sensitivity 165 (RNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15200 insertion sequence from SARA17 15805 transposase (tnpA) 15805 transposase (tnpA)	33.3% 21.2% 21.2% 38.2% 21.1% 42.1% 37.7% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 25.6% 35.5% 25.6% 33.9% 37.7% 27.0% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.3.4%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP09315 HP09315 HP09315 HP0935 HP0935 HP0985 Colicin-relat HP0428 Drug and ai HP126 HP0428 Drug and ai HP1426 HP0428 Drug and ai HP0606 HP1476 HP1066 HP1043 HP0988 HP09888 HP09888 HP09888 HP09888 HP09888 HP09888 HP09888 HP09888 HP09888 HP0980 HP0980 HP0980 HP0980 HP0980 HP0980 HP0980 HP0980 HP0980 HP128 HP128 HP	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) <i>ef functions</i> collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster terY protein nalog sensitivity transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mde66) phenylacvylica ecid decarboxylase tetracycline resistance from SARA17 IS200 insertion sequence from SARA17	33.3% 212% 212% 38.2% 211% 42.1% 37.7% 28.9% 37.7% 28.9% 37.7% 28.9% 35.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 23.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 27.
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP0950 HP0315 HP0967 HP1248 HP0485 <i>Colicin-relat</i> HP1484 HP1484 HP1428 <i>Drug and a</i> HP1431 HP0428 <i>Drug and a</i> HP1431 HP0606 HP1476 HP1431 HP0608 HP1476 HP1048 HP1639 HP0479 HP1639 HP0987 HP0987 HP0987 HP0937 HP1634 HP0433 HP	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hease survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) dividence factor mviN protein (mviN) virulence factor mviN protein (mviN) ef functions collicin tolerance-like protein (toIB) phage/collicin/fellurite resistance cluster terY protein raidog sensitivity transferase (ksgA) membrane fusion protein (mrtC) modulator of drug activity (mda66) pherylacrylic acid decarboxylase tetracycline resistance protein tetX(P), putative related functions 15200 insertion sequence from SARA17 15806 transposase (tnpA) 15806 transposase (tnpB) 15806 transposase (tnpB)	33.3% 22.8% 27.2% 38.2% 21.1% 42.1% 37.7% 28.9% 35.5% 25.6% 25.6% 25.6% 25.6% 25.6% 25.6% 25.6% 23.9% 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% 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% 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% 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%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% 33.3%33.3% 33.3%34% 33.3%34% 33.3%34% 33.3%34% 33.3% 34% 33.3%34% 33.3%34% 33.3%34% 33.3%34% 33.3%34% 33.3%34% 33.3%34%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1424 HP0970 HP128 HP09315 HP0947 HP1248 HP0945 Colicin-relat HP0947 HP1428 HP0428 Drug and ai HP0428 HP0428 HP0428 HP0428 HP0428 HP04535 HP04555 HP05555 HP0555555 HP05555	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) <i>ef functions</i> collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster terY protein nalog sensitivity transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mde66) phenylacvylica ecid decarboxylase tetracycline resistance from SARA17 IS200 insertion sequence from SARA17	33.3% 212% 212% 38.2% 211% 42.1% 37.7% 28.9% 37.7% 28.9% 37.7% 28.9% 35.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 23.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 27.
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1228 HP09370 HP0350 HP0315 HP0947 HP1248 HP0985 <i>Colicin-relat</i> HP0428 <i>Drug and a</i> HP1431 HP1431 HP1451 <i>Transposon</i> HP1457 <i>Transposon</i> HP1456 HP1456 HP1456 HP1456 HP1457 HP0988 HP097 HP0988 HP0987 HP0988 HP0997 HP1096 HP1096 HP1096 HP1097 HP1	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hease survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mvIN) ad functions collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster terY protein membrane fusion protein (mrIC) modulator of drug activity (mda66) phenylacrylic add decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15206 franciposase (tmpA) 15206 franciposase (tmpA) 1	33.3% 22.2% 27.2% 38.2% 21.2% 42.1% 37.7% 28.9% 26.9% 25.5% 25.5% 25.5% 25.5% 25.5% 24.2% 35.5% 24.2% 35.5% 24.2% 33.9%33.9% 33.9%33.9% 33.9% 33.9% 33.9%33.0% 33.9% 33.9%33.0% 33.0% 33.0%33.0% 33.0%33.0% 33.0% 33.0%33.0% 33.0%33.0% 33.0%33.0% 33.0%33.0% 33.0%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1228 HP09370 HP0350 HP0315 HP0947 HP1248 HP0985 <i>Colicin-relat</i> HP0428 HP0485 <i>Colicin-relat</i> HP0428 HP1431 HP1431 HP1431 HP1451 Transposon HP1407 HP1455 HP0478 HP1455 HP0478 HP1036 HP0388 HP0478 HP0388 HP0478 HP0388 HP0478 HP0388 HP0478 HP0388 HP0478 HP037 HP0388 HP0471 HP0471 HP0381 HP0471 H	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein L (vapD) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence associated protein to(B) phage/colicin/tellurite resistance cluster terY protein raiog sensitivity 155 (rRN/ aclenosine-N6,N6+-dimethyl- transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mde66) phenylacylic acid decarboxylase tetracycline resistance protein tetA(P), putative related functions 15200 insertion sequence from SARA17 15305 transposase (tnpA) 15305 transposase (tnpA) 15305 transposase (tnpA) 15305 transposase (tnpA) 15305 transposase (tnpA) 15305 transposase (tnpA) 15305 transposase (tnpB) 15305 transposase (tnpB) 1530	32.3% 22.8% 27.2% 27.2% 32.8% 21.1% 42.1% 70.2% 28.9% 23.5% 25.7% 25.7% 25.6% 25.7% 25.6% 25.7% 25.7% 25.6% 23.9% 27.2% 39.7% 27.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.4%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1228 HP09370 HP1248 HP0985 <i>Colicin-relat</i> HP0428 HP0885 <i>Colicin-relat</i> HP0428 HP1426 HP1426 HP1426 HP1426 HP1427 <i>Transposon</i> HP1431 HP1451 HP1451 HP1451 HP1454 HP1454 HP1455 HP0478 HP1098 HP0988 HP0988 HP0988 HP0987 HP1096 HP1096 HP10987 HP1096 HP1097 HP10	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence associated protein homolog (wacB) virulence factor mviN protein (mvIN) <i>ed functions</i> collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster terY protein nalog sensitivity 155 (rRNA (adenosine-N6,N6+)-dimethyl- transferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15200 insertion sequence from SARA17 15605 transposase (tnpA) 15605 transposase (tnpB) 15605 transpo	32.3% 22.8% 27.2% 27.2% 32.8% 27.7% 70.2% 28.9% 23.5% 25.7% 25.7% 25.6% 25.7% 25.6% 25.7% 25.6% 25.7% 26.9% 27.0% 33.9% 27.0% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4%
HP1483 HP0927 HP0280 HP0970 HP1228 HP0970 HP1228 HP0970 HP1248 HP0985 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 HP0485 <i>Transposon</i> HP1495 HP0474 HP1455 <i>Transposon</i> HP1495 HP0474 HP1495 HP0474 HP1096 HP1097 HP1097 HP1097 HP1097 HP1097 HP1097 HP1097 HP07312 HP0086 HP00812 HP0081 HP0081 HP0081 HP0081 HP0081 HP0081 HP0081 HP0081 HP0081 HP008	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein NoNolog (wacB) virulence associated protein homolog (wacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurtle resistance cluster terY protein nalog sensitivity ransferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative "related functions StoBo transposase (tnpA) ISBOB transposase (tnpB) ISBOB transposase (tn	32.3% 22.8% 27.2% 27.2% 27.2% 28.9% 27.7% 70.2% 28.9% 23.5% 25.7% 25.6% 25.7% 25.6% 25.7% 25.6% 23.9% 23.9% 27.2% 39.7% 33.9% 27.2% 33.9% 33.9% 33.9% 33.9% 33.4% 33.3%
HP1483 HP0927 HP0220 HP0220 HP0220 HP0370 HP1424 HP0970 HP1228 HP0985 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Colicin-relat</i> HP0485 <i>Transposon</i> HP1431 HP0486 HP1457 <i>Transposon</i> HP1497 HP1451 <i>Transposon</i> HP0488 HP0488 HP0488 HP0488 HP0488 HP0488 HP0488 HP0488 HP0497 HP0497 HP0497 HP1096 HP1096 HP1097 HP1097 HP0739 HP0973 HP007312 HP0086 HP0086 HP0087	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-heas survival protein (surE) virulence associated protein D (vapD) virulence associated protein Nonolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurtle resistance cluster terY protein nalog sensitivity transferase (ksgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative "related functions Sta00 insertion sequence from SARA17 IS800 transposase (tnpA) IS800 transposase (tnpB) IS800 tra	32.3% 22.8% 27.2% 27.2% 23.8% 27.7% 70.2% 28.9% 23.5% 25.7% 25.6% 25.7% 25.6% 25.7% 25.6% 25.7% 25.6% 25.7% 26.3% 39.7% 39.7% 39.9% 39.7% 33.9% 33.9% 33.9% 33.4%33.4% 33.4% 33.4%33.3%33.3%
HP1483 HP0927 HP02280 HP09270 HP1228 HP0970 HP1228 HP09370 HP1248 HP09370 HP1248 HP0935 <i>Colicin-relat</i> HP0428 <i>Colicin-relat</i> HP0428 HP1426 HP1426 HP1426 HP1426 HP1426 HP1426 HP1427 HP1427 HP1421 HP0414 HP1431 HP0438 HP1435 HP1435 HP1435 HP1435 HP1435 HP1435 HP0437 HP0457 H	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein Nonolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurite resistance cluster terY protein alog sensitivity resistance-Nik-Ne}-dimethyl- transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions Si200 insertion sequence from SARA17 IS200 transposase (tnpA) IS200 transposase (tnpA) IS200 transposase (tnpA) IS200 transposase (tnpA) IS200 transposase (tnpA) IS200 transposase (tnpA) IS200 transposase (tnpB) IS200	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 28.9% 25.7% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.9% 33.9% 27.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.9% 33.9% 33.3%
HP1483 HP0927 HP02280 HP09270 HP1228 HP0970 HP1228 HP09370 HP1248 HP09370 HP0267 HP1248 HP0935 <i>Colicin-relat</i> HP0428 <i>Colicin-relat</i> HP0428 <i>Drug and a</i> HP1431 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0430 HP0430 HP0431 HP1457 HP1457 HP1457 HP1453 HP0434 HP0434 HP	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein Nonolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurtle resistance cluster terY protein alog sensitivity renderase (kgA) membrane tusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative related functions (Sto6 transposase (tnpA) (Sto6 transposase (tnpB) (Sto6 transposase (tnpB)	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 28.9% 25.7% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.9% 33.9% 27.2% 97.2% 97.2% 97.2% 97.2% 97.2% 33.9% 33.9% 33.3%
HP1483 HP0927 HP02280 HP09270 HP1228 HP0970 HP1228 HP09370 HP1248 HP0935 <i>Colicin-relat</i> HP0428 <i>Colicin-relat</i> HP0428 <i>Drug and a</i> HP1431 HP0428 <i>Drug and a</i> HP0431 HP1451 <i>Transposon</i> HP1457 <i>Transposon</i> HP1456 HP1456 HP1456 HP1458 HP0414 HP0448 HP1457 HP1457 HP1457 HP1035 HP1035 HP1035 HP10312 HP1033 HP103	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) <i>ad functions</i> collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster terY protein alog sensitivity remembrane fusion protein (mrC) modulator of drug activity (mda66) phenylacrylic aid decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15200 insertion sequence from SARA17 15205 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpB) 15605 transposase (tnp	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 28.9% 25.7% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.3%
HP1483 HP0927 HP02280 HP0970 HP1228 HP0970 HP1228 HP0970 HP1228 HP09370 HP1248 HP0935 <i>Colicin-relat</i> HP0428 <i>Colicin-relat</i> HP0428 HP0428 <i>Drug and a</i> HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0430 HP0430 HP0431 HP0434 HP1450 HP0434 HP1450 HP0434 HP0434 HP1035 HP0437 HP04	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein Novel (sacB) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurite resistance cluster terY protein alog sensitivity resistance-N8,N6-}-dimethyl- transforase (kgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic aid decarboxylase tetracycline resistance protein tetA(P), putative -related functions 15200 insertion sequence from SARA17 15205 insertions sequence from	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 28.9% 25.7% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.3%
HP1483 HP0927 HP02280 HP0970 HP1228 HP0970 HP1228 HP0970 HP1228 HP09370 HP1248 HP0935 <i>Colicin-relat</i> HP0947 HP1248 HP0947 HP1248 HP0947 HP1248 HP0428 HP0428 HP0428 HP0431 HP0454 HP1450 HP1450 HP1450 HP1450 HP1454 HP1454 HP1455 HP0437 HP0438 HP0437 HP0438 HP0437 HP0438 HP0437 HP0438 HP048	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein Lo (vapD) virulence associated protein lo (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence associated protein (toIB) phage/colicin/tellurite resistance cluster terY protein alog sensitivity resistance-N8,N6-}-dimethyl- transformase (kgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacytic aid decarboxylase tetracycline resistance protein tetA(P), putative -related functions S200 insertion sequence from SARA17 IS205 fransposase (tnpA) IS205 fransposase (tnpA) IS205 fransposase (tnpA) IS205 fransposase (tnpA) IS205 transposase (tnpB) IS305 transp	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.3%
HP1483 HP0927 HP02280 HP0970 HP1228 HP0970 HP1228 HP0970 HP1228 HP09370 HP1248 HP0935 <i>Colicin-relat</i> HP0428 <i>Colicin-relat</i> HP0428 HP0428 <i>Drug and a</i> HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP0430 HP0430 HP0431 HP0434 HP1450 HP0434 HP1450 HP0434 HP0434 HP1035 HP0437 HP04	gerC2 protein (gerC2) heat shock protein (htpX) heat shock protein (htpX) heat shock protein (htpX) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-hase survival protein (surE) virulence associated protein D (vapD) virulence associated protein (surE) virulence associated protein homolog (vacB) virulence associated protein (noW) af <i>functions</i> colicin tolerance-like protein (noB) phage/colicin/fellurite resistance cluster terY protein alog sensitivity transferase (kgA) membrane tusion protein (mtrC) modulator of drug activity (mde66) phenylacytic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>related functions</i> 15206 fransposase (tnpA) 15806 fransposase (tnpB) 15806 fransposase (tnpB	32.3% 22.8% 27.2% 27.2% 27.2% 27.7% 70.2% 28.9% 28.9% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.3%

HP0258	conserved protein	hypothetical	integral	membrane	32.7%	H H
HP0284	conserved protein	hypothetical	integral	membrane	29.2%	H H
HP0362	conserved protein	hypothetical	integral	membrane	28.8%	H H
HP0415	conserved protein	hypothetical			44.4%	H H
HP0467	conserved protein	hypothetical	integral	membrane	100.0%	H H
HP0571	conserved protein	hypothetical	integral	membrane	29.5%	H H
HP0644	conserved protein	hypothetical	integral	membrane	30.3%	H H
HP0677	conserved protein	hypothetical	integral	membrane	28.5%	H H
HP0693	protein	hypothetical			46.7%	H H
HP0718	protein	hypothetical			33.5%	H H
HP0737	conserved protein	hypothetical	integral	membrane	33.3%	H H
HP0758	conserved protein	hypothetical	integral	membrane	47.6%	H H
HP0759	conserved protein	hypothetical	integral	membrane	31.1%	H H
HP0787	conserved protein	hypothetical	integral	membrane	25.2%	H H
HP0851	protein	hypothetical			37.3%	H H
HP0920	protein	hypothetical			36.3%	H H
HP0946	conserved protein	hypothetical			35.9%	H H
HP0952	protein	hypothetical			38.5%	H H
HP0983	protein	hypothetical			32.8%	H
HP1044	protein	hypothetical			30.6%	H
HP1061	protein	hypothetical			35.0%	H H
HP1080	protein	hypothetical			44.0%	H
HP1162	protein	hypothetical			27.6%	H H
HP1175	protein	hypothetical			40.6%	H H
HP1184	protein	hypothetical	- N.		23.5%	H H
HP1185	conserved protein	hypothetical	integral	membrane	55.5%	H H
HP1225	conserved protein	hypothetical	integral	membrane	31.6%	H H
HP1234	conserved protein	hypothetical	integral	membrane	29.0%	H H
HP1235	conserved protein	hypothetical	integral	membrane	30.9%	H H
HP1330	protein	hypothetical			41.7%	Н
HP1331	protein	hypothetical			33.6%	H
HP1343	protein	hypothetical			49.1%	H H
HP1363	protein	hypothetical			33.1%	H
HP1407	protein	hypothetical			22.4%	H H
HP1466	protein	hypothetical			30.9%	H H
HP1484	protein	hypothetical			41.2%	H H
HP1486	protein	hypothetical			23.8%	H H
HP1487	protein	hypothetical			30.7%	H H
HP1509	protein	hypothetical			34.3%	H H
HP1548	protein	hypothetical			30.6%	H H
HP0138 HP1438	conserved	hypothetical hypothetical	lipoprot	ein	41.2% 32.0%	H H
	conserved	hypothetical hypothetical	membra	ane protein	21.8% 38.8%	Н
	protein 4	hypothetical			23.2%	U G
HP0032	conserved	hypothetical hypothetical	protein	protein	48.2% 37.0%	H H
HP0035 HP0086	conserved conserved	hypothetical hypothetical	protein protein		34.1% 28.7%	H H
HP0094 HP0100	conserved	hypothetical hypothetical	protein		29.8% 32.0%	H H
HP0102 HP0105	conserved	hypothetical hypothetical hypothetical hypothetical	protein		29.3% 39.7%	H
HP0117 HP0162					34.2% 36.7%	H H
HP0233	conserved	hypothetical hypothetical	protein		33.9% 30.5%	H H
HP0248 HP0274	conserved	hypothetical hypothetical	protein		30.7% 38.5%	H H
HP0285 HP0309	conserved	hypothetical hypothetical hypothetical hypothetical hypothetical	protein		30.8% 31.3%	H H
HP0310 HP0318					33.7% 47.2%	H H
HP0318 HP0328 HP0334 HP0347 HP0373	conserved	hypothetical hypothetical hypothetical	protein protein		30.7% 30.8%	H H
	conserved	hypothetical	protein		31.8% 31.4%	H H
HP0374 HP0388	conserved	hypothetical hypothetical hypothetical	protein		24.7% 39.8%	Н
HP0396	conserved	hypothetical	protein		39.9% 33.7%	
HP0447	conserved	hypothetical hypothetical	protein		45.6% 38.2%	
HP0465	conserved	hypothetical hypothetical	protein		95.5% 95.7%	
HP0469	conserved	hypothetical hypothetical	protein		97.1% 95.1%	
	conserved conserved	hypothetical hypothetical	protein protein		99.2% 37.2%	
HP0552	conserved	hypothetical hypothetical	protein		95.3% 37.8%	
HP0639	conserved	hypothetical hypothetical	protein		30.0% 41.0%	
	conserved	hypothetical	protein		32.0% 36.0%	
HP0656 HP0707 HP0709	conserved	hypothetical hypothetical	protein		40.1% 49.6%	
HP0710 HP0716	conserved	hypothetical hypothetical	protein protein		33.7% 30.2%	

HP0728	conserved hypoth	netical	protein	29.3%
HP0734	conserved hypoth	netical	protein	31.0%
HP0741	conserved hypoth			30.2%
HP0745	conserved hypoth	netical	protein	33.7%
HP0747	conserved hypoth	netical	protein	32.4%
HP0760	conserved hypoth	netical	protein	36.1%
HP0810	conserved hypoth	netical	protein	31.0%
HP0813	conserved hypoth	netical	protein	32.5%
HP0823	conserved hypoth	netical	protein	27.8%
HP0860	conserved hypoth	netical	protein	52.1%
HP0890 HP0891	conserved hypoth			32.2% 33.8%
HP0891 HP0892	conserved hypoth conserved hypoth	letical	protein	33.8%
HP0894	conserved hypoth	notical	protein	39.8%
HP0926	conserved hypoth	notical	protein	30.7%
HP0934	conserved hypoth			33.6%
HP0956	conserved hypoth	netical	protein	36.2%
HP0959	conserved hypoth	netical	protein	31.1%
HP0966	conserved hypoth	netical	protein	29.1%
HP0975	conserved hypoth	netical	protein	25.0%
HP1020	conserved hypoth	netical	protein	31.5%
HP1037	conserved hypoth	netical	protein	95.9%
HP1046	conserved hypoth	netical	protein	32.6%
HP1049 HP1066	conserved hypoth	netical	protein	39.7% 41.3%
HP 1066 HP 1149	conserved hypoth	retical	protein	24.7%
HP1160	conserved hypoth conserved hypoth	notical	protein	34.7%
HP1182	conserved hypoth			34.6%
HP1214	conserved hypoth			21.5%
HP1221	conserved hypoth	netical	protein	42.4%
HP1240	conserved hypoth	netical	protein	22.5%
HP1242	conserved hypoth	netical	protein	42.3%
HP1259	conserved hypoth	netical	protein	44.6%
HP1284	conserved hypoth	netical	protein	36.8%
HP1291	conserved hypoth	netical	protein	26.3%
HP1335	conserved hypoth	netical	protein	33.9%
HP1337	conserved hypoth	netical	protein	27.2%
HP1338	conserved hypoth	netical	protein	36.2%
HP1394 HP1401	conserved hypoth conserved hypoth	netical	protein	33.6% 27.5%
HP1401	conserved hypoth	retical	protein	27.5% 41.6%
HP1413	conserved hypoth			27.4%
HP1417	conserved hypoth	netical	protein	23.7%
HP1423	conserved hypoth	netical	protein	40.3%
HP1426	conserved hypoth			40.0%
HP1428	conserved hypoth	netical	protein	37.8%
HP1443	conserved hypoth	netical	protein	37.9%
HP1449	conserved hypoth	netical	protein	39.0%
HP1453	conserved hypoth	netical	protein	26.8%
HP1459	conserved hypoth			30.1%
HP1504	conserved hypoth	netical	protein	23.9%
HP1510 HP1533	conserved hypoth	netical	protein	30.6% 25.4%
HP1533 HP1570	conserved hypoth conserved hypoth	1etical	protein	25.4% 40.5%
HP1570 HP1573	conserved hypoth			40.5%
HP1587	conserved hypoth	notical	protein	39.0%
HP1588	conserved hypoth	netical	protein	32.0%
HP1589	conserved hypoth			35.1%
HP0713	conserved hypoth	netical	protein	
	(plasmid pHPM18	(0)		41.8%
HP0028	conserved hypoth	netical	secreted protein	42.1%
HP0139	conserved hypoth	netical	secreted protein	37.1%
HP0160	conserved hypoth			30.6%
HP0190	conserved hypoth	netical	secreted protein	31.4%
HP0211 HP0235	conserved hypoth	netical	secreted protein	24.3% 31.5%
HP0235 HP0257	conserved hypoth conserved hypoth	1etical	secreted protein	29.2%
HP0237	conserved hypoth			36.4%
HP0506	conserved hypoth	netical	secreted protein	29.8%
HP0518	conserved hypoth	netical	secreted protein	96.9%
HP0785	conserved hypoth			26.6%
HP0949	conserved hypoth	netical	secreted protein	39.7%
HP0977	conserved hypoth	netical	secreted protein	29.4%
HP0980	conserved hypoth	netical	secreted protein	57.4%
HP1075	conserved hypoti			42.9%
HP1098	conserved hypoti	netical	secreted protein	27.0%
HP1117	conserved hypoth	netical	secreted protein	32.3%
HP1216 HP1285	conserved hypoti conserved hypoti	ieucal	secreted protein	31.9% 38.0%
HP1286	conserved hypoti	optical	secreted protein	37.5%
HP1464	conserved hypoti	netical	secreted protein	27.4%
HP1488	conserved hypoth	netical	secreted protein	29.8%
HP1551	conserved hypoti	netical	secreted protein	42.7%
UNKNOWN				
General				
HP0390				
	adhesin-thiol perc	xidase	e (tagD)	38.3%
HP1193	aldo-keto reducta	se, pu	tative	46.6%
HP1193 HP0872	aldo-keto reducta alkylphosphonate	se, pu uptak	tative e protein (phnA)	46.6% 61.1%
HP1193 HP0872 HP0207	aldo-keto reducta alkylphosphonate ATP-binding prote	se, pu uptak in (mp	tative e protein (phnA) or)	46.6% 61.1% 38.9%
HP1193 HP0872 HP0207 HP0136	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co	se, pu uptak in (mp migrat	tative e protein (phnA) or)	46.6% 61.1% 38.9% 35.5%
HP1193 HP0872 HP0207 HP0136 HP0485	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote	se, pu uptak in (mp migrat ein	tative e protein (phnA) or) ory protein (bcp)	46.6% 61.1% 38.9%
HP1193 HP0872 HP0207 HP0136	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol	se, pu uptak in (mp migrat ein	tative e protein (phnA) or) ory protein (bcp)	46.6% 61.1% 38.9% 35.5% 30.8%
HP1193 HP0872 HP0207 HP0136 HP0485	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad)	se, pu uptak in (mp migrat ein dehyd	tative e protein (phnA) ory protein (bcp) rogenase	46.6% 61.1% 38.9% 35.5% 30.8% 44.0%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote	se, pu uptak in (mp migrat in dehyd ke pro in (gtp	tative e protein (phnA) rr) ory protein (bcp) rogenase tein (xseA) 11)	46.6% 61.1% 38.9% 35.5% 30.8%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0981 HP0569 HP0303	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote	se, pu uptak in (mp migrat ein dehyd ke pro ein (gtp ein (ob	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) o1) g)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0981 HP0569 HP0303 HP0834	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote	se, pu uptak in (mp migrat in dehyd ke pro in (gtp in (ob in hor	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0981 HP0981 HP0303 HP0303 HP0834 HP0480	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote	se, pu uptak in (mp migrat in dehyd ke pro in (gtp in (ob in hor	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) o1) g)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0981 HP0569 HP0303 HP0834 HP0480 HP0480 HP1489	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote fipase-like protein	se, pu uptak in (mp migrat in dehyd ke pro in (gtp in (ob in hor	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 21.7%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0881 HP0569 HP0303 HP0834 HP0480 HP0480 HP0480 HP0495	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote lipase-like protein niS-like protein	se, pu uptak in (mp migrat in dehyd ke pro in (gtp in (ob in hor	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 611% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 21.7% 27.3%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0881 HP0881 HP0303 HP0834 HP0480 HP1489 HP0480 HP0480 HP0421	aldo-keto reducta alkyphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote lipase-like protein nifS-like protein	se, pu uptak in (mp migrat in dehyd ke pro in (gt in (ob in hor in hor in, fus	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 54.1% 54.1% 54.1% 54.1% 54.3% 37.3%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1104 HP0881 HP0569 HP0303 HP0834 HP0480 HP1489 HP0405 HP0221 HP0658	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-II GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote inilS-like protein nilS-like protein nilU-like protein	se, pu uptak in (mp migrat in dehyd ke pro in (gt in (ob in hor in hor in, fus	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 611% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 21.7% 54.1% 27.3% 37.3%
HP1193 HP0872 HP0372 HP0136 HP0485 HP1104 HP0981 HP0569 HP0303 HP0834 HP0480 HP0480 HP0480 HP0480 HP0495 HP0221 HP0658 HP0269	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote lipase-like protein miK-like protein miK-like protein PET112-like protein pEs protein (pls)	se, pu uptak in (mp migrat ein dehyd ke pro ein (gtp ein (ob ein hor ein, fus n	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 21.7% 27.3% 37.3% 37.3% 37.3% 345.4% 34.5%
HP1193 HP0872 HP0372 HP0136 HP0485 HP1104 HP0981 HP0569 HP0303 HP0834 HP0480 HP0480 HP0480 HP0480 HP0495 HP0221 HP0658 HP0269	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) (I=4 GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote innilS-like protein nilS-like protein nilS-like protein nilU-like protein pfs protein (pfs) poly E-rich protein poly E-rich protei	se, pu uptak in (mp migrat ein dehyd ke pro ein (gtp ein (ob ein hor ein, fus n	tative e protein (phnA) r) ory protein (bcp) rogenase tein (xseA) 1) g) mologue (yphC)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 48.2% 36.7% 54.1% 27.3% 37.3% 45.4% 28.7%
HP1193 HP0872 HP0207 HP0136 HP0485 HP1485 HP0480 HP0393 HP0393 HP0394 HP0480 HP0480 HP0480 HP0480 HP0480 HP0485 HP0658 HP0658 HP0625	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like protei cinnamyl-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding protei Til-Jike protein PET112-like protein PET12-like protein protein E (gcpE)	se, pu uptak in (mp migrat in dehyd ke pro in (gt in (ob in hor in hor in, fus n	tative e protein (phnA) yr) ory protein (bcp) rogenase tein (xseA) 31) 9) nologue (yphC) nologue (yihK)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 54.1% 54.1% 54.1% 21.7% 54.1% 27.3% 45.4% 37.3% 45.4% 34.5% 28.7%
HP1193 HP0872 HP0267 HP0136 HP0485 HP10485 HP10485 HP10480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0481 HP0480 HP0421 HP0658 HP0322 HP0625 HP0625	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote innamyl-alcohol ELI3-2 (cad) II di GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote inil-Like protein nil'S-like protein nil'S-like protein pls protein (pls) poly E-rich protein protein E (gopE) protein ptosphat	se, pu uptak in (mp migrat ein dehyd ke pro ein (gtp ein (ob ein hor ein, fus n n ase 20	tative e protein (phnA) y) ory protein (bcp) orogenase tein (xseA) 1) g) nologue (yphC) AA-homolog (yihK)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 36.7% 54.1% 48.2% 36.7% 54.1% 27.3% 37.3% 45.4% 28.7%
HP1193 HP0872 HP0267 HP0136 HP0485 HP10485 HP10485 HP10480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0481 HP0480 HP0421 HP0658 HP0322 HP0625 HP0625	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like protein cinnamy-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding protein III-Silke protein nIIS-like protein PET112-like protein PET12-like protein protein (pls) protein (pls) protein (pls)	se, pur uptak in (mp migrat ain dehyd ke pro ain (gtp ain (ob ain hor ain hor ain fus n n ase 20 nature	tative e protein (phnA) yr) ory protein (bcp) orogenase tein (xseA) J1) g) mologue (yphC) AA-homolog (yihK)	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 36.7% 36.7% 36.7% 37.3% 37.3% 45.4% 28.7% 37.3% 45.4% 28.7% 30.7%
HP1193 HP0872 HP0267 HP0136 HP0485 HP10485 HP10485 HP10480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0480 HP0481 HP0480 HP0421 HP0658 HP0322 HP0625 HP0625	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like prote cinnamyl-alcohol ELI3-2 (cad) ETP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding prote injl/Sike protein nif/Sike protein nif/Like protein pls protein (pfs) poly E-rich protein protein (posphat solute-binding signature protein	se, pu uptak in (mg migrat ein dehyd ke proc ein (ob ein (ob ein hor ein, fus n n ase 2C nature (aspB)	tative e protein (phnA) y) ory protein (bcp) orogenase tein (xseA) 1) g) nologue (yphC) A-homolog (yihK) c homolog (ptc1) and mitochondrial	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 48.2% 54.1% 54.1% 54.1% 21.7% 54.1% 27.3% 45.4% 37.3% 45.4% 34.5% 28.7%
HP1103 HP0872 HP0277 HP0136 HP0485 HP1104 HP0485 HP1104 HP0486 HP1104 HP0480 HP0480 HP0480 HP0480 HP0480 HP0490 HP0491 HP0628 HP0431 HP0624	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like protein cinnamy-alcohol ELI3-2 (cad) exonuclease VII-li GTP-binding prote GTP-binding prote GTP-binding prote GTP-binding protein III-Silke protein nIIS-like protein PET112-like protein PET12-like protein protein (pls) protein (pls) protein (pls)	se, pu uptak in (mg migrat ein dehyd ke proc ein (ob ein (ob ein hor ein, fus n n ase 2C nature (aspB)	tative e protein (phnA) y) ory protein (bcp) orogenase tein (xseA) 1) g) nologue (yphC) A-homolog (yihK) c homolog (ptc1) and mitochondrial	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 48.1% 36.7% 36.7% 36.7% 37.3% 37.3% 45.4% 28.7% 37.3% 45.4% 28.7% 30.7%
HP1103 HP0872 HP0277 HP0136 HP0485 HP1104 HP0485 HP1104 HP0486 HP1104 HP0480 HP0480 HP0480 HP0480 HP0480 HP0490 HP0491 HP0628 HP0431 HP0624	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like protein cinnamyi-alcohol ELI3-2 (cad) exonuclease VILII GTP-binding prote GTP-binding prote GTP-binding protein GTP-binding protein GTP-binding protein GTP-binding protein miKJ-like protein miKJ-like protein miKJ-like protein miKJ-like protein protein E (gopE) protein phosphatu solute-binding sig signature protein hiodiasulfide inte	se, pu uptak in (mg migrat ein dehyd ke proc ein (ob ein (ob ein hor ein, fus n n ase 2C nature (aspB)	tative e protein (phnA) y) ory protein (bcp) orogenase tein (xseA) 1) g) nologue (yphC) A-homolog (yihK) c homolog (ptc1) and mitochondrial	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 42.5% 42.5% 54.1% 54.1% 54.1% 54.1% 54.1% 54.1% 54.4% 37.3% 45.4% 37.3% 45.4% 30.7% 26.4%
HP1103 HP0872 HP0277 HP0136 HP0485 HP1104 HP0485 HP1104 HP0486 HP1104 HP0480 HP0480 HP0480 HP0480 HP0480 HP0490 HP0491 HP0628 HP0431 HP0624	aldo-keto reducta alkylphosphonate ATP-binding prote bacterioferritin co catalase-like protein cinnamyi-alcohol ELI3-2 (cad) exonuclease VILII GTP-binding prote GTP-binding prote GTP-binding protein GTP-binding protein GTP-binding protein GTP-binding protein miKJ-like protein miKJ-like protein miKJ-like protein miKJ-like protein protein E (gopE) protein phosphatu solute-binding sig signature protein hiodiasulfide inte	se, pu uptak in (mg migrat ein dehyd ke proc ein (ob ein (ob ein hor ein, fus n n ase 2C nature (aspB)	tative e protein (phnA) y) ory protein (bcp) orogenase tein (xseA) 1) g) nologue (yphC) A-homolog (yihK) c homolog (ptc1) and mitochondrial	46.6% 61.1% 38.9% 35.5% 30.8% 44.0% 42.5% 42.5% 42.5% 54.1% 54.1% 54.1% 54.1% 54.1% 54.1% 54.4% 37.3% 45.4% 37.3% 45.4% 30.7% 26.4%