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MICROBIAL GENOMICS

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SUPPLEMENTARY TEXT

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3 **METHODS**

4 Quality assessment of genomes

5 Three additional quality control steps were performed on all genomes. First, the genomes were BLASTed (blastn v2.2.26+) [1] against a filtered version of the RDP database (v11.1) [2] that 6 included only complete or near-complete 16S rRNA genes (>1400 bp) annotated to species level. This 7 8 was carried out to confirm that the top hit for each assembly was an L. salivarius sequence in the RDP 9 database and also to make sure that no other good hit (>1000 bp; identity >= 97%) was found, which would indicate possible contamination. Second, 39 universal marker genes [3] were BLASTed 10 (tblastn) against the contigs of each genome. The reasoning here was that all 39 marker genes should 11 12 be fully assembled in a high-quality genome (which they were). Third, the contigs of each genome 13 were assessed using Kraken (v0.10.6) [4] as a further test for possible contamination. The results of all 43 Kraken runs are shown in Table S4. 14

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16 Assigning contigs to replicons

A common problem when analysing genes of interest in draft genomes is being able to tell whether a particular gene is present on the chromosome or on a plasmid. Since all of a contig must either be part of the chromosome or part of a plasmid, once a contig has been assigned to a replicon the genes present on the contig can also be assigned to the same replicon. We describe here the method used in this study to assign each contig to its most likely replicon.

A database of 92 plasmids (10 megaplasmids and 82 plasmids) from 16 *Lactobacillus* species was generated from complete genomes available on NCBI. Each draft genome was BLASTed (blastn v2.2.26+) against this database and the results were filtered in order to assign each contig to a plasmid or, failing plasmid assignment, to the chromosome. Megaplasmids (>10 kb; both circular and linear) and smaller plasmids (<10 kb) were included in the database so four categories of replicon were possible (including the chromosome).

28 To justify BLAST thresholds for assigning contigs to replicon categories, 4 complete genomes (UCC118, CECT5713, Ren and NIAS840) were broken up into contigs using a randomly 29 generated chi-squared distribution with Degrees of Freedom equal to 1. This distribution was chosen 30 because its median Spearman correlation with the distribution of lengths of contigs for each draft 31 32 genome in our study was 0.96 (Q1 = 0.9; Q3 = 0.98; n = 38), ensuring that the artificial draft genomes 33 would resemble the draft genomes in our dataset in terms of contig length distributions. The values of 34 this distribution were then converted to proportions and randomly permuted in order to avoid a bias 35 between contig length and genome region. Each genome was divided up based on the order of the 36 randomly permuted proportions where each proportion is a fraction of the total number of base pairs in the genome. For each of the 4 complete genomes, each replicon was broken up into 50 contigs and 37 38 contigs less than 200 bp were excluded. The FASTA header for each contig was labelled with the

replicon from which it was taken so that the specificity and sensitivity of the contig assignment
method could be tested. The R (v3.2.3) code uploaded to figshare (Data Bibliography of main text;
data file 5) shows the steps for generating 50 draft contigs from the complete chromosome sequence
of UCC118.

43 The 4 artificial draft genomes were then BLASTed (blastn) against the database of 92 plasmids. This was done for each genome separately so that the complete plasmids from each genome 44 being BLASTed could be removed from the database beforehand. This ensured that draft plasmid 45 46 contigs were not just aligning to the complete version of their own plasmids. An unfiltered evaluation of the BLAST results showed that the highest % alignment length of a chromosomal contig against 47 the plasmid database was 23.7% (490/2,070). An alignment length of 25% against the plasmid 48 database was therefore chosen as the cut-off for assigning contigs to plasmids. BLAST hits between 49 two sequences can have multiple high-scoring pairs (HSPs) so the sum of the non-overlapping length 50 51 of all HSPs between each contig and reference plasmid was calculated. The reference plasmid 52 sequence with the highest % alignment to the contig was chosen and all alignments of less than 25% 53 were excluded. Depending on their top hit, these remaining contigs were assigned to one of three 54 categories: plasmid, circular megaplasmid or linear megaplasmid. It should be noted that small 55 contigs representing transposases or other small repetitive regions may be present on both the 56 chromosome and the plasmid(s) so the assignment of these contigs is less reliable. The sensitivity and 57 specificity of the BLAST results for the 4 artificial draft genomes against the plasmid database are 58 shown in Table S5. Code for calculating the sum of the non-overlapping length of HSPs between each 59 contig and each reference plasmid has been uploaded to figshare (Data Bibliography of main text; data file 6). 60

As an additional quality check, three genes identified as being specific to the *L. salivarius* circular megaplasmid(5) - *repA* (LSL_1739), *repE* (LSL_1740) and *parA* (LSL_1741) – were BLASTed (tblastn) against the contigs for each genome assembly to see if all top hits were to predicted megaplasmid contigs. Results are in Table S2.

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66 Specific functional groups

67 COG categories for genes were predicted by BLASTing (blastp) amino acid sequences 68 against a COG database (ftp://ftp.ncbi.nih.gov/pub/COG/COG2014/data) with thresholds of 40% 69 identity, 50% alignment length of the query gene and a BLAST bit score of 60. Any gene match that 70 fell below these thresholds was added to the COG category 'unknown function'. For each genome, 71 genes were assigned to their respective replicons.

Peptidases were predicted by BLASTing (blastp) amino acid sequences against full sequences
from the MEROPS database (https://merops.sanger.ac.uk). BLAST thresholds used were 40%
identity, 50% alignment length of the query gene and a BLAST bit score of 60.

75 Sortase genes were predicted using hmmscan from the HMMER3 (v3.1b1) [6] toolkit with 76 the following downloaded sortase family HMM profiles: 77 http://nihserver.mbi.ucla.edu/Sortase/sortase_family_classification.hmm. A cut-off score of >30 was 78 chosen to balance false positive and false negative predictions based on comparisons with the non-79 redundant NCBI and KEGG annotations. Genes with an LPXTG motif were predicted using hmmscan 80 with a TIGRFAM [7] HMM profile (TIGR01167) and an e-value cut-off of 1e-05. The LOCP [8] 81 webserver was used to locate putative pilus operons using default parameters. All three methods used 82 amino acid sequences as input.

Glycosyl hydrolases and glycosyl transferases were predicted using hmmscan with DBcan [9]
 HMM profiles (http://csbl.bmb.uga.edu/dbCAN/). For each genome, GH and GT genes were assigned

to their respective replicons. A cut-off score of >30 was chosen to balance false positive and false
 negative predictions based on comparisons with non-redundant NCBI and KEGG annotation.

87 The Bagel3 [10] webserver was used to predict genetic loci for bacteriocin production and
88 surrounding areas of interest (AOIs) using marker genes. For each genome, AOIs were sorted into
89 their respective replicons.

90 CRISPRs were predicted using MinCED (v0.2.0), which was downloaded from the following
91 link: https://github.com/ctSkennerton/minced. To predict cas genes associated with each CRISPR,
92 hmmscan was used with cas-specific HMMs from TIGRFAM. CRISPRs that had no associated cas
93 genes were labelled as 'undefined'. The same method used to build the core-gene phylogenetic tree
94 was also used to build a tree from the amino acid sequences of the cas 1 (type-II and type-III) gene.

95 Genes involved in exopolysaccharide biosynthesis were predicted using the two EPS clusters 96 of UCC118 as references. This was the only functional group that relied on a reference genome and it was used in order to give an overview of EPS genetic diversity in L. salivarius since a much larger, 97 98 more detailed study is being conducted on the intra-specific diversity and functionality of EPS 99 clusters in L. salivarius (Bourin et al; in preparation). Amino acid sequences of the UCC118 EPS genes were BLASTed (tblastn) against contigs with thresholds of 40% identity, 50% alignment length 100 101 of the query gene and a BLAST bit score of 60. BLAST hits were then manually curated, taking note 102 of UCC118 EPS genes present in multiple copies (in the case of transposases) and genes that passed the thresholds but were located in very different regions of the genome than the other predicted EPS 103 104 genes.

Signal peptides were predicted using SignalP (v4.1) [11] with default parameters for grampositive bacteria. Transmembrane domains were predicted using TMHMM (v2.0) [12] and all predictions with more than 10 expected amino acids in transmembrane helices in the first 60 amino acids were excluded from the results due to their likelihood of being signal peptides (see Instructions at http://www.cbs.dtu.dk/services/TMHMM/).

110 Antibiotic resistance (AR) genes were predicted using an AR reference gene set from the 111 Comprehensive Antibiotic Resistance Database (CARD; v1.09) [13]. Within the CARD database, the 112 FASTA file denoted 'protein homolog model' was filtered to include only complete genes and then 113 genes were translated from nucleotide to amino acid sequences. Amino acid sequences for each 114 genome were BLASTed against this database and filtered at 40% identity, 50% alignment length of 115 the query gene and a BLAST score of 60.

116 Potential virulence factors (VF) were predicted using a version of the virulence factor (VFDB) which downloaded from the following 117 database [14]. was link: 118 http://www.mgc.ac.cn/VFs/Down/VFDB_setA_pro.fas.gz. This database is the core dataset and 119 contains virulence factor genes that have been experimentally verified only - the full database was not used in order to minimise the number of false positive gene predictions. Amino acid sequences for 120 each genome were BLASTed against the database and filtered at 70% identity and 90% alignment 121 122 length of the query gene. More stringent cut-off values were used for virulence factors compared with antibiotic resistance genes because using BLAST to identify homologous genes based on the VF 123 124 database is known to produce false positives at lower cut-off values.

Prophages were predicted using VIRSorter (v1.0.2) [15] where predicted regions with the lowest confidence (category 3; 'not so sure') for both complete phage contigs and prophages were excluded. Predicted phage genes for the remaining categories were assigned to COG categories (the same COG database used for the general COG analysis) using blastp with thresholds of 40% identity, 50% alignment length of the query gene and a BLAST bit score of 60. Any gene that fell below these thresholds was added to the COG category 'unknown function'. Transposases were predicted using hmmscan with TnpPred [16] HMM profiles downloaded from the following link: http://www.mobilomics.cl/. An e-value cut-off of 1e-05 was used. For each genome, predicted transposases were assigned to their respective replicons.

Bile salt hydrolase genes were predicted using a subset of the KEGG database where the EC number 3.5.1.24 was used to select bile salt hydrolase genes. Amino acid sequences were BLASTed (blastp) against this database with thresholds of 40% identity, 50% alignment length of the query (and reference) gene and a BLAST bit score of 60. These genes were then BLASTed against each other to give a pairwise BLAST score for each pair of bile salt hydrolase genes.

All statistics and data visualisation were carried out in R (v3.2.3) [17]. R packages used
during this study were MADE4 [18] and SeqinR [19].

RESULTS AND DISCUSSION

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145The core-gene phylogenetic tree of L. salivarius has similar sub-clade146topology to POCP clusters, but overall tree topology is dissimilar

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Percentage of Conserved Proteins (POCP) [20] calculates a similarity score based on 148 149 percentage of genes in common between all the amino acid sequences in two genomes. POCP was designed as a method to identify whether a particular species belongs within a genus. We were not 150 interested in applying this threshold since all strains obviously fall within a single genus; instead, the 151 152 goal was to assess the congruency of a core-gene phylogeny with a method that clustered the strains 153 based on the presence and absence of genes. Fig. S3 shows a heatmap of POCP values, where 154 clustering of strains is in reasonable agreement with the core-gene phylogeny of Fig. 2 in terms of 155 sub-clades. Several strains cluster apart from their core-gene sub-clades including CECT5713 and CCUG38008. A greater difference between POCP and the core-gene tree versus ANI and the core-156 gene tree is expected because POCP value calculations ignore homologous regions, using similarity 157 based on gene presence and absence distributions to cluster strains. This is a rough approximation of 158 the combined effect of gene decay and HGT since a gene that is present in one strain and absent in 159 another has either acquired a deleterious mutation or else has been horizontally transferred by one of 160 several mechanisms. The reason why many of the sub-clades in Fig. S3 agree with the core-gene 161 phylogeny is that the probability of gene decay or HGT events having occurred after two strains start 162 163 to diverge from a common ancestor increases with time. Adaptation to different niches and differing 164 selection pressures then start to disrupt the correlation between core-gene phylogeny and clustering of 165 shared/unshared genes [21]. We found no general association of clusters from any tree generated in this study with the isolation sources of the strains (Table S1), but members of several small clusters 166 167 were all isolated from the same source. This overall lack of niche-strain association may be due to the transient appearance of L. salivarius in niches associated with the gastro-intestinal tract (food, 168 169 opportunistic infection of body sites, etc.) and it would be a mistake to assume that every strain has acquired niche-specific adaptations to its source of primary isolation. 170

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Protease genes show no variation or considerable variation depending on MEROPS protease family

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Proteases are a large group of proteins, divided into many families that are involved in the
hydrolysis of peptides. Fig. S4 shows 53 protease families that display variation across the 43

genomes in this dataset. Genes for eighteen additional protease families were predicted in *L. salivarius*, but these families showed no variation across the strains, with 17 represented by a single gene per strain (A01A, C108, C14B, C19, C46, I04, I87, M02, M10A, M13, M15D, M20B, M20D, M24A, S09A, S09B, T05, T06) and one, a cysteine protease (C19) described as 'ubiquitin-specific' by the MEROPS database (Table S6), represented by two genes per strain. It can be speculated that these 18 families are subjected to purifying selection since the remaining 53 protease families vary both in gene count and in presence and absence across the strains.

184 Out of the 53 protease families that vary in their distributions, 33 are present in all 43 genomes, but have variable gene counts; genes for thirty of these are found on the chromosome only 185 while the remaining three are present on multiple replicons. The gene count per protease family 186 ranges from 0 to 24 where some families are present in all but a single genome and other families are 187 present in one only (usually DSM18933 - the strain of L. hayakitensis used in this study). The 188 protease family with the most genes in L. salivarius (4-24) is M23B, which is annotated as a 189 lysostaphin in the MEROPS database (Table S6), an antibacterial enzyme that degrades peptidoglycan 190 191 in the cell walls of certain bacteria, staphylococci in particular.

192 There are a number of protease families and protease inhibitors that are rare in the dataset of 193 L. salivarius annotations, with representatives belonging to one or several genomes only. JCM1046 194 has gene products in two families that the other strains do not have - I75 and S26B - both relevant genes predicted to reside on the chromosome. The gene encoding I75 is on a small contig of 964 bp 195 196 that has a 99% match over its full length to a phage from E. coli, suggesting recent acquisition of this 197 sequence as a prophage. The only other predicted protease inhibitor, I63, is an inhibitor of pappalysin-1 and it is present in all L. salivarius genomes but absent from L. hayakitensis DSM18933. S26B is a 198 199 signal peptidase that cleaves signal peptides from a secreted protein as it is being translated. 200 DSM18933 has 2 protease families that are not present in L. salivarius, which suggests that they were 201 either horizontally acquired by L. hayakitensis after the split from its common ancestor with L. 202 salivarius or else that L. salivarius subsequently lost these families through gene decay, whether through genetic drift or active selection pressure. These two families are M42 and M60, a glutamyl 203 204 aminopeptidase and an enhancin, respectively.

Sun *et al* conducted a genus-wide, comparative genomic study of lactobacilli and found
 considerable variation in cell-envelope proteases [22]. Our study shows that a more general overview
 of protease families reflects the high levels of variation seen in *Lactobacillus*, at the species level, in
 L. salivarius.

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Prophages, CRISPRs and insertion sequences are widely distributed across *L. salivarius* but no obvious association exists between them

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Two agents of HGT that affect both the bacterial chromosome and extrachromosomal 213 replicons are bacteriophages and insertion sequences (consisting primarily of a transposase gene). 214 Bacteriophages are ubiquitous among bacterial communities and phage-host dynamics has been 215 shown to stabilise diversity within a community [23] as well as to drive the arms race between the 216 217 evolution of bacterial defences (often in the form of CRISPR-cas systems) and the counter-evolution 218 of phage structures that neutralise those defences [24]. Insertion sequences (IS) have been implicated 219 in the horizontal transfer of a wide range of functions and are noted for their role in conferring niche-220 specific advantages to bacteria, allowing the persistence of strains or species in new environments that were previously uninhabitable [25]. 221

Fig. S5 shows a heatmap of predicted prophage genes (COGs) and Fig. S6 shows a barplot of prophage counts. Nine strains (2 sub-clades of 4 strains each and JCM1230) lack predicted 224 prophages; it is unlikely that these 9 strains have no history of interacting with bacteriophages -225 instead, VirSorter has failed to predict relatively intact prophages in the genomes of these strains. Canchaya et al summarise the relationship between bacteria and prophages by writing that prophages 226 227 are lost from bacterial genomes as easily as they are acquired [26]. There is no clear association of the 228 two sub-clades with a single niche, although the human oral cavity is the isolation source of 5 of these strains and the other 4 were isolated from the mammalian intestine. It is tempting to suggest that the 229 oral environment selects against the persistence of prophages; however, Edlund et al describe the oral 230 231 cavity as the perfect portal for viruses to access the oral microbial community [27] and previous 232 studies have shown that it is host to a diverse community of phages [28, 29].

The COG category in Fig. S5 with by far the most genes is 'Function unknown' (S) with a 233 mean average gene count of 61.3 compared with the second highest - 'General function prediction 234 only' - of 3. The size of these categories emphasises the limits of current knowledge regarding 235 bacteriophage gene function. There is a correlation between number of predicted prophages and 236 237 number of prophage genes (Spearman; rho = 0.78; p < 0.001), which is largely expected and 238 highlights the size constraints on phages that infect L. salivarius since number of prophages, not 239 phage type, approximately accounts for number of prophage genes. Some of the COG categories that 240 are least abundant in predicted prophages are those involved in cell-specific functions such as cell 241 motility (N) and secretion (U). The distribution of the remaining COG categories across the strains is indicative of the dynamic nature between bacteria and their phages, with considerable intra-species 242 243 variation suggesting that the prophage complement of the ancestor of L. salivarius does not resemble any of the currently extant strains since their repertoire of prophages is so distinct. 244

Table S7 describes the distribution of CRISPRs across the 43 genomes as well as their 245 246 associated cas genes. All CRISPRs are located on the chromosome, highlighting their role in 247 protecting against extrachromosomal sequences. Almost all strains in this dataset have either the type-248 II or type-III CRISPR-cas system (or both), identified by the cas 9 or cas 10 gene, respectively, and 6 249 strains have no identified CRISPRs. The presence of either type-II or type-III CRISPR-cas systems show some clustering on the core-gene tree in Fig. 2: the DSM20555^T sub-clade consisting of 4 strains 250 all have the type-III system only while the CECT5713 (6 strains) and UCC118 (4 strains) sub-clades 251 252 have the type-II system only; the AH43348 sub-clade (6 strains), in contrast, has both type-II and type-III systems. The partial clustering of CRISPR-cas systems according to the core-gene tree is 253 254 supported by Fig. S7, which shows a maximum-likelihood tree of the cas 1 gene for type-II CRISPR-255 cas, providing evidence of CRISPR-cas systems being acquired and maintained in the common 256 ancestors of these sub-clades. The 6 strains with no CRISPRs show some clustering on the core-gene 257 tree in Fig. 2, but JCM1045 and DSM18933 are singletons. The absence of CRISPR-cas systems does 258 not have an obvious association with niche or the presence of prophages, suggesting that the 259 interaction between CRISPR-cas systems, bacteriophages and the environment is far from straightforward. There are also 6 undefined CRISPRs from 4 strains that could not be described due to 260 261 the absence of cas genes in close proximity. These CRISPRs are probably degraded systems that are no longer functional since all functioning CRISPR-cas systems have the cas 1 gene, which is involved 262 263 in recognition and cleavage of invading DNA.

Fig. S8 shows a heatmap of gene counts for insertion sequences across the 43 strains, divided 264 265 up into their respective replicons. The most striking thing about this figure is the inter-strain diversity 266 of transposases, both within and between replicons. The gene counts for each transposase family in a specific strain on a particular replicon range from 0 to 52, highlighting the considerable variation in 267 copy number displayed by these horizontally transferred sequences. The majority of transposases have 268 copies on the chromosome and the plasmids, suggesting that they utilise the conjugative ability of 269 270 plasmids to increase their abundance within and between species. The distributions of the IS families follow different patterns, from being widely spread over all three replicon groups (IS3) to being 271

272 limited to the chromosome and megaplasmid (IS21) to being confined to the smaller plasmid(s)
273 (IS256). The only IS family confined to the chromosome is IS1 in a single strain - NIAS840.

The multi-replicon distribution of IS families implies that there is strong selection pressure on 274 insertion sequences to transpose regularly from chromosomes to plasmids and vice versa, perhaps 275 276 being partly responsible for the fact that transposases are currently considered to account for the most abundant gene families in both prokaryotes and eukaryotes [30]. The widespread distribution of IS3 in 277 L. salivarius replicons is mirrored by its abundance (539 genes across the 43 strains); it is also the 278 279 only family to consist of two sub-families - IS3 and IS150. Similarly, the other IS families with the widest distributions - ISL3, IS21 and IS200 - also have the greatest abundances after IS3, although 280 IS21 is absent from the smaller plasmids even if it is ubiquitous on the *L. salivarius* chromosome. 281

Overall, IS families with a higher copy number in this dataset show a strong correlation with how many strains (and replicons per strain) harbour them (Spearman; rho = 0.95; p < 0.001), showing that insertion sequences do not have a tendency to just replicate within a single replicon without undergoing regular HGT. Out of the 19 IS families present in the TnpPred database (http://www.mobilomics.cl/), 14 are identified in *L. salivarius* in this study. This emphasises the ability of transposases to transfer themselves within and between species, leading to greater sequence diversity and, when they carry additional genes with them, greater functional diversity as well.

Protein secretion and membrane-anchoring gene richness are not associated with strain isolation source

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Fig. S9 shows a barplot with the number of genes containing signal peptides and trans-293 294 membrane domains in the 43 strains. Proteins belonging to these two functional groups play an important role in the interaction of a bacterium with its environment since they are either secreted 295 296 from the cell or function as membrane-bound structures. The number of predicted genes with signal 297 peptides and with trans-membrane domains range from 56 to 84 and from 33 to 54, respectively. There is no association between niche and the number of either of these functional groups, which is 298 299 not entirely surprising. These results highlight once more the point made earlier that certain isolation 300 sources of L. salivarius strains shouldn't be interpreted as the niches that each strain has adapted to 301 over time - some strains might be acting as opportunists that don't persist in a given environment for long such as the Lactobacillus species from a 2007 study (mainly L. rhamnosus) that were isolated 302 303 from the blood, cerebrospinal fluid, peritoneal fluid and intestinal fistula of immuno-compromised 304 children [31].

305 306

307 Most *L. salivarius* strains harbour genes for two bile salt hydrolases

308 Fig. S10 shows a heatmap of BLAST scores for all the predicted bile salt hydrolase (Bsh) genes in the 42 L. salivarius strains. The ability to hydrolyse bile salts is a necessary trait for any 309 310 bacterium that is adapted to traversing the initial sections of the gastro-intestinal tract in order to 311 colonise the intestine. It is also a required function for probiotics since a potential probiotic without 312 the ability to reach its target area (usually the colon) will be ineffective. All 42 L. salivarius strains have at least one Bsh gene while L. hayakitensis DSM18933 has none, suggesting that the common 313 314 ancestor of L. salivarius and L. hayakitensis did not possess a Bsh gene, although it is possible that another strain of L. hayakitensis does harbour one or more; if this is the case then gene decay of the 315 Bsh gene in DSM18933 is a likely explanation. Two Bsh genes - one on the chromosome and one on 316 the megaplasmid - seems to be the typical organisation in L. salivarius as described by Claesson et al 317

318 [32] since 36 out of 42 strains fit this description. Four strains - CECT5713, JCM1230, LMG14476
319 and LMG14477 - have a single Bsh gene located on the chromosome while 2 strains - cp400 and
320 JCM1046 - have three BSH genes, both having two on the megaplasmid and one on the chromosome.

321 The presence of at least one Bsh in all 42 L. salivarius strains reinforces the point that this 322 species is commonly isolated from the GIT of humans and animals. The variable number of Bsh genes and their presence on both the chromosome and the megaplasmid suggests that there is variability in 323 bile resistance across the strains. This was shown in a study by Fang *et al*, but they cautioned that bile 324 325 resistance is independent of the bsh1 allele type (the Bsh on the megaplasmid of most strains) and 326 they go on to show that, upon exposure to bile and cholate, a transcriptome analysis reveals the upregulation of numerous stress response and efflux proteins, which might mask the variable influence 327 328 of Bsh allele types [33].

It should be noted that for the BLAST analysis of this category, a stricter cut-off value of 50% 329 330 for coverage of both the query and reference genes was used. This was done because the number of 331 BLAST hits to Bsh genes in the database contradicted previous literature so a closer agreement in protein length between query and reference sequences was enforced. It is possible that large 332 discrepancies between the lengths of sequences in the database and sequences in the predicted L. 333 334 salivarius gene repertoire led to false negative Bsh predictions. When the criteria are relaxed to include only 50% coverage of the query gene (and not the reference) an extra Bsh is predicted in some 335 strains and these might actually be genuine Bsh genes that this study has excluded. 336

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338 Summary survey of virulence factors and antibiotic resistance genes

Fig. S11 shows a barplot of the predicted number of putative antibiotic resistance genes (AR) and virulence factors (VF) across the 43 strains. VFs range from 2 to 3 genes and ARs range from 7 to 16. Virulence and antibiotic resistance are two traits that are screened for when assessing the suitability of a strain to act as a probiotic [34] and these traits are particularly dangerous in clinical settings. Table S8 and Table S9 give a more detailed summary of these results for ARs and VFs, respectively, while data file 7 and data file 8 give the corresponding amino acid sequences in FASTA format (figshare; Data Bibliography of main text).

The most commonly predicted function for AR genes in this dataset is transport, specifically a subset of efflux pumps for such antibiotics as tetracycline, elfamycin, bacitracin, clindamycin, fosfomycin, dalfopristin and others. Efflux pumps evolved long before the advent of antibiotic usage in modern medicine and probably originated as a defence against toxic substances entering the cell [35] – a strategy that has more recently been used to confer antibiotic resistance to microbes from multiple drugs, leading to a health crisis in the effective treatment of infection with antibiotics.

352 Virulence factor identification depends very much on context; a probiotic trait in one setting can be labelled as a virulence factor in another - for instance, when a pathogen acquires the ability to 353 354 survive intestinal transit in order to colonise the human colon. The most commonly predicted functions for VF genes in our dataset are for an ATP-dependent protease and a UDP-glucose 355 pyrophosphorylase. Overall, there is a wide variety of functions for these potential VFs, both in the 356 357 VF database and in the predicted functions for L. salivarius. This highlights the ongoing evolutionary competition between hosts and microbes, the defensive and counter-defensive adaptive traits that arise 358 from unrelated proteins with an overlapping strategy - to evade host mechanisms and successfully 359 colonise the host environment. 360

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	JCM1040
- 87	01M14315
	Ren
	778
	CECT5713
Ц <u>58</u>	CCuG38008
	NIAS840
	JCM1046
	LMG14477
	LMG14476
	NCIMB702343
62 00	NCIMB8817
	JCM1045
	UCC119
	AH43324
	UCC118
52	NCIMB8818
	CCuG47171
	cp400
	JCM1230
65	GJ24
73	JCM1047
80	SMXD51
	JCM1042
	CCuG2753OB
90	JCM1044
I	NCIMB8816
	CCuG44481
	ATCC11741
	DSM20555
	DSM20554
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)	gul1
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	L21 CCuG47825 CCuG47826 ACS116 CCuG45735













Translation, ribosomal structure and biogenesis Transcription Replication, recombination and repair Cell cycle control, cell division, chromosome partitioning Defense mechanisms Signal transduction mechanisms Cell wall/membrane/envelope biogenesis Cell motility Intracellular trafficking, secretion and vesicular transport Posttranslational modification, protein turnover and chaperones Energy production and conversion Carbohydrate transport and metabolism Amino acid transport and metabolism Nucleotide transport and metabolism Coenzyme transport and metabolism Lipid transport and metabolism Inorganic ion transport and metabolism Secondary metabolites biosynthesis, transport and catabolism Mobilome: prophages, transposons General function prediction only Function unknown



Fig. S7	F ^m					NCIMB702343
						JCM1230
			 99			NCIMB8818
				5		UCC118
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						CCuG47825
						CCuG2753OB
				22		JCM1044
			- 36			JCM1042
				25		NCIMB8816
						CECT5713
						CCuG38008
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			41		97	NCIMB8817
						SMXD51
						DSM20492
						AH4231
70						AH43348
16						866
δ						AH4331
						CCuG45735









778 JCM1040 01M14315 cp400 JCM1046 DSM20554 SMXD51 CCuG47171 JCM1047 NIAS840 NCIMB702343 AH4331 AH4331 AH4331 AH4331 AH4334 NIAS840 JCM1045 JCM1042 CCuG47735 866 AH43324 JCM1045 JCM1045 JCM1045 JCM1042 JCM1

Fig. S11



gene count

	contigs	total size (bp)	max contig size (bp)	N50	GC %	gene count	circular megaplasmids	linear megaplasmids	small plasmids	isolation source	BioSample accession
ACS116	154	2044600	71067	28667	32.7	2210	1	0	0	human_vaginal_cavity	SAMN00017035
CCuG47825	120	1921003	93995	30969	32.8	2041	1	0	1	human_blood,55-year-old_female	SAMN06163258
LMG14477	243	2080357	139646	31335	32.8	2238	1	0	1	parakeet_with_sepsis	SAMN06163272
LMG14476	238	2087383	139606	38865	32.8	2243	1	0	1	cat_with_myocarditis	SAMN06163271
DSM18933	216	1699788	420945	47652	34	1844	0	0	0	faeces_of_thoroughbred_horse	SAMD00008721
cp400	89	2148103	152599	48732	32.8	2286	1	0	0	pre-weaned_piglet_faeces	SAMEA3138854
AH4331	177	2090404	196933	51266	32.9	2254	1	0	2	human_ileo-cecal_region	SAMN06163250
AH4231	186	2095546	196492	51450	32.9	2260	1	0	2	human_ileo-cecal_region	SAMN06163249
AH43324	114	2176341	196739	53856	32.8	2319	1	0	1	human_ileo-cecal_region	SAMN06163251
CCuG45735	77	1949679	199587	61326	32.7	1982	1	0	1	human_blood	SAMN06163256
CCuG44481	119	1946114	255195	63223	32.7	2013	1	0	1	bird	SAMN06163255
866	82	1973474	239143	67307	32.6	2019	1	0	0	clinical_isolate_ICU	SAMN03198074
AH43348	109	2026883	186083	73962	32.6	2177	1	1	1	human_ileo-cecal_region	SAMN06163252
01M14315	87	1933921	212516	78580	33	1965	1	0	1	human_gallbladder_pus	SAMN06163248
DSM20555	63	1982794	244105	80533	32.4	2000	1	0	0	human_saliva	SAMN02369414
L21	74	1956328	215606	95624	32.7	2015	1	0	1	human_faeces	SAMN06163270
NCIMB8816	77	1859216	465152	106164	32.8	1886	1	0	2	human_saliva	SAMN06163274
JCM1044	59	1800424	465193	115042	32.6	1799	1	0	0	human_intestine	SAMN06163266
JCM1042	60	1802147	465022	115144	32.6	1800	1	0	0	human_intestine	SAMN06163265
CCuG2753OB	48	1801346	465248	115144	32.6	1799	1	0	0	human_abdomen_abcess	SAMN06163253
NCIMB702343	83	1922903	646361	119088	32.8	1953	1	0	0	unknown	SAMN06163273
CCuG38008	91	1936298	463867	122107	32.7	1972	1	0	2	human_gall,73-year-old_male	SAMN06163254
gul-2	81	2002733	521962	126351	32.5	2027	1	0	0	root_canal	SAMN06163263
ATCC11741	54	1995868	274210	126392	32.5	2011	1	0	0	human_HMP_ref	SAMN00001483
JCM1040	66	1922028	421976	133271	32.8	1951	1	0	1	human_intestine	SAMN06163264
CCuG47171	140	2040146	353585	136925	32.9	2152	1	0	2	human_tooth_plaque	SAMN06163257
CCuG47826	71	1980366	279863	142710	32.8	2044	1	0	1	human_blood,55-year-old_female	SAMN06163259
JCM1230	82	1723361	400300	151438	32.6	1719	0	0	0	chicken_intestine	SAMN06163269
JCM1045	69	1928686	331541	153948	32.7	1964	1	0	0	human_intestine	SAMN06163267
gul-1	75	2001390	521857	162200	32.5	2026	1	0	0	root_canal	SAMN06163262
778	44	1942335	332399	164413	32.7	1947	1	0	1	clinical_isolate_ICU	SAMN03197988
DSM20554	74	1975060	334317	170258	32.6	2026	1	0	1	human_saliva	SAMN06163261
JCM1047	147	2222264	475807	178703	32.4	2345	1	1	1	swine_intestine	SAMN06163268
NCIMB8818	79	2013336	250622	180395	32.9	2103	1	0	1	St_lvel_cheese	SAMN06163276
DSM20492	32	1889334	481851	240870	32.6	1892	1	0	0	human_saliva	SAMN06163260
NCIMB8817	56	1831814	777665	294813	32.6	1852	1	0	1	turkey_faeces	SAMN06163275
GJ24	11	1995968	754247	502388	33	2028	1	0	1	human_intestine	SAMN02470918
SMXD51	10	1967688	1019433	1019433	32.9	1992	1	0	2	chicken_cecum	SAMN02470767
NIAS840	4	2046557	1705688	1705688	33	2032	2	0	1	chicken_faeces	SAMN02470897
Ren	3	1978364	1751565	1751565	33	2019	1	0	1	human_centanarian_faeces	SAMN02584770
UCC118	4	2133977	1827111	1827111	33	2264	1	0	2	human_ileo-cecal_region	SAMN02604111
CECT5713	4	2136138	1828169	1828169	33.1	2345	1	0	2	human_breast_milk/infant_faeces	SAMN02604101
JCM1046	5	2320461	1836297	1836297	32.9	2296	2	1	1	swine_intestine	SAMN02711722

strain	aene	contia	replicon	% identity	alignment length	e-value	BLAST score	aene lenath
779	ronA 1511720		мр	00 21	25 <i>1</i>	2 00E 165	507	25A
770	ropE_LSL1740	NODE 46		00.00	204	0.001 105	507	234
778	nept_L3L1740	NODE 46		99.09	330	2 005 170	550	330
//8	parA_LSL1741	NODE_46	IVIP	99.63	270	2.00E-179	550	270
866	repA_LSL1739	NODE_//	MP	99.21	254	8.00E-165	507	254
866	repE_LSL1740	NODE_77	MP	96.06	330	0	644	330
866	parA_LSL1741	NODE_77	MP	99.63	270	2.00E-179	550	270
01M14315	repA_LSL1739	contig_34	MP	99.21	254	7.00E-165	507	254
01M14315	repE_LSL1740	contig_34	MP	99.09	330	0	665	330
01M14315	parA_LSL1741	contig_34	MP	99.63	270	1.00E-179	550	270
ACS116	repA_LSL1739	contig_13	MP	98.82	254	1.00E-166	505	254
ACS116	repE_LSL1740	contig_13	MP	99.09	330	0	667	330
ACS116	parA LSL1741	contig 139	MP	99.16	239	1.00E-169	484	270
AH4231	repA LSL1739	contig 95	MP	99.21	254	8.00E-165	507	254
AH4231	repE_LSL1740	contig 95	MP	98.79	330	0	664	330
AH4231	narA ISI1741	contig 95	MP	99.63	270	2 00F-179	550	270
AH/331	ron / 1511730	contig_101	MD	99.09	254	2.00E 175	507	250
AH4331	ropE ISI1740	contig_101		09.21	204	0.001-105	507	234
AH4331		contig_101		98.79	330	2 005 170	504	350
AH4331	parA_LSL1741	contig_101	IVIP	99.63	270	2.00E-179	550	270
AH43324	repA_LSL1739	contig_44	MP	99.61	254	5.00E-166	510	254
AH43324	repE_LSL1740	contig_44	MP	95.45	330	0	644	330
AH43324	parA_LSL1741	contig_44	MP	100	270	3.00E-180	551	270
AH43348	repA_LSL1739	contig_70	MP	99.21	254	9.00E-165	507	254
AH43348	repE_LSL1740	contig_70	MP	98.79	330	0	664	330
AH43348	parA_LSL1741	contig_70	MP	99.63	270	2.00E-179	550	270
AH43348	parA_LSL1741	contig_69	MPL	93.7	270	3.00E-169	520	270
ATCC11741	repA_LSL1739	contig_37	MP	99.21	254	9.00E-165	506	254
ATCC11741	repE_LSL1740	contig 37	MP	96.06	330	0	644	330
ATCC11741	parA LSL1741	contig 37	MP	99.63	270	1.00E-179	550	270
CCuG2753OB	repA_LSI1739	contig 21	MP	99.21	254	7.00F-165	507	254
CCuG27530B	renF_ISI1740	contig 21	MP	98 79	330	0	663	330
CCuG27530B	$nar \Lambda S 17/1$	contig_21	MD	98.79	270	3 00F-178	546	270
CCuG27550B	ronA 1511720	contig_21		98.89	270	5.00L-178	507	270
CCuG38008	repA_LSL1739	contig_40		99.21	204	J.00L-10J	507	234
CCuG38008		contig_40		97.27	330	1 005 170	059	350
CCuG38008	parA_LSL1741	contig_40		99.63	270	1.00E-179	550	270
CCuG44481	repA_LSL1739	contig_46	MP	99.21	254	7.00E-165	507	254
CCuG44481	repE_LSL1740	contig_46	MP	96.36	330	0	646	330
CCuG44481	parA_LSL1741	contig_39	MP	99.63	270	0	550	270
CCuG45735	repA_LSL1739	contig_51	MP	99.21	254	8.00E-165	507	254
CCuG45735	repE_LSL1740	contig_51	MP	99.39	330	0	668	330
CCuG45735	parA_LSL1741	contig_51	MP	99.63	270	2.00E-179	550	270
CCuG47171	repA_LSL1739	contig_58	MP	98.43	254	3.00E-163	503	254
CCuG47171	repE_LSL1740	contig_58	MP	96.97	330	0	650	330
CCuG47171	parA_LSL1741	contig_58	MP	100	270	4.00E-180	551	270
CCuG47825	repA_LSL1739	contig_92	MP	99.21	254	7.00E-165	507	254
CCuG47825	repE LSL1740	contig 92	MP	99.39	330	0	668	330
CCuG47825	parA LSL1741	contig 91	MP	99.63	270	0	550	270
CCuG47826	repA LSL1739	contig 36	MP	99.21	254	8.00E-165	507	254
CCuG47826	repF_LSL1740	contig 36	MP	99 39	330	0	668	330
CCuG47826	$nar \Delta I SI 1741$	contig 36	MP	99.63	270	2 00F-179	550	270
CECT5713	ron / 1511730	contig_30	MD	99.03	254	9 00F-165	507	250
CECTE 712	ropE ISI1740	contig_4		07.27	204	9.00L-105	507	234
CECT5713	nept_L3L1740	contig_4		97.27	330	2 005 170	039	330
CEC15/13	parA_LSL1741	contig_4	IVIP	99.63	270	2.00E-179	550	270
cp400	repA_LSL1739	contig_16	MP	99.21	254	7.00E-165	507	254
cp400	repE_LSL1740	contig_16	MP	96.36	330	0	646	330
cp400	parA_LSL1741	contig_16	MP	99.63	270	2.00E-179	550	270
DSM18933	repA_LSL1739	NODE_63	С	78.74	254	3.00E-132	413	254
DSM18933	parA_LSL1741	NODE_63	С	86.62	269	8.00E-157	484	270
DSM20492	repA_LSL1739	contig_14	MP	98.82	254	3.00E-164	505	254
DSM20492	repE_LSL1740	contig_14	MP	95.76	330	0	644	330
DSM20492	parA_LSL1741	contig_14	MP	99.63	270	2.00E-179	550	270

DSM20554	repA_LSL1739	contig_26	MP	99.21	254	8.00E-165	507	254
DSM20554	repE_LSL1740	contig_26	MP	92.73	330	0	626	330
DSM20554	parA_LSL1741	contig_26	MP	99.26	270	1.00E-178	547	270
DSM20555	repA_LSL1739	Scaffold29	MP	99.21	254	6.00E-165	506	254
DSM20555	repE_LSL1740	Scaffold29	MP	96.06	330	0	644	330
DSM20555	parA LSL1741	Scaffold33	MP	99.63	270	3.00E-180	550	270
GJ24	repA LSL1739	contig 9	MP	99.61	254	2.00E-165	509	254
GJ24	repE_LSL1740	contig 9	MP	95.15	330	0	641	330
GI24	narA SI 1741	contig 9	MP	99.63	270	2 00F-179	550	270
aul1	ren 1 SI 1730	contig_17	MD	00 21	250	0.00E-165	506	250
gul1	rope 1511740	contig_17		06.06	234	9.00L-105	500	234
guii		contig_17		90.00	350	1 005 170	044	350
gui	parA_LSL1741	contig_17	IVIP	99.03	270	1.00E-179	550	270
guiz	repA_LSL1739	contig_18	MP	99.21	254	9.00E-165	506	254
gul2	repE_LSL1740	contig_18	MP	96.06	330	0	644	330
gul2	parA_LSL1/41	contig_18	MP	99.63	270	1.00E-179	550	270
JCM1040	repA_LSL1739	contig_30	MP	99.21	254	7.00E-165	507	254
JCM1040	repE_LSL1740	contig_30	MP	99.7	330	0	671	330
JCM1040	parA_LSL1741	contig_30	MP	99.26	270	7.00E-179	548	270
JCM1042	repA_LSL1739	contig_27	MP	99.21	254	7.00E-165	507	254
JCM1042	repE_LSL1740	contig_27	MP	98.79	330	0	663	330
JCM1042	parA_LSL1741	contig_27	MP	98.89	270	3.00E-178	546	270
JCM1044	repA_LSL1739	contig_23	MP	99.21	254	7.00E-165	507	254
JCM1044	repE LSL1740	contig 23	MP	98.79	330	0	663	330
JCM1044	parA LSL1741	contig 23	MP	98.89	270	3.00E-178	546	270
JCM1045	repA LSL1739	contig 30	MP	99.21	254	8.00E-165	507	254
JCM1045	repE_LSL1740	contig 30	MP	99.39	330	0	668	330
ICM1045	narA SI 1741	contig 30	MP	99.63	270	2 00F-179	550	270
ICM1046	ren Δ ISI1739	contig_65	MP	99.21	254	8 00F-166	507	254
JCM1046	repF_LSL1740	contig_65	MD	96.67	330	0.001 100	648	330
JCM1040	$repl_lsl1740$	contig_65		90.67	270	0	550	270
JCIVI1040	parA_L3L1741	contig_03		99.03	270	2 005 162	500	270
JCIVI1047	repA_LSL1739	contig_34	IVIP	98.43	254	3.00E-103	503	254
JCIVI1047	repE_LSL1740	contig_34	IVIP	95.45	330	0	642	330
JCM1047	parA_LSL1741	contig_34	MP	99.63	270	2.00E-179	550	270
L21	repA_LSL1739	contig_44	MP	99.21	254	8.00E-165	507	254
L21	repE_LSL1740	contig_44	MP	99.39	330	0	668	330
L21	parA_LSL1741	contig_44	MP	99.63	270	2.00E-179	550	270
LMG14476	repA_LSL1739	contig_42	MP	98.82	254	3.00E-164	505	254
LMG14476	repE_LSL1740	contig_42	MP	95.15	330	0	640	330
LMG14476	parA_LSL1741	contig_42	MP	99.63	270	2.00E-179	550	270
LMG14477	repA_LSL1739	contig_41	MP	98.82	254	3.00E-164	505	254
LMG14477	repE_LSL1740	contig_41	MP	95.15	330	0	640	330
LMG14477	parA_LSL1741	contig_41	MP	99.63	270	2.00E-179	550	270
NCIMB702343	repA_LSL1739	NODE_62	MP	99.61	254	2.00E-165	509	254
NCIMB702343	repE LSL1740	NODE 62	MP	95.45	330	0	644	330
NCIMB702343	parA LSL1741	NODE 62	MP	99.63	270	2.00E-179	550	270
NCIMB8816	repA LSL1739	contig_35	MP	99.21	254	7.00E-165	507	254
NCIMB8816	repF_LSI1740	contig 35	MP	98.79	330	0	663	330
NCIMB8816	$nar\Delta ISI1741$	contig 35	MP	98.89	270	3 00F-178	546	270
NCIMB8817	renA \$11739	contig 19	MP	99.05	250	7.00E-165	507	250
	ropE_LSL1740	contig_19	MD	06.26	234	7.002 105	645	224
		contig_19		90.30	330	2 OOE 170	04J	330
		contig_19		99.05	270	2.00E-179	530	270
	repA_LSL1739	contig_33		99.21	254	8.00E-105	507	254
	rept_LSL1740	contig_33		99.39	330	0	668 	330
NCIMB8818	parA_LSL1/41	contig_33	IVIP MD	99.63	270	2.00E-1/9	550	270
NIAS840	repA_LSL1739	contig_3	MP	98.43	254	3.00E-163	503	254
NIAS840	repE_LSL1740	contig_3	MP	95.45	330	0	642	330
NIAS840	parA_LSL1741	contig_3	MP	100	270	4.00E-180	551	270
Ren	repA_LSL1739	plasmid_1	MP	99.21	254	8.00E-165	507	254
Ren	repE_LSL1740	plasmid_1	MP	99.09	330	0	665	330
Ren	parA_LSL1741	plasmid_1	MP	99.63	270	2.00E-179	550	270
SMXD51	repA_LSL1739	contig_7	MP	99.44	179	8.00E-140	357	254

SMXD51	repE_LSL1740	contig_7	MP	96.36	330	0	646	330
SMXD51	parA_LSL1741	contig_7	MP	99.63	270	2.00E-179	550	270
UCC118	repA_LSL1739	contig_4	MP	100	254	2.00E-166	511	254
UCC118	repE_LSL1740	contig_4	MP	95.45	330	0	644	330
UCC118	parA_LSL1741	contig_4	MP	100	270	5.00E-180	551	270

strain	AOI	replicon	bacteriocin	class
778	AOI 1	chromosome	enterolysin A	III
778	AOI 1	chromosome	enterolysin A	Ш
866	AOI 1	chromosome	enterolysin A	III
866	AOI 1	chromosome	enterolysin A	III
866	AOI 1	megaplasmid	salivaricin P	П
01M14315	AOI 1	chromosome	enterolysin A	III
01M14315	AOI 1	chromosome	enterolysin A	Ш
ACS116	AOI 1	chromosome	enterolysin A	III
ACS116	AOI 1	chromosome	enterolysin A	III
ACS116	AOI 1	chromosome	enterolysin A	III
ACS116	AOI 1	chromosome	enterolysin A	111
ACS116	AOI 1	megaplasmid	salivaricin P	II
AH4231	AOI 1	chromosome	enterolysin A	Ш
AH4231	AOI 1	chromosome	enterolysin A	Ш
AH4231	AOI 1	chromosome	enterolysin A	111
AH4231	AOI 1	megaplasmid	salivaricin P	II
AH4331	AOI 1	chromosome	enterolysin A	III
AH4331	AOI 1	chromosome	enterolysin A	III
AH4331	AOI 1	chromosome	enterolysin A	111
AH4331	AOI 1	megaplasmid	salivaricin P	II
AH43324	AOI 1	chromosome	enterolysin A	III
AH43324	AOI 1	chromosome	enterolysin A	111
AH43324	AOI 1	chromosome	enterolysin A	111
AH43324	AOI 1	megaplasmid	salivaricin P	II
AH43348	AOI 1	chromosome	enterolysin A	111
AH43348	AOI 1	chromosome	enterolysin A	111
AH43348	AOI 1	chromosome	enterolysin A	111
AH43348	AOI 1	megaplasmid	salivaricin P	II
ATCC11741	AOI 1	chromosome	enterolysin A	111
CCUG2753OB	AOI 1	chromosome	enterolysin A	III
CCUG2753OB	AOI 1	megaplasmid	LS2	II
CCUG38008	AOI 1	chromosome	enterolysin A	III
CCUG38008	AOI 1	chromosome	enterolysin A	III
CCUG38008	AOI 1	megaplasmid	salivaricin P	II
CCUG44481	AOI 1	chromosome	enterolysin A	III
CCUG44481	AOI 1	megaplasmid	plantaricin S	II
CCUG44481	AOI 2	megaplasmid	plantaricin NC8	II
CCUG44481	AOI 2	megaplasmid	lactacin F	Ш
CCUG44481	AOI 2	megaplasmid	acidocin LF221B	Ш
CCUG44481	AOI 2	megaplasmid	salivaricin P	II
CCUG45735	AOI 1	chromosome	enterolysin A	111
CCUG45735	AOI 1	chromosome	enterolysin A	111
CCUG45735	AOI 1	megaplasmid	salivaricin P	II
CCUG47171	AOI 1	chromosome	enterolysin A	III
CCUG47171	AOI 1	chromosome	enterolysin A	III
CCUG47171	AOI 1	megaplasmid	plantaricin NC8	II
CCUG47171	AOI 1	megaplasmid	lactacin F	II
CCUG47171	AOI 1	megaplasmid	acidocin LF221B	II
CCUG47171	AOI 1	megaplasmid	salivaricin P	II

CCUG47825	AOI 1	chromosome	enterolysin A	111
CCUG47825	AOI 1	chromosome	enterolysin A	III
CCUG47826	AOI 1	chromosome	enterolysin A	Ш
CCUG47826	AOI 1	chromosome	enterolysin A	Ш
CCUG47826	AOI 1	chromosome	enterolysin A	III
CCUG47826	AOI 1	megaplasmid	salivaricin P	П
CECT5713	AOI 2	chromosome	enterolysin A	111
CECT5713	AOI 3	chromosome	enterolysin A	111
CECT5713	AOI 4	chromosome	enterolysin A	Ш
CECT5713	AOI 1	megaplasmid	salivaricin P	П
cp400	AOI 1	chromosome	enterolysin A	Ш
cp400	AOI 1	chromosome	enterolysin A	Ш
cp400	AOI 1	megaplasmid	salivaricin P	П
DSM18933	AOI 1	chromosome	enterolysin A	Ш
DSM18933	AOI 1	chromosome	enterolysin A	Ш
DSM20492	AOI 1	chromosome	enterolysin A	Ш
DSM20554	AOI 1	chromosome	enterolysin A	Ш
DSM20554	AOI 1	chromosome	enterolysin A	Ш
DSM20554	AOI 1	small plasmid	MR10B	П
DSM20555	AOI 1	chromosome	enterolysin A	Ш
GJ24	AOI 1	chromosome	enterolysin A	Ш
GJ24	AOI 1	megaplasmid	plantaricin S	П
GJ24	AOI 2	megaplasmid	plantaricin NC8	Ш
GJ24	AOI 2	megaplasmid	salivaricin P	П
gul1	AOI 1	chromosome	enterolysin A	Ш
gul2	AOI 1	chromosome	enterolysin A	Ш
JCM1040	AOI 1	chromosome	enterolysin A	Ш
JCM1040	AOI 1	chromosome	enterolysin A	Ш
JCM1042	AOI 1	chromosome	enterolysin A	Ш
JCM1042	AOI 1	megaplasmid	LS2	Ш
JCM1044	AOI 1	chromosome	enterolysin A	Ш
JCM1044	AOI 1	megaplasmid	LS2	П
JCM1045	AOI 1	chromosome	enterolysin A	Ш
JCM1045	AOI 1	megaplasmid	enterolysin A	Ш
JCM1046	AOI 1	chromosome	enterolysin A	Ш
JCM1046	AOI 1	megaplasmid	salivaricin P	Ш
JCM1046	AOI 1	linear megaplasmid	enterolysin A	Ш
JCM1046	AOI 1	small plasmid	MR10B	П
JCM1047	AOI 1	chromosome	enterolysin A	Ш
JCM1047	AOI 1	small plasmid	MR10B	Ш
JCM1047	AOI 1	megaplasmid	salivaricin P	Ш
JCM1047	AOI 1	linear megaplasmid	enterolysin A	Ш
JCM1230	AOI 1	chromosome	enterolysin A	Ш
L21	AOI 1	chromosome	enterolysin A	Ш
L21	AOI 1	chromosome	enterolysin A	Ш
L21	AOI 1	megaplasmid	salivaricin P	П
LMG14476	AOI 1	chromosome	enterolysin A	Ш
LMG14476	AOI 1	chromosome	enterolysin A	Ш
LMG14476	AOI 1	megaplasmid	salivaricin P	П
LMG14477	AOI 1	chromosome	enterolysin A	Ш

LMG14477	AOI 1	chromosome	enterolysin A	
LMG14477	AOI 1	megaplasmid	salivaricin P	Ш
NCIMB702343	AOI 1	chromosome	enterolysin A	III
NCIMB702343	AOI 1	chromosome	enterolysin A	111
NCIMB702343	AOI 1	megaplasmid	salivaricin P	Ш
NCIMB8816	AOI 1	megaplasmid	LS2	Ш
NCIMB8816	AOI 1	chromosome	enterolysin A	III
NCIMB8817	AOI 1	chromosome	enterolysin A	III
NCIMB8818	AOI 1	chromosome	enterolysin A	III
NCIMB8818	AOI 1	chromosome	enterolysin A	III
NCIMB8818	AOI 1	megaplasmid	salivaricin P	Ш
NIAS840	AOI 1	chromosome	enterolysin A	III
Ren	AOI 1	chromosome	enterolysin A	III
Ren	AOI 2	chromosome	enterolysin A	III
SMXD51	AOI 1	chromosome	enterolysin A	III
SMXD51	AOI 1	megaplasmid	LS2	П
UCC118	AOI 1	chromosome	enterolysin A	
UCC118	AOI 2	chromosome	enterolysin A	III
UCC118	AOI 3	chromosome	enterolysin A	III
UCC118	AOI 1	megaplasmid	salivaricin P	П

strain	classification	taxon nucleotide %	taxon nucleotides	contig count
01M14315	Lactobacillus_salivarius	97.9012	1755411	67
01M14315	unclassified	1.96655	35261	6
01M14315	Lactobacillus_fermentum	0.124593	2234	1
01M14315	Lactobacillus_casei_group	0.00764064	137	1
778	Lactobacillus_salivarius	99.3133	1921066	36
778	unclassified	0.686742	13284	1
866	Lactobacillus salivarius	100	1963667	75
ACS116	 Lactobacillus salivarius	100	1956854	132
AH4231	 Lactobacillus salivarius	97.1495	1950134	121
AH4231	unclassified	2.45587	49298	32
AH4231	Lactobacillus casei group	0.212867	4273	9
AH4231	Lactobacillus fermentum	0.181732	3648	2
AH4331	Lactobacillus salivarius	97.1714	1947771	115
AH4331	unclassified	2 47302	49571	
AH4331	Lactobacillus casei group	0 181594	3640	8
ΔΗ4331	Lactobacillus fermentum	0.101004	3488	1
AH/332/	Lactobacillus salivarius	98 / 57/	19/2606	87
AH43324 AH43324	unclassified	1 5/250	20426	1
AH43324 AH43324	Lactobacillus salivarius	1.04255	2028360	100
ATTC11741		00 0019	100777	109
ATCC11741		0.01010	105/727	40
ATCC11741	Convoltation autimusosum	0.0464641	921	4
ATCC11741	Corynebacterium_aurimucosum	0.0243730	403	2
ATCC11741	Erysipelotnix_musiopathiae	0.0126869	241	1
ATCC11/41	Rhodococcus_equi	0.0126869	241	1
CCUG2753OB		100	1790291	42
CCuG38008	Lactobacillus_salivarius	98.1458	1895829	67
CCuG38008	unclassified	1.82684	35288	10
CCuG38008	Lactobacillus_casei_group	0.0273342	528	2
CCuG44481	Lactobacillus_salivarius	96.0994	1812482	54
CCuG44481	unclassified	2.94823	55605	5
CCuG44481	Lactobacillus_reuteri	0.738793	13934	1
CCuG44481	Clostridium_spSY8519	0.213621	4029	1
CCuG45735	Lactobacillus_salivarius	99.9105	1947895	69
CCuG45735	Lactobacillus_helveticus	0.0802713	1565	1
CCuG45735	unclassified	0.00918119	179	1
CCuG47171	Lactobacillus_salivarius	97.6392	1974695	82
CCuG47171	unclassified	1.87664	37954	22
CCuG47171	Lactobacillus_casei_group	0.32352	6543	7
CCuG47171	Lactobacillus_plantarum	0.160598	3248	1
CCuG47825	Lactobacillus_salivarius	99.8319	1786862	97
CCuG47825	unclassified	0.114757	2054	3
CCuG47825	Streptococcus_dysgalactiae_group	0.0323487	579	2
CCuG47825	Citrobacter_rodentium_ICC168	0.0209512	375	1
CCuG47826	Lactobacillus_salivarius	99.1878	1940444	50
CCuG47826	unclassified	0.783915	15336	5
CCuG47826	Lactobacillus_sanfranciscensis	0.0221332	433	3
CCuG47826	Lactobacillus_casei_group	0.00618504	121	1
CECT5713	Lactobacillus_salivarius	100	2136138	4
cp400	Lactobacillus_salivarius	98.7922	2016437	72
cp400	Lactobacillus_reuteri	1.20779	24652	2
DSM18933	unclassified	93.4389	6964	18
DSM18933	Lactobacillus_salivarius	6.56112	489	3
DSM20492	Lactobacillus_salivarius	100	1890069	30
DSM20554	Lactobacillus_salivarius	100	1949872	51
DSM20555	Lactobacillus_salivarius	100	1874089	44

GJ24	Lactobacillus_salivarius	99.7466	1986988	8
GJ24	unclassified	0.253359	5047	1
gul1	Lactobacillus_salivarius	100	1907028	62
gul2	Lactobacillus_salivarius	99.982	1908848	68
gul2	unclassified	0.011628	222	1
gul2	Lactobacillus_johnsonii	0.00633776	121	1
JCM1040	Lactobacillus_salivarius	98.5093	1822228	46
JCM1040	unclassified	1.48416	27454	7
JCM1040	Lactobacillus_casei_group	0.00654124	121	1
JCM1042	Lactobacillus_salivarius	100	1789991	54
JCM1044	Lactobacillus_salivarius	100	1788967	53
JCM1045	Lactobacillus_salivarius	100	1928808	64
JCM1046	Lactobacillus_salivarius	94.2248	1802918	91
JCM1046	unclassified	4.7194	90302	6
JCM1046	Lactobacillus_reuteri	1.0558	20202	3
JCM1047	Lactobacillus_salivarius	98.613	2040949	81
JCM1047	unclassified	1.38704	28707	1
JCM1230	Lactobacillus_salivarius	100	1656507	38
L21	Lactobacillus_salivarius	99.7884	1927838	60
L21	unclassified	0.195349	3774	5
L21	Lactobacillus_sanfranciscensis	0.0162532	314	2
LMG14476	Lactobacillus_salivarius	100	1887993	157
LMG14477	Lactobacillus_salivarius	99.99	1822244	144
LMG14477	unclassified	0.00998669	182	1
NCIMB702343	Lactobacillus_salivarius	99.9607	1884140	42
NCIMB702343	unclassified	0.0393128	741	2
NCIMB8816	Lactobacillus_salivarius	99.0933	1820558	61
NCIMB8816	unclassified	0.785101	14424	7
NCIMB8816	Lactobacillus_casei_group	0.121597	2234	1
NCIMB8817	Lactobacillus_salivarius	100	1814802	45
NCIMB8818	Lactobacillus_salivarius	97.8194	1970529	67
NCIMB8818	unclassified	1.99051	40098	9
NCIMB8818	Lactobacillus_casei_group	0.120231	2422	2
NCIMB8818	Streptococcus_anginosus_group	0.0698948	1408	1
NIAS840	Lactobacillus_salivarius	100	1866462	3
Ren	Lactobacillus_salivarius	100	1978364	3
SMXD51	Lactobacillus_salivarius	98.4374	1928066	8
SMXD51	unclassified	1.56264	30607	1
UCC118	Lactobacillus_salivarius	100	2133977	4

	UCC118 +	UCC118 -	CECT5713 +	CECT5713 -	NIAS840 +	NIAS840 -	Ren +	Ren -
chromosome	100	0	100	0	100	0	100	0
megaplasmid 1	100	0	100	0	97.5	2.5	85.3	14.7
megaplasmid 2	NA	NA	NA	NA	8.3	91.7	NA	NA
small plasmid 1	100	0	100	0	0	100	90.7	9.3
small plasmid 2	100	0	100	0	NA	NA	NA	NA

Aspartic (A) Peptidases		
FAMILY	SUBFAMILY	TYPE ENZYME
A1	A1A	pepsin A (Homo sapiens)
۵2	A1B A2A	nepentnesin (Nepentnes gracilis) HIV-1 retronensin (human immunodeficiency virus 1)
n£	A2B	Tv3 transposon pertidas (Saccharomyces cerevisiae)
	A2C	Gypsy transposon peptidase (Drosophila melanogaster)
	A2D	Osvaldo retrotransposon peptidase (Drosophila buzzatii)
A3	A3A	cauliflower mosaic virus-type peptidase (cauliflower mosaic virus)
45	A3B	bacilliform virus peptidase (rice tungro bacilliform virus)
AS		tnermopsin (suitoioous aciaocaidarius)
A9		signa pepulase in (Eschara con) soumapensin (human soumaretrovirus)
A11	A11A	Copia transposon peptidase (Drosophila melanogaster)
	A11B	Ty1 transposon peptidase (Saccharomyces cerevisiae)
A22	A22A	presenilin 1 (Homo sapiens)
	A22B	impas 1 peptidase (Homo sapiens)
A24	A24A	type 4 prepilin peptidase 1 (Pseudomonas aeruginosa)
۵25	AZ4B	riak peptuase (ivietnanococcus maripaluuis) anr nentifase (Barillus megaterium)
A26		omptin (Escherichia coli)
A28	A28A	DNA-damage inducible protein 1 (Saccharomyces cerevisiae)
	A28B	skin SASPase (Mus musculus)
A31		HybD peptidase (Escherichia coli)
A32		PerP peptidase (Caulobacter crescentus)
A36 Oustaine (C) Pentidases		sporulation factor SpoligA (Bacilius subtilis)
FAMILY	SUBFAMILY	TYPE ENZYME
C1	C1A	papain (Carica papaya)
	C1B	bleomycin hydrolase (Saccharomyces cerevisiae)
C2	C2A	calpain-2 (Homo sapiens)
C3	C3A	poliovirus-type picornain 3C (human poliovirus 1)
	C3B	enterovirus picornain 2A (human poliovirus 1)
	C3C	toot-and-mouth disease virus picornain 3C (toot-and-mouth disease virus)
	C3D	cowpea mosaic comovinus-type promiamise (cowpea mosaic virus) henastitis A virus-type promiamise (cowpea mosaic virus)
	C3F	parechovirus picornain 3C (human parechovirus 1)
	C3G	rice tungro spherical virus-type peptidase (rice tungro spherical virus)
	C3H	grapevine fanleaf-type nepovirus picornain 3C (grapevine fanleaf virus)
C4		nuclear-inclusion-a peptidase (plum pox virus)
C5		adenain (human adenovirus type 2)
C6		potato virus Y-type helper component peptidase (potato virus Y)
C7		Chestnut bilgin Lungus virus p29 peptidase (Cryphonectria hypovirus)
C9		sindbis virus-tvoe nsP2 peptidase (Sindbis virus)
C10		streptopain (Streptococcus pyogenes)
C11		clostripain (Clostridium histolyticum)
C12		ubiquitinyl hydrolase-L1 (Homo sapiens)
C13		legumain (Canavalia ensiformis)
C14	C14A	caspase-1 (Rattus norvegicus)
C15	C14B	metadaspase (cal (Saccharomyces cerevisiae)
C16	C16A	pyroginaliny peptiador (because any composition of the pentides of the pentid
	C16B	murine hepatitis coronavirus papain-like peptidase 2 (murine hepatitis virus)
C18		hepatitis C virus peptidase 2 (hepatitis C virus)
C19		ubiquitin-specific peptidase 14 (Homo sapiens)
C21		tymovirus peptidase (turnip yellow mosaic virus)
C23		carlavirus peptidase (apple stem pitting virus)
C24		rabbit hemorrhagit disease virus sc-inke peptidase (rabbit hemorrhagit disease virus) anaginan RenA (Pornhyromonas a anagina)
C26		amma-gutamvl hydrolase (Ratus norvegicus)
C27		rubella virus peptidase (Rubella virus)
C28		foot-and-mouth disease virus L-peptidase (foot-and-mouth disease virus)
C30		porcine transmissible gastroenteritis virus-type main peptidase (transmissible gastroenteritis virus)
C31		porcine reproductive and respiratory syndrome arterivirus-type cysteine peptidase alpha (lactate-dehydrogenase-elevating virus)
C32		equine arteritis virus-type cysteine peptidase (porcine reproductive and respiratory syndrome virus)
C36		equine arterius virus vsp2-type cysteme pepudase (equine arterius virus) heat necrofic vallow vain furovirus,two enable-like pentidase (heat necrofic vallow vein virus)
C37		calicivitin (Southamor virus)
C39		bacteriocin-processing peptidase (Pediococcus acidilactici)
C40		dipeptidyl-peptidase VI (Lysinibacillus sphaericus)
C42		beet yellows virus-type papain-like peptidase (beet yellows virus)
C44		amidophosphoribosyltransferase precursor (Homo sapiens)
C45		acyl-coenzyme A:b-aminopenicillanic acid acyl-transferase precursor (Penicillium chrysogenum) bodarbog protein (Desconbile melopagastor)
C48		reciping proceim (process) and interaction and a set of the set of
C48		Ulp1 peptidase (Saccharomyces cerevisiae)
C50		separase (Saccharomyces cerevisiae)
C51		D-alanyl-glycyl peptidase (Staphylococcus aureus)
C53		pestivirus Npro peptidase (classical swine fever virus)
C54		autophagin-1 (Homo sapiens)
C55		ropi protein (retsilla pseudotuberculosis) Pfol paptidase (Pyrocoscy furiosus)
C57		vaccinia virus I7L processing peptidase (Vaccinia virus)
C58	C58A	YopT peptidase (Yersinia pestis)
	C58B	HopN1 peptidase (Pseudomonas syringae)
C59		penicillin V acylase precursor (Lysinibacillus sphaericus)
C60	C60A	sortase A (Staphylococcus aureus)
	C60B	sortase B (Staphylococcus aureus)
C62		gill-associated virus 3C-like peptidase (gill-associated virus)
C64		Annan swine rever virus processing peptidase (Annan swine rever VIPUS) Cezanne nentidase (Homo saniens)
C65		otubain-1 (Homo sapiens)
C66		IdeS peptidase (Streptococcus pyogenes)
C67		CylD peptidase (Homo sapiens)
C69		dipeptidase A (Lactobacillus helveticus)

C71		Avirpiz peptidase (rseudononas synngae)
		pseudomurein endoisopeptidase Pei (Methanobacterium phage psiM2)
C74		pestivirus NS2 peptidase (bovine viral diarrhea virus 1)
C75		AgrB peptidase (Staphylococcus aureus)
C76		viral tegument protein deubiquitinylating peptidase (human herpesvirus 1)
C78		UfSP1 peptidase (Mus musculus)
C79		ElaD peptidase (Escherichia coli)
C80		RTX self-cleaving toxin (Vibrio cholerae)
C82	C82A	L,D-transpeptidase (Enterococcus faecium)
C83		gamma-glutamylcysteine dipeptidyltranspeptidase (Nostoc sp. PCC 7120)
C84		prtH peptidase (Tannerella forsythia)
C85	C85A	OTLD1 deubiguitinylating enzyme (Homo sapiens)
	C85B	OTU1 peptidase (Saccharomyces cerevisiae)
C86		ataxin-3 (Homo saniens)
C87		nairovirus deubiquitinylating pentidase (Crimean-Congo bemorrhagic fever virus)
(89		acid ceramidase precursor (Homo sapiens)
683		
C95		Lapo peptidase (Pseudonionas nuorescens)
695		No in a second de la contraction de la contracti
095		McjB peptidase (Escherichia coli)
(97		DeSI-1 peptidase (Mus musculus)
098		USPL1 peptidase (Homo sapiens)
C99		iflavirus processing peptidase (Ectropis obliqua picorna-like virus)
C101		OTULIN peptidase (Homo sapiens)
C102		GtgE peptidase (Salmonella enterica)
C104		PlyC phage lysin (Streptococcus phage C1)
C105		papain-like peptidase 1 alpha (simian hemorrhagic fever virus)
C107		alphamesonivirus 3C-like peptidase (Cavally virus)
C108		Prp peptidase (Staphylococcus aureus)
C110		kyphoscoliosis peptidase (Mus musculus)
C111		coagulation factor XIIIa (Homo sapiens)
C113		IgdE peptidase (Streptococcus suis)
Glutamic (G) Peptidases		
FAMILY	SUBFAMILY	TYPE ENZYME
61	5051741121	scytalidoglutamic pentidase (Scytalidium lignicolum)
63		pro pock appondage protoin (bactorionhage nhi 20)
Gz Matella (M) Deptideses		pre-neck appendage protein (bacteriophage prii-25)
Metallo (M) Peptidases	CUREARANY	
FAMILY	SUBFAIVILLY	ITPE ENZIVE
		aminopeptidase N (Homo sapiens)
M2		angiotensin-converting enzyme peptidase unit 1 (Homo sapiens)
M3	M3A	thimet oligopeptidase (Rattus norvegicus)
	M3B	oligopeptidase F (Lactococcus lactis)
M4		thermolysin (Bacillus thermoproteolyticus)
M5		mycolysin (Streptomyces cacaoi)
M6		immune inhibitor A peptidase (Bacillus thuringiensis)
M7		snapalysin (Streptomyces lividans)
M8		leishmanolysin (Leishmania major)
M9	M9A	bacterial collagenase V (Vibrio alginolyticus)
	M9B	bacterial collagenase H (Clostridium histolyticum)
M10	M10A	matrix metallopeptidase-1 (Homo sapiens)
	M10B	serralysin (Serratia marcescens)
	M10C	fragilysin (Bacteroides fragilis)
M11	WILDC	aamatalucin (Chlamudamanac rainhardtii)
M11		gametorysin (chianiyuononas rennarutii)
M12	MIZA	astacin (Astacus astacus)
	M12B	adamalysin (Crotalus adamanteus)
M13		neprilysin (Homo sapiens)
M14	M14A	carboxypeptidase A1 (Homo sapiens)
	M14B	carboxypeptidase E (Bos taurus)
	M14C	gamma-D-glutamylmeso-diaminopimelate peptidase I (Lysinibacillus sphaericus)
	M14D	cytosolic carboxypeptidase 6 (Homo sapiens)
M15	M15A	zinc D-Ala-D-Ala carboxypeptidase (Streptomyces albus)
	M15B	vanY D-Ala-D-Ala carboxypeptidase (Enterococcus faecium)
	M15C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118)
	M15C M15D	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium)
M16	M15C M15D M16A	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli)
M16	M15C M15D M16A M16B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing pontidase bata-subunit (Saccharomycar caravisiae)
M16	M15C M15D M16A M16B M16C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitidikris (Longo canienc)
M16	M15C M15D M16A M16B M16C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) Jeurine aminopentidase 3 (Bos taurus)
M16	M15C M15D M16A M16B M16C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) minopentidase 1 (Saccharomyces cerevicine)
M16 M17 M18	M15C M15D M16A M16B M16C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) emphrone dineatidase (Homo capienc)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) euptirilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) aminopeptidase I (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) guitamate carbovanentidase (Recordences cere)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C M20A	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C M20A M20B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C M20A M20A M20B M20C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C M20A M20A M20B M20C M20D	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Caa-His dipeptidase (Escherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus)
M16 M17 M18 M19 M20	M15C M16A M16A M16B M16C M20A M20B M20C M20D M20F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase 5s1 (Sulfolobus sofataricus) carnosine dipeptidase II (Mus musculus)
M16 M17 M18 M19 M20 M23	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20F M23A	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 3 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase I (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus)
M16 M17 M18 M19 M20	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20F M23A M23B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans)
M16 M17 M18 M19 M20 M23 M24	M15C M15D M16A M16B M16C M20B M20B M20B M20C M20D M20F M23A M23B M23A	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Carboxypeptidase Ss1 (Sulfolobus solfataricus) caroosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase I (Aromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24	M15C M15D M16A M16A M16B M16C M20A M20B M20C M20D M20D M20D M20D M20D M20A M23A M23A M23A M23A M24A M24B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase (Sscherichia coli) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24 M26	M15C M15D M16A M16B M16C M20B M20B M20B M20C M20D M20F M23A M238 M24A M248	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bostaurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bost aurus) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24 M26 M27	M15C M15D M16A M16A M16B M16C M20B M20B M20C M20D M20D M20D M20D M20A M23B M23A M23B M24A M24B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pltrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bos taurus) aminopeptidase (Escheromyces cerevisiae) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) gla1-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16A M16B M16C M20A M20B M20C M20D M20C M20D M20C M20D M20C M23B M24A M24B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Sscherichia coli) carboxypeptidase S1 (Sulfolobus sofataricus) carboxypeptidase S1 (Sulfolobus sofataricus) teat-lytic metallopeptidase (Acromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) (gA1-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20F M23A M23A M23A M24B M24A M24B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bost aurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase 7 (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) Carboxypeptidase (Escherichia coli) Carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) tentoxilysin (Clostridium tetani) aminopeptidase I (Streptoroccus griseus) glutamate carboxypeptidase II (Homo sapiens)
M16 M17 M18 M19 M20 M23 M24 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20A M20B M20B M20C M20D M20C M20D M20C M20D M20A M23A M23A M23A M23A M23A M23B M28A M28B M28C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bos taurus) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Carboxypeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) caronsine dipeptidase II (Mus musculus) beta-lytic metallopeptidase 1 (Escherichia coli) glutamatin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) gA1-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase II (Homo sapiens)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20B M20B M20C M20D M20C M20D M20C M20D M20F M23A M23B M24A M23B M24A M28B M28C M28D	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pltrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carosine dipeptidase I (Mus musculus) beta-lytic metallopeptidase (Acromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase S (Streptoonyces griseus) glutamate carboxypeptidase (Streptooccus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptoomyces griseus) glutamate carboxypeptidase (I-Momo sapiens) IAP aminopeptidase (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20C M20D M20A M23A M23B M24A M24B M24B M24B M28B M28C M28E M28E	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase 1 (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) lgA1-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase (Streptonyces griseus) glutamate carboxypeptidase (Escherichia coli) APA minopeptidase (Escherichia coli) aminopeptidase (Sterpetidase (Interpetidase) IAP aminopeptidase (Escherichia coli) aminopeptidase (Sterpetidase (Interpetidase) APA minopeptidase (Sterpetidase (Interpetidase) APA minopeptidase (Sterpetichia coli)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20B M20B M20B M20B M20C M20D M20F M23A M23B M24A M23B M24A M24B M28B M28C M28D M28C M28C M28C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bos taurus) membrane dipeptidase (Foeudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) glutamate carboxypeptidase S1 (Sulfolobus solfataricus) certosilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase IS (Streptonyces using) aminopeptidase S (Streptoroliticus) aminopeptidase S (Streptoricus) aminopeptidase S-62 (Acanthocheilonema viteae) aminopeptidase A (Vibrio proteolyticus)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20B M20B M20C M20D M20C M20D M20C M20D M20C M20D M20F M23A M24A M238 M238 M28A M28B M28C M28D M28E M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pltrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Sacherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguins) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase II (Sulfis)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20C M20D M20F M23A M23A M23B M24A M24B M24B M28A M28B M28C M28B M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Saccharomyces coffactione) carboxypeptidase (Saccharomyces coffactione) carboxypeptidase (Saccharomyces offacticus) carboxypeptidase (Saccharomyces offacticus) carboxypeptidase (Saccharomobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) lgA1-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase 5 (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase Ap1 (Vibrio proteolyticus) ywaD peptidase Ap1 (Vibrio proteolyticus) ywaD peptidase (Bacillus subtilis) aminopeptidase (Bacillus subtilis)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30	M15C M15D M16A M16A M16B M16C M20B M20B M20B M20B M20D M20F M23A M23B M24A M23B M24A M24B M28B M28B M28C M28D M28E M28E M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-O-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase II (Homo sapiens) IAP aminopeptidase (Scherichia coli) aminopeptidase S-62 (Acanthocheilonema viteae) aminopeptidase (Saclus ubilis) wwaD peptidase (Bacillus subtilis) wwaD peptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30 M32	M15C M15D M16A M16A M16B M16C M20B M20B M20C M20D M20C M20D M20C M20D M20C M20D M20F M23A M23B M23A M23B M23B M23B M23B M28B M28B M28C M28D M28B M28C M28D M28B M28C	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Sactaromyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) caronsine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguins) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase (Ischerichia coli) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase T (Thermus aquaticus)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30 M32 M34	M15C M15D M16A M16B M16C M20A M20B M20C M20D M20C M20D M20F M23A M23A M23B M24A M24B M24B M28A M28B M28A M28B M28C M28B M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) plrtilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Ischerichia coli) carboxypeptidase S1 (Sulfolobus softaricus) carboxypeptidase S1 (Sulfolobus softaricus) carboxypeptidase I (Sulfolobus softaricus) teat-ytic metallopeptidase (Acmonbacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) aminopeptidase S (Streptorocccus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase (I (Homo sapiens) IAP aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase S-63 (Acanthocheilonema viteae) aminopeptidase Ta (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase Taq (Thermus aquaticus) anthrax lethal factor (Bacillus anthracis)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30 M32 M34 M34 M35	M15C M15D M16A M16B M16C M20B M20B M20B M20B M20F M23A M23B M23A M23B M24A M24B M24B M28A M28B M28B M28B M28E M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-O-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase (St. (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase (Escherichia coli) aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase foli (Staphylococcus shutius) ywaD peptidase foli (Staphylococcus shutius) picolysin (Staphylococcus shutius) aminopeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase Taq (Thermus aquaticus) anthrax lethal factor (Bacillus anthracis) deuterolysin (Aspergillus flavus)
M16 M17 M18 M19 M20 M23 M24 M24 M26 M27 M28 M29 M30 M32 M34 M35 M35 M36	M15C M15D M16A M16A M16B M16C M20B M20B M20C M20D M20C M20D M20C M20D M20C M20D M20A M20A M20A M20A M20A M20A M23A M23A M23A M23A M23B M23A M28B M28C M28D M28E M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Escherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguins) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase I (Homo sapiens) IAP aminopeptidase T (Hermus aquaticus) aminopeptidase T (Achromcka coli) aminopeptidase T (Achromcka coli) aminopeptidase T (Maremus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase T (Thermus aquaticus) anthrax lethal factor (Bacillus subtilis) aminopeptidase T (Mermus aquaticus) anthrax lethal factor (Bacillus subtilis) aminopeptidase T (Mermus aquaticus) anthrax lethal factor (Bacillus subtilis) fungalysin (Aspergillus finuigatus)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M30 M30 M32 M34 M35 M36 M38	M15C M15D M16A M16B M16C M20A M20B M20B M20C M20D M20D M20D M20C M20D M20D M20P M20A M20B M20A M20B M20A M20A M20A M20A M20A M20A M20A M20A	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-D-Ala dipeptidase (Enterococcus faecium) plitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Bos taurus) aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase (Homo sapiens) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) Xaa-His dipeptidase (Escherichia coli) carboxypeptidase (St. Gulfolobus solfataricus) caronsine dipeptidase (I (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase 5 (Streptomyces griseus) glutamate carboxypeptidase (Escherichia coli) aminopeptidase 5 (Acanthocheilonema viteae) aminopeptidase 5 (Acanthocheilonema viteae) aminopeptidase 7 (Thermus aquaticus) hycolysin (Staphylococcus hycus) ywaD peptidase Taq (Thermus aquaticus) hycolysin (Aspergillus subtilis) anthrax lethal factor (Bacillus anthracis) deuterolysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) isoaspartyl dipeptidase (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30 M32 M34 M34 M35 M36 M38 M41	M15C M15D M16A M16B M16C M20B M20B M20B M20B M20C M20D M20F M23A M23A M23B M23A M24B M23A M24B M28A M28B M28B M28B M28B M28B M28B M28B M28B	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-O-la dipeptidase (Enterococcus faecium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase (Sscherichia coli) carboxypeptidase S1 (Sulfolobus solfataricus) carnosine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) aminopeptidase P (Escherichia coli) glutamate carboxypeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) LAP aminopeptidase (Streptovaccus sanjunis) tentoxilysin (Clostridium tetani) aminopeptidase F2 (Escherichia coli) aminopeptidase S1 (Vibro porteolyticus) ywaD peptidase (Stareptococcus supiens) LAP aminopeptidase (Streptovacy) aminopeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase T (Thermus aquaticus) anthrax lethal factor (Bacillus subtilis) authrax lethal factor (Bacillus subtilis) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fisoaspartyl dipeptidase (Escherichia coli)
M16 M17 M18 M19 M20 M23 M24 M26 M27 M28 M29 M30 M32 M34 M35 M36 M38 M41 M41 M42	M15C M15D M16A M16A M16B M16C M20B M20B M20B M20B M20D M20F M23A M23B M24A M23B M24A M24B M28A M28B M28C M28D M28E M28F	Ply118 L-Ala-D-Glu peptidase (bacteriophage A118) vanX D-Ala-O-la dipeptidase (Enterococcus facium) pitrilysin (Escherichia coli) mitochondrial processing peptidase beta-subunit (Saccharomyces cerevisiae) eupitrilysin (Homo sapiens) leucine aminopeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) membrane dipeptidase 1 (Saccharomyces cerevisiae) glutamate carboxypeptidase (Pseudomonas sp.) peptidase T (Escherichia coli) carboxypeptidase (Escherichia coli) carboxypeptidase (Sactaricus) caronsine dipeptidase (Ischerichia coli) carboxypeptidase Ss1 (Sulfolobus solfataricus) caronsine dipeptidase II (Mus musculus) beta-lytic metallopeptidase (Achromobacter lyticus) lysostaphin (Staphylococcus simulans) methionyl aminopeptidase 1 (Escherichia coli) galta-specific metallopeptidase (Streptococcus sanguinis) tentoxilysin (Clostridium tetani) aminopeptidase S (Streptomyces griseus) glutamate carboxypeptidase II (Homo sapiens) IAP aminopeptidase (Escherichia coli) aminopeptidase ES-62 (Acanthocheilonema viteae) aminopeptidase T (Thermus aquaticus) hyicolysin (Staphylococcus shvilus) carboxypeptidase Taq (Thermus aquaticus) hyicolysin (Staphylococcus hyicus) carboxypeptidase Taq (Thermus aquaticus) hyicolysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus) fungalysin (Aspergillus flavus)

	M43B	pappalysin-1 (Homo sapiens)
M44		pox virus metallopeptidase (Vaccinia virus)
M48	M48A	Ste24 peptidase (Saccharomyces cerevisiae)
	M48B	HtpX peptidase (Escherichia coli)
	M48C	Oma1 peptidase (Saccharomyces cerevisiae)
M49		dipeptidyl-peptidase III (Rattus norvegicus)
M50	M50A	site 2 peptidase (Homo sapiens)
N/54	IVI50B	sporulation factor SpolvFB (Bacillus subtilis)
M22		drenderysin (Meenanocaldococcus Janiaschin)
M56		PlaP1 pentidase (Staphylococcus aureus)
M57		prtR a p (Myrococcus xanthus)
M60		enhancin (Tymantria dispar nucleonolyhedrovirus)
M60		glycyl aminonentidase (Snhingomonas cansulata)
M64		IgA peptidase (Clostridium ramosum)
M66		StcE peptidase (Escherichia coli)
M67	M67A	BPN11 peptidase (Saccharomyces cerevisiae)
	M67B	JAMM-like protein (Archaeoglobus fulgidus)
	M67C	STAMBP isopeptidase (Homo sapiens)
M72		peptidyl-Asp metallopeptidase (Pseudomonas aeruginosa)
M73		camelysin (Bacillus cereus)
M74		murein endopeptidase (Escherichia coli)
M75		imelysin (Pseudomonas aeruginosa)
M76		Atp23 peptidase (Homo sapiens)
M77		tryptophanyl aminopeptidase 7-DMATS-type peptidase (Aspergillus fumigatus)
M78		ImmA peptidase (Bacillus subtilis)
M79		RCE1 peptidase (Saccharomyces cerevisiae)
M80		Wss1 peptidase (Saccharomyces cerevisiae)
M81		microcystinase MIrC (Sphingomonas sp. ACM-3962)
M82		PrsW peptidase (Bacillus subtilis)
M84		MpriBi peptidase (Bacillus intermedius)
M85		NIeC peptidase (Escherichia coli)
		rgnr gamma-polygiutamate hydrolase (Bacillus phage phiNIT1)
M87		chloride channel accessory protein 1 (Homo sapiens)
M88		IMPa peptidase (Pseudomonas aeruginosa)
M90		Mith peptidase (Escherichia coli)
M03		NED peptidase (Escherichia coll)
M95		selecase (Methanocaldococcus iannaschii)
M95		Tiki1 pentidace (Homo sapiens)
M97		EcxAB pentidase (Eccherichia coli)
M98		Yahl a n. (Escherichia coli)
M99		Csd4 pentidase (Helicobacter pylori)
Asparagine (N) Peptide Lyases		
FAMILY	SUBFAMILY	TYPE ENZYME
N1		nodavirus peptide lyase (flock house virus)
N2		tetravirus coat protein (Nudaurelia capensis omega virus)
N4		Tsh-associated self-cleaving domain and similar (Escherichia coli)
N5		picobirnavirus self-cleaving protein (Human picobirnavirus)
N6		YscU protein (Yersinia pseudotuberculosis)
N7		reovirus type 1 coat protein (Mammalian orthoreovirus 1)
N7 N8		reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1)
N7 N8 N9		reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae)
N7 N8 N9 N10		reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803)
N7 N8 N9 N10 N11		reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos)
N7 N8 N9 N10 N11 Mixed (P) Peptidases		reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos)
N7 N8 N10 N11 Mixed (P) Peptidases FAMILY	SUBFAMILY	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1	SUBFAMILY	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2	SUBFAMILY P2A	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2	SUBFAMILY P2A P2B	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases	SUBFAMILY P2A P2B	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY	SUBFAMILY P2A P2B SUBFAMILY	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1P	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) elutamul denoentidate J (Staphylococcur aurour)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) Dord pontidase (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1E S1C S1D S1F	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos tarrus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) strentoreixia A (Strentomyces griacus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D S1E S1E S1F	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coll) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D S1E S1F	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) toreavirin (Sindbis virus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D S1E S1F	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1C S1C S1C S1E S1F	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (Vellow fever virus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D S1E S1F S1F S8A S88	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flaviviru (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9	SUBFAMILY P2A P2B SUBFAMILY S1A S1B S1C S1D S1E S1F S1F S8A S8B S9A	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia colii) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirui (Sindbis virus) [gA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Sus scrofa)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1D S1E S1F S1F S8A S8B S9A S9B	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Sus forfa) dipeptidyl-peptidase I (Memo sapiens)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9C	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Su scrofa) dipeptidyl-peptidase (Ivmo sapiens)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Sus scrofa) dipeptidyl-peptidase IV (Homo sapiens) glutamyl endopeptidase (Mamastrovis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Sus scrofa) dipeptidyl-peptidase (Momo sapiens) glutamyl endopeptidase (Carbaidopsis thaliana)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (I Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Mamastrovirus 1) togavirni (Sindbis virus) glutamyl (Sindbis virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase I (Homo sapiens) glutamyl endopeptidase I (Homo sapiens) glutamyl endopeptidase I (Homo sapiens) glutamyl endopeptidase (I Arabidopsis thaliana) carboxypeptidase Y (Saccharomyces cerevisiae)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11	SUBFAMILY P2A P2B SUBFAMILY S1A S1E S1C S1D S1E S1F S1F S8A S88 S98 S99 S99 S90 S90	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (Yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (U Homo sapiens) acylaminoacyl-peptidase (Homo sapiens) acylaminoacyl-peptidase (Carbidopsis thaliana) carboxypeptidase Y (Saccharomyces cerevisiae) D-Aa-D-Ala carboxypeptidase A (Geobacillus stearothermophilus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1C S1D S1E S1F S8A S8B S9A S9B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Umo sapiens) acylaminoacyl-peptidase (Momo sapiens) glutamyl endopeptidase (Varbidopsis thaliana) carboxypeptidase (Saccharomyces cerevisiae) prolyl oligopetidase (Sacserofa) dipeptiday-peptidase (Momo sapiens) glutamyl endopeptidase (Varbidopsis thaliana) carboxypeptidase (Saccharomyces cerevisiae) p-Aab-OA acarboxypeptidase B (Streptomyces lividans)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S13	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coll) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Vinomo sapiens) glutamyl endopeptidase (Vinomo sapiens) glutamyl endopeptidase (Vinomo sapiens) glutamyl endopeptidase (Komo sapiens) glutamyl endopeptidase (Mamastrovirus 1) togavirni (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Vinomo sapiens) glutamyl endopeptidase ((Arabidopsis thaliana) carboxypeptidase C (Arabidopsis thaliana) carboxypeptidase C (Sceharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala peptidase C (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S13 S14	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S1F S8A S88 S9A S98 S9A S99 S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase 1 (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirn (Sindbis virus) IgA1-specific serine peptidase (Namastrovirus 1) togavirn (Sindbis virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase ((Jemos sapiens) acylaminoacyl-peptidase ((Jemos sapiens) acylaminoacyl-peptidase ((Jemos sapiens) glutamyl endopeptidase (Jemos sapiens) acylaminoacyl-peptidase (Jemos sapiens) acylaminoacyl-peptidase (Jemos sapiens) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala ceptokypeptidase C (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S13 S14 S13 S14 S15	SUBFAMILY P2A P2B SUBFAMILY S1A S1E S1C S1D S1E S1F S8A S88 S98 S99 S99 S90 S90	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (Yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Lormo sapiens) acylaminoacyl-peptidase (Momo sapiens) acylaminoacyl-peptidase (Carbidopsis thaliana) carboxypeptidase (Saccharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase S (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase (Sterptomyces lividans) D-Ala-D-Ala peptidase C (Escherichia coli) peptidase C (Escherichia coli) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase A (Sterptomyces lividans) D-Ala-D-Ala carboxypeptidase C (Escherichia coli) peptidase C (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S12 S13 S12 S13 S14 S14 S15 S15 S16	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME Chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP petidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) [gA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Carbaigens) glutamyl endopeptidase (Lomo sapiens) acylaminoacyl-peptidase (Homo sapiens) glutamyl endopeptidase (Carbaidopsis thaliana) carboxypeptidase (Sacstrofa) dipeptidyl-peptidase (Homo sapiens) glutamyl endopeptidase (Carbaidopsis thaliana) carboxypeptidase (Carbaidopsis thaliana) carboxypeptidase C (Escherichia coli) p-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala peptidase C (Escherichia coli) peptidase C (Escherichia coli) peptidase C (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S13 S14 S12 S13 S14 S15 S16 S12 S13 S14 S15 S16 S12 S16 S16 S12 S17 S18 S18 S18 S18 S18 S18 S18 S18 S18 S18	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coll) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Vitomo sapiens) glutamyl endopeptidase (Vitomo sapiens) glutamyl endopeptidase (Komospiens) glutamyl endopeptidase (Jong Streptomyces Jong Streptomyces) prolyl oligopeptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (Yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Jong Sapiens) glutamyl endopeptidase (Carabidopsis thaliana) carboxypeptidase V (Saccharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase Lococccus lactis) Lon-A peptidase (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S12 S13 S14 S12 S13 S14 S15 S14 S15 S16 S12 S14 S15 S16 S12 S14 S16 S21 S24 S24	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing V-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase (IStaphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Victomo sapiens) acylaminoacyl-peptidase (Momo sapiens) acylaminoacyl-peptidase (Momo sapiens) glutamyl endopeptidase (Victomo sapiens) acylaminoacyl-peptidase (Momo sapiens) acylaminoacyl-peptidase (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase C (Escherichia coli) peptidase (Descherichia coli) Peptidase (Descherichia coli) Peptidase (Descherichia coli) Peptidase (Escherichia coli) Con-A peptidase (Escherichia coli) peptidase (Escherichia coli) Peptidase (Escherichia coli) Pata-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala cerboxypeptidase (Escherichia coli) peptidase (Escherichia coli) Pertomase (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1C S1C S1F S1F S8A S8B S9A S9B S9C S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing vetype proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Scherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (Yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Jaconospiens) acylaminoacyl-peptidase (Carbidopsis thaliana) carboxypeptidase C (Arabidopsis thaliana) carboxypeptidase C (Saccharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase C (Escherichia coli) peptidase C [Escherichia coli) Xaa-Pro dipeptidyl-peptidase L (Escherichia coli) Svaa-Pro dipeptidyl-peptidase L (Escherichia coli) cytomegalovirus assemblin (human herpesvirus 5) repressor LexA (Escherichia coli) signal peptidase L (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S13 S14 S12 S13 S14 S15 S15 S16 S21 S24 S26	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) [gA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Carbaigens) glutamyl endopeptidase (Lomo sapiens) acylaminoacyl-peptidase (Homo sapiens) glutamyl endopeptidase (Carbaidopsis thaliana) carboxypeptidase (Sus corfa) dipeptidyl-peptidase (Homo sapiens) glutamyl endopeptidase A (Geobacillus sterarthermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala peptidase C (Escherichia coli) peptidase C (Escherichia coli) cytomegalovirus assemblin (human herpesvirus 5) repressor LexA (Escherichia coli) signal peptidase 1 (Escherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S13 S14 S12 S13 S14 S15 S15 S16 S21 S24 S26	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1C S1D S1F S1F S8A S8B S9A S9B S9A S9B S9C S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME Chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coll) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (vellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces crevisiae) prolyl oligopeptidase (Su scrofa) dipeptidase (Su scrofa) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala peptidase (Lescherichia coli) peptidase (Escherichia coli) cytomegalovirus assemblin (human herpesvirus 5) repressor LexA (Escherichia coli) signalaez 11 kDa component (Saccharomyces cerevisiae) TraF peptidase (12 scherichia coli) signalaez 11 kDa component (Saccharomyces cerevisiae) TraF peptidase (12 scherichia coli)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S12 S13 S14 S12 S13 S14 S15 S12 S13 S14 S15 S12 S13 S14 S15 S12 S13 S14 S15 S12 S13 S14 S15 S12 S13 S14 S15 S14 S15 S15 S15 S15 S15 S15 S15 S15 S15 S15	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase (IScherichia coli) lysyl endopeptidase (Escherichia coli) lysyl endopeptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) lgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Vienon sapiens) acylaminoacyl-peptidase (Momo sapiens) glutamyl endopeptidase (Carbabis sthaliana) carboxypeptidase ((Streptomyces griseus) acylaminoacyl-peptidase ((Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase C (Escherichia coli) peptidase C (Jarbidopsis thaliana) carboxypeptidase C (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli) peptidase (Escherichia coli) signalase 21 kDa component (Saccharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala cerboxypeptidase (Escherichia coli) signalase 21 kDa component (Saccharomyces cerevisiae) TraF peptidase (Escherichia coli) signalase 21 kDa component (Saccharomyces cerevisiae) TraF peptidase (Escherichia coli) signalase 21 kDa component (Saccharomyces cerevisiae)
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N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S10 S11 S12 S13 S12 S13 S14 S12 S13 S14 S15 S15 S16 S21 S24 S26 S28 S29 S30 S10 S11	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunit A (Saccharomyces cerevisiae) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) [gA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (yellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Carbaidopsis thaliana) carboxypeptidase (Carbaidopsis thaliana) cardoxypeptidase (Carbaidopsis thaliana) cardoxypeptidase (Carbaidopsis thaliana) carboxypeptidase (Carbaidopsis thaliana) carboxypeptidase C (Scherichia coli) peptidase C (Escherichia coli) cytomegalovirus assemblin (human herpesvirus 5) repressor LexA (Escherichia coli) signal peptidase (Ischerichia coli) signal apetidase (Escherichia coli) signal apetidase (Escherichia coli) signal peptidase (Ischerichia coli) signal peptidase
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S14 S15 S16 S12 S13 S14 S15 S16 S21 S24 S26 S27 S28 S29 S30 S31 S14 S22 S28 S29 S30 S31 S22 S28 S29 S30 S31 S31 S28 S29 S30 S31 S31 S32 S32 S33 S42 S42 S42 S42 S42 S42 S42 S42 S42 S42	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9A S9B S9C S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME Chymotrypsin A (Bos taurus) glutamyl endopeptidase 1 (Staphylococcus aureus) DegP peptidase (Escherichia coll) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Mamastrovirus 1) togavirni (Sindbis virus) IgA1-specific serine peptidase (Neisseria gonorrhoeae) flavivirin (vellow fever virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Lomo sapiens) glutamyl endopeptidase (Lomo sapiens) glutamyl endopeptidase (Momo sapiens) acryonypeptidase (Su scrofa) dipeptidyl-peptidase (Momo sapiens) glutamyl endopeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala peptidase C (Escherichia coli) peptidase C [Escherichia coli] cytomegalovirus assemblin (human herpesvirus 5) repressor LexA (Escherichia coli) signala ez 11 kDa component (Saccharomyces cerevisiae) TraF peptidase C 1 (Escherichia coli) lysosomal Pro-Xaa carboxypeptidase (Homo sapiens) signala ez 11 kDa component (Saccharomyces cerevisiae) TraF peptidase C 1 (Escherichia coli) lysosomal Pro-Xaa carboxypeptidase (Homo sapiens) potyvirus P1 peptidase (plum pox virus) pestivirus NS3 polyprotein peptidase (bovine viral diarrhea virus 1) evuine addressi Pustina menterice (ounine at-thetic virus)
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S12 S13 S14 S12 S13 S14 S15 S12 S13 S14 S15 S12 S13 S14 S15 S15 S16 S12 S13 S14 S15 S16 S12 S13 S14 S15 S16 S12 S13 S14 S15 S16 S12 S13 S14 S15 S14 S15 S14 S15 S14 S15 S14 S15 S14 S15 S15 S15 S15 S15 S15 S15 S15 S15 S15	SUBFAMILY P2A P2B SUBFAMILY S1A S1D S1C S1D S1E S1F S8A S8B S9A S9B S9C S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing replicative DNA helicase precursor (Synechocystis sp. PCC 6803) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Scherichia coli) lysyl endopeptidase (Achromobacter lyticus) streptogrisin A (Streptomyces griseus) astrovirus serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) IgA1-specific serine peptidase (Mamastrovirus 1) togavirin (Sindbis virus) subtilisin Carlsberg (Bacillus licheniformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Sus csrofa) dipeptidyl-peptidase (Komo sapiens) acylaminoacyl-peptidase (Homo sapiens) acylaminoacyl-peptidase (Homo sapiens) glutamyl endopeptidase C (Arabidopsis thaliana) carboxypeptidase C (Jachidopsis thaliana) carboxypeptidase C (Jaccharomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase (Latcococcus lactis) L
N7 N8 N9 N10 N11 Mixed (P) Peptidases FAMILY P1 P2 Serine (S) Peptidases FAMILY S1 S3 S6 S7 S8 S9 S9 S10 S11 S12 S13 S6 S7 S8 S9 S9 S10 S11 S12 S13 S12 S13 S12 S13 S12 S13 S13 S13 S13 S13 S13 S13 S13 S13 S13	SUBFAMILY P2A P2B SUBFAMILY S1A S1C S1C S1C S1F S8A S8B S9A S9B S9C S9D S9D S9D	reovirus type 1 coat protein (Mammalian orthoreovirus 1) poliovirus capsid VPO-type self-cleaving protein (human poliovirus 1) intein-containing v-type proton ATPase catalytic subunut A (Saccharomyces cerevisiae) intein-containing chloroplast ATP-dependent peptide lyase (Chlamydomonas eugametos) TYPE ENZYME DmpA aminopeptidase (Ochrobactrum anthropi) EGF-like module containing mucin-like hormone receptor-like 2 (Homo sapiens) polycystin-1 (Homo sapiens) TYPE ENZYME Chymotrypsin A (Bos taurus) glutamyl endopeptidase I (Staphylococcus aureus) DegP peptidase (Escherichia coli) lysyl endopeptidase (Scherichia coli) lysyl endopeptidase (Kamostorius 1) togavirus serine peptidase (Mamastrovirus 1) togavirus serine peptidase (Mamastrovirus 1) togavirus (Sindbis virus) glutamyl endopeptidase (Neisseria gonorrhoeae) flavivirin (Yellow fever virus) subtilisin Carlsberg (Bacillus lichenformis) kexin (Saccharomyces cerevisiae) prolyl oligopeptidase (Landoroses cerevisiae) prolyl oligopeptidase (Vanidomos spiens) acylaminoacyl-peptidase (Momo sapiens) glutamyl endopeptidase (Venos spiens) acylaminoacyl-peptidase (Momo sapiens) glutamyl endopeptidase (Venos spiens) acylaminoacyl-peptidase (Karomyces cerevisiae) D-Ala-D-Ala carboxypeptidase A (Geobacillus stearothermophilus) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase B (Streptomyces lividans) D-Ala-D-Ala carboxypeptidase C (Escherichia coli) signalage 21 kDa component (Saccharomyces cerevisiae) TraF peptidase (Ifcencichia coli) signalase 21 kDa component (Saccharomyces cerevisiae) TraF peptidase (Escherichia coli) signalase 21 kDa compon

\$39	S39A	sobemovirus peptidase (cocksfoot mottle virus)
	S39B	luteovirus peptidase (potato leaf roll luteovirus)
S41	S41A	C-terminal processing peptidase-1 (Escherichia coli)
	S41B	tricorn core peptidase (Thermoplasma acidophilum)
S45		penicillin G acylase precursor (Escherichia coli)
S46		dipeptidyl-peptidase 7 (Porphyromonas gingivalis)
S48		HetR putative peptidase (Anabaena variabilis)
S49	S49A	signal peptide peptidase A (Escherichia coli)
	S49B	protein C (bacteriophage lambda)
	S49C	archaean signal peptide peptidase 1 (Pyrococcus horikoshii)
S50		infectious pancreatic necrosis birnavirus Vp4 peptidase (infectious pancreatic necrosis virus)
S51		dipeptidase E (Escherichia coli)
S53		sedolisin (Pseudomonas sp. 101)
S54		rhomboid-1 (Drosophila melanogaster)
S55		SpoIVB peptidase (Bacillus subtilis)
S59		nucleoporin 145 (Homo sapiens)
S60		lactoferrin (Homo sapiens)
S62		influenza A PA peptidase (influenza A virus)
S64		Ssy5 peptidase (Saccharomyces cerevisiae)
S65		picornain-like cysteine peptidase (Breda virus)
S66		murein tetrapeptidase LD-carboxypeptidase (Pseudomonas aeruginosa)
S68		PIDD auto-processing protein unit 1 (Homo sapiens)
S69		Tellina virus 1 VP4 peptidase (Tellina virus 1)
S71		MUC1 self-cleaving mucin (Homo sapiens)
S72		dystroglycan (Homo sapiens)
S73		gpO peptidase (Enterobacteria phage P2)
S74		Escherichia coli phage K1F endosialidase CIMCD self-cleaving protein (Enterobacteria phage K1F)
S75		White bream virus serine peptidase (White bream virus)
S77		prohead peptidase gp21 (Enterobacteria phage T4)
S78		prohead peptidase (Enterobacteria phage HK97)
S79		CARD8 self-cleaving protein (Homo sapiens)
S80		prohead peptidase gp175 (Pseudomonas phage phiKZ)
S81		destabilase (Hirudo medicinalis)
Threonine (T) Peptidases		
FAMILY	SUBFAMILY	TYPE ENZYME
T1	T1A	archaean proteasome, beta component (Thermoplasma acidophilum)
	T1B	HsIV component of HsIUV peptidase (Escherichia coli)
Τ2		glycosylasparaginase precursor (Homo sapiens)
тз		gamma-glutamyltransferase 1 (Escherichia coli)
Т5		ornithine acetyltransferase precursor (Saccharomyces cerevisiae)
Τ7		CwpV self-cleaving threonine peptidase (Peptoclostridium difficile)
Peptidases of Unknown Catalytic Type		· · · · · · · · · · · · · · · · · · ·
FAMILY	SUBFAMILY	TYPE ENZYME
U32		collagenase (Porphyromonas gingivalis)
U40		protein P5 murein endopeptidase (bacteriophage phi-6)
U49		Lit peptidase (Escherichia coli)
U56		homomultimeric peptidase (Thermotoga maritima)
U57		vabG protein (Bacillus subtilis)
U62		microcin-processing peptidase 1 (Escherichia coli)
U69		AIDA-I self-cleaving autotransporter protein (Escherichia coli)
U72		Dop isopeptidase (Mycobacterium tuberculosis)
U73		small protease (Pseudomonas aeruginosa)

strain	replicon	CRISPR type	CRISPR sub-type	repeat number	repeat length	n repeat sequence	avg. length of spacers	cas 1	cas 3	cas 9	cas 10
//8	chromosome		II-A	/	3		32	Y		Y	
800	chromosome		II-A	59	5		30	ř V		Ŷ	v
01M1/315	chromosome		II-A	13	3		30	v		v	1
01M14315	chromosome		III-A	12	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	39	v			v
ACS116	chromosome		II-A	17	3	6 GTTTCAGAAGGATGTTAAATCAATTAGGTTAAGACT	29	Ŷ		Y	
ACS116	chromosome		III-A	9	3	5 TTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Ŷ			
AH4231	chromosome	П	II-A	60	3	6 GTTTCAGAAGGATGTTAAATCAATTAGGTTAAGACT	30	Y		Y	
AH4231	chromosome	III	III-A	26	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			Y
AH4331	chromosome	П	II-A	60	3	6 GTTTCAGAAGGATGTTAAATCAATTAGGTTAAGACT	30	Y		Y	
AH4331	chromosome	111	III-A	26	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			Y
AH43324	chromosome	П	II-A	28	3	6 GTTTCAGAAGTATGTTAAATCAATAAGGTTAAGACC	30	Y		Y	
AH43348	chromosome	П	II-A	62	3	6 GTTTCAGAAGGATGTTAAATCAATTAGGTTAAGACT	30	Y		Y	
AH43348	chromosome	III	III-A	31	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			Y
ATCC11741	chromosome		III-A	12	3	6 GTTTTCGTCTCCTTCATTCGGAGATATGTTCTTATT	37	Y			Y
CCuG2753OB	chromosome		II-A	19	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Y	
CCUG38008	chromosome		II-A	29	5		30	Ŷ		Ŷ	
CCUG44481	NA	NA	NA	0	2		0	v		v	
CCuG45735	chromosomo		II-A	40	3		30	T V		T	v
CCuG43733	chromosome		III-A	15	3		38	v			v
CCuG47825	chromosome		11-A	23	3		30	v		v	
CCuG47825	chromosome	undefined	undefined	12	3	7 AGTITICGTCTCCTATATICGGAGATATGTTCTTACT	40				
CCuG47826	chromosome		II-A	22	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Y	
CCuG47826	chromosome		III-A	19	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	37	Ŷ			Y
CECT5713	chromosome	П	II-A	28	3	6 GTTTCAGAAGTATGTTAAATCAATAAGGTTAAGACC	30	Y		Y	
cp400	chromosome	III	III-A	28	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			Y
DSM18933	NA	NA	NA	0		0 NA	0				
DSM20492	chromosome	Ш	II-A	17	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Υ	
DSM20492	chromosome	111	III-A	22	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			Y
DSM20554	chromosome	111	III-A	22	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	37	Y			Y
DSM20555	chromosome	111	III-A	12	3	6 GTTTTCGTCTCCTTCATTCGGAGATATGTTCTTATT	37	Y			Y
GJ24	NA	NA	NA	0		0 NA	0				
gul1	chromosome	111	III-A	12	3	6 GTTTTCGTCTCCTTCATTCGGAGATATGTTCTTATT	37	Y			Y
gul2	chromosome		III-A	12	3	6 GTTTTCGTCTCCTTCATTCGGAGATATGTTCTTATT	37	Y			Y
JCM1040	chromosome		II-A	15	3		29	Y		Y	v
JCIVI1040	chromosome		III-A	10	3		30	T		v	T
JCM1042	chromosomo		II-A	19	3		30	v		v	
ICM1044	NΔ	NA	NΔ	19	3		30	'			
ICM1046	chromosome		III-A	27	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	38	Y			v
JCM1047	NA	NA	NA	0	-	0 NA	0				
JCM1230	chromosome	Ш	II-A	40	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGGCC	29	Y		Y	
L21	chromosome	Ш	II-A	26	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	29	Y		Y	
L21	chromosome	111	III-A	50	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	37	Y			Y
LMG14476	NA	NA	NA	0		0 NA	0				
LMG14477	NA	NA	NA	0		0 NA	0				
NCIMB702343	chromosome	П	II-A	41	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Y	
NCIMB702343	chromosome	undescribed	undescribed	11	2	4 GTTTCAGAAGTATGTTAAATCAAT	41				
NCIMB702343	chromosome	111	III-A	20	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	37	Y			Y
NCIMB702343	chromosome	undescribed	undescribed	6	3	5 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGAC	31				
NCIMB8816	chromosome	11	II-A	8	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Y	
NCIMB8817	chromosome		II-A	50	3	6 GTTTCAGAAGTATGTTAAATCAATTAGGTTAAGACC	30	Y		Y	
NCIMB8818	chromosome	11	II-A	8	3		30	Ŷ		Ŷ	
NIAS840	chromosome	undefined	undefined	18	3		40	v			v
NIA5840	megaplasmid	undefined	III-A undefined	9	5		30	T			т
Ren	chromosomo	II	ILA		3		29	v			v
Ren	chromosome		III-A	11	3	6 GTTTTCGTCTCCTATATTCGGAGATATGTTCTTACT	29	,			I
SMXD51	chromosome		II-A	25	3		29	Y		Y	
UCC118	chromosome		II-A	23	3		2.9	Ŷ		Ŷ	
	anomosome			20	5		50				

query gene	% identity	query coverage	e-value	query gene length	functional annotation
01M14315_ORF_49	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
01M14315_ORF_69 01M14315_ORF_212	49 48	498	2.00E-170 2.00E-70	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRE is a vanR variant found in the vanE gene cluster
01M14315_ORF_611	46	418	8.00E-123	440	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
01M14315_ORF_653	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
01M14315_ORF_938	45	569	4.00E-147	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
01M14315_ORF_1128	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
01M14315_ORF_1278 01M14315_ORF_1354	62 40	61 222	2.00E-22 7.00E-47	73 224	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
01M14315_ORF_1416	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
01M14315_ORF_1628	43	219	2.00E-53	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
778_ORF_72	50	500	2.00E-172	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
778_ORF_226	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
778_ORF_512 778_ORF_610	46	418 396	1.00E-120 0	440 395	Mycobacterium tuberculosis murA conters intrinsic resistance to tostomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
778_ORF_828	40	573	2.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
778_ORF_832 778_ORF_1079	45 41	648	0 3.00F-54	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster
778_ORF_1272	40	222	8.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
778_ORF_1335	44	222	1.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
866_ORF_51	43	221	1.00E-62	233	vanRM is a vanR variant found in the vanM gene cluster
866_ORF_106	55	95	7.00E-31	99	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
866_ORF_107 866_ORF_271	49	391 233	5.00E-131 1.00E-70	387	LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster
866_ORF_642	46	418	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
866_ORF_682 866_ORF_913	69 40	396	0 9 00E-146	395 578	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
866_ORF_917	40	648	0.002	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
866_ORF_1176	41	233	6.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
866_ORF_1362 866_ORF_1373	40	219 302	1.00E-46 2.00E-80	302	MacB is an AIP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance
866_ORF_1455	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
866_ORF_1663	43	219	4.00E-53	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ACS116_ORF_71	45	95	7.00E-31	99	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
ACS116_ORF_72	49	391	5.00E-131	387	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
ACS116_ORF_228 ACS116 ORF 651	48	418	1.00E-70 1.00E-120	441	Wanker is a varie variant found in the varie gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
ACS116_ORF_722	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
ACS116_ORF_1019 ACS116_ORF_1023	40	583	9.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
ACS116_ORF_1271	40	187	3.00E-41	191	vanRA, also known as vanR, is a vanR variant found in the vanA gene cluster
ACS116_ORF_1293	40	223	2.00E-49	223	vanRE is a vanR variant found in the vanE gene cluster
ACS116_ORF_1328 ACS116_ORF_1482	45 40	286	1.00E-80 1.00E-46	299	MprF is a integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ACS116_ORF_1493	45	302	2.00E-80	302	bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance
ACS116_ORF_1575	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH4231_ORF_45	45	215	4.00E-53	235	vanRM is a vanR variant found in the vanM gene cluster
AH4231_ORF_65	55	95	7.00E-31	99	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
AH4231_ORF_66 AH4231 ORF 231	49	233	5.00E-131 1.00E-70	387	LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster
AH4231_ORF_639	46	418	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
AH4231_ORF_680	69	396	0 00E-146	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
AH4231_ORF_1027	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
AH4231_ORF_1288	41	233	6.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
AH4231_OKF_1471 AH4231 ORF 1482	40	302	2.00E-80	302	bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance
AH4231_ORF_1564	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH4231_ORF_1777 AH4231_ORF_1862	43 40	219	4.00E-53 1.00E-54	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones vanRM is a vanR variant found in the vanM gene cluster
AH4331_ORF_45	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
AH4331_ORF_63	55	95	7.00E-31	99	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
AH4331_ORF_230	49	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
AH4331_ORF_647	46	418	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
AH4331_ORF_687 AH4331_ORF_994	69 40	396 583	0 9.00F-146	395 578	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that conter resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
AH4331_ORF_998	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
AH4331_ORF_1263	41	233	6.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
AH4331_ORF_1440 AH4331_ORF_1457	40	302	2.00E-80	302	bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance
AH4331_ORF_1539	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH4331_OKF_1752 AH4331 ORF 1832	43	219	4.00E-53 1.00E-54	233	vanRM is an ATP-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones vanRM is a vanR variant found in the vanM gene cluster
AH43324_ORF_52	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
AH43324_ORF_70	50	498	3.00E-171	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
AH43324_ORF_630	46	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
AH43324_ORF_670	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
AH43324_ORF_969 AH43324 ORF 973	40	583	1.00E-145 0	578	Adec is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
AH43324_ORF_1227	41	233	4.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
AH43324_ORF_1280	40	400	2.00E-90	415	MprF is a integral membrane protein that modifies the negatively-charged phosphatidylglycerol on the membrane surface
AH43324_ORF_1428 AH43324_ORF_1439	40	305	1.00E-79	302	bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracion resistance
AH43324_ORF_1522	44	222	1.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH43324_ORF_1765 AH43348 ORF 45	43	219	5.00E-53 1.00E-62	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones vanRM is a vanR variant found in the vanM gene cluster
AH43348_ORF_64	55	95	7.00E-31	99	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
AH43348_ORF_65	49	391	5.00E-131	387	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
AH43348_ORF_640	48	233	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
AH43348_ORF_680	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
AH43348_ORF_992 AH43348 ORF 996	40	583 648	9.00E-146 0	578 772	Adec. is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
AH43348_ORF_1259	41	233	6.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
AH43348_ORF_1447	40	219	1.00E-46	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH43348_ORF_1539	45 44	302	2.00E-80 4.00E-62	302 227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
AH43348_ORF_1755	43	219	4.00E-53	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ATCC11/41_ORF_54 ATCC11741 ORF 71	45	225 498	1.00E-62 3.00E-172	236 493	vanкки is a vank variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis
ATCC11741_ORF_216	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster

ATCC11741_ORF_559	46	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
ATCC11741_ORF_600	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
ATCC11741_ORF_824	41	573	9.00E-147	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
ATCC11741_ORF_828	45 41	233	4 00E-54	233	Versia is a penicillin-binding protein found in Streptococcus pneumoniae
ATCC11741 ORF 1264	40	222	2.00E-46	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ATCC11741_ORF_1327	44	222	2.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ATCC11741_ORF_1544	43	221	1.00E-56	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG2753OB_ORF_53	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
CCUG2753OB_ORF_73	49	233	1.00E-171 1.00E-70	493 220	LSBA IS an ABC efflux pump expressed in Enterococcus raecalis
CCuG27530B_ORF_506	48	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
CCuG2753OB_ORF_546	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG2753OB_ORF_777	40	583	4.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
CCuG2753OB_ORF_782	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
CCuG2753OB_ORF_1031	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG2753OB_ORF_1212	40	222	7.00E-47 1.00E-61	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG2753OB ORF 1501	43	221	2.00E-56	244	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG38008_ORF_55	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
CCuG38008_ORF_70	49	500	2.00E-171	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
CCuG38008_ORF_221	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
CCuG38008_ORF_546	4b 69	418	2.00E-121	305	Mycobacterium tuberculosis mura conters intrinsic resistance to tostomycin Sequence variants of Strentomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG38008_ORF_380	40	583	9.00F-147	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
CCuG38008_ORF_889	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
CCuG38008_ORF_1140	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG38008_ORF_1286	60	63	1.00E-22	67	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
CCuG38008_ORF_1389	44	222	2.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCUG38008_ORF_1606	43	221	2.00E-56 2.00E-54	244	Macb is an ATP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones vanBM is a vanB variant found in the vanM gene cluster.
CCuG44481 ORF 44	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanW gene cluster
CCuG44481_ORF_96	50	498	2.00E-172	490	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
CCuG44481_ORF_246	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
CCuG44481_ORF_661	46	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
CCuG44481_ORF_702	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG44481_ORF_911	40	583	7.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
CCuG44481_ORF_915	45	648 222	1 005 52	1/2	PBP1a is a peniciliin-binding protein found in Streptococcus pneumoniae
CCuG44481_ORF_1148	41	233	7.00E-47	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG44481_ORF_1401	44	222	1.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG44481_ORF_1700	58	67	8.00E-24	84	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
CCuG44481_ORF_1782	99	458	0	458	TetL is a tetracycline efflux protein found in many species of Gram-negative and Gram-positive bacteria
CCuG44481_ORF_1931	90	641	0	646	TetM is a ribosomal protection protein that confers tetracycline resistance
CCuG44481_ORF_1937	99	215	4.00E-156	215	cat is used to describe many variants of the chloramphenicol acetyltransferase gene in a range of organisms
CCuG44481_ORF_1974	51	306	8.00E-109	326	bcrA is an ABC transporter found in Bacillus lichenitormis that confers bacitracin resistance
CCuG45735_ORF_51	45	225	1.00E-62	230	Vankin is a vank variant found in the vanimi gene cluster
CCuG45735_ORF_70	49	391	5 00E-131	387	IsaA is an ABC efflux nump expressed in Enterococcus faecalis
CCuG45735_ORF_227	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
CCuG45735_ORF_644	46	418	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
CCuG45735_ORF_685	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG45735_ORF_918	40	583	9.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
CCuG45735_ORF_922	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
CCuG45735_ORF_1183	41	233	6.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG45735_ORF_1365	40	219	1.00E-46 2.00E-80	224	Macb Is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance.
CCuG45735_ORF_1461	43	222	4.00E-62	227	MacB is an ADP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG45735_ORF_1681	43	219	4.00E-53	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG45735_ORF_1865	58	67	8.00E-24	84	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
CCuG47171_ORF_51	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
CCuG47171_ORF_73	49	498	2.00E-171	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
CCuG47171_ORF_217	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
CCuG47171_ORF_594	4b 69	418	2.00E-121	305	Mycobacterium tuberculosis mura conters intrinsic resistance to tostomycin Sequence variants of Strentomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG47171 ORF 889	40	583	2.00E-145	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
CCuG47171_ORF_893	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
CCuG47171_ORF_1141	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG47171_ORF_1371	40	222	7.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47171_ORF_1434	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47171_ORF_1663	44	204	3.00E-51	219	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47171_ORF_1918	58	231	8.00E-24 2.00E-53	84 220	Vanu is a transcriptional activator of the vanu operon of vancomycin resistance genes MacR is an ATP-binding cassette (ARC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825 ORF 286	41	136	4.00E-26	154	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825_ORF_287	49	81	1.00E-20	102	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825_ORF_505	43	90	4.00E-21	94	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825_ORF_506	47	122	3.00E-30	128	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825_ORF_570	40 46	222	7.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47825_URF_//3	46 69	418	1.UUE-122	438 30⊏	iviycouscientum tuberculosis mura conters intrinsic resistance to fostomycin Sequence variants of Strentomyces cinnamoneus elongation factor. Tu that confer resistance to elfonyce antibiotics
CCuG47825_ORF_017	41	590 493	7.00E-129	395 494	AdeC is the outer membrane factor of the AdeARC multidrug efflux complex
CCuG47825_ORF_1080	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
CCuG47825_ORF_1351	45	225	1.00E-62	248	vanRM is a vanR variant found in the vanM gene cluster
CCuG47825_ORF_1369	50	498	7.00E-174	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
CCuG47825_ORF_1449	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG47825_ORF_1451	44	77	0.00E+00	93	vanSL is a vanS variant found in the vanL gene cluster
CCuG47825_ORF_1688	4U 48	164	3.UUE-32 1.00E-70	1/2	A type III ABC transporter, identified on the novobiocin biosynthetic gene cluster vanRE is a vanR variant found in the vanE gene cluster
CCuG47825_ORF_1830	40 58	233	1.00E-70 8.00F-24	229 81	value is a transcriptional activator of the vanG operon of vancomycin resistance genes
CCuG47826_ORF 51	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
CCuG47826_ORF_68	50	498	7.00E-174	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
CCuG47826_ORF_234	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
CCuG47826_ORF_242	40	164	3.00E-32	172	A type III ABC transporter, identified on the novobiocin biosynthetic gene cluster
CCuG47826_ORF_556	46	418	8.00E-123	440	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
CLUG47826_ORF_596	69 41	396	U 3 00E-147	395 570	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
CCuG47826_ORF_907	41 45	509 . 648	0	5/8 777	Aueu is the outer memorane ractor or the AueAbu multiorug emux complex PRP1a is a penicillin-binding protein found in Strentococcus pneumoniae
CCuG47826 ORF 1164	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
CCuG47826_ORF_1452	40	222	7.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47826_ORF_1514	43	222	3.00E-60	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47826_ORF_1724	43	219	5.00E-53	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CCuG47826_ORF_1842	58	67	8.00E-24	84	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
CECT5713_ORF_44		0,			
UEU15/13 URE 64	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
CECT5713 OPE 240	45 50 48	225 500	1.00E-62 6.00E-172 4.00E-70	236 493	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanBE is a vange variant found in the vanE and enterococcus faecalis
CECT5713_ORF_249 CECT5713_ORF_699	45 50 48 46	225 500 231 418	1.00E-62 6.00E-172 4.00E-70 2.00E-121	236 493 229 441	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mvcrbacterium tuberculosis murk confers intrinsic resistance to fosformurin
CECT5713_ORF_249 CECT5713_ORF_699 CECT5713_ORF_742	45 50 48 46 69	225 500 231 418 396	1.00E-62 6.00E-172 4.00E-70 2.00E-121 0	236 493 229 441 395	vanRM is a vanR variant found in the vanM gene cluster LSA is an ABC efflux pume perpresed in Entercococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamvcin antihintirs
CECT5713_ORF_249 CECT5713_ORF_699 CECT5713_ORF_742 CECT5713_ORF_1052	45 50 48 46 69 41	225 500 231 418 396 127	1.00E-62 6.00E-172 4.00E-70 2.00E-121 0 3.00E-28	236 493 229 441 395 136	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex

CEC15/13_ORF_1057	45	040		772	The same performance protect to the most epiceoccus preamonace
CECI5/13_ORF_1328	41	233	3.00E-54	233	vanke is a vank variant found in the vane gene cluster
CECT5/13_ORF_1549	40	222	7.00E-47	224	MacB is an AIP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
CECT5713_ORF_1563	45	305	1.00E-79	302	DCFA is an ABC transporter round in Bacilius lichenitormis that conters bacitracin resistance MacR is an ATR binding cascette (APC) transporter that experts macrolides with 14, or 15, membered lactones
CECT5713_ORF_1047	44	222	5.00E-53	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
cp400_OBE_61	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
cp400_ORF_244	48	233	1.00F-70	229	vanRE is a vanR variant found in the vanE gene cluster
cp400 ORF 747	46	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
cp400_ORF_789	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
cp400_ORF_799	40	583	2.00E-147	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
cp400_ORF_803	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
cp400_ORF_1294	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
cp400_ORF_1551	40	222	1.00E-45	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
cp400_ORF_1615	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
cp400_ORF_2079	60	60	2.00E-20	71	VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
cp400_ORF_2106	50	498	8.00E-168	493	LsaA is an ABC ettlux pump expressed in Enterococcus faecalis
DSM18933_ORF_149	42	107	3.00E-23	110	EmrE is a small multidrug transporter that functions as a homodimer
DSM18933_ORF_286	47	220	1.00E-67	233	MacB is an ATP-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones
DSM18935_ORF_502	44	225	1.00E-59 2.00E-70	230	valike is a valik variant found in the valie gene cluster
DSM18933_ORE 1243	43	417	7.00E-115	122	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
DSM18933_ORE 1422	46	645	0	766	PRP1a is a penicillin-hinding protein found in Streptococcus pneumoniae
DSM18933_ORF_1449	68	396	0	395	Sequence variants of Strentomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
DSM20492 ORF 47	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
DSM20492 ORF 69	50	500	5.00E-172	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
DSM20492_ORF_218	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
DSM20492_ORF_577	46	418	3.00E-121	440	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
DSM20492_ORF_617	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
DSM20492_ORF_862	40	583	9.00E-148	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
DSM20492_ORF_866	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
DSM20492_ORF_1098	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
DSM20492_ORF_1287	40	222	7.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20492_ORF_1350	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20492_ORF_1554	43	221	1.00E-56	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20554_ORF_46	45	225	1.00E-62	236	vankM is a vank variant found in the vanM gene cluster
	10	500	3.UUE-1/2 1.00E-70	495	LSAA IS AIL ADD EIHUX PUMP EXPRESSED IN ENTEROCOCCUS TAECAIIS
DSM20554_ORF_208	48	233	1.00E-70	229	Vankr is a vank variant found in the vanr gene cluster
DSM20554_ORF_505	40	306	5.00E-121	305	Mycobacterium tuberculosis mura comens municipalities factor Tu that confer resistance to elfamycin antibiotics
DSM20554_ORE 910	40	583	9 00F-148	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
DSM20554_ORE 914	45	648	0	772	PRP1a is a penicillin-binding protein found in Streptococcus pneumoniae
DSM20554_ORE_1106	41	233	3.00F-54	233	vanRE is a vanR variant found in the vanE gene cluster
DSM20554 ORF 1298	40	222	7.00E-47	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20554 ORF 1361	44	222	4.00E-62	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20554_ORF_1581	43	221	1.00E-56	233	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20555_ORF_55	45	225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
DSM20555_ORF_72	50	498	3.00E-172	493	LsaA is an ABC efflux pump expressed in Enterococcus faecalis
DSM20555_ORF_212	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
DSM20555_ORF_554	46	418	2.00E-121	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
DSM20555_ORF_594	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
DSM20555_ORF_815	41	573	9.00E-147	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
DSM20555_ORF_819	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
DSM20555_ORF_1069	41	233	4.00E-54	233	vanke is a vank variant found in the vane gene cluster
DSM20555_ORF_1257	40	222	2.00E-40	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
DSM20555_ORE 1535	44	222	1.00E-56	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
GI24 ORE 21	50	498	2.00F-171	493	IsaA is an ABC efflux nump expressed in Enterococcus faecalis
GJ24 ORF 180	48	233	1.00E-70	229	vanRF is a vanR variant found in the vanF gene cluster
GJ24 ORF 620	46	418	1.00E-120	441	Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
GJ24_ORF_661	69	396	0	395	Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
GJ24_ORF_870	40	583	6.00E-146	578	AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
GJ24_ORF_874	45	648	0	772	PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
GJ24_ORF_1110	41	233	3.00E-54	233	vanRE is a vanR variant found in the vanE gene cluster
GJ24_ORF_1344	40	222	2.00E-46	224	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
GJ24_ORF_1407	44	222	1.00E-61	227	MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
			1 00E 62	236	vanRM is a vanR variant found in the vanM gene cluster
GJ24_ORF_1736	45	225	1.001-02		
GJ24_ORF_1736 gul1_ORF_54	45 45	225 225	1.00E-62	236	vanRM is a vanR variant found in the vanM gene cluster
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71	45 45 50	225 225 498	1.00E-62 3.00E-172	236 493	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_215	45 45 50 48	225 225 498 233	1.00E-02 1.00E-62 3.00E-172 1.00E-70	236 493 229	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_215 gul1_ORF_519 gul1_ORF_560	45 45 50 48 46 60	225 225 498 233 418 206	1.00E-02 1.00E-62 3.00E-172 1.00E-70 2.00E-121	236 493 229 441 205	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Entercococcus faecalis vanRF is a vanR Variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Secures undrafter of Expensioner clanapation forter Tu that conferenciations to elformicin antibiation
G124_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_215 gul1_ORF_519 gul1_ORF_560 gul1_ORF_783	45 45 50 48 46 69 41	225 225 498 233 418 396 573	1.00E-02 1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147	236 493 229 441 395 578	vanRM is a vanR variant found in the vanM gene cluster LsA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces clinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics Add ic it he outer membrane factor of the AddBC multifum afflux complex.
GJ24_ORF_1736 gull_ORF_54 gull_ORF_71 gull_ORF_71 gull_ORF_519 gull_ORF_560 gull_ORF_783 gull_ORF_787	45 45 50 48 46 69 41 45	225 225 498 233 418 396 573 648	1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147 0	236 493 229 441 395 578 777	vanRM is a vanR variant found in the vanM gene cluster LsAA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a pencillin-binding protein found in Strentococcus neurunniae
Gl24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_215 gul1_ORF_519 gul1_ORF_560 gul1_ORF_783 gul1_ORF_787 gul1_ORF_787	45 45 50 48 46 69 41 45 41	225 225 498 233 418 396 573 648 233	1.00E-02 1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147 0 4.00E-54	236 493 229 441 395 578 772 233	vanRM is a vanR variant found in the vanM gene cluster LsAA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_71 gul1_ORF_519 gul1_ORF_560 gul1_ORF_783 gul1_ORF_783 gul1_ORF_783 gul1_ORF_1039 gul1_ORF_1226	45 45 50 48 46 69 41 45 41 45 41 40	225 225 498 233 418 396 573 648 233 222	1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147 0 4.00E-54 2.00E-46	236 493 229 441 395 578 772 233 224	vanRM is a vanR variant found in the vanM gene cluster LsaA is an ABC efflux pump expressed in Enterococus faecalis vanRF is a vanR Variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics Addec is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster MacB is an ATP-binding castet (ABC) transporter that exports macrolides with 14- or 15- membered lactones
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_71 gul1_ORF_519 gul1_ORF_560 gul1_ORF_783 gul1_ORF_787 gul1_ORF_787 gul1_ORF_1039 gul1_ORF_1226 gul1_ORF_1288	45 45 50 48 46 69 41 45 41 45 41 40 44	225 225 498 233 418 396 573 648 233 222 222	1.00E-62 3.00E-172 1.00E-70 2.00E-172 0 9.00E-147 0 4.00E-54 2.00E-61	236 493 229 441 395 578 772 233 224 227	vanRM is a vanR variant found in the vanM gene cluster LsA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
Gl24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_71 gul1_ORF_519 gul1_ORF_560 gul1_ORF_783 gul1_ORF_787 gul1_ORF_1039 gul1_ORF_1226 gul1_ORF_1288 gul1_ORF_1505	45 45 50 48 46 69 41 45 41 40 40 44 43	225 225 498 233 418 396 573 648 233 222 222 221	1.00E-62 3.00E-172 1.00E-70 2.00E-171 0 9.00E-147 0 4.00E-54 2.00E-61 1.00E-56	236 493 229 441 395 578 772 233 224 227 233	vanRM is a vanR variant found in the vanM gene cluster LsAA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a pencillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
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Gl24_OFF_1736 gul1_OFF_54 gul1_OFF_71 gul1_OFF_71 gul1_OFF_519 gul1_OFF_560 gul1_OFF_787 gul1_OFF_787 gul1_OFF_787 gul1_OFF_1226 gul1_OFF_1226 gul1_OFF_1288 gul1_OFF_1505 gul2_OFF_55 gul2_OFF_72	45 45 50 48 46 69 41 45 41 40 44 43 43 50	225 225 498 233 418 396 573 648 233 222 221 225 221 225 498	1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147 0 4.00E-54 2.00E-61 1.00E-62 3.00E-172	236 493 229 441 395 578 772 233 224 227 233 236 493	vanRM is a vanR variant found in the vanM gene cluster LsA is an ABC efflux pump expressed in Entercocccus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics Addc is the outer membrane factor of the AdeABC multifurg efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones vanRM is a vanR variant found in the vanB gene cluster MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones vanRM is a vanR variant found in the vanB gene cluster SAA is an ABC- efflux pump expressed in Entercoccus faecalis
GJ24_ORF_1736 gul1_ORF_54 gul1_ORF_71 gul1_ORF_71 gul1_ORF_519 gul1_ORF_500 gul1_ORF_783 gul1_ORF_787 gul1_ORF_727 gul1_ORF_1226 gul1_ORF_1228 gul1_ORF_1255 gul2_ORF_55 gul2_ORF_72 gul2_ORF_72	45 45 50 48 46 69 41 45 41 45 41 40 44 43 45 50 48	225 225 498 233 418 396 573 648 233 222 222 221 225 498 233	1.00E-62 3.00E-172 1.00E-70 2.00E-121 0 9.00E-147 0 4.00E-54 2.00E-61 1.00E-56 1.00E-62 3.00E-172 1.00E-70	236 493 229 441 395 578 772 233 224 227 233 236 493 229	vanRM is a vanR variant found in the vanM gene cluster LSA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae vanRE is a vanR variant found in the vanE gene cluster MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones VanRH is a vanR variant found in the vanM gene cluster LSA is an ABC efflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanF gene cluster
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JCM1042_ORF_1252	40	222 7.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1042_ORF_1315	44	222 1.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1042_ORF_1545	43	221 2.00E-56 225 1.00E-62	244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 236 yanBM is a yanB variant found in the yanM gene cluster.
JCM1044_ORF_71	49	500 1.00E-171	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
JCM1044_ORF_216	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
JCM1044_ORF_504	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
JCM1044_ORF_544	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
JCM1044_ORF_778	40	583 4.00E-146	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
ICM1044_ORF_785	45	233 3.00F-54	233 vanRE is a vanR variant found in the vanE gene cluster
JCM1044_ORF_1210	40	222 7.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1044_ORF_1273	44	222 1.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1044_ORF_1498	43	221 2.00E-56	244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1045_ORF_56	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
JCM1045_ORF_74	50	498 3.00E-1/2	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
JCM1045_ORF_215	46	418 4.00E-121	440 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
JCM1045_ORF_649	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
JCM1045_ORF_886	41	583 2.00E-148	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
JCM1045_ORF_890	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
JCM1045_ORF_1145	41	233 4.00E-54	233 vanRE is a vanR variant found in the vanE gene cluster
JCM1045_ORF_1343	40	222 5.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ICM1045_0RF_1411	44	225 1.00E-62	227 Walls is an Arr-binding casselle (Abc) transporter that exports macronices with 14° of 13° membered factories
JCM1046_ORF_75	50	498 8.00E-168	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
JCM1046_ORF_220	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
JCM1046_ORF_569	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
JCM1046_ORF_609	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
JCM1046_ORF_874	40	583 2.00E-147	578 Adec is the outer membrane factor of the AdeABC multidrug efflux complex
ICM1046_ORF_1099	43	233 3.00F-54	233 vanRE is a vanR variant found in the vanE gene cluster
JCM1046_ORF_1251	62	61 2.00E-22	73 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
JCM1046_ORF_1320	40	222 1.00E-45	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1046_ORF_1382	44	222 1.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1046_ORF_1829	90	639 0	644 TetM is a ribosomal protection protein that confers tetracycline resistance
JCM1047_ORF_54	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
JCM1047_ORF_91	49	496 8.00E-1/2	492 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
JCM1047_ORF_241	46	418 7.00E-122	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
JCM1047_ORF_720	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
JCM1047_ORF_1061	40	579 2.00E-144	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
JCM1047_ORF_1065	45	648 0	766 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
JCM1047_ORF_1301	41	233 1.00E-53	233 vanRE is a vanR variant found in the vanE gene cluster
JCM1047_ORF_1485	40	222 1.00E-46	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1047_ORF_1547	44	222 1.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
JCM1047_ORF_2131	58	67 8.00E-24	84 Vanu is a transcriptional activator or the vang operon or vancomycin resistance genes
ICM1230 ORF 72	45	225 1 00E-62	use relations a noosonna protection protein that comes tetracycline resistance
JCM1230_ORF 93	50	498 4.00E-172	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
JCM1230_ORF_258	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
JCM1230_ORF_548	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
JCM1230_ORF_588	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
JCM1230_ORF_798	40	583 7.00E-145	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
JCM1230_ORF_802	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
ICM1230_ORF_1046	41	233 3.00E-54 222 1.00E-46	233 Vanke is a vank variant found in the vane gene cluster 234 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
ICM1230_ORF_1288	40	222 1.00E-40	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
L21 ORF 50	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
L21_ORF_67	50	498 7.00E-174	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
L21_ORF_222	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
L21_ORF_688	46	418 8.00E-123	440 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
L21_ORF_728	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
L21_ORF_969	41	573 4.00E-147	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
L21_ORF_975	45	233 3.00F-54	233 vanRE is a vanR variant found in the vanE gene cluster
L21 ORF 1405	40	222 7.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
L21_ORF_1467	44	222 2.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
L21_ORF_1675	43	219 5.00E-53	233 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
L21_ORF_1986	58	67 8.00E-24	84 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
LMG14476_ORF_69	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
LMG14476_ORF_90	50	498 8.00E-1/3	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
LMG14476_ORF_251	40	263 1 00E-59	327 vanHA also known as vanH is a vanH variant in the vanA gene cluster
LMG14476 ORF 549	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
LMG14476_ORF_589	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
LMG14476_ORF_968	40	583 7.00E-145	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
LMG14476_ORF_972	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
LIVIG14476_ORF_1201	41	233 3.00E-54	233 Vankt is a vank variant found in the vanEigene cluster
LWIG14470_OKF_1347	60 40	01 3.UUE-23 222 6.00F-47	voice shares a transcriptional activation of the value operan of vancomyclin resistance genes 224 MacR is an ATP-binding cassette (ARC) transporter that exports macrolides with 14, or 15, membered lactopor
LMG14476_ORF 1480	-10	LLL 0.00L 4/	2
LMG14476_ORE_1711	44	222 2.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
	44 43	222 2.00E-61 221 4.00E-56	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
LMG14477_ORF_52	44 43 45	222 2.00E-61 221 4.00E-56 225 1.00E-62	227 MacB is an AIP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 MacB is an AIP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster
LMG14477_ORF_52 LMG14477_ORF_73	44 43 45 50	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173	227 MacB is an AIP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_211	44 43 45 50 48	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70	227 MacB is an AIP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_248	44 43 45 50 48 40	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59	227 Mack is an AIP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 Mack is an AIP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRH is a vanR variant found in the vanF gene cluster 327 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_248 LMG14477_ORF_243 LMG14477_ORF_543	44 43 45 50 48 40 46 69	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 306	227 Mack is an AIP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 Mack is an AIP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 327 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 411 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 305 sonuere variante of forenouverse cinganopaus elegonation for the Tuber confer recitance to alformatic antibilation
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_241 LMG14477_ORF_543 LMG14477_ORF_543 LMG14477_ORF_952	44 43 45 50 48 40 46 69 40	222 2.00E-61 221 4.00E-66 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145	227 Mack is an ATP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 244 Mack is an ATP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 327 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 411 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics 578 AdeC is the outer membrane factor of the Ad-ABC multifruine efflux commlex
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_248 LMG14477_ORF_543 LMG14477_ORF_553 LMG14477_ORF_952 LMG14477_ORF_955	44 43 45 50 48 40 46 69 40 45	222 2.00E-61 221 4.00E-62 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145 648 0	 227 MacB is an ATP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABU) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 414 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics 578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex 772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_248 LMG14477_ORF_543 LMG14477_ORF_583 LMG14477_ORF_552 LMG14477_ORF_956 LMG14477_ORF_956	44 43 45 50 48 40 46 69 40 45 41	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145 648 0 233 3.00E-54	 224 Mack is an A1P-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones 234 Mack is an A1P-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 239 usnRF is a vanR variant found in the vanF gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 247 Mack is a undercluster cluster 248 vanH variant found in the vanF gene cluster 257 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 258 vanRe is a set of Streptomyces clinnamous elongation factor Tu that confer resistance to elfamycin antibiotics 258 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex 270 PBP1a is a vanR variant found in the vanE gene cluster 231 vanRE is a vanR variant found in the vanE gene cluster
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_73 LMG14477_ORF_248 LMG14477_ORF_543 LMG14477_ORF_543 LMG14477_ORF_553 LMG14477_ORF_955 LMG14477_ORF_1135 LMG14477_ORF_1330	44 43 45 50 48 40 46 69 40 45 41 60	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145 648 0 233 3.00E-54 61 3.00E-23	 227 Mack is an AIP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 234 Mack is an AIP-binding cassette (ABC) transporter that exports macroiides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 327 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 327 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 41 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics 578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex 772 PBP1a is a pancillin-binding protein found in Streptococcus pneumoniae 233 vanRE is a vanR variant found in the vanE gene cluster 68 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_73 LMG14477_ORF_211 LMG14477_ORF_543 LMG14477_ORF_543 LMG14477_ORF_952 LMG14477_ORF_956 LMG14477_ORF_1330 LMG14477_ORF_1330	44 43 45 50 48 40 46 69 40 45 41 60 40	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 533 7.00E-145 648 0 233 3.00E-54 61 3.00E-23 222 6.00E-47	 224 MacB is an ATP-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 493 IsaA Is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 414 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 395 Sequence variants of Streptomyces cinnamoneus elongation factor 10 that confer resistance to elfamycin antibiotics 578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex 772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae 233 vanRE is a vanR variant found in the vanE gene cluster 68 VanD is a transcriptional activator of the vanG operon of vancomycin resistance genes 244 MacB is an ATP-binding cassette (ABC) transporter that exports macroildes with 14- or 15- membered lactones
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LMG14477_ORF_52 LMG14477_ORF_73 LMG14477_ORF_73 LMG14477_ORF_248 LMG14477_ORF_543 LMG14477_ORF_543 LMG14477_ORF_552 LMG14477_ORF_555 LMG14477_ORF_1185 LMG14477_ORF_1185 LMG14477_ORF_1401 LMG14477_ORF_1464 LMG14477_ORF_1464 LMG14477_ORF_1464	44 43 45 50 48 40 46 69 40 45 41 60 40 44 43 45	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145 648 0 233 3.00E-54 61 3.00E-54 61 3.00E-54 61 3.00E-54 222 2.00E-61 221 4.00E-56	 224 Mack is an A1P-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 234 Mack is an A1P-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 236 vanRM is a vanR variant found in the vanM gene cluster 231 saA is an ABC efflux pump expressed in Enterococcus faecalis 232 vanRF is a vanR variant found in the vanF gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 237 vanHA, also known as vanH, is a vanH variant in the vanA gene cluster 238 vanRE is a vanR variant found in the vanE gene cluster 233 vanRE is a vanR variant found in the vanE gene cluster 234 vanRE is a vanR variant found in the vanE gene cluster 234 vanRE is a vanR variant found in the vanE gene cluster 234 vanRE is a vanR variant found in the vanE gene cluster 234 vanRE is a vanR variant found in the vanG operon of vancomycin resistance genes 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 MacB is
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LING14477_ORF_52 LING14477_ORF_73 LING14477_ORF_73 LING14477_ORF_543 LING14477_ORF_543 LING14477_ORF_543 LING14477_ORF_553 LING14477_ORF_153 LING14477_ORF_1185 LING14477_ORF_1401 LING14477_ORF_1404 LING14477_ORF_1404 LING14477_ORF_1697 NCIMB702343_ORF_53 NCIMB702343_ORF_53 NCIMB702343_ORF_58 NCIMB702343_ORF_58 NCIMB702343_ORF_58 NCIMB702343_ORF_854 NCIMB702343_ORF_854 NCIMB702343_ORF_854 NCIMB702343_ORF_1243 NCIMB702343_ORF_1243 NCIMB702343_ORF_1315 NCIMB702343_ORF_1381	44 43 50 48 40 46 69 40 45 41 60 40 45 41 40 44 45 52 48 69 40 45 52 48 69 40 41 52 40 44	222 2.00E-61 221 4.00E-56 225 1.00E-62 498 8.00E-173 231 2.00E-70 263 1.00E-59 418 2.00E-121 396 0 583 7.00E-145 648 0 233 3.00E-54 61 3.00E-52 222 6.00E-47 222 2.00E-61 221 4.00E-56 223 3.00E-62 233 1.00E-70 396 0 418 2.00E-121 418 2.00E-62 223 1.00E-56 225 1.00E-62 233 1.00E-70 396 0 418 2.00E-142 583 2.00E-145 648 0 233 3.00E-54 62 7.00E-23 333 3.00E-54 62 7.00E-47 222 7.00E-47 222 7.00E-62 <	 Mack is an AIP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones san AIP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones usak is an APC defflux pump expressed in Enterococcus faecalis vanRF is a vanR variant found in the vanR gene cluster tay canRF is a vanR variant fourd in the van gene cluster wanRF is a vanR variant fourd in the van gene cluster wanRF is a vanR variant of the vanG gene cluster wanRF is a vanR variant of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics AdeC is the outer membrane factor of the AdeABC multidrug efflux complex a vanR variant found in the vanG gene cluster vanRE is a vanR variant found in the vanG generon of vancomycin resistance genes wanRE is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones kas an ABC efflux pump expressed in Enterococcus faecalis usaR is an ABC efflux pump expressed in Enterococcus faecalis usaR is an ABC efflux pump expressed in Enterococcus faecalis usaR is an ABC efflux pump expressed in Enterococcus faecalis sa vanR variant found in the vanG gene cluster AdeC is the outer membrane factor of the AdeABC multidrug efflux complex R

NCIMB702343_ORF_1779	58	67 8.00E-24	84 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
NCIMB8816_ORF_55	45	225 1.00E-62 500 1.00E-171	236 vanKM is a vank variant found in the vanMigene cluster 493 LisaA is an ABC efflux numn expressed in Enterococcus faecalis
NCIMB8816_ORF_221	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
NCIMB8816_ORF_507	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
NCIMB8816_ORF_547	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
NCIMB8816_ORF_782	40	583 4.00E-146	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
NCIMB8816 ORF 1032	41	233 3.00E-54	233 vanRE is a vanR variant found in the vanE gene cluster
NCIMB8816_ORF_1253	40	222 7.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
NCIMB8816_ORF_1317	44	222 1.00E-61	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
NCIMB8816_ORF_1545 NCIMB8816_ORF_1605	43 40	221 2.00E-56 227 1.00E-54	244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 233 vanBM is a vanB variant found in the vanM gene cluster
NCIMB8817_ORF_60	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
NCIMB8817_ORF_79	50	498 7.00E-171	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
NCIMB8817_ORF_221	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
NCIMB8817_ORF_610	46 69	418 2.00E-121 396 0	441 Mycobacterium tuberculosis mura conters intrinsic resistance to fostomycin 395. Sequence variants of Strentomyces cinnamoneus elongation factor. Tu that confer resistance to elfamycin antibiotics
NCIMB8817_ORF_880	41	579 2.00E-148	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
NCIMB8817_ORF_884	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
NCIMB8817_ORF_1133	41	233 3.00E-54	233 vanRE is a vanR variant found in the vanE gene cluster 234 MacR is an ATR binding correction (ARC) transporter that expects macrolides with 14, or 15, membered lactoper
NCIMB8817_ORF_1305	40	222 9.00E-62	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactories
NCIMB8818_ORF_51	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
NCIMB8818_ORF_71	50	498 2.00E-171	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
NCIMB8818_ORF_226 NCIMB8818_ORF_452	49 43	231 3.00E-71 219 5.00E-53	229 vanRF is a vanR variant found in the vanF gene cluster 233 MarR is an ΔTP-binding cassette (ΔRC) transporter that exports macrolides with 14- or 15- membered lactones
NCIMB8818_ORF_740	46	418 2.00E-121	441 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
NCIMB8818_ORF_780	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
NCIMB8818_ORF_1075	40	583 4.00E-146	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
NCIMB8818_ORF_1079 NCIMB8818_ORF_1330	45 41	648 U 233 4 00E-54	7/2 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
NCIMB8818_ORF_1484	62	61 6.00E-22	73 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
NCIMB8818_ORF_1530	40	222 7.00E-47	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
NCIMB8818_ORF_1541	45	305 1.00E-79	302 bcrA is an ABC transporter found in Bacillus licheniformis that confers bacitracin resistance
NCIMB8818_ORF_1650 NCIMB8818_ORF_1908	44	222 1.00E-61 77 0.00E+00	227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 76. A type III ABC transporter identified on the powobiocin biosynthetic gene cluster.
NIAS840_ORF_88	48	233 1.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
NIAS840_ORF_241	49	498 3.00E-171	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
NIAS840_ORF_403	40	222 1.00E-46	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
NIAS840_ORF_403	98	164 9.00E-119	164 InuC is a transposon-mediated nucleotidyltransferase found in Streptococcus agalactiae
NIAS840_ORF_661	99	216 1.00E-158	216 vatH is a plasmid-mediated acetyltransferase found in Enterococcus faecium
NIAS840_ORF_662	99	525 0	525 vgaD is an efflux protein expressed in Enterococcus faecium that confers resistance to streptogramin A antibiotics
NIAS840_ORF_793	45	225 1.00E-62	236 vanRM is a vanR variant found in the vanM gene cluster
NIAS840_ORF_1168	69	396 0	395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
NIAS840_ORF_1378	41	583 1.00E-148	578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
NIAS840_ORF_1382	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
NIAS840_ORF_1588 Rep_ORF_41	41	233 3.00E-54 225 1.00E-62	233 VanKE is a vanK variant found in the vanE gene cluster
Ren_ORF_63	50	498 4.00E-171	493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis
Ren_ORF_230	48	233 2.00E-70	229 vanRF is a vanR variant found in the vanF gene cluster
Ren_ORF_651	46	418 8.00E-123	440 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin
Ren ORF 929	41	569 4.00E-147	595 Sequence variants of streptomyces clinianoneus elongation factor fu that complex 578 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
Ren_ORF_933	45	648 0	772 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae
Ren_ORF_1188	41	233 3.00E-54	233 vanRE is a vanR variant found in the vanE gene cluster
Ren_ORF_1386 Ren_ORF_1448	40 44	222 3.00E-47 222 4.00E-62	224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
Ren_ORF_1680	49	81 7.00E-21	102 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14 or 15- membered lactones
Ren_ORF_1681	46	110 1.00E-26	131 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
Ren_ORF_1761	58	67 8.00E-24	84 VanU is a transcriptional activator of the vanG operon of vancomycin resistance genes
SMXD51_ORF_100	40		222 we DMA is a set D we should be the set of set o
SMXD51_ORF_205	40	227 1.00E-54 225 1.00E-62	233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster
SMXD51_ORF_366	43 50	227 1.00E-54 225 1.00E-62 498 1.00E-171	233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Entercoccus faecalis
01 D/D E / 0 D E /01	45 50 48	227 1.00E-34 225 1.00E-62 498 1.00E-171 233 1.00E-70	233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 493 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster
SMXD51_ORF_691	45 50 48 44	227 1.00E-54 225 1.00E-62 498 1.00E-171 233 1.00E-70 222 1.00E-61 233 2.00E-61	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 249 LsaA is an ABC efflux pump expressed in Enterococcus facealis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an AT-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 236 MacB is an ATD-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones
SMXD51_ORF_691 SMXD51_ORF_758 SMXD51_ORF_1013	45 50 48 44 40 46	227 1.00E-54 225 1.00E-62 498 1.00E-70 222 1.00E-61 222 2.00E-46 418 2.00E-121	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 439 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 424 Mycobacterium tuberculosis murk confers intrinsic resistance to fosfomycin
SMXD51_ORF_691 SMXD51_ORF_758 SMXD51_ORF_1013 SMXD51_ORF_1055	45 50 48 44 40 46 69	225 1.00E-54 225 1.00E-62 498 1.00E-171 233 1.00E-70 222 2.00E-61 222 2.00E-46 418 2.00E-121 396 0	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 439 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 431 Mycobacterium tuberculosis murk confers intrinsic resistance to fosfomycin 395 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics
SMXD51_ORF_091 SMXD51_ORF_758 SMXD51_ORF_1013 SMXD51_ORF_1055 SMXD51_ORF_1276	45 50 48 44 40 46 69 40	225 1.00E-54 428 1.00E-62 428 1.00E-61 222 1.00E-61 222 2.00E-61 222 2.00E-64 418 2.00E-121 396 0 583 6.00E-146	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 249 LsaA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 245 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 241 Mycobacterium tuberculosis murA confers intrinsic resistance to fosfomycin 255 Sequence variants of Streptomyces cinnamoneus elongation factor Tu that confer resistance to elfamycin antibiotics 278 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex
SMXD51_ORF_091 SMXD51_ORF_758 SMXD51_ORF_1013 SMXD51_ORF_1055 SMXD51_ORF_1276 SMXD51_ORF_1280 SMXD51_ORF_1513	45 50 48 44 40 46 69 40 45 41	225 1.00E-54 225 1.00E-62 498 1.00E-70 222 1.00E-61 222 2.00E-61 222 2.00E-61 233 6.00E-121 396 0 583 6.00E-146 648 0 233 3.00E-54	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 231 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 224 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 258 valce is an arb-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 259 Sequence variants of Streptomyces cinnamoneus elongation factor. Tu that confer resistance to elfamycin antibiotics 258 AdeC is the outer membrane factor of the AdeABC multidrug efflux complex 232 VanB is a panRicillin-binding protein found in Streptococcus pneumoniae 233 vanBE is a vanB variant found in the vanF gene cluster
SMXD51_ORF_758 SMXD51_ORF_758 SMXD51_ORF_1013 SMXD51_ORF_1055 SMXD51_ORF_1280 SMXD51_ORF_1280 SMXD51_ORF_1513 SMXD51_ORF_1702	45 50 48 44 40 46 69 40 45 41 97	225 1.00E-54 225 1.00E-62 498 1.00E-171 233 1.00E-61 222 2.00E-61 222 2.00E-61 222 2.00E-61 233 6.00E-121 396 0 583 6.00E-146 648 0 233 3.00E-54 242 5.00E-173	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 231 vanRA is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 245 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 246 VacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 247 MacB is a vanR variant found in the vanF gene cluster 258 ErnG is a vanR variant found in the vanE gene cluster 258 ErnG is a methyltransferase that catalyzes the methylation of A2058 of the 235 ribosomal RNA in two steps
SMXD51_ORF_758 SMXD51_ORF_758 SMXD51_ORF_1013 SMXD51_ORF_1013 SMXD51_ORF_1276 SMXD51_ORF_1276 SMXD51_ORF_1270 SMXD51_ORF_1702 SMXD51_ORF_1702	45 50 48 44 46 69 40 45 41 97 89	225 1.00E-54 225 1.00E-62 498 1.00E-70 222 1.00E-61 222 2.00E-61 222 2.00E-61 233 3.00E-121 396 0 583 6.00E-146 648 0 233 3.00E-54 242 5.00E-173 639 0	 233 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 236 vanRM is a vanR variant found in the vanM gene cluster 239 task is an ABC efflux pump expressed in Enterococcus faecalis 229 vanRF is a vanR variant found in the vanF gene cluster 227 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 245 MacB is an ATP-binding cassette (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding consent (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 MacB is an ATP-binding consent (ABC) transporter that exports macrolides with 14- or 15- membered lactones 245 MacB is an ATP-binding consent (ABC) transporter that exports macrolides with 14- or 15- membered lactones 244 macB is an ATP-binding consent (ABC) transporter that exports macrolides with 14- or 15- membered lactones 245 Ref is the outer membrane factor of the AdeBC multidrug efflux complex 276 PBP1a is a penicillin-binding protein found in Streptococcus pneumoniae 233 vanRE is a vanR variant found in the vanE gene cluster 258 ErmC is a methytransferase that castlyzes the methylation of A2058 of the 235 ribosomal RNA in two steps 264 TetM is a ribosomal protection protein that confers tetracycline resistance
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gene	functional annotation	% identity	query coverage	e-value	query length
01M14315_ORF_1114	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
01M14315_ORF_1197	UDP-glucose_pyrophosphorylase	72.7	293	4.00E-151	290
778_ORF_1065 778_ORF_1147	ATP-dependent_Cip_protease_proteolytic_subunit	72.59	197	1.00E-105 2.00E-151	197 290
866_ORF_1162	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
866_ORF_1246	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
ACS116_ORF_1278	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
ACS116_ORF_1363	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
AH4231_ORF_1274 AH4231_ORF_1357	UDP-glucose pyrophosphorylase	72.39	293	2.00E-103	290
AH4331 ORF 1249	ATP-dependent Clp protease proteolytic subunit	72.59	197	1.00E-105	197
AH4331_ORF_1331	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
AH4331_ORF_2194	cell_wall_surface_anchor_family_protein,_Plasminogenand_Fibronectin-binding_protein_B	70.3	101	9.00E-43	105
AH43324_ORF_1245	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
AH43324_ORF_1326 AH43348_ORF_1213	UDP-giucose_pyropnosphorylase ATP-denendent Clin protease proteolytic subunit	72.7	293	2.00E-151 1.00E-105	290
AH43348 ORF 1315	UDP-glucose pyrophosphorylase	72.55	293	2.00E-151	290
ATCC11741_ORF_1065	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
ATCC11741_ORF_1147	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
CCuG2753OB_ORF_1016	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
CCuG2753OB_ORF_1100	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
CCuG38008_ORF_1120	UDP-glucose nyronhosnhorylase	72.33	293	2 00E-103	290
CCuG44481 ORF 1134	ATP-dependent Clp protease proteolytic subunit	72.59	197	1.00E-105	197
CCuG44481_ORF_1217	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
CCuG45735_ORF_1169	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
CCuG45735_ORF_1251	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
CCuG47171_ORF_1127	A IP-dependent_CIp_protease_proteolytic_subunit	/2.59	197	1.00E-105 2.00E-151	197
CCuG47825 ORF 396	polysaccharide biosynthesis protein CpsF	73.63	91	5.00E-46	93
CCuG47825 ORF 1465	ATP-dependent Clp protease proteolytic subunit	72.59	197	1.00E-105	197
CCuG47825_ORF_2004	UDP-glucose_pyrophosphorylase	72.35	293	7.00E-151	290
CCuG47826_ORF_1150	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
CCuG47826_ORF_1339	UDP-glucose_pyrophosphorylase	72.35	293	7.00E-151	290
CECT5713_ORF_1313	ATP-dependent_CIp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
cp400 ORF 1280	ATP-dependent Clp protease proteolytic subunit	72.59	293 197	1.00E-105	197
cp400_ORF_1413	UDP-glucose_pyrophosphorylase	73.04	293	4.00E-152	290
DSM18933_ORF_62	UDP-glucose_pyrophosphorylase	73.04	293	7.00E-153	300
DSM18933_ORF_219	polysaccharide_biosynthesis_protein_CpsF	74.5	149	7.00E-86	149
DSM18933_ORF_1644	ATP-dependent_Clp_protease_proteolytic_subunit	73.58	193	1.00E-104	196
DSWI20492_ORF_1084	ATP-dependent_CIP_protease_proteorytic_subunit	72.59	197	2.00E-105	290
DSM20492_ORF_1456	polysaccharide biosynthesis protein CpsF	75	132	5.00E-73	132
DSM20554_ORF_1092	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
DSM20554_ORF_1174	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
DSM20554_ORF_1467	polysaccharide_biosynthesis_protein_CpsF	75	132	5.00E-73	132
DSM20555_ORF_1055	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
GI24 ORE 1096	ATP-dependent Clp protease proteolytic subunit	72.7	293	2.00E-151 1.00E-105	290
GJ24 ORF 1189	UDP-glucose pyrophosphorylase	72.7	293	2.00E-151	290
gul1_ORF_1025	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
gul1_ORF_1107	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
gul2_ORF_1067	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
GUIZ_ORF_1150	ODP-giucose_pyrophosphorylase	72.7	293	2.00E-151	290
JCM1040_ORF_1192	UDP-glucose pyrophosphorylase	72.55	293	2.00E-151	290
JCM1042_ORF_1056	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
JCM1042_ORF_1141	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
JCM1044_ORF_1016	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
JCM1044_ORF_1100	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
JCM1045_ORF_1131	A IP-dependent_cip_protease_proteolytic_subunit	72.59	197	2.00E-105	290
JCM1046 ORF 1085	ATP-dependent Clp protease proteolytic subunit	72.59	197	1.00E-105	197
JCM1046_ORF_1167	UDP-glucose_pyrophosphorylase	73.04	293	4.00E-152	290
JCM1046_ORF_1500	polysaccharide_biosynthesis_protein_CpsF	75.17	149	9.00E-84	152
JCM1047_ORF_1287	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
JCM1047_ORF_1370	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
JCM1230_ORF_1032	A IP-dependent_CIP_protease_proteorytic_subunit	72.59	197	2.00E-105	290
L21 ORF 1211	ATP-dependent Clp protease proteolytic subunit	72.59	197	1.00E-105	197
L21_ORF_1294	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
LMG14476_ORF_1187	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
LMG14476_ORF_1272	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
LMG14477_ORF_1171	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
NCIMB702343 ORF 1073	ATP-dependent Clp protease proteolytic subunit	72.7	293	1.00F-105	290 197
NCIMB702343_ORF 1158	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
NCIMB702343_ORF_1488	polysaccharide_biosynthesis_protein_CpsF	77.14	140	7.00E-79	141
NCIMB8816_ORF_1018	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
NCIMB8816_ORF_1141	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
NCIMB8815_ORF_1869	ceii_waii_surrace_anchor_tamiiy_protein_Plasminogenand_Fibronectin-binding_protein_B	70	110	4.00E-47	110
NCIMB8817 ORF 1201	UDP-glucose pyrophosphorylase	72.59	293	2.00E-105	290
NCIMB8818_ORF_1316	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197	1.00E-105	197
NCIMB8818_ORF_1399	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
NIAS840_ORF_276	UDP-glucose_pyrophosphorylase	72.7	293	2.00E-151	290
NIAS840_ORF_577	polysaccharide_biosynthesis_protein_CpsF	75	132	5.00E-73	132

NIAS840_ORF_1603	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197 1.00E-105	197
Ren_ORF_1171	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197 1.00E-105	197
Ren_ORF_1266	UDP-glucose_pyrophosphorylase	72.35	293 4.00E-150	290
SMXD51_ORF_1498	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197 1.00E-105	197
SMXD51_ORF_1595	UDP-glucose_pyrophosphorylase	72.7	293 2.00E-151	290
UCC118_ORF_1257	ATP-dependent_Clp_protease_proteolytic_subunit	72.59	197 1.00E-105	197
UCC118_ORF_1367	UDP-glucose_pyrophosphorylase	72.7	293 2.00E-151	290