猪链球菌全基因组序列比较分析

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摘要 2005 年, 在四川局部地区爆发的人感染猪链球菌疫情导致 200 多人感染, 30 多人死亡. 为了研究猪链球菌的致病机理, 以达到防止细菌传播和人畜感染的目的, 对已测序的猪链球菌(*Streptococcus suis*)的 2 个菌株(P1/7, 89-1591)进行了全面的功能注释和分析. 猪链球菌 P1/7 的基因组全长为 2.007 Mb, 共有 1969 个可读框(ORF), 而部分测序的猪链球菌 89-1591 序列包含在 177 个连接群(contig)中, 长为 1.98 Mb, 含有 1918 个 ORF. 两菌株基因组比较结果表明, 其平均编码区(CDS)的长度非常接近. 在所有 ORF 中, 同源 ORF 数为 1306 个. 两菌株中可能的毒性因子大多数具同源性. 但也存在例外, 如在 P1/7 中存在于一个基因岛内, 编码与毒性相关的荚膜多糖的 11 个毒性因子(CPS2A-2K)中, 4 个基因 *cps*2A, 2B, 2I, 2J 未在 89-159 菌株中发现. 同时, P1/7 中编码细胞外因子(EF)和溶血素(Haemolysin)的基因也未在 89-159 菌株中发现. 另外, 两菌株中与 DNA 复制、修复及重组相关的基因组成上存在着明显的差异, 并且在表面蛋白质组成上也同样存在着一定的差异. 这些特性表明两菌株为了适应不同的环境压力而演化出特有的功能单位, 暗示着 2 个菌株在毒性机理上存在着一定的差异. 以上分析结果为系统地研究猪链球菌以及防治、疫苗的开发、治疗药物的设计提供了广泛的基因组学信息.

关键词 猪链球菌(***Streptococcus suis***) 菌株 **P1/7** 菌株 **89-1591** 毒性因子

2005 年, 在四川局部地区爆发的人感染猪链球菌疫情导致 200 多人感染, 30 多人死亡[1]. 猪链球菌是厌氧性的革兰氏阳性球菌, 是多年来困扰全世界猪肉生产的一种特异病原体. 尽管在过去的十几年中, 猪链球菌研究一直为人们所关注, 但对于这种病原体还知道得不多. 已有的研究表明, 根据其荚膜多糖抗原特性的差异, 可将猪链球菌分为 35 种血清型(1~34 型及 1/2 型)及相当数量无法定型的菌株[2,3]. 不同血清群对不同的动物宿主有不同的致病性, 而且并非所有的血清型均有致病性, 同一血清型不同菌株之间以及不同血清型菌株之间其毒力也存在差异[4,5]. 有些血清群可引起猪发病; 有的血清群, 如R及F群等既可引起猪发病, 也可同时感染人群, 是重要的人畜共患病病原体. 猪感染后可引起脑膜炎、关节炎、肺炎、败血症、心内膜炎、流产和脓疮脑等疾病[6].

在所有的猪链球菌中, 血清 2 型呈全球性分布, 致病力强, 临床检出率最高. 但 2 型也有致病株和非致病株之分. 按兰氏分群, 猪链球菌 2 型为R群, 1 型为S群, 有的血清型不能分群, 有的属S-T群或T群. 人感染 2 型猪链球菌通常表现为化脓性脑膜炎、伴有耳聋、运动功能紊乱, 严重的病例发生中毒性休克综合症, 导致多脏器衰竭及死亡[7~13]. 一般认为, 猪链球菌中重要的毒力相关因子有荚膜多糖(CPS)、溶菌酶释放蛋白(MRP)、胞外因子(EF)、溶血素(suilysin)、黏附素(FBP)等[2,14,15]. 但已有的研究结果表明, 在血清 2 型中与高毒性相关的毒性因子溶血素只存在于近 70%的各种血清型的猪链球菌分离群中[6,16]. 而且溶血素的产生并不总是与毒性相匹配. 从来源于欧洲的猪中分离的许多猪链球菌都能产生溶血素, 而大多数来源于北美的菌株则不产生溶血素. 有证据表明, 在不同的国家, 猪链球菌的菌株具有相当大的差异[2]. 而且在其他细菌中用于判断毒性因子的标准在猪链球菌中不一定是必须的, 如荚膜的存在不一定就决定了菌株的毒性, 具有弱的溶血性的菌株也可能有极高的毒性[17]. 除了以上的一些毒性因子外, 相关的一些研究还报道了一些其他潜在的候选毒性因子, 如细胞壁和胞外蛋白质在一些野生型的猪链球菌中也与毒性相关, 但研究结果发现一些不产生这些蛋白质的突变菌株具有与野生型菌株相当的毒性[18]. 一些表面蛋白已经作为潜在的毒性因子进行了研究, 从荷兰的猪中分离出来的猪链球菌 2 型具有

的一些蛋白明显与毒性相关，甚至认为这些蛋白就是使得猪链球菌在被巨噬细胞吞噬后具有抵抗消化的功能，但从加拿大的病猪所分离的大多数猪链球菌 2 型却不产生这些蛋白[19]. 因此，毒性因子与猪链球菌致病性之间的关系现在还不是十分清楚.

到目前为止，猪链球菌如何生存、繁殖并感染宿主的机制还不清楚. 因此通过基因组的比较分析，在基因组水平上确定和注释与细菌和宿主相互作用相关的特异基因有可能帮助我们了解细菌的感染过程和致病机理. 关系邻近的病原微生物的种间或菌株之间的比较基因组学是用来确定与宿主特异性和毒性相关的基因的重要工具. 因此在两个猪链球菌的菌株间的基因组比较能够给我们提供线索去寻找参与宿主-病原体相互作用的菌株间共同具有的和菌株特异的基因，为系统地研究猪链球菌以及防治、疫苗的开发、治疗药物的设计提供广泛的基因组学信息. 据此，我们对来自欧洲的菌株 P1/7 (*Streptococcus suis* P1/7)的基因组序列进行了详细的功能注释，同时将其与来自北美的猪链球菌株 89-1591 (*Streptococcus suis* 89-1591)的部分基因组序列进行了系统的比较基因组学的研究，分析结果不仅揭示了两个菌株之间保守的组成部分，还发现了各自基因组中特异的组成成份，这些结果可为系统、详细地研究猪链球菌的致病机理、疾病防治提供基因组学基础.

1 材料与方法

(ⅰ) 基因组序列样本来源. 菌株 89-1591 是从病猪中分离出来的 2 型猪链球菌，来自于北美，相关的序列来自美国能源部的联合基因组研究院(US Department of Energy Joint Genome Institute, ftp://ftp.jgi-psf.org/pub/JGI_data /Microbial/streptococcus_suis/)，为未完成的序列，共有 177 个连接群(contig)，长度为 1.98 Mb. 菌株 P1/7 来自于欧洲，也属于 2 型猪链球菌，来自英国 Wellcome Trust Sanger 研究中心(ftp://ftp.sanger.ac.uk/pub/pathogens/ss/)，全长序列为 2007491 bp.

(ⅱ) 基因预测和注释. 菌株 89-1591 的基因预测与注释信息从美国国立生物技术信息中心(National Center for Biotechnology Information, NCBI, http://www.ncbi.nlm.nih.gov/genomes/framik.cgi?gi=5245&db=G/)得到. NCBI 对其 1918 个 ORF 做了简单的功能标注. 菌株 P1/7 共发现有 1969 个 ORF, ORF 的功能注释是通过将所有预测的蛋白序列用 BlastP 在本地大型服务器上搜索非冗余的蛋白库而得到.

(ⅲ) 两株*Streptococcus suis* 的蛋白分析. 两株猪链球菌的蛋白分类分别用Pfam RELEASE 18.0 数据库，用HMMPfam搜索其Pfam分类. 将两种菌株的蛋白质序列剔除信号肽的干扰后，用ConPred Ⅱ进行在线预测[20]，得到所有蛋白的跨膜区域. 用RPS-Blast[21]和CDD库[22](2005 年 7 月 6 日发布的版本)对蛋白序列进行序列联配，得到相应的功能域注释信息以及COG分类信息. 对数据分布的差异进行了Fisher确切检验.

另外，我们还利用自己开发的Seq2GO对 2 株猪链球菌的基因进行了基于GO系统的功能分类[23]. 相比于同类软件[24]，Seq2GO人为参数少，充分利用Blast结果，基于超几何分布概率模型得到预测功能分类的P值，具有严格的统计学意义，预测也较为准确和稳定. 用 Seq2GO 进行蛋白功能分类的流程如下:

对未知功能序列做Blast(使用GenBank的nr库)分析，在给定的E值($E<1\times10^{-10}$)标准下可筛选得到一组相似性序列，将这些序列的名称转换为Gene 数据库中的GeneId号[25]，根据Gene 数据库提供的gene2go注释表，将这些GeneId号投射到GO的功能结点. 假设这些GeneId号共有k个能投射到GO上，而其中有x个投射到某个特定的GO功能结点. 如果这组基因Id并不由Blast而来，而是从全基因组序列中等概率地随机抽取得到，则该功能结点上抽到的基因数目服从超几何分布[26]，x/k成为一个较大百分比的可能性较小，可计算该结点的P值. 由于序列相似导致的功能相似，这组基因将在某些功能上出现积聚现象，从而这些相关功能结点的x/k百分比能大到随机抽取不太可能达到的程度. 根据人为给定的显著性水平，选择出一组P值较小的功能结点. 最后，对这组结点根据父子关系筛选，去除那些祖先结点(冗余结果)，保留最具体的功能分类.

(ⅳ) 比较基因组分析. 用Blastn[27]将*Streptococcus suis* 89-1591 的每个连接群与*Streptococcus suis* P1/7 的整个基因组进行序列联配，根据最高的同源性决定每个连接群相对于整个基因组的位置. 应用MUMmer[28]对每个 89-1591 的连接群与P1/7 基因组进行序列联配.

对 *Streptococcus suis* 89-1591 和 *Streptococcus suis* P1/7 已预测的 CDSs 的序列进行比较分析. 首先，

用两者蛋白序列进行双向 BlastP 序列联配，选取 $E \leqslant 10^{-5}$，一致性≥35%以及匹配长度≥75%的一对基因作为同源性的基因，同源性基因以外的为各自的特异基因. 在这些同源基因对里面，将互为最佳匹配的一对基因作为直系同源基因对，然后，再将这些直系同源基因对的核酸序列去做 Blastn 序列联配，找出序列完全相同的基因、序列长度相同但碱基存在差异的基因以及存在插入/删除的基因.

(v) 毒性因子及表面蛋白的分析. 根据文献报道的相关毒性因子，经过 BlastP 序列联配在两菌株中寻找这些因子. 同时，有的蛋白质具有革兰氏阳性细菌表面蛋白所特有的功能域，这些表面蛋白被列为是潜在的毒性因子.

(vi) 基因岛分析. 对 *Streptococcus suis* P1/7 所有的 1969 个 ORF，将每 6 个作为一个聚类群(cluster)，每次移动一个 ORF，最终得到 1964 个聚类群，然后每个分别计算 GC 含量和各种二核苷酸在基因组中出现频率的差异，并计算平均值，将每个聚类群的值与平均值比较得到了一些特异的区域，并同时根据 tRNA 以及转座酶的分布，经过人工确定，得到基因岛.

(vii) 猪链球菌蛋白质相互作用预测与分析. 应用系统发生谱方法[29~31]、基因邻居方法[32]、基因融合方法[33]以及操纵子[34]方法分别预测了 *Streptococcus suis* P1/7 和 *Streptococcus suis* 89-1591 两个菌株基因组范围内的蛋白质相互作用，然后应用Sun等人[29]建立的InPrePPI方法整合上面预测的结果(结果未显示).

2 结果

2.1 基因组总体结构和特征

Streptococcus suis P1/7 基因组是由一个环状的染色体组成(图 1). 基因组中总共找到了 1969 个 ORF，编码蛋白质的 ORF 是 1874 个. 对其中 1447 个 CDSs 给出了预测的功能，占总的 CDSs 的 73.5%，含有 448 个操纵子(operon). 而在 *Streptococcus suis* 89/1591 中

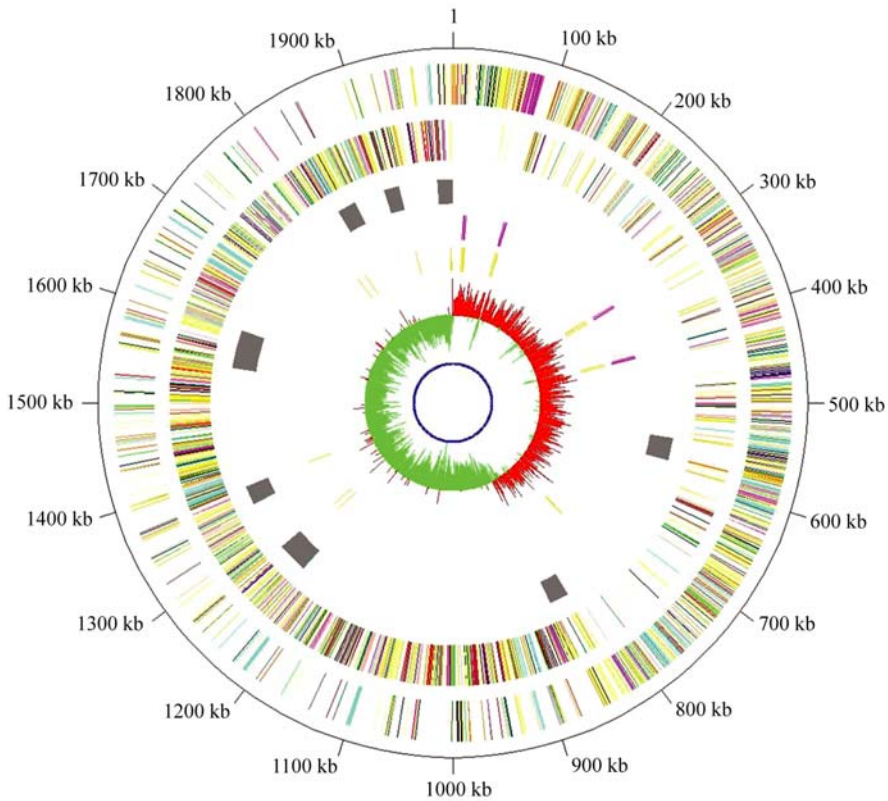

图 1 *S. suis* P1/7 基因组圈图

最外圈的刻度代表基因组长度，以 bp 计. 从外到内各圈分别表示: 1，正义链上的所有基因; 2，反义链上的所有基因; 3，我们找到的 8 个基因岛; 4, tRNA 基因; 5, rRNA 基因; 6, GC 偏差(GC bias, (G–C)/(G+C))；红色表示值>0，绿色表示值<0; 7, GC 含量. 第 1, 2 圈基因按 COG 分类用不同的颜色表示

预测的 ORF 是 1918 个，其中 1486 个赋予了功能注释，占总数的 77.5%. 将 *Streptococcus suis* 89-1591 中所有的连接群与 *Streptococcus suis* P1/7 整个基因组进行序列联配，在 177 个 contig 中，与 P1/7 基因组序列具有相似性的连接群有 152 个，总长为 1788339 bp，占总长的 90.4%，含有 418 个操纵子(图 2).

Streptococcus suis 89-1591 与 *Streptococcus suis* P1/7 基因组的基本特征见表 1. 两者基因组的 GC 含量相似，编码蛋白区的 GC 含量均低于整个基因组. 在已知的注释信息中可以看出 *Streptococcus suis* 89-1591 与 *Streptococcus suis* P1/7 大部分的 CDS 具有一定的相似性，这不仅表现在蛋白质水平，同样也表现在核苷酸水平，同长碱基差异序列对共有 848 对，占了 CDS 总数的 43%左右. 直系同源分析的结果表明，89-1591 和 P1/7 中属于直系同源的 CDS 数是 1306，因此，两菌株间有很高的同源性. 除此之外，核酸序列完全相同的基因和存在插入/删除的基因分别有 31 对和 427 对. *Streptococcus suis* P1/7 具有 12 个 rRNA 和 56 个 tRNA，但在已知的 89-1591 序列中却没有找到相关编码 rRNA 和 tRNA 的基因.

2.2　基因功能分类

两菌株中基因根据它们预测的功能进行了分类(图 3). 统计数据结果表明在 COG 分类中只有 L 功能类(DNA 复制，重排和修复)在两个菌株间有明显差异(P = 0.01299, Fisher 确切检验). 仔细分析 L 类的蛋白质组成发现，该组分差异主要来源于其中的转座酶(transposase)，因为两菌株中所含的转座酶差异相当大，其中 P1/7 中含有 25 个转座酶，而 89-1591 中则含有 51 个.

在利用 GO 对两菌株进行功能预测过程中(BlastP 的 $E < 1\times10^{-10}$，功能节点的 $P < 0.01$)，89-1591 中有 874 条序列注释到 1198 个 GO 功能结点中，共得到 2856 条注释；P1/7 中有 988 条序列注释到 1310 个 GO 功能结点中，共 3281 条注释，同时我们绘制了两套数据的预测结果在 GO 上的分布图，详细结果见网络版附表表 1 和 2.

比较两个基因组序列的注释分布情况发现两者的注释情况非常的相似，对每个有注释的功能结点作四格表 χ^2 检验(四格表考虑因素为数据集 89-1591/P1/7，功能有/否)，3 个体系中仅发现少数几个结点 $P < 0.01$，且全部与核糖体有关(网络版附图 1).

比较预测结果与其他物种 GO 分布的差异. 我们使用超几何分布来比较 89-1591 预测结果和 GenBank 的 nr 库(所有基因不分物种)在 GO 上的分布情况差异

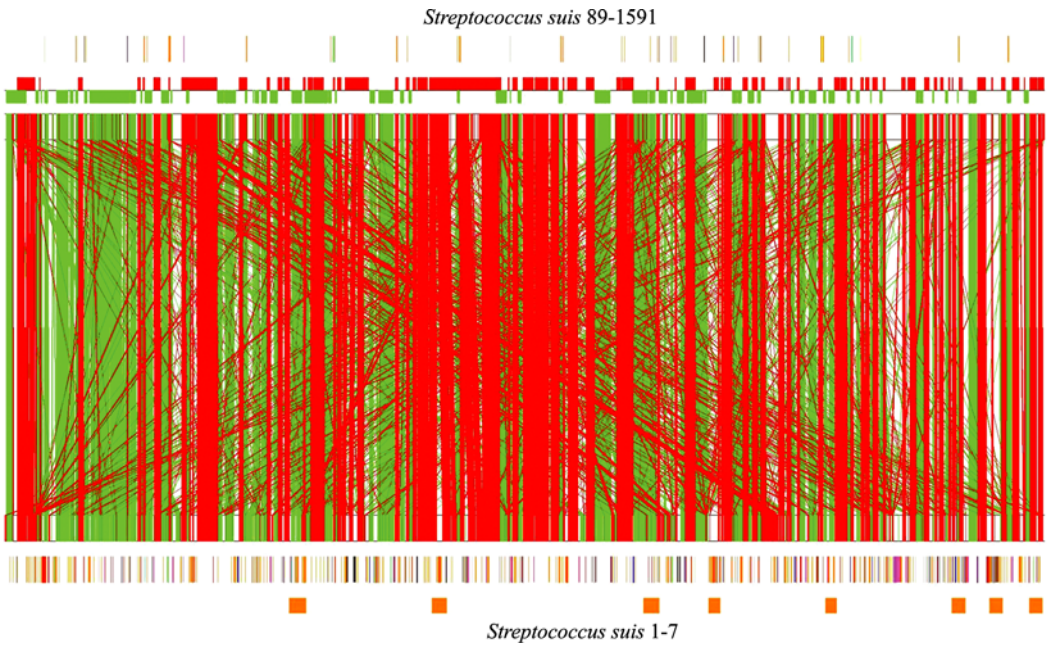

图 2　两 *S. suis* 菌株基因组比较图

两菌株基因组的线性比较. 不连续的片段表示 89-1591 的连接群，红色表示正义链，绿色表示反义链. 89-1591 的连接群和 P1/7 基因组序列联配上的部分用线连接，红色和绿色分别表示正向序列联配上和反向序列联配上. 垂直的短线代表两菌株各自特异的基因，按照 COG 分类用不同的颜色表示. 最下面 8 个橙色的不连续片段表示我们预测的基因岛

表 1 *S. suis* P1/7 与 89-1581 菌株基因组基本信息比较

	Streptococcus suis 89-1591	*Streptococcus suis* 1-7
染色体基本信息		
基因组大小/bp	1978218	2007491
(G+C)含量(%)		
整个基因组	41.03	41.30
编码蛋白区域	35.45	34.18
核糖体 RNAs		12
转运 RNAs		56
转座酶	51	25
CDS 总数	1918	1969
CDS 平均长度/bp	883	902
CDSs 按序列变化分类		
所有同源基因	1351	1341
直系同源基因总数	1306	1306
核酸序列完全相同	31	31
核酸序列长度相同，具 SNPs	848	848
核酸序列有插入或缺失	427	427
旁系同源基因总数	45	35
各自特有的基因	567	628

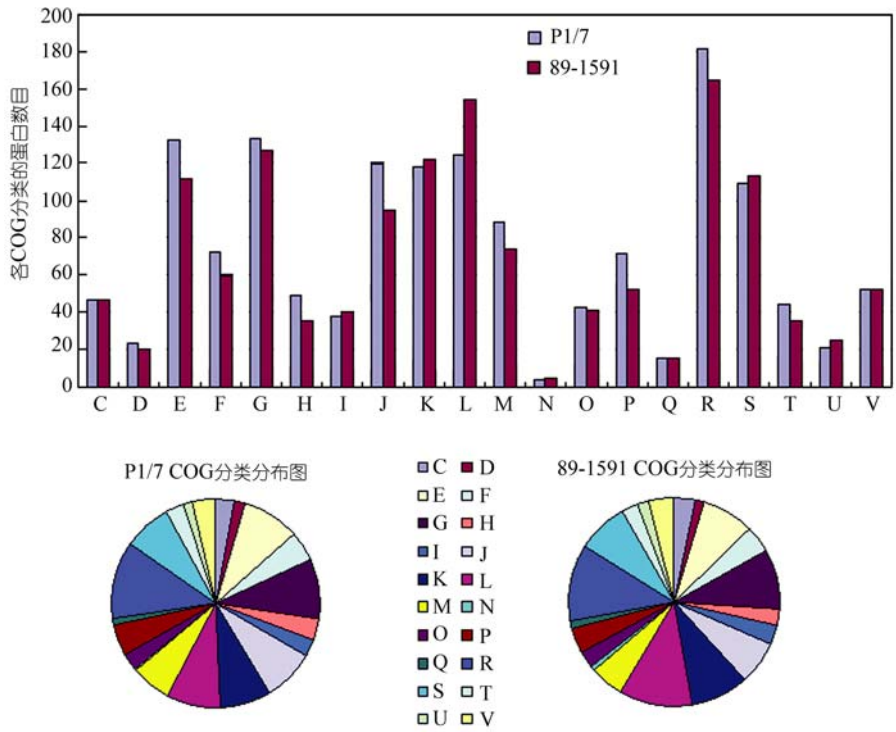

图 3 两 *S. suis* 菌株蛋白 COG 分类比较图

各字母分别代表以下 COG 分类: C, Energy production and conversion; D, Cell cycle control, cell division, chromosome partitioning; E, Amino acid transport and metabolism; F, Nucleotide transport and metabolism; G, Carbohydrate transport and metabolism; H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; J, Translation, ribosomal structure and biogenesis; K, Transcription; L, Replication, recombination and repair; M, Cell wall/membrane/envelope biogenesis; N, Cell motility; O, Posttranslational modification, protein turnover, chaperones; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis, transport and catabolism; R, General function prediction only; S, Function unknown; T, Signal transduction mechanisms; U, Intracellular trafficking, secretion, and vesicular transport; V, Defense mechanisms

($P < 0.01$, 且注释基因数目超过 5), 采用的方法与比较 89-1591/ P1/7 时采用的方法相同(网络版附表 3 及附图 2). 我们发现 89-1591 基因功能注释的分布情况和其他物种的平均分布情况有较大差异, 相比之下, 89-1591 和 P1/7 的基因功能注释分布情况差异是非常微小的.

在ConPred Ⅱ进行跨膜结构的预测结果中, 定义存在至少一次跨膜结构的蛋白为跨膜蛋白. 2 个菌株在跨膜蛋白比率上有显著差异($P = 0.01164$, Fisher确切检验)(网络版附图 3), 其中P1/7 的跨膜蛋白比率为 30.40%, 89-1591 的跨膜蛋白比率则为 26.72%. 这种差异主要是由两者跨膜蛋白中功能未定蛋白的数目差异造成, 这类蛋白在P1/7 中有 117 个而 89-1591 仅有 44 个. 两菌株中相当部分的跨膜蛋白是ABC类型的转运系统, 包括多种药物、糖类、金属离子(如金属钴, Fe^{3+}, Mn^{2+}/Zn^{2+}等)以及其他无机元素的转运系统. 其中我们发现了两个非常有意思的ABC类型细菌素转运系统的蛋白. 因为细菌素是一类能抑制周围其他细菌生长的化学物质, 在一些细菌的自然防御系统中发挥着主要作用, 而 2 型猪链球菌能产生类似细菌素的物质[35].

2.3 毒性因子

在两菌株的基因组中发现的相关毒性因子, 其组成上也存在着一定的差异. 如编码荚膜多糖的基因, 在 P1/7 中一共有 11 个, 而在 89-1591 中则缺失其中的 *cps2A-2B* 和 *cps2I-2J* 基因(表 2). 两个菌株中都具有编码溶菌酶释放蛋白的基因、纤维原结合因子(FBP)、谷氨酸脱氢酶(GDH)、甘油醛-3-磷酸脱氢酶(GAPDH)以及与其他细菌如格氏链球菌(*Streptococcus gordonii*), 肺炎链球菌(*Streptococcus pneumoniae*)以及化脓性链球菌(*Streptococcus pyogenes*)等具同源性的双肽酰肽酶Ⅳ(Dipeptidyl peptidase Ⅳ, DPPⅣ). 但 P1/7 中的胞外蛋白因子(EF)和溶血素在 89-1591 菌株中却未被发现. 此外, 在 P1/7 所编码的可能的表面蛋白质(surface protein)中有 11 个具有革兰氏阳性锚定蛋白功能域, 其中有两个(SSU1474, SSU1886)未能 89-1591 中找到相应的同源基因(表 3). 同时, P1/7 所含有的 7 个具有 YSIRK 功能域蛋白质有三个(SSU1715, SSU1773, SSU1849)未在 89-1591 中发现. 对于具有转肽酶(sortase)功能域的蛋白, 89-1591 中只找到 4 个可能与 P1/7 相关蛋白质匹配的基因, 而缺失与 SSU1882 和 SSU1883 的同源基因.

2.4 基因岛与菌株特异的基因

通过分析, 在 P1/7 菌株中一共找到了 8 个基因岛(图 1 和 2, 表 4), 其中第一个基因岛总长度为 33.5 kb, 包括了毒性因子中的所有 CPS, 并包含 8 个转座

表 2　*S. suis* P1/7 与 89-1581 两菌株中毒性因子的分布

毒性因子		*Streptococcus suis* 89-1591		*Streptococcus suis* 1-7
		Gi 号	菌株特有编号	菌株特有编号
荚膜多糖 (CPS)	Cps2A			SSU0515
	Cps2B			SSU0516
	Cps2C	50590876	Ssui801001141	SSU0517
	Cps2D	50590875	Ssui801001140	SSU0518
	Cps2E	50590874	Ssui801001139	SSU0519
	Cps2F	50590873	Ssui801001138	SSU0520
	Cps2G	50590872	Ssui801001137	SSU0521
	Cps2H	50590871	Ssui801001136	SSU0523
	Cps2I			SSU0524
	Cps2J			SSU0525
	Cps2K	50590870	Ssui801001135	SSU0526
溶菌酶释放蛋白(MRP)		50591404	Ssui801000600	SSU0706
胞外蛋白因子(EF)				SSU0171
溶血素(suilysin)				SSU1231
纤维原结合因子(FBP)		50591472	Ssui801000506	SSU1311
谷氨酸脱氢酶(GDH)		50590027	Ssui801001956	SSU0234
甘油醛-3-磷酸脱氢酶(GAPDH)		50590586	Ssui801001403	SSU0153
双肽酰肽酶Ⅳ(DPPⅣ)		50591872	Ssui801000154	SSU0187

表 3 *S. suis* P1/7 与 89-1581 菌株可能的表面蛋白的分布

表面蛋白特有功能域	*Streptococcus suis* 89-1591		*Streptococcus suis* 1-7
	Gi 号	菌株特有编号	菌株特有编号
Gram_pos_anchor	50591904	Ssui801000026	SSU0172
	50591776	Ssui801000197	SSU0253
	50591419	Ssui801000567	SSU0427
	50591074	Ssui801000941	SSU0706
	50590819	Ssui801001178	SSU0757
	50590495	Ssui801001508	SSU0860
	50590352	Ssui801001643	SSU1050
	50590286	Ssui801001711	SSU1143
	50590038	Ssui801001948	SSU1215
			SSU1474
			SSU1886
YSIRK_signal	50591873	Ssui801000156	SSU0186
	50590352	Ssui801001643	SSU0757
	50590198	Ssui801001801	SSU0879
	50590079	Ssui801001908	SSU1053
			SSU1715
			SSU1773
			SSU1849
Sortase	50591963	Ssui801000088	SSU0428
	50590820	Ssui801001179	SSU0453
	50590530	Ssui801001467	SSU0925
	50589897	Ssui801002068	SSU1881
			SSU1882
			SSU1883

表 4 *S. suis* P1/7 菌株中的可能的基因岛的分布

基因岛	起始位置	终止位置	GC 含量	双核苷酸特性	转座酶	tRNA	整合酶
基因岛 1	550621	584181	0.375	0.069	+		
基因岛 2	826635	856045	0.368	0.059			+
基因岛 3	1235671	1266771	0.439	0.044		+	
基因岛 4	1361730	1385142	0.397	0.105		+	+
基因岛 5	1587302	1610122	0.430	0.055			+
基因岛 6	1831238	1859237	0.458	0.040			
基因岛 7	1904491	1930596	0.431	0.062		+	
基因岛 8	1981167	2007289	0.398	0.055		+	

酶和 20 个功能未定蛋白，表明这个基因岛很可能是一个毒性岛. 第四个基因岛长度为 23.4 kb 左右，GC 含量较低，其中含有 tRNA，噬菌体整合酶(integrase)和可能的噬菌体蛋白，显示其可能来源于噬菌体.

基于现有序列，两个菌株序列联配的结果表明，89-1591 菌株中含有 567 个特异基因，而 P1/7 中则有 628 个特异基因.

2.5 蛋白质相互作用的结果

根据生物信息学方法预测得到的蛋白质相互作用网络中，P1/7 菌株蛋白质组范围内的蛋白质相互作

用网络共包含 3763 个连接，涉及到 1327 个蛋白质(网络版附图 4). 而 89-1591 菌株蛋白质组范围内的蛋白质相互作用网络共包含 5119 个连接，涉及到 1374 个蛋白质(网络版附图 5). 在 P1/7 的蛋白质相互作用网络中，大多数 CPS 蛋白质组成了一个功能模块.

2.6 代谢途径分析结果

在总共 628 个特异的 P1/7 蛋白质中，有 278 个预测的功能未定蛋白质，而其中只有 15 个是保守的，其余的为这个菌株所特有. 而 89-1591 中 567 个特异的蛋白质，有 202 个是预测的功能未定蛋白质. 在这个菌株中，还存在有一些特异的代谢途径组成成份，其中的主要是 ABC 转运系统，包括 3 类：第 1 类是与细胞色素 bd 生物合成相关的 ABC-类型的转运系统(COG4987, COG4988)；第 2 类是 ABC 类型的多药物转运系统，主要是 ATP 酶和通透酶的组成成份；第 3 类是抗微生物多肽的转运系统. 另外还有主要易化超家族中的透性酶(permeases of the major facilitator superfamily). 这些特异成份的组成提示 89-1591 菌株可能具有较强的、相当广泛的抗药性. 另外, 89-1591 还有很多特异的转座酶. 在 P1/7 及 89-1591 菌株的基因组中，还发现了一些蛋白水解酶的存在，其中有类似胰蛋白酶的丝氨酸蛋白酶和金属蛋白酶(metalloprotease)等. II 型的分泌途径主要存在于在宿主表面形成克隆的生物体中，大多数情况下，具有 II 型分泌途径的生物体并不侵染细胞. 在猪链球菌 89-1591 菌株基因组中，发现了编码 II 型分泌途径的相关基因 *pilB*, *pulG*, *pulO*, *pulA* 以及 *pulF* 等组成成分.

3 讨论

3.1 功能分类结果的讨论

以上我们利用已有的两株来源于不同地区的猪链球菌序列，从生物信息学的角度对其作了较全面的比较、分析. 尽管 89-1591 菌株的序列还未完全完成，但从序列联配的结果来看，其测序的部分已覆盖了整个基因组的 90%以上.

两菌株都属于血清 2 型，而且它们的基因接近 60%是同源的. GO 功能分类显示，两菌株中近一半的 ORF 可以同时定位到相关的功能位置中，统计两菌株在 GO 功能分类中每个节点的分布发现只有很少几个节点的 $P < 0.01$，而且这些全部是与组成核糖体的成分有关. 同时，两菌株之间的功能注释的分布相似性远远超过整个 GenBank 里平均功能分布的相关性. 至于两菌株在组成核糖体成份上的差异可能与 89-1591 的序列未完全测序有关. 综上所述，这表明两个菌株之间的功能分布具有很好的一致性，预测结果的可信度高. 在以 COG 为标准的分类中，功能已知的最大的一类是 L，是与细胞中 DNA 复制，修复及重组相关的，如果除去这一类中含的转座酶，实际上碳水化合物的转运和代谢(G)及氨基酸的转运和代谢(E)两类在整个功能分类所占有的比例是最高的，这与细菌的生活方式直接相关，功能完备的能量及物质转运系统是细菌快速繁殖的根本保证. 同样，与蛋白质翻译，核糖体结构和生物合成相关的 J 类以及与转录相关的 K 类蛋白质也具有相当高的比例.

在对两菌株的功能注释中，还有一部分的基因因为没有相关的同源性而无法解析其功能，这种情况下，蛋白质相互作用为编码蛋白质的基因功能的注释提供了另一个有效的途径. 其原理是在生命活动中，相互作用的蛋白质具有功能上的相关性[36,37]. 依据此原理，我们对菌株中有些未知功能的蛋白质进行了功能的注释，如SSU1053 编码了透明质酸酶(hyaluronidase). 透明质酸酶是能特异性分解细胞外基质成分——透明质酸(HA)的一种蛋白水解酶，通过作用于细胞外基质影响细胞的增殖、分化及迁移. 与 SSU1053 邻近的其他三个基因，SSU1051, SSU1052, SSU1054 在蛋白质相互作用中与SSU1053 形成一个小的模块，之间都有功能的相关性，因此，可以推测这四个基因都是与透明质酸的代谢相关.

两菌株基因比较的结果显示，它们的转座酶数量差异很大，菌株 89-1591 中所含的转座酶的数量是菌株 P1/7 的一倍多. 同时，在 P1/7 基因组中，没有功能注释的有 537 个，其中在其他物种中有同源基因的为 206 个, P1/7 所特有的为 223 个，占到总数的 41.5%. 这预示着两菌株在进化过程中为了适应不同的环境，各自进化出了许多新的功能.

在已知的特异基因中，还发现两菌株的有些基因具有相类似的功能，但它们基因之间却没有序列上的同源性，这类功能相似而不具有同源性的基因在细菌的转运系统中表现最为明显，如属于 ABC 类型的 ATP 酶和通透酶组成成份的多药物转运系统(COG1131, COG1132)中，在已注释 25 个不同的 ATP 酶和通透酶成分中，有 8 种是 89-1591 菌株所特有的，比例高达 30%多. 许多与 ABC 类型相关的转运系统

都出现了新的特异的组成成份，这预示着这两个菌株在进化中针对各自生长的环境演化出了一系列新的基因，以适应环境的变化．这种组成上的差异还在糖类的转运系统中得到体现，同时89-1591中还具有特异的属于ABC类型的与细胞色素bd生物合成相关的转运系统．细胞色素 bd 是在催化由氧气还原为水的呼吸链中的两个终端泛醌氧化酶之一，这种酶在低氧情况下表达．同样，感受外界刺激的细胞趋化因子的组成系统也存在差异，如89-1591菌株中存在特异的甲基接受趋化蛋白，属于主要易化超家族的通透酶，此外还有转录调控因子，膜蛋白质，表面抗原等．因此，这些特异的基因功能从基本的生物功能(如能量代谢)到与感受特异环境的因子等都有体现．

3.2 病理分析结果的讨论

荚膜多糖在很多革兰氏阳性病原体的病原形成中起着主要的作用[38~40]．在无乳链球菌(*S. agalactiae*)病原形成过程中被认为是单一的最重要的毒性因子，并可以抑制吞噬作用[41]．相似地，在以小鼠为模型的病原形成中，荚膜是肺炎链球菌的克隆形成及系统感染所必要的因子[42]．化脓性链球菌(*S. pyogenes*)透明质酸(hyaluronic acid)荚膜也是菌株抵抗吞噬作用所必须的，同时还起到粘附素的作用与表达在咽上皮细胞表面的CD44 结合[43,44]．当双组分调节系统CsrR/CsrS (CovR/CovS) 被抑制时荚膜的合成得以活化，从而导致形成高包被的菌株，这种菌株在小鼠模型中具有强化的毒性．在鱼链球菌(*S. iniae*)中，荚膜基因的突变体减弱了菌株抗吞噬作用的能力以及致病能力[45]．以上结果表明荚膜在链球菌毒性中的重要性．

对以上两个来源于不同地区的猪链球菌基因组结构及组成的分析结果表明不同来源的猪链球菌株的一些组成具有相当大的差异，这些与以前的研究结果具有一致性[46]．尽管对猪链球菌各个菌株中相关的毒性因子了解有限，已有的研究结果显示2型猪链球菌中最重要的毒性因子是荚膜多糖，它同时也是细菌防止被巨嗜细胞吞噬并被杀死所需要的结构成份．在人类中除了少数几例已报道被血清1型和14型感染的病例外，引起感染的主要是血清 2 型菌株．与其他的链球菌相比，尽管荚膜与猪链球菌的毒性具有相关性，但荚膜的存在不一定就决定了菌株的毒性．有些结果显示有毒的与无毒性的菌株都可以同时具有荚膜多糖以及唾液酸，并具有相似的内吞过程，这些结果提示了在猪链球菌中还有其他的重要因子与毒性相关．在血清2型中与高毒性相关的另一个毒性因子是形成孔状结构的溶血素，它存在于近 70%的各种血清型的猪链球菌的分离群中[16]，此类溶血素是硫醇活化的、胆固醇结合和成孔的溶细胞素的成员．但溶血素的产生并不总是与毒性相匹配，从来源于欧洲的猪中分离的许多猪链球菌都产生溶菌素时，大多数来源于北美的菌株则不产生溶菌素，来自于欧洲P1/7的菌株与来自于北美洲的89-1591菌株的基因组序列的序列联配进一步证实了这个结果．而且有些研究显示具有弱的溶血性的菌株能有极高的毒性[17]．以上结果表明在其他细菌中决定毒性因子的标准在猪链球菌中不一定是必须的，同时，还有证据表明溶血素释放因子(MRP)及细胞外因子(EF)也与猪链球菌的毒性相关[2]．总之，毒性因子与猪链球菌之间的关系现在还不十分清楚，有待进一步的探讨．

在两个菌株中都存在有编码转肽酶的基因，转肽酶与表面蛋白的分泌定位有关．已有的研究结果表明,该酶缺陷株不能表达表面蛋白，从而大大减弱对宿主的粘附性和致病性[17]．转肽酶基因几乎存在于所有革兰氏阳性细菌中，因此，它是一种很有价值的新药靶标，能抑制转肽酶形成的药物预计可能有效预防革兰氏阳性细菌引起的感染．

我们对全长猪链球菌 P1/7 的基因组进行了注释分析，并与89-1591序列进行了比较; P1/7 1969个可读框1486个赋予了功能注释，占总数的77.5%．两株猪链球菌的序列有比较大的保守性，89-1591 中 177 个连接群中有90.4%的连接群与P1/7具有相似性；而且两者有 1306 对基因属于直系同源．荚膜多糖，溶菌酶释放蛋白，纤维原结合因子等毒性因子都在两株菌中鉴定到，但编码荚膜多糖的 *cps2A-2B* 和 *cps2I-2J* 基因以及胞外蛋白因子和溶血素却没有9-1591 菌株中发现，说明两者在致病性上存在一定的差异．有些蛋白具有革兰氏阳性菌锚定在细胞壁上的功能域，YSIRK功能域和转肽酶功能域的可能表面蛋白，极有可能与毒性有关，这些潜在的毒性因子也在两株菌中鉴定得到，两株菌也表现出了比较大的差异．以上分析结果为系统地研究猪链球菌，以及防治、疫苗的开发、治疗药物的设计提供了广泛的基因组学信息基础．

快速检测猪链球菌可以采用芯片，抗体等方法．

PCR 检测可以利用猪链球菌中的荚膜基因. 通过 DNA 指纹法可以显示细菌的感染和传播的模型. 疫苗作为一种控制病原体感染的方法已广泛应用在日常生活中. 疫苗可以防止死亡但一般不会阻止感染. 目前, 大多数的针对猪链球菌感染的疫苗是菌株特异的自体疫苗, 仅含有从源头农场分离出来的猪链球菌的病原菌株, 因此由疫苗产生的免疫性具有差异性, 开发高效、广谱的防治猪链球菌的疫苗将是下一个研究的重点之一, 特异存在于猪链球菌中的分泌蛋白及表面蛋白是疫苗设计中抗原表位候选目标, 我们的研究结果为这方面的工作提供了有重要价值的信息.

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参 考 文 献

1 Normile D. Infectious diseases. WHO probes deadliness of China's pig-borne disease. Science, 2005, 309(5739): 1308－1309[DOI]

2 Wisselink H J, Smith H E, Stockhofe-Zurwieden N, et al. Distribution of capsular types and production of muramidase-released protein (MRP) and extracellular factor (EF) of *Streptococcus suis* strains isolated from diseased pigs in seven European countries. Vet Microbiol, 2000, 74(3): 237－248[DOI]

3 Higgins R, Gottschalk M, Boudreau M, et al. Description of six new capsular types (29-34) of *Streptococcus suis*. J Vet Diagn Invest, 1995, 7(3): 405－406

4 Vecht U, Arends J P, van der Molen E J, et al. Differences in virulence between two strains of *Streptococcus suis* type Ⅱ after experimentally induced infection of newborn germ-free pigs. Am J Vet Res, 1989, 50(7): 1037－1043

5 Heath P J, Hunt B, Harwood D J, et al. Isolation and identification of *Streptococcus suis* serotypes 3, 4 and 7. Vet Rec, 1995, 136(21): 547

6 King S J, Heath P J, Luque I, et al. Distribution and genetic diversity of suilysin in *Streptococcus suis* isolated from different diseases of pigs and characterization of the genetic basis of suilysin absence. Infect Immun, 2001, 69(12): 7572－7582[DOI]

7 Vilaichone R K, Mahachai V, Nunthapisud P. *Streptococcus suis* peritonitis: Case report. J Med Assoc Thai, 2000, 83(10): 1274－1277

8 Strangmann E, Froleke H, Kohse K P. Septic shock caused by *Streptococcus suis*: Case report and investigation of a risk group. Int J Hyg Environ Health, 2002, 205(5): 385－392[DOI]

9 Spiss H K, Kofler M, Hausdorfer H, et al. *Streptococcus suis* meningitis and neurophysiology of the acoustic system. First case report from Austria. Nervenarzt, 1999, 70(8): 738－741[DOI]

10 Leelarasamee A, Nilakul C, Tien-Grim S, et al. *Streptococcus suis* toxic-shock syndrome and meningitis. J Med Assoc Thai, 1997, 80(1): 63－68

11 Ibaraki M, Fujita N, Tada M, et al. A Japanese case of *Streptococcus suis* meningitis associated with lumbar epidural abscess. Rinsho Shinkeigaku, 2003, 43(4): 176－179

12 Grebe T, Bergenthal D, Fahr A M, et al. Meningitis caused by *Streptococcus suis* type 2 in an adult. Dtsch Med Wochenschr, 1997, 122(41): 1244－1247

13 Chotmongkol V, Janma J, Kawamatawong T. *Streptococcus suis* meningitis: Report of a case. J Med Assoc Thai, 1999, 82(9): 922－924

14 Vecht U, Wisselink H J, Jellema M L, et al. Identification of two proteins associated with virulence of *Streptococcus suis* type 2. Infect Immun, 1991, 59(9): 3156－3162

15 Staats J J, Feder I, Okwumabua O, et al. *Streptococcus suis*: Past and present. Vet Res Commun, 1997, 21(6): 381－407[DOI]

16 Jacobs A A, Loeffen P L, van den Berg A J, et al. Identification, purification, and characterization of a thiol-activated hemolysin (suilysin) of *Streptococcus suis*. Infect Immun, 1994, 62(5): 1742－1748

17 Gottschalk M, Segura M. The pathogenesis of the meningitis caused by *Streptococcus suis*: The unresolved questions. Vet Microbiol, 2000, 76(3): 259－272[DOI]

18 Smith H E, Wisselink H J, Stockhofe-Zurwieden N, et al. Virulence markers of *Streptococcus suis* type 1 and 2. Adv Exp Med Biol, 1997, 418: 651－655

19 Gottschalk M, Lebrun A, Wisselink H, et al. Production of virulence-related proteins by Canadian strains of *Streptococcus suis* capsular type 2. Can J Vet Res, 1998, 62(1): 75－79

20 Arai M, Mitsuke H, Ikeda M, et al. ConPred Ⅱ: A consensus prediction method for obtaining transmembrane topology models with high reliability. Nucleic Acids Res, 2004, 32(Web server issue): W390－W393

21 Schaffer A A, Wolf Y I, Ponting C P, et al. IMPALA: Matching a protein sequence against a collection of PSI-BLAST-constructed position-specific score matrices. Bioinformatics, 1999, 15(12): 1000－1011[DOI]

22 Marchler-Bauer A, Anderson J B, Cherukuri P F, et al. CDD: A conserved domain database for protein classification. Nucleic Acids Res, 2005, 33(Database issue): D192－D196[DOI]

23 Ashburner M, Ball C A, Blake J A, et al. Gene ontology: Tool for the unification of biology. The Gene Ontology Consortium. Nat Genet, 2000, 25(1): 25－29[DOI]

24 Conesa A, Gotz S, Garcia-Gomez J M, et al. Blast2GO: A universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics, 2005, 21(18): 3674－3676[DOI]

25 Maglott D, Ostell J, Pruitt K D, et al. Entrez gene: Gene-centered information at NCBI. Nucleic Acids Res, 2005, 33(Database issue): D54－D58[DOI]

26 Segal E, Friedman N, Koller D, et al. A module map showing conditional activity of expression modules in cancer. Nat Genet, 2004, 36(10): 1090－1098

27 Altschul S F, Madden T L, Schaffer A A, et al. Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucleic Acids Res, 1997, 25(17): 3389－3402[DOI]

28 Delcher A L, Phillippy A, Carlton J, et al. Fast algorithms for large-scale genome alignment and comparison. Nucleic Acids Res, 2002, 30(11): 2478－2483[DOI]

29 Sun J, Xu J, Liu Z, et al. Refined phylogenetic profiles method for predicting protein-protein interactions. Bioinformatics, 2005, 21(16): 3409－3415[DOI]

30 Date S V, Marcotte E M. Discovery of uncharacterized cellular systems by genome-wide analysis of functional linkages. Nat Biotechnol, 2003, 21(9): 1055－1062[DOI]

31 Pellegrini M, Marcotte E M, Thompson M J, et al. Assigning protein functions by comparative genome analysis: Protein phylogenetic profiles. Pro Natl Acad Sci USA, 1999, 96(8): 4285－4288[DOI]

32 Dandekar T, Snel B, Huynen M, et al. Conservation of gene order: A fingerprint of proteins that physically interact. Trends Biochem Sci, 1998, 23(9): 324－328[DOI]

33 Marcotte E M, Pellegrini M, Thompson M J, et al. A combined algorithm for genome-wide prediction of protein function. Nature, 1999, 402(6757): 83－86[DOI]

34 Strong M, Mallick P, Pellegrini M, et al. Inference of protein function and protein linkages in *Mycobacterium tuberculosis* based on prokaryotic genome organization: A combined computational approach. Gen Biol, 2003, 4(9): R59[DOI]

35 Melancon D, Grenier D. Production and properties of bacteriocin-like inhibitory substances from the swine pathogen *Streptococcus suis* serotype 2. Appl Environ Microbiol, 2003, 69(8): 4482－4488[DOI]

36 Schwikowski B, Uetz PFields S. A network of protein-protein interactions in yeast. Nat Biotechnol, 2000, 18(12): 1257－1261[DOI]

37 Oliver S. Guilt-by-association goes global. Nature, 2000, 403(6770): 601－603[DOI]

38 Bisno A L, Brito M O, Collins C M. Molecular basis of group A streptococcal virulence. Lancet Infect Dis, 2003, 3(4): 191－200[DOI]

39 Hava D L, LeMieux J, Camilli A. From nose to lung: The regulation behind *Streptococcus pneumoniae* virulence factors. Mol Microbiol, 2003, 50(4): 1103－1110[DOI]

40 Rubens C E, Haft R F, Wessels M R. Characterization of the capsular polysaccharide genes of group B streptococci. Dev Biol Stand, 1995, 85: 237－244

41 Spellerberg B. Pathogenesis of neonatal *Streptococcus agalactiae* infections. Microbes Infect, 2000, 2(14): 1733－1742[DOI]

42 Magee A D, Yother J. Requirement for capsule in colonization by *Streptococcus pneumoniae*. Infect Immun, 2001, 69(6): 3755－3761[DOI]

43 Cywes C, Stamenkovic I, Wessels M R. CD44 as a receptor for colonization of the pharynx by group A Streptococcus. J Clin Invest, 2000, 106(8): 995－1002

44 Schrager H M, Alberti S, Cywes C, et al. Hyaluronic acid capsule modulates M protein-mediated adherence and acts as a ligand for attachment of group A *Streptococcus* to CD44 on human keratinocytes. J Clin Invest, 1998, 101(8): 1708－1716

45 Miller J D, Neely M N. Large-scale screen highlights the importance of capsule for virulence in the zoonotic pathogen *Streptococcus iniae*. Infect Immun, 2005, 73(2): 921－934[DOI]

46 Chatellier S, Gottschalk M, Higgins R, et al. Relatedness of *Streptococcus suis* serotype 2 isolates from different geographic origins as evaluated by molecular fingerprinting and phenotyping. J Clin Microbiol, 1999, 37(2): 362－366

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表 1 菌株 89-1591 的蛋白序列 Gene Ontology 功能预测结果列表 [a)]

gi	acc	name	term_type
50589882	GO:0006289	nucleotide-excision repair	biological_process
50589882	GO:0030163	protein catabolism	biological_process
50589884	GO:0015808	L-alanine transport	biological_process
50589886	GO:0006310	DNA recombination	biological_process
50589886	GO:0009432	SOS response	biological_process
50589891	GO:0000050	urea cycle	biological_process
50589891	GO:0006526	arginine biosynthesis	biological_process
50589891	GO:0006527	arginine catabolism	biological_process
50589892	GO:0006526	arginine biosynthesis	biological_process
50589906	GO:0015758	glucose transport	biological_process
50589909	GO:0006313	DNA transposition	biological_process
50589914	GO:0006099	tricarboxylic acid cycle	biological_process
50589914	GO:0006118	electron transport	biological_process
50589914	GO:0009061	anaerobic respiration	biological_process
50589914	GO:0009094	L-phenylalanine biosynthesis	biological_process
50589918	GO:0008654	phospholipid biosynthesis	biological_process
50589927	GO:0006260	DNA replication	biological_process
50589930	GO:0015833	peptide transport	biological_process
50589933	GO:0005980	glycogen catabolism	biological_process
50589939	GO:0006817	phosphate transport	biological_process
50589940	GO:0006817	phosphate transport	biological_process
50589944	GO:0008643	carbohydrate transport	biological_process
50589946	GO:0006805	xenobiotic metabolism	biological_process
50589946	GO:0006808	regulation of nitrogen utilization	biological_process
50589946	GO:0010044	response to aluminum ion	biological_process
50589947	GO:0000271	polysaccharide biosynthesis	biological_process
50589947	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50589949	GO:0009410	response to xenobiotic stimulus	biological_process
50589949	GO:0015893	drug transport	biological_process
50589952	GO:0006072	glycerol-3-phosphate metabolism	biological_process
50589952	GO:0008654	phospholipid biosynthesis	biological_process
50589954	GO:0000154	rRNA modification	biological_process
50589954	GO:0009636	response to toxin	biological_process
50589954	GO:0046677	response to antibiotic	biological_process
50589962	GO:0006259	DNA metabolism	biological_process
50589962	GO:0009166	nucleotide catabolism	biological_process
50589966	GO:0042891	antibiotic transport	biological_process
50589966	GO:0046677	response to antibiotic	biological_process
50589967	GO:0042891	antibiotic transport	biological_process
50589967	GO:0046677	response to antibiotic	biological_process
50589970	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	biological_process
50589971	GO:0006144	purine base metabolism	biological_process
50589971	GO:0006152	purine nucleoside catabolism	biological_process
50589971	GO:0006166	purine ribonucleoside salvage	biological_process
50589975	GO:0009255	Entner-Doudoroff pathway	biological_process
50589978	GO:0006633	fatty acid biosynthesis	biological_process

续表 1

gi	acc	name	term_type
50589978	GO:0006633	fatty acid biosynthesis	biological_process
50589980	GO:0006067	ethanol metabolism	biological_process
50589980	GO:0006113	fermentation	biological_process
50589981	GO:0006427	histidyl-tRNA aminoacylation	biological_process
50589984	GO:0000004	biological process unknown	biological_process
50589989	GO:0006810	transport	biological_process
50589998	GO:0006313	DNA transposition	biological_process
50589999	GO:0006796	phosphate metabolism	biological_process
50589999	GO:0006817	phosphate transport	biological_process
50590000	GO:0006817	phosphate transport	biological_process
50590001	GO:0006817	phosphate transport	biological_process
50590002	GO:0006817	phosphate transport	biological_process
50590004	GO:0006828	manganese ion transport	biological_process
50590004	GO:0006829	zinc ion transport	biological_process
50590004	GO:0007155	cell adhesion	biological_process
50590004	GO:0009405	pathogenesis	biological_process
50590007	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590016	GO:0016576	histone dephosphorylation	biological_process
50590019	GO:0006012	galactose metabolism	biological_process
50590019	GO:0009225	nucleotide-sugar metabolism	biological_process
50590020	GO:0006012	galactose metabolism	biological_process
50590020	GO:0009225	nucleotide-sugar metabolism	biological_process
50590023	GO:0006810	transport	biological_process
50590024	GO:0048473	D-methionine transport	biological_process
50590025	GO:0006508	proteolysis and peptidolysis	biological_process
50590027	GO:0006537	glutamate biosynthesis	biological_process
50590027	GO:0009083	branched chain family amino acid catabolism	biological_process
50590033	GO:0006412	protein biosynthesis	biological_process
50590034	GO:0006414	translational elongation	biological_process
50590044	GO:0009290	cellular DNA import	biological_process
50590044	GO:0030420	establishment of competence for transformation	biological_process
50590049	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
50590055	GO:0006457	protein folding	biological_process
50590055	GO:0006605	protein targeting	biological_process
50590055	GO:0006836	neurotransmitter transport	biological_process
50590058	GO:0006810	transport	biological_process
50590061	GO:0006810	transport	biological_process
50590064	GO:0006412	protein biosynthesis	biological_process
50590064	GO:0007046	ribosome biogenesis	biological_process
50590065	GO:0006412	protein biosynthesis	biological_process
50590065	GO:0007046	ribosome biogenesis	biological_process
50590068	GO:0006306	DNA methylation	biological_process
50590070	GO:0005975	carbohydrate metabolism	biological_process
50590071	GO:0009631	cold acclimation	biological_process
50590072	GO:0006118	electron transport	biological_process

续表 1

gi	acc	name	term_type
50590073	GO:0005975	carbohydrate metabolism	biological_process
50590073	GO:0008655	pyrimidine salvage	biological_process
50590073	GO:0009058	biosynthesis	biological_process
50590073	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50590073	GO:0046108	uridine metabolism	biological_process
50590075	GO:0006081	aldehyde metabolism	biological_process
50590075	GO:0006113	fermentation	biological_process
50590075	GO:0051144	propanediol catabolism	biological_process
50590076	GO:0009088	threonine biosynthesis	biological_process
50590083	GO:0006426	glycyl-tRNA aminoacylation	biological_process
50590084	GO:0006426	glycyl-tRNA aminoacylation	biological_process
50590088	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
50590089	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
50590090	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
50590091	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
50590093	GO:0006730	one-carbon compound metabolism	biological_process
50590094	GO:0006281	DNA repair	biological_process
50590096	GO:0009394	2'-deoxyribonucleotide metabolism	biological_process
50590097	GO:0006810	transport	biological_process
50590099	GO:0000910	cytokinesis	biological_process
50590099	GO:0043093	binary fission	biological_process
50590100	GO:0000910	cytokinesis	biological_process
50590101	GO:0009252	peptidoglycan biosynthesis	biological_process
50590102	GO:0009252	peptidoglycan biosynthesis	biological_process
50590104	GO:0006508	proteolysis and peptidolysis	biological_process
50590105	GO:0006289	nucleotide-excision repair	biological_process
50590106	GO:0015693	magnesium ion transport	biological_process
50590108	GO:0006313	DNA transposition	biological_process
50590109	GO:0006313	DNA transposition	biological_process
50590110	GO:0006313	DNA transposition	biological_process
50590115	GO:0006464	protein modification	biological_process
50590115	GO:0042254	ribosome biogenesis and assembly	biological_process
50590116	GO:0000004	biological process unknown	biological_process
50590122	GO:0000918	selection of site for barrier septum formation	biological_process
50590123	GO:0006545	glycine biosynthesis	biological_process
50590123	GO:0006564	L-serine biosynthesis	biological_process
50590124	GO:0005975	carbohydrate metabolism	biological_process
50590125	GO:0009436	glyoxylate catabolism	biological_process
50590140	GO:0006354	RNA elongation	biological_process
50590141	GO:0000004	biological process unknown	biological_process
50590145	GO:0006508	proteolysis and peptidolysis	biological_process
50590145	GO:0007218	neuropeptide signaling pathway	biological_process
50590145	GO:0007267	cell-cell signaling	biological_process
50590145	GO:0010002	cardioblast differentiation	biological_process
50590145	GO:0016486	peptide hormone processing	biological_process
50590145	GO:0042310	vasoconstriction	biological_process

续表 1

gi	acc	name	term_type
50590146	GO:0006414	translational elongation	biological_process
50590148	GO:0006040	amino sugar metabolism	biological_process
50590151	GO:0006810	transport	biological_process
50590152	GO:0006810	transport	biological_process
50590154	GO:0000271	polysaccharide biosynthesis	biological_process
50590157	GO:0009097	isoleucine biosynthesis	biological_process
50590157	GO:0009099	valine biosynthesis	biological_process
50590173	GO:0009294	DNA mediated transformation	biological_process
50590174	GO:0006265	DNA topological change	biological_process
50590174	GO:0006268	DNA unwinding	biological_process
50590176	GO:0000154	rRNA modification	biological_process
50590179	GO:0045941	positive regulation of transcription	biological_process
50590181	GO:0006420	arginyl-tRNA aminoacylation	biological_process
50590181	GO:0040019	positive regulation of embryonic development	biological_process
50590183	GO:0006298	mismatch repair	biological_process
50590186	GO:0009097	isoleucine biosynthesis	biological_process
50590186	GO:0009099	valine biosynthesis	biological_process
50590187	GO:0009097	isoleucine biosynthesis	biological_process
50590187	GO:0009099	valine biosynthesis	biological_process
50590188	GO:0009097	isoleucine biosynthesis	biological_process
50590188	GO:0009099	valine biosynthesis	biological_process
50590189	GO:0006566	threonine metabolism	biological_process
50590189	GO:0009097	isoleucine biosynthesis	biological_process
50590192	GO:0015860	purine nucleoside transport	biological_process
50590193	GO:0008015	circulation	biological_process
50590193	GO:0009086	methionine biosynthesis	biological_process
50590194	GO:0009086	methionine biosynthesis	biological_process
50590201	GO:0006865	amino acid transport	biological_process
50590203	GO:0008643	carbohydrate transport	biological_process
50590204	GO:0008643	carbohydrate transport	biological_process
50590205	GO:0008643	carbohydrate transport	biological_process
50590207	GO:0006414	translational elongation	biological_process
50590209	GO:0006353	transcription termination	biological_process
50590210	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590211	GO:0005976	polysaccharide metabolism	biological_process
50590212	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590212	GO:0015759	beta-glucoside transport	biological_process
50590212	GO:0015771	trehalose transport	biological_process
50590214	GO:0006567	threonine catabolism	biological_process
50590217	GO:0016226	iron-sulfur cluster assembly	biological_process
50590217	GO:0016259	selenocysteine metabolism	biological_process
50590218	GO:0009228	thiamin biosynthesis	biological_process
50590219	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
50590224	GO:0009435	NAD biosynthesis	biological_process
50590226	GO:0000004	biological process unknown	biological_process
50590229	GO:0006878	copper ion homeostasis	biological_process

续表 1

gi	acc	name	term_type
50590232	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590235	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590235	GO:0015761	mannose transport	biological_process
50590240	GO:0000910	cytokinesis	biological_process
50590240	GO:0009252	peptidoglycan biosynthesis	biological_process
50590241	GO:0006099	tricarboxylic acid cycle	biological_process
50590248	GO:0006772	thiamin metabolism	biological_process
50590249	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50590250	GO:0000004	biological process unknown	biological_process
50590253	GO:0006281	DNA repair	biological_process
50590254	GO:0006310	DNA recombination	biological_process
50590255	GO:0006298	mismatch repair	biological_process
50590258	GO:0006821	chloride transport	biological_process
50590259	GO:0015847	putrescine transport	biological_process
50590259	GO:0015848	spermidine transport	biological_process
50590260	GO:0015847	putrescine transport	biological_process
50590260	GO:0015848	spermidine transport	biological_process
50590261	GO:0015847	putrescine transport	biological_process
50590261	GO:0015848	spermidine transport	biological_process
50590262	GO:0015847	putrescine transport	biological_process
50590262	GO:0015848	spermidine transport	biological_process
50590263	GO:0009252	peptidoglycan biosynthesis	biological_process
50590267	GO:0009252	peptidoglycan biosynthesis	biological_process
50590268	GO:0000004	biological process unknown	biological_process
50590272	GO:0007059	chromosome segregation	biological_process
50590272	GO:0030261	chromosome condensation	biological_process
50590273	GO:0007059	chromosome segregation	biological_process
50590273	GO:0030261	chromosome condensation	biological_process
50590274	GO:0000154	rRNA modification	biological_process
50590276	GO:0006826	iron ion transport	biological_process
50590277	GO:0006826	iron ion transport	biological_process
50590278	GO:0006826	iron ion transport	biological_process
50590279	GO:0006826	iron ion transport	biological_process
50590280	GO:0006750	glutathione biosynthesis	biological_process
50590280	GO:0006982	response to lipid hydroperoxide	biological_process
50590280	GO:0009636	response to toxin	biological_process
50590281	GO:0000154	rRNA modification	biological_process
50590286	GO:0006334	nucleosome assembly	biological_process
50590286	GO:0006938	sarcomere alignment	biological_process
50590286	GO:0006942	regulation of striated muscle contraction	biological_process
50590286	GO:0007638	mechanosensory behavior	biological_process
50590286	GO:0008366	nerve ensheathment	biological_process
50590286	GO:0045104	intermediate filament cytoskeleton organization and biogenesis	biological_process
50590286	GO:0045214	sarcomere organization	biological_process
50590300	GO:0000004	biological process unknown	biological_process
50590303	GO:0015833	peptide transport	biological_process

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gi	acc	name	term_type
50590307	GO:0006396	RNA processing	biological_process
50590308	GO:0006413	translational initiation	biological_process
50590311	GO:0006353	transcription termination	biological_process
50590315	GO:0019563	glycerol catabolism	biological_process
50590316	GO:0006260	DNA replication	biological_process
50590326	GO:0006260	DNA replication	biological_process
50590326	GO:0006281	DNA repair	biological_process
50590326	GO:0006310	DNA recombination	biological_process
50590326	GO:0009432	SOS response	biological_process
50590329	GO:0006084	acetyl-CoA metabolism	biological_process
50590329	GO:0006090	pyruvate metabolism	biological_process
50590329	GO:0006096	glycolysis	biological_process
50590330	GO:0006090	pyruvate metabolism	biological_process
50590330	GO:0006096	glycolysis	biological_process
50590330	GO:0006099	tricarboxylic acid cycle	biological_process
50590331	GO:0006090	pyruvate metabolism	biological_process
50590331	GO:0006554	lysine catabolism	biological_process
50590332	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
50590332	GO:0006118	electron transport	biological_process
50590332	GO:0006546	glycine catabolism	biological_process
50590332	GO:0006550	isoleucine catabolism	biological_process
50590332	GO:0006552	leucine catabolism	biological_process
50590332	GO:0006564	L-serine biosynthesis	biological_process
50590332	GO:0006574	valine catabolism	biological_process
50590332	GO:0006748	lipoamide metabolism	biological_process
50590336	GO:0008033	tRNA processing	biological_process
50590337	GO:0006094	gluconeogenesis	biological_process
50590337	GO:0006565	L-serine catabolism	biological_process
50590338	GO:0006094	gluconeogenesis	biological_process
50590338	GO:0006565	L-serine catabolism	biological_process
50590340	GO:0006824	cobalt ion transport	biological_process
50590341	GO:0006824	cobalt ion transport	biological_process
50590342	GO:0006824	cobalt ion transport	biological_process
50590344	GO:0005975	carbohydrate metabolism	biological_process
50590344	GO:0009438	methylglyoxal metabolism	biological_process
50590345	GO:0006096	glycolysis	biological_process
50590345	GO:0006941	striated muscle contraction	biological_process
50590346	GO:0006629	lipid metabolism	biological_process
50590347	GO:0006554	lysine catabolism	biological_process
50590347	GO:0006695	cholesterol biosynthesis	biological_process
50590347	GO:0006696	ergosterol biosynthesis	biological_process
50590347	GO:0006700	C21-steroid hormone biosynthesis	biological_process
50590347	GO:0007548	sex differentiation	biological_process
50590347	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
50590347	GO:0046951	ketone body biosynthesis	biological_process
50590352	GO:0006508	proteolysis and peptidolysis	biological_process

续表 1

gi	acc	name	term_type
50590353	GO:0000004	biological process unknown	biological_process
50590354	GO:0006281	DNA repair	biological_process
50590358	GO:0006055	CMP-N-acetylneuraminate biosynthesis	biological_process
50590358	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50590360	GO:0006047	UDP-N-acetylglucosamine metabolism	biological_process
50590360	GO:0007155	cell adhesion	biological_process
50590360	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50590360	GO:0046380	N-acetylneuraminate biosynthesis	biological_process
50590361	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50590361	GO:0009631	cold acclimation	biological_process
50590361	GO:0042309	homoiothermy	biological_process
50590361	GO:0050826	response to freezing	biological_process
50590375	GO:0006812	cation transport	biological_process
50590388	GO:0006858	extracellular transport	biological_process
50590389	GO:0006810	transport	biological_process
50590391	GO:0009086	methionine biosynthesis	biological_process
50590391	GO:0009088	threonine biosynthesis	biological_process
50590391	GO:0009097	isoleucine biosynthesis	biological_process
50590392	GO:0006549	isoleucine metabolism	biological_process
50590392	GO:0006555	methionine metabolism	biological_process
50590392	GO:0009088	threonine biosynthesis	biological_process
50590392	GO:0009092	homoserine metabolism	biological_process
50590396	GO:0006457	protein folding	biological_process
50590397	GO:0006260	DNA replication	biological_process
50590397	GO:0006281	DNA repair	biological_process
50590397	GO:0006310	DNA recombination	biological_process
50590399	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
50590401	GO:0006979	response to oxidative stress	biological_process
50590403	GO:0006508	proteolysis and peptidolysis	biological_process
50590404	GO:0046654	tetrahydrofolate biosynthesis	biological_process
50590408	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590409	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590410	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
50590410	GO:0006526	arginine biosynthesis	biological_process
50590410	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590411	GO:0006353	transcription termination	biological_process
50590411	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590415	GO:0006412	protein biosynthesis	biological_process
50590415	GO:0007046	ribosome biogenesis	biological_process
50590416	GO:0006413	translational initiation	biological_process
50590417	GO:0006172	ADP biosynthesis	biological_process
50590417	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50590417	GO:0046083	adenine metabolism	biological_process
50590418	GO:0006886	intracellular protein transport	biological_process
50590418	GO:0015628	type II protein secretion system	biological_process
50590419	GO:0006412	protein biosynthesis	biological_process

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gi	acc	name	term_type
50590421	GO:0006412	protein biosynthesis	biological_process
50590422	GO:0006412	protein biosynthesis	biological_process
50590422	GO:0007046	ribosome biogenesis	biological_process
50590423	GO:0006412	protein biosynthesis	biological_process
50590423	GO:0007046	ribosome biogenesis	biological_process
50590424	GO:0006412	protein biosynthesis	biological_process
50590424	GO:0007046	ribosome biogenesis	biological_process
50590425	GO:0006412	protein biosynthesis	biological_process
50590425	GO:0007046	ribosome biogenesis	biological_process
50590426	GO:0006412	protein biosynthesis	biological_process
50590427	GO:0006412	protein biosynthesis	biological_process
50590427	GO:0007046	ribosome biogenesis	biological_process
50590429	GO:0030245	cellulose catabolism	biological_process
50590432	GO:0006810	transport	biological_process
50590432	GO:0051189	prosthetic group metabolism	biological_process
50590436	GO:0009252	peptidoglycan biosynthesis	biological_process
50590436	GO:0019408	dolichol biosynthesis	biological_process
50590437	GO:0008654	phospholipid biosynthesis	biological_process
50590438	GO:0006508	proteolysis and peptidolysis	biological_process
50590439	GO:0006433	prolyl-tRNA aminoacylation	biological_process
50590440	GO:0006833	water transport	biological_process
50590440	GO:0006863	purine transport	biological_process
50590440	GO:0006970	response to osmotic stress	biological_process
50590440	GO:0007588	excretion	biological_process
50590440	GO:0009935	nutrient import	biological_process
50590440	GO:0010033	response to organic substance	biological_process
50590440	GO:0015722	canalicular bile acid transport	biological_process
50590440	GO:0015793	glycerol transport	biological_process
50590440	GO:0015837	amine transport	biological_process
50590440	GO:0015855	pyrimidine transport	biological_process
50590440	GO:0030104	water homeostasis	biological_process
50590440	GO:0046689	response to mercury ion	biological_process
50590442	GO:0019563	glycerol catabolism	biological_process
50590443	GO:0019563	glycerol catabolism	biological_process
50590445	GO:0015768	maltose transport	biological_process
50590448	GO:0006423	cysteinyl-tRNA aminoacylation	biological_process
50590451	GO:0006535	cysteine biosynthesis from serine	biological_process
50590452	GO:0006402	mRNA catabolism	biological_process
50590455	GO:0000154	rRNA modification	biological_process
50590458	GO:0009306	protein secretion	biological_process
50590462	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50590463	GO:0006260	DNA replication	biological_process
50590466	GO:0006564	L-serine biosynthesis	biological_process
50590466	GO:0008615	pyridoxine biosynthesis	biological_process
50590466	GO:0009113	purine base biosynthesis	biological_process
50590468	GO:0006564	L-serine biosynthesis	biological_process

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gi	acc	name	term_type
50590468	GO:0007420	brain development	biological_process
50590468	GO:0031102	neurite regeneration	biological_process
50590469	GO:0006281	DNA repair	biological_process
50590482	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50590482	GO:0009252	peptidoglycan biosynthesis	biological_process
50590489	GO:0009405	pathogenesis	biological_process
50590489	GO:0019835	cytolysis	biological_process
50590491	GO:0006401	RNA catabolism	biological_process
50590494	GO:0000917	barrier septum formation	biological_process
50590494	GO:0030187	melatonin biosynthesis	biological_process
50590495	GO:0009166	nucleotide catabolism	biological_process
50590496	GO:0009166	nucleotide catabolism	biological_process
50590496	GO:0009225	nucleotide-sugar metabolism	biological_process
50590497	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
50590501	GO:0000731	DNA synthesis during DNA repair	biological_process
50590501	GO:0030174	regulation of DNA replication initiation	biological_process
50590502	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
50590504	GO:0009166	nucleotide catabolism	biological_process
50590504	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50590505	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
50590518	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
50590519	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
50590521	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590522	GO:0006012	galactose metabolism	biological_process
50590522	GO:0046835	carbohydrate phosphorylation	biological_process
50590526	GO:0006508	proteolysis and peptidolysis	biological_process
50590527	GO:0006508	proteolysis and peptidolysis	biological_process
50590529	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590535	GO:0000105	histidine biosynthesis	biological_process
50590535	GO:0001718	conversion of met-tRNAf to fmet-tRNA	biological_process
50590535	GO:0009086	methionine biosynthesis	biological_process
50590535	GO:0009113	purine base biosynthesis	biological_process
50590535	GO:0009257	10-formyltetrahydrofolate biosynthesis	biological_process
50590535	GO:0015940	pantothenate biosynthesis	biological_process
50590535	GO:0019415	acetate biosynthesis from carbon monoxide	biological_process
50590535	GO:0019653	purine fermentation	biological_process
50590535	GO:0046656	folic acid biosynthesis	biological_process
50590538	GO:0006825	copper ion transport	biological_process
50590541	GO:0045449	regulation of transcription	biological_process
50590543	GO:0000004	biological process unknown	biological_process
50590546	GO:0006313	DNA transposition	biological_process
50590552	GO:0006961	antibacterial humoral response (sensu Protostomia)	biological_process
50590552	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50590552	GO:0009405	pathogenesis	biological_process
50590552	GO:0030260	entry into host cell	biological_process
50590555	GO:0006401	RNA catabolism	biological_process

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gi	acc	name	term_type
50590555	GO:0009631	cold acclimation	biological_process
50590555	GO:0042255	ribosome assembly	biological_process
50590569	GO:0000004	biological process unknown	biological_process
50590571	GO:0007046	ribosome biogenesis	biological_process
50590572	GO:0006270	DNA replication initiation	biological_process
50590572	GO:0006271	DNA strand elongation	biological_process
50590574	GO:0006412	protein biosynthesis	biological_process
50590577	GO:0016049	cell growth	biological_process
50590578	GO:0006281	DNA repair	biological_process
50590579	GO:0015937	coenzyme A biosynthesis	biological_process
50590582	GO:0006396	RNA processing	biological_process
50590582	GO:0006401	RNA catabolism	biological_process
50590583	GO:0006450	regulation of translational fidelity	biological_process
50590586	GO:0006094	gluconeogenesis	biological_process
50590586	GO:0006096	glycolysis	biological_process
50590587	GO:0006096	glycolysis	biological_process
50590590	GO:0006542	glutamine biosynthesis	biological_process
50590594	GO:0006464	protein modification	biological_process
50590594	GO:0042254	ribosome biogenesis and assembly	biological_process
50590596	GO:0006090	pyruvate metabolism	biological_process
50590596	GO:0006096	glycolysis	biological_process
50590604	GO:0006412	protein biosynthesis	biological_process
50590604	GO:0007046	ribosome biogenesis	biological_process
50590605	GO:0006412	protein biosynthesis	biological_process
50590608	GO:0000910	cytokinesis	biological_process
50590609	GO:0005987	sucrose catabolism	biological_process
50590612	GO:0008643	carbohydrate transport	biological_process
50590614	GO:0006810	transport	biological_process
50590615	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
50590616	GO:0016126	sterol biosynthesis	biological_process
50590616	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
50590617	GO:0006695	cholesterol biosynthesis	biological_process
50590617	GO:0006696	ergosterol biosynthesis	biological_process
50590617	GO:0016310	phosphorylation	biological_process
50590617	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
50590619	GO:0006855	multidrug transport	biological_process
50590624	GO:0042891	antibiotic transport	biological_process
50590624	GO:0046677	response to antibiotic	biological_process
50590625	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50590626	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50590628	GO:0009073	aromatic amino acid family biosynthesis	biological_process
50590630	GO:0015697	quaternary ammonium group transport	biological_process
50590630	GO:0018987	osmoregulation	biological_process
50590631	GO:0015697	quaternary ammonium group transport	biological_process
50590631	GO:0018987	osmoregulation	biological_process
50590636	GO:0009152	purine ribonucleotide biosynthesis	biological_process

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gi	acc	name	term_type
50590637	GO:0006750	glutathione biosynthesis	biological_process
50590640	GO:0006457	protein folding	biological_process
50590640	GO:0006979	response to oxidative stress	biological_process
50590640	GO:0050821	protein stabilization	biological_process
50590641	GO:0006400	tRNA modification	biological_process
50590649	GO:0006281	DNA repair	biological_process
50590649	GO:0006310	DNA recombination	biological_process
50590652	GO:0006508	proteolysis and peptidolysis	biological_process
50590661	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
50590661	GO:0006430	lysyl-tRNA aminoacylation	biological_process
50590668	GO:0006747	FAD biosynthesis	biological_process
50590668	GO:0009231	riboflavin biosynthesis	biological_process
50590668	GO:0009398	FMN biosynthesis	biological_process
50590669	GO:0006400	tRNA modification	biological_process
50590680	GO:0006364	rRNA processing	biological_process
50590680	GO:0042255	ribosome assembly	biological_process
50590688	GO:0006532	aspartate biosynthesis	biological_process
50590689	GO:0006421	asparaginyl-tRNA aminoacylation	biological_process
50590689	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
50590692	GO:0006281	DNA repair	biological_process
50590694	GO:0006438	valyl-tRNA aminoacylation	biological_process
50590716	GO:0009166	nucleotide catabolism	biological_process
50590716	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50590719	GO:0009252	peptidoglycan biosynthesis	biological_process
50590720	GO:0016226	iron-sulfur cluster assembly	biological_process
50590722	GO:0016226	iron-sulfur cluster assembly	biological_process
50590722	GO:0016261	selenocysteine catabolism	biological_process
50590723	GO:0016226	iron-sulfur cluster assembly	biological_process
50590724	GO:0016226	iron-sulfur cluster assembly	biological_process
50590725	GO:0009243	O antigen biosynthesis	biological_process
50590725	GO:0009252	peptidoglycan biosynthesis	biological_process
50590727	GO:0046677	response to antibiotic	biological_process
50590729	GO:0006800	oxygen and reactive oxygen species metabolism	biological_process
50590730	GO:0000004	biological process unknown	biological_process
50590731	GO:0006826	iron ion transport	biological_process
50590733	GO:0009306	protein secretion	biological_process
50590733	GO:0009405	pathogenesis	biological_process
50590734	GO:0019358	nicotinate nucleotide salvage	biological_process
50590734	GO:0019363	pyridine nucleotide biosynthesis	biological_process
50590735	GO:0009435	NAD biosynthesis	biological_process
50590737	GO:0000004	biological process unknown	biological_process
50590741	GO:0006820	anion transport	biological_process
50590749	GO:0006810	transport	biological_process
50590756	GO:0006633	fatty acid biosynthesis	biological_process
50590757	GO:0006633	fatty acid biosynthesis	biological_process
50590758	GO:0006633	fatty acid biosynthesis	biological_process

续表 1

gi	acc	name	term_type
50590759	GO:0006633	fatty acid biosynthesis	biological_process
50590760	GO:0006633	fatty acid biosynthesis	biological_process
50590761	GO:0006633	fatty acid biosynthesis	biological_process
50590762	GO:0006633	fatty acid biosynthesis	biological_process
50590763	GO:0006633	fatty acid biosynthesis	biological_process
50590764	GO:0008654	phospholipid biosynthesis	biological_process
50590766	GO:0006633	fatty acid biosynthesis	biological_process
50590769	GO:0000004	biological process unknown	biological_process
50590773	GO:0000004	biological process unknown	biological_process
50590776	GO:0000018	regulation of DNA recombination	biological_process
50590776	GO:0006338	chromatin remodeling	biological_process
50590776	GO:0009117	nucleotide metabolism	biological_process
50590776	GO:0016584	nucleosome spacing	biological_process
50590776	GO:0042766	nucleosome mobilization	biological_process
50590776	GO:0045941	positive regulation of transcription	biological_process
50590776	GO:0051260	protein homooligomerization	biological_process
50590777	GO:0006348	chromatin silencing at telomere	biological_process
50590777	GO:0016584	nucleosome spacing	biological_process
50590777	GO:0046020	negative regulation of transcription from RNA polymerase II promoter by pheromones	biological_process
50590779	GO:0009252	peptidoglycan biosynthesis	biological_process
50590784	GO:0006464	protein modification	biological_process
50590786	GO:0009252	peptidoglycan biosynthesis	biological_process
50590788	GO:0006555	methionine metabolism	biological_process
50590788	GO:0006556	S-adenosylmethionine biosynthesis	biological_process
50590789	GO:0006206	pyrimidine base metabolism	biological_process
50590789	GO:0006220	pyrimidine nucleotide metabolism	biological_process
50590789	GO:0009165	nucleotide biosynthesis	biological_process
50590792	GO:0009102	biotin biosynthesis	biological_process
50590792	GO:0018054	peptidyl-lysine biotinylation	biological_process
50590798	GO:0006281	DNA repair	biological_process
50590799	GO:0006561	proline biosynthesis	biological_process
50590800	GO:0006561	proline biosynthesis	biological_process
50590801	GO:0006118	electron transport	biological_process
50590801	GO:0006561	proline biosynthesis	biological_process
50590801	GO:0008652	amino acid biosynthesis	biological_process
50590804	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590807	GO:0006313	DNA transposition	biological_process
50590811	GO:0009307	DNA restriction-modification system	biological_process
50590815	GO:0006304	DNA modification	biological_process
50590816	GO:0006434	seryl-tRNA aminoacylation	biological_process
50590821	GO:0009299	mRNA transcription	biological_process
50590826	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590826	GO:0045013	negative regulation of transcription by carbon catabolites	biological_process
50590827	GO:0009249	protein-lipoylation	biological_process
50590829	GO:0006631	fatty acid metabolism	biological_process
50590831	GO:0006532	aspartate biosynthesis	biological_process

续表 1

gi	acc	name	term_type
50590831	GO:0009088	threonine biosynthesis	biological_process
50590831	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
50590832	GO:0009252	peptidoglycan biosynthesis	biological_process
50590834	GO:0015628	type II protein secretion system	biological_process
50590836	GO:0005985	sucrose metabolism	biological_process
50590839	GO:0006810	transport	biological_process
50590842	GO:0000004	biological process unknown	biological_process
50590843	GO:0006508	proteolysis and peptidolysis	biological_process
50590844	GO:0000910	cytokinesis	biological_process
50590845	GO:0006270	DNA replication initiation	biological_process
50590845	GO:0006275	regulation of DNA replication	biological_process
50590846	GO:0006260	DNA replication	biological_process
50590850	GO:0006012	galactose metabolism	biological_process
50590852	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590852	GO:0015761	mannose transport	biological_process
50590853	GO:0008645	hexose transport	biological_process
50590853	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590854	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50590855	GO:0005975	carbohydrate metabolism	biological_process
50590855	GO:0035071	salivary gland cell death	biological_process
50590855	GO:0045045	secretory pathway	biological_process
50590856	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590857	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590861	GO:0001510	RNA methylation	biological_process
50590861	GO:0006400	tRNA modification	biological_process
50590870	GO:0000271	polysaccharide biosynthesis	biological_process
50590872	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50590875	GO:0045227	capsule polysaccharide biosynthesis	biological_process
50590891	GO:0006535	cysteine biosynthesis from serine	biological_process
50590893	GO:0006457	protein folding	biological_process
50590893	GO:0006605	protein targeting	biological_process
50590893	GO:0006836	neurotransmitter transport	biological_process
50590895	GO:0007165	signal transduction	biological_process
50590900	GO:0009408	response to heat	biological_process
50590901	GO:0006457	protein folding	biological_process
50590901	GO:0006950	response to stress	biological_process
50590902	GO:0006950	response to stress	biological_process
50590903	GO:0006457	protein folding	biological_process
50590903	GO:0009408	response to heat	biological_process
50590906	GO:0006865	amino acid transport	biological_process
50590907	GO:0006865	amino acid transport	biological_process
50590912	GO:0006825	copper ion transport	biological_process
50590912	GO:0015691	cadmium ion transport	biological_process
50590930	GO:0006118	electron transport	biological_process
50590931	GO:0006744	ubiquinone biosynthesis	biological_process
50590931	GO:0009234	menaquinone biosynthesis	biological_process

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gi	acc	name	term_type
50590933	GO:0009228	thiamin biosynthesis	biological_process
50590941	GO:0000004	biological process unknown	biological_process
50590943	GO:0009252	peptidoglycan biosynthesis	biological_process
50590944	GO:0009252	peptidoglycan biosynthesis	biological_process
50590950	GO:0000004	biological process unknown	biological_process
50590951	GO:0007155	cell adhesion	biological_process
50590951	GO:0008544	epidermis development	biological_process
50590954	GO:0006400	tRNA modification	biological_process
50590954	GO:0009636	response to toxin	biological_process
50590961	GO:0015768	maltose transport	biological_process
50590962	GO:0015768	maltose transport	biological_process
50590963	GO:0008643	carbohydrate transport	biological_process
50590966	GO:0005980	glycogen catabolism	biological_process
50590968	GO:0000004	biological process unknown	biological_process
50590969	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
50590971	GO:0006813	potassium ion transport	biological_process
50590976	GO:0008655	pyrimidine salvage	biological_process
50590976	GO:0009116	nucleoside metabolism	biological_process
50590977	GO:0000025	maltose catabolism	biological_process
50590977	GO:0005993	trehalose catabolism	biological_process
50590978	GO:0005987	sucrose catabolism	biological_process
50590979	GO:0008643	carbohydrate transport	biological_process
50590980	GO:0008643	carbohydrate transport	biological_process
50590983	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50590985	GO:0009086	methionine biosynthesis	biological_process
50590985	GO:0019344	cysteine biosynthesis	biological_process
50590985	GO:0019346	transsulfuration	biological_process
50590990	GO:0009086	methionine biosynthesis	biological_process
50590990	GO:0009088	threonine biosynthesis	biological_process
50590990	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
50590990	GO:0009097	isoleucine biosynthesis	biological_process
50590991	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
50590992	GO:0006313	DNA transposition	biological_process
50590994	GO:0000154	rRNA modification	biological_process
50590997	GO:0006464	protein modification	biological_process
50590999	GO:0009098	leucine biosynthesis	biological_process
50591000	GO:0009098	leucine biosynthesis	biological_process
50591001	GO:0009098	leucine biosynthesis	biological_process
50591002	GO:0009098	leucine biosynthesis	biological_process
50591003	GO:0009098	leucine biosynthesis	biological_process
50591009	GO:0006457	protein folding	biological_process
50591013	GO:0009062	fatty acid catabolism	biological_process
50591013	GO:0009395	phospholipid catabolism	biological_process
50591014	GO:0042572	retinol metabolism	biological_process
50591014	GO:0045494	photoreceptor maintenance	biological_process
50591015	GO:0016042	lipid catabolism	biological_process

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gi	acc	name	term_type
50591016	GO:0006113	fermentation	biological_process
50591016	GO:0016049	cell growth	biological_process
50591021	GO:0009228	thiamin biosynthesis	biological_process
50591022	GO:0006400	tRNA modification	biological_process
50591023	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591025	GO:0001678	cell glucose homeostasis	biological_process
50591025	GO:0005977	glycogen metabolism	biological_process
50591025	GO:0006002	fructose 6-phosphate metabolism	biological_process
50591025	GO:0006110	regulation of glycolysis	biological_process
50591026	GO:0006260	DNA replication	biological_process
50591027	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591028	GO:0006810	transport	biological_process
50591030	GO:0006146	adenine catabolism	biological_process
50591030	GO:0006155	adenosine deaminase reaction	biological_process
50591030	GO:0009168	purine ribonucleoside monophosphate biosynthesis	biological_process
50591030	GO:0019735	antimicrobial humoral response (sensu Vertebrata)	biological_process
50591030	GO:0045187	regulation of circadian sleep/wake cycle, sleep	biological_process
50591030	GO:0046085	adenosine metabolism	biological_process
50591032	GO:0006313	DNA transposition	biological_process
50591033	GO:0006313	DNA transposition	biological_process
50591035	GO:0006352	transcription initiation	biological_process
50591036	GO:0006269	DNA replication, synthesis of RNA primer	biological_process
50591042	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591047	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591049	GO:0006098	pentose-phosphate shunt	biological_process
50591051	GO:0009405	pathogenesis	biological_process
50591054	GO:0006508	proteolysis and peptidolysis	biological_process
50591060	GO:0006793	phosphorus metabolism	biological_process
50591063	GO:0019350	teichoic acid biosynthesis	biological_process
50591065	GO:0000271	polysaccharide biosynthesis	biological_process
50591065	GO:0042941	D-alanine transport	biological_process
50591065	GO:0046374	teichoic acid metabolism	biological_process
50591066	GO:0009252	peptidoglycan biosynthesis	biological_process
50591066	GO:0017000	antibiotic biosynthesis	biological_process
50591066	GO:0019290	siderophore biosynthesis	biological_process
50591073	GO:0000271	polysaccharide biosynthesis	biological_process
50591074	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50591076	GO:0006865	amino acid transport	biological_process
50591077	GO:0006865	amino acid transport	biological_process
50591078	GO:0006868	L-glutamine transport	biological_process
50591079	GO:0006865	amino acid transport	biological_process
50591081	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591081	GO:0015759	beta-glucoside transport	biological_process
50591081	GO:0019533	cellobiose transport	biological_process
50591083	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591083	GO:0015759	beta-glucoside transport	biological_process

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gi	acc	name	term_type
50591084	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591084	GO:0015759	beta-glucoside transport	biological_process
50591084	GO:0019533	cellobiose transport	biological_process
50591085	GO:0000004	biological process unknown	biological_process
50591087	GO:0030245	cellulose catabolism	biological_process
50591089	GO:0006429	leucyl-tRNA aminoacylation	biological_process
50591090	GO:0006508	proteolysis and peptidolysis	biological_process
50591090	GO:0007218	neuropeptide signaling pathway	biological_process
50591090	GO:0007267	cell-cell signaling	biological_process
50591090	GO:0010002	cardioblast differentiation	biological_process
50591090	GO:0016486	peptide hormone processing	biological_process
50591090	GO:0042310	vasoconstriction	biological_process
50591093	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591095	GO:0006099	tricarboxylic acid cycle	biological_process
50591096	GO:0006099	tricarboxylic acid cycle	biological_process
50591096	GO:0006113	fermentation	biological_process
50591096	GO:0019629	propionate catabolism, 2-methylcitrate cycle	biological_process
50591097	GO:0006447	regulation of translational initiation by iron	biological_process
50591097	GO:0006879	iron ion homeostasis	biological_process
50591097	GO:0008652	amino acid biosynthesis	biological_process
50591097	GO:0016478	negative regulation of translation	biological_process
50591097	GO:0019643	reductive tricarboxylic acid cycle	biological_process
50591099	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
50591100	GO:0008340	determination of adult life span	biological_process
50591100	GO:0009186	deoxyribonucleoside diphosphate metabolism	biological_process
50591100	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
50591100	GO:0040035	hermaphrodite genital morphogenesis	biological_process
50591101	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591104	GO:0006413	translational initiation	biological_process
50591105	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50591111	GO:0000271	polysaccharide biosynthesis	biological_process
50591114	GO:0000271	polysaccharide biosynthesis	biological_process
50591117	GO:0015777	teichoic acid transport	biological_process
50591117	GO:0015920	lipopolysaccharide transport	biological_process
50591118	GO:0015777	teichoic acid transport	biological_process
50591122	GO:0006955	immune response	biological_process
50591125	GO:0006816	calcium ion transport	biological_process
50591125	GO:0006828	manganese ion transport	biological_process
50591125	GO:0006874	calcium ion homeostasis	biological_process
50591125	GO:0006942	regulation of striated muscle contraction	biological_process
50591125	GO:0009612	response to mechanical stimulus	biological_process
50591125	GO:0015992	proton transport	biological_process
50591125	GO:0045932	negative regulation of muscle contraction	biological_process
50591127	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50591131	GO:0006012	galactose metabolism	biological_process
50591132	GO:0030245	cellulose catabolism	biological_process

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gi	acc	name	term_type
50591133	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591133	GO:0015759	beta-glucoside transport	biological_process
50591133	GO:0019533	cellobiose transport	biological_process
50591137	GO:0006419	alanyl-tRNA aminoacylation	biological_process
50591143	GO:0006508	proteolysis and peptidolysis	biological_process
50591146	GO:0006431	methionyl-tRNA aminoacylation	biological_process
50591148	GO:0009423	chorismate biosynthesis	biological_process
50591149	GO:0009423	chorismate biosynthesis	biological_process
50591150	GO:0009423	chorismate biosynthesis	biological_process
50591151	GO:0009423	chorismate biosynthesis	biological_process
50591155	GO:0030245	cellulose catabolism	biological_process
50591158	GO:0030245	cellulose catabolism	biological_process
50591159	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591159	GO:0015759	beta-glucoside transport	biological_process
50591159	GO:0019533	cellobiose transport	biological_process
50591161	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591161	GO:0015759	beta-glucoside transport	biological_process
50591162	GO:0000004	biological process unknown	biological_process
50591162	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591166	GO:0030245	cellulose catabolism	biological_process
50591168	GO:0030245	cellulose catabolism	biological_process
50591169	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591172	GO:0001523	retinoid metabolism	biological_process
50591172	GO:0006805	xenobiotic metabolism	biological_process
50591173	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591173	GO:0015759	beta-glucoside transport	biological_process
50591173	GO:0015770	sucrose transport	biological_process
50591173	GO:0015771	trehalose transport	biological_process
50591176	GO:0006508	proteolysis and peptidolysis	biological_process
50591177	GO:0006835	dicarboxylic acid transport	biological_process
50591177	GO:0015810	L-aspartate transport	biological_process
50591177	GO:0015813	L-glutamate transport	biological_process
50591178	GO:0006835	dicarboxylic acid transport	biological_process
50591180	GO:0006448	regulation of translational elongation	biological_process
50591181	GO:0006810	transport	biological_process
50591182	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50591182	GO:0009252	peptidoglycan biosynthesis	biological_process
50591187	GO:0000154	rRNA modification	biological_process
50591189	GO:0006810	transport	biological_process
50591192	GO:0006644	phospholipid metabolism	biological_process
50591196	GO:0006313	DNA transposition	biological_process
50591200	GO:0006855	multidrug transport	biological_process
50591202	GO:0030488	tRNA methylation	biological_process
50591203	GO:0000105	histidine biosynthesis	biological_process
50591204	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591205	GO:0006096	glycolysis	biological_process

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gi	acc	name	term_type
50591206	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591206	GO:0015755	fructose transport	biological_process
50591209	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
50591210	GO:0006626	protein-mitochondrial targeting	biological_process
50591210	GO:0042780	tRNA 3'-processing	biological_process
50591211	GO:0006810	transport	biological_process
50591214	GO:0006206	pyrimidine base metabolism	biological_process
50591214	GO:0006231	dTMP biosynthesis	biological_process
50591214	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
50591215	GO:0046654	tetrahydrofolate biosynthesis	biological_process
50591216	GO:0006510	ATP-dependent proteolysis	biological_process
50591217	GO:0000004	biological process unknown	biological_process
50591218	GO:0006165	nucleoside diphosphate phosphorylation	biological_process
50591218	GO:0006183	GTP biosynthesis	biological_process
50591218	GO:0006228	UTP biosynthesis	biological_process
50591218	GO:0006241	CTP biosynthesis	biological_process
50591218	GO:0006917	induction of apoptosis	biological_process
50591218	GO:0007427	tracheal epithelial cell migration (sensu Insecta)	biological_process
50591218	GO:0008285	negative regulation of cell proliferation	biological_process
50591218	GO:0018105	peptidyl-serine phosphorylation	biological_process
50591218	GO:0045786	negative regulation of progression through cell cycle	biological_process
50591219	GO:0000004	biological process unknown	biological_process
50591223	GO:0006855	multidrug transport	biological_process
50591224	GO:0000002	mitochondrial genome maintenance	biological_process
50591224	GO:0000294	mRNA catabolism, endonucleolytic cleavage-dependent decay	biological_process
50591224	GO:0006449	regulation of translational termination	biological_process
50591224	GO:0009097	isoleucine biosynthesis	biological_process
50591224	GO:0017148	negative regulation of protein biosynthesis	biological_process
50591225	GO:0000004	biological process unknown	biological_process
50591230	GO:0019546	arginine deiminase pathway	biological_process
50591232	GO:0000050	urea cycle	biological_process
50591232	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
50591232	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
50591232	GO:0006526	arginine biosynthesis	biological_process
50591233	GO:0019546	arginine deiminase pathway	biological_process
50591235	GO:0006508	proteolysis and peptidolysis	biological_process
50591238	GO:0008616	queuosine biosynthesis	biological_process
50591240	GO:0006002	fructose 6-phosphate metabolism	biological_process
50591240	GO:0006046	N-acetylglucosamine catabolism	biological_process
50591240	GO:0007340	acrosome reaction	biological_process
50591240	GO:0046370	fructose biosynthesis	biological_process
50591242	GO:0009396	folic acid and derivative biosynthesis	biological_process
50591243	GO:0006559	L-phenylalanine catabolism	biological_process
50591243	GO:0006727	ommochrome biosynthesis	biological_process
50591243	GO:0006729	tetrahydrobiopterin biosynthesis	biological_process
50591243	GO:0006809	nitric oxide biosynthesis	biological_process

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gi	acc	name	term_type
50591243	GO:0042133	neurotransmitter metabolism	biological_process
50591243	GO:0046654	tetrahydrofolate biosynthesis	biological_process
50591249	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
50591251	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
50591252	GO:0009254	peptidoglycan turnover	biological_process
50591252	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50591254	GO:0009254	peptidoglycan turnover	biological_process
50591254	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
50591256	GO:0008152	metabolism	biological_process
50591259	GO:0009255	Entner-Doudoroff pathway	biological_process
50591260	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591261	GO:0006027	glycosaminoglycan catabolism	biological_process
50591266	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591266	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591267	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591267	GO:0006817	phosphate transport	biological_process
50591268	GO:0007528	neuromuscular junction development	biological_process
50591270	GO:0015937	coenzyme A biosynthesis	biological_process
50591272	GO:0000002	mitochondrial genome maintenance	biological_process
50591272	GO:0001525	angiogenesis	biological_process
50591272	GO:0006206	pyrimidine base metabolism	biological_process
50591272	GO:0006220	pyrimidine nucleotide metabolism	biological_process
50591272	GO:0006935	chemotaxis	biological_process
50591272	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50591273	GO:0009264	deoxyribonucleotide catabolism	biological_process
50591274	GO:0006206	pyrimidine base metabolism	biological_process
50591274	GO:0006216	cytidine catabolism	biological_process
50591274	GO:0006217	deoxycytidine catabolism	biological_process
50591280	GO:0000004	biological process unknown	biological_process
50591283	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
50591283	GO:0015940	pantothenate biosynthesis	biological_process
50591285	GO:0006412	protein biosynthesis	biological_process
50591286	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
50591286	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50591288	GO:0006412	protein biosynthesis	biological_process
50591289	GO:0006350	transcription	biological_process
50591290	GO:0000002	mitochondrial genome maintenance	biological_process
50591290	GO:0006412	protein biosynthesis	biological_process
50591290	GO:0007046	ribosome biogenesis	biological_process
50591292	GO:0006414	translational elongation	biological_process
50591292	GO:0006415	translational termination	biological_process
50591293	GO:0015693	magnesium ion transport	biological_process
50591295	GO:0009252	peptidoglycan biosynthesis	biological_process
50591296	GO:0006810	transport	biological_process
50591299	GO:0009252	peptidoglycan biosynthesis	biological_process
50591300	GO:0006281	DNA repair	biological_process

续表 1

gi	acc	name	term_type
50591300	GO:0006310	DNA recombination	biological_process
50591301	GO:0009252	peptidoglycan biosynthesis	biological_process
50591302	GO:0006810	transport	biological_process
50591305	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591306	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591306	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591314	GO:0009306	protein secretion	biological_process
50591315	GO:0009297	fimbriae biogenesis	biological_process
50591315	GO:0009405	pathogenesis	biological_process
50591315	GO:0015628	type II protein secretion system	biological_process
50591318	GO:0006350	transcription	biological_process
50591320	GO:0009252	peptidoglycan biosynthesis	biological_process
50591321	GO:0006437	tyrosyl-tRNA aminoacylation	biological_process
50591325	GO:0006828	manganese ion transport	biological_process
50591325	GO:0006829	zinc ion transport	biological_process
50591325	GO:0007155	cell adhesion	biological_process
50591325	GO:0009405	pathogenesis	biological_process
50591326	GO:0006828	manganese ion transport	biological_process
50591326	GO:0006829	zinc ion transport	biological_process
50591327	GO:0006826	iron ion transport	biological_process
50591327	GO:0006828	manganese ion transport	biological_process
50591327	GO:0006829	zinc ion transport	biological_process
50591362	GO:0006260	DNA replication	biological_process
50591362	GO:0006281	DNA repair	biological_process
50591362	GO:0006310	DNA recombination	biological_process
50591369	GO:0009252	peptidoglycan biosynthesis	biological_process
50591372	GO:0001321	age-dependent general metabolic decline during replicative cell aging	biological_process
50591372	GO:0015986	ATP synthesis coupled proton transport	biological_process
50591373	GO:0015986	ATP synthesis coupled proton transport	biological_process
50591374	GO:0015986	ATP synthesis coupled proton transport	biological_process
50591376	GO:0015986	ATP synthesis coupled proton transport	biological_process
50591380	GO:0006260	DNA replication	biological_process
50591380	GO:0006281	DNA repair	biological_process
50591380	GO:0006310	DNA recombination	biological_process
50591383	GO:0006010	glucose 6-phosphate utilization	biological_process
50591383	GO:0006098	pentose-phosphate shunt	biological_process
50591383	GO:0006749	glutathione metabolism	biological_process
50591383	GO:0045767	regulation of anti-apoptosis	biological_process
50591386	GO:0009306	protein secretion	biological_process
50591389	GO:0000067	DNA replication and chromosome cycle	biological_process
50591389	GO:0000910	cytokinesis	biological_process
50591389	GO:0007001	chromosome organization and biogenesis (sensu Eukaryota)	biological_process
50591389	GO:0007076	mitotic chromosome condensation	biological_process
50591390	GO:0006396	RNA processing	biological_process
50591394	GO:0009082	branched chain family amino acid biosynthesis	biological_process
50591396	GO:0006260	DNA replication	biological_process

续表 1

gi	acc	name	term_type
50591396	GO:0006265	DNA topological change	biological_process
50591399	GO:0000910	cytokinesis	biological_process
50591400	GO:0006260	DNA replication	biological_process
50591400	GO:0006265	DNA topological change	biological_process
50591401	GO:0000004	biological process unknown	biological_process
50591402	GO:0006310	DNA recombination	biological_process
50591407	GO:0000004	biological process unknown	biological_process
50591408	GO:0006289	nucleotide-excision repair	biological_process
50591409	GO:0006814	sodium ion transport	biological_process
50591412	GO:0009252	peptidoglycan biosynthesis	biological_process
50591414	GO:0006400	tRNA modification	biological_process
50591415	GO:0000004	biological process unknown	biological_process
50591417	GO:0008033	tRNA processing	biological_process
50591418	GO:0006703	estrogen biosynthesis	biological_process
50591420	GO:0008654	phospholipid biosynthesis	biological_process
50591421	GO:0006310	DNA recombination	biological_process
50591423	GO:0006166	purine ribonucleoside salvage	biological_process
50591423	GO:0006168	adenine salvage	biological_process
50591424	GO:0009086	methionine biosynthesis	biological_process
50591425	GO:0006269	DNA replication, synthesis of RNA primer	biological_process
50591427	GO:0000004	biological process unknown	biological_process
50591428	GO:0030001	metal ion transport	biological_process
50591429	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50591429	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
50591430	GO:0009243	O antigen biosynthesis	biological_process
50591430	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
50591432	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50591432	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
50591433	GO:0009243	O antigen biosynthesis	biological_process
50591433	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
50591435	GO:0009253	peptidoglycan catabolism	biological_process
50591435	GO:0016998	cell wall catabolism	biological_process
50591436	GO:0009253	peptidoglycan catabolism	biological_process
50591436	GO:0016998	cell wall catabolism	biological_process
50591442	GO:0006825	copper ion transport	biological_process
50591442	GO:0009873	ethylene mediated signaling pathway	biological_process
50591443	GO:0006979	response to oxidative stress	biological_process
50591445	GO:0006810	transport	biological_process
50591448	GO:0006313	DNA transposition	biological_process
50591450	GO:0006260	DNA replication	biological_process
50591450	GO:0006308	DNA catabolism	biological_process
50591454	GO:0008033	tRNA processing	biological_process
50591454	GO:0008616	queuosine biosynthesis	biological_process
50591455	GO:0006508	proteolysis and peptidolysis	biological_process
50591456	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591457	GO:0007339	binding of sperm to zona pellucida	biological_process

续表 1

gi	acc	name	term_type
50591457	GO:0008037	cell recognition	biological_process
50591458	GO:0000271	polysaccharide biosynthesis	biological_process
50591458	GO:0042493	response to drug	biological_process
50591459	GO:0006506	GPI anchor biosynthesis	biological_process
50591459	GO:0016036	cellular response to phosphate starvation	biological_process
50591459	GO:0046506	sulfolipid biosynthesis	biological_process
50591462	GO:0006435	threonyl-tRNA aminoacylation	biological_process
50591463	GO:0006868	L-glutamine transport	biological_process
50591465	GO:0006096	glycolysis	biological_process
50591471	GO:0019660	glycolytic fermentation	biological_process
50591472	GO:0009405	pathogenesis	biological_process
50591473	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591474	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591474	GO:0015759	beta-glucoside transport	biological_process
50591474	GO:0015771	trehalose transport	biological_process
50591475	GO:0030245	cellulose catabolism	biological_process
50591476	GO:0000004	biological process unknown	biological_process
50591478	GO:0015847	putrescine transport	biological_process
50591478	GO:0015848	spermidine transport	biological_process
50591481	GO:0006313	DNA transposition	biological_process
50591494	GO:0006304	DNA modification	biological_process
50591504	GO:0009152	purine ribonucleotide biosynthesis	biological_process
50591505	GO:0006532	aspartate biosynthesis	biological_process
50591505	GO:0009073	aromatic amino acid family biosynthesis	biological_process
50591507	GO:0008610	lipid biosynthesis	biological_process
50591509	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591509	GO:0009113	purine base biosynthesis	biological_process
50591510	GO:0006144	purine base metabolism	biological_process
50591510	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591510	GO:0006541	glutamine metabolism	biological_process
50591511	GO:0005996	monosaccharide metabolism	biological_process
50591511	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591511	GO:0006541	glutamine metabolism	biological_process
50591511	GO:0008340	determination of adult life span	biological_process
50591511	GO:0009113	purine base biosynthesis	biological_process
50591511	GO:0009116	nucleoside metabolism	biological_process
50591511	GO:0040016	embryonic cleavage	biological_process
50591512	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591512	GO:0009113	purine base biosynthesis	biological_process
50591513	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591513	GO:0009113	purine base biosynthesis	biological_process
50591514	GO:0009152	purine ribonucleotide biosynthesis	biological_process
50591515	GO:0006304	DNA modification	biological_process
50591519	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591519	GO:0009113	purine base biosynthesis	biological_process
50591520	GO:0006144	purine base metabolism	biological_process

续表 1

gi	acc	name	term_type
50591520	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591521	GO:0006144	purine base metabolism	biological_process
50591521	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591523	GO:0006144	purine base metabolism	biological_process
50591523	GO:0006189	'de novo' IMP biosynthesis	biological_process
50591523	GO:0009712	catechol metabolism	biological_process
50591524	GO:0006810	transport	biological_process
50591529	GO:0006810	transport	biological_process
50591531	GO:0006810	transport	biological_process
50591532	GO:0006310	DNA recombination	biological_process
50591538	GO:0006315	homing of group II introns	biological_process
50591538	GO:0006396	RNA processing	biological_process
50591555	GO:0006306	DNA methylation	biological_process
50591557	GO:0000154	rRNA modification	biological_process
50591557	GO:0001510	RNA methylation	biological_process
50591557	GO:0006400	tRNA modification	biological_process
50591559	GO:0019274	phenylalanine biosynthesis, prephenate pathway	biological_process
50591560	GO:0009423	chorismate biosynthesis	biological_process
50591561	GO:0009423	chorismate biosynthesis	biological_process
50591561	GO:0018920	glyphosate metabolism	biological_process
50591576	GO:0006333	chromatin assembly or disassembly	biological_process
50591576	GO:0007350	blastoderm segmentation	biological_process
50591576	GO:0007379	segment specification	biological_process
50591591	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591593	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50591594	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50591598	GO:0000004	biological process unknown	biological_process
50591599	GO:0009423	chorismate biosynthesis	biological_process
50591600	GO:0009073	aromatic amino acid family biosynthesis	biological_process
50591601	GO:0019274	phenylalanine biosynthesis, prephenate pathway	biological_process
50591607	GO:0006532	aspartate biosynthesis	biological_process
50591608	GO:0006950	response to stress	biological_process
50591611	GO:0006530	asparagine catabolism	biological_process
50591611	GO:0006995	cellular response to nitrogen starvation	biological_process
50591613	GO:0006268	DNA unwinding	biological_process
50591613	GO:0006310	DNA recombination	biological_process
50591616	GO:0000910	cytokinesis	biological_process
50591617	GO:0006164	purine nucleotide biosynthesis	biological_process
50591617	GO:0006166	purine ribonucleoside salvage	biological_process
50591617	GO:0007610	behavior	biological_process
50591617	GO:0019835	cytolysis	biological_process
50591617	GO:0046651	lymphocyte proliferation	biological_process
50591618	GO:0006166	purine ribonucleoside salvage	biological_process
50591618	GO:0006400	tRNA modification	biological_process
50591622	GO:0006283	transcription-coupled nucleotide-excision repair	biological_process
50591623	GO:0006412	protein biosynthesis	biological_process

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gi	acc	name	term_type
50591624	GO:0000004	biological process unknown	biological_process
50591628	GO:0006520	amino acid metabolism	biological_process
50591628	GO:0006865	amino acid transport	biological_process
50591640	GO:0005996	monosaccharide metabolism	biological_process
50591642	GO:0009651	response to salt stress	biological_process
50591642	GO:0015937	coenzyme A biosynthesis	biological_process
50591642	GO:0015939	pantothenate metabolism	biological_process
50591643	GO:0015937	coenzyme A biosynthesis	biological_process
50591643	GO:0015939	pantothenate metabolism	biological_process
50591644	GO:0000105	histidine biosynthesis	biological_process
50591644	GO:0006730	one-carbon compound metabolism	biological_process
50591644	GO:0009086	methionine biosynthesis	biological_process
50591644	GO:0009113	purine base biosynthesis	biological_process
50591644	GO:0009257	10-formyltetrahydrofolate biosynthesis	biological_process
50591644	GO:0015940	pantothenate biosynthesis	biological_process
50591647	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
50591647	GO:0006546	glycine catabolism	biological_process
50591647	GO:0006550	isoleucine catabolism	biological_process
50591647	GO:0006552	leucine catabolism	biological_process
50591647	GO:0006564	L-serine biosynthesis	biological_process
50591647	GO:0006574	valine catabolism	biological_process
50591653	GO:0006113	fermentation	biological_process
50591653	GO:0006800	oxygen and reactive oxygen species metabolism	biological_process
50591654	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591655	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591655	GO:0009204	deoxyribonucleoside triphosphate catabolism	biological_process
50591657	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591657	GO:0015759	beta-glucoside transport	biological_process
50591657	GO:0019533	cellobiose transport	biological_process
50591658	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591658	GO:0015759	beta-glucoside transport	biological_process
50591658	GO:0019533	cellobiose transport	biological_process
50591659	GO:0006113	fermentation	biological_process
50591659	GO:0015942	formate metabolism	biological_process
50591660	GO:0006098	pentose-phosphate shunt	biological_process
50591664	GO:0006313	DNA transposition	biological_process
50591665	GO:0006428	isoleucyl-tRNA aminoacylation	biological_process
50591671	GO:0000004	biological process unknown	biological_process
50591671	GO:0006522	alanine metabolism	biological_process
50591672	GO:0000910	cytokinesis	biological_process
50591672	GO:0046785	microtubule polymerization	biological_process
50591674	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50591675	GO:0006415	translational termination	biological_process
50591676	GO:0006306	DNA methylation	biological_process
50591680	GO:0006730	one-carbon compound metabolism	biological_process
50591680	GO:0009396	folic acid and derivative biosynthesis	biological_process

续表 1

gi	acc	name	term_type
50591680	GO:0019264	glycine biosynthesis from serine	biological_process
50591683	GO:0008152	metabolism	biological_process
50591690	GO:0009152	purine ribonucleotide biosynthesis	biological_process
50591690	GO:0046037	GMP metabolism	biological_process
50591691	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591691	GO:0015771	trehalose transport	biological_process
50591693	GO:0006617	SRP-dependent cotranslational protein-membrane targeting, signal sequence recognition	biological_process
50591693	GO:0009306	protein secretion	biological_process
50591697	GO:0006310	DNA recombination	biological_process
50591697	GO:0015074	DNA integration	biological_process
50591698	GO:0005975	carbohydrate metabolism	biological_process
50591699	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591700	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591700	GO:0006817	phosphate transport	biological_process
50591732	GO:0000154	rRNA modification	biological_process
50591736	GO:0000910	cytokinesis	biological_process
50591742	GO:0006414	translational elongation	biological_process
50591749	GO:0015684	ferrous iron transport	biological_process
50591750	GO:0000910	cytokinesis	biological_process
50591751	GO:0000910	cytokinesis	biological_process
50591751	GO:0006810	transport	biological_process
50591752	GO:0006415	translational termination	biological_process
50591753	GO:0006118	electron transport	biological_process
50591759	GO:0006323	DNA packaging	biological_process
50591763	GO:0006281	DNA repair	biological_process
50591763	GO:0006310	DNA recombination	biological_process
50591765	GO:0009405	pathogenesis	biological_process
50591765	GO:0019836	hemolysis	biological_process
50591766	GO:0016114	terpenoid biosynthesis	biological_process
50591766	GO:0045337	farnesyl diphosphate biosynthesis	biological_process
50591768	GO:0006308	DNA catabolism	biological_process
50591774	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
50591774	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591780	GO:0006289	nucleotide-excision repair	biological_process
50591780	GO:0042026	protein refolding	biological_process
50591781	GO:0005980	glycogen catabolism	biological_process
50591782	GO:0005980	glycogen catabolism	biological_process
50591783	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591783	GO:0015771	trehalose transport	biological_process
50591785	GO:0015758	glucose transport	biological_process
50591788	GO:0000004	biological process unknown	biological_process
50591792	GO:0000004	biological process unknown	biological_process
50591794	GO:0006824	cobalt ion transport	biological_process
50591795	GO:0006824	cobalt ion transport	biological_process
50591796	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591796	GO:0009409	response to cold	biological_process

续表 1

gi	acc	name	term_type
50591797	GO:0000004	biological process unknown	biological_process
50591798	GO:0009252	peptidoglycan biosynthesis	biological_process
50591804	GO:0009372	quorum sensing	biological_process
50591806	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
50591808	GO:0006260	DNA replication	biological_process
50591809	GO:0006431	methionyl-tRNA aminoacylation	biological_process
50591810	GO:0000154	rRNA modification	biological_process
50591810	GO:0001510	RNA methylation	biological_process
50591815	GO:0042891	antibiotic transport	biological_process
50591815	GO:0046677	response to antibiotic	biological_process
50591827	GO:0006979	response to oxidative stress	biological_process
50591827	GO:0030091	protein repair	biological_process
50591828	GO:0006631	fatty acid metabolism	biological_process
50591829	GO:0006118	electron transport	biological_process
50591838	GO:0006298	mismatch repair	biological_process
50591841	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591841	GO:0015771	trehalose transport	biological_process
50591842	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591842	GO:0015759	beta-glucoside transport	biological_process
50591842	GO:0015771	trehalose transport	biological_process
50591843	GO:0000025	maltose catabolism	biological_process
50591843	GO:0005993	trehalose catabolism	biological_process
50591845	GO:0006118	electron transport	biological_process
50591846	GO:0006401	RNA catabolism	biological_process
50591847	GO:0006508	proteolysis and peptidolysis	biological_process
50591847	GO:0009306	protein secretion	biological_process
50591848	GO:0006281	DNA repair	biological_process
50591848	GO:0006310	DNA recombination	biological_process
50591849	GO:0006825	copper ion transport	biological_process
50591849	GO:0009873	ethylene mediated signaling pathway	biological_process
50591850	GO:0006825	copper ion transport	biological_process
50591850	GO:0006878	copper ion homeostasis	biological_process
50591850	GO:0007622	rhythmic behavior	biological_process
50591850	GO:0015694	mercury ion transport	biological_process
50591853	GO:0006002	fructose 6-phosphate metabolism	biological_process
50591853	GO:0006043	glucosamine catabolism	biological_process
50591853	GO:0006044	N-acetylglucosamine metabolism	biological_process
50591853	GO:0007340	acrosome reaction	biological_process
50591853	GO:0046370	fructose biosynthesis	biological_process
50591860	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591860	GO:0015759	beta-glucoside transport	biological_process
50591860	GO:0019533	cellobiose transport	biological_process
50591861	GO:0006047	UDP-N-acetylglucosamine metabolism	biological_process
50591861	GO:0007155	cell adhesion	biological_process
50591861	GO:0009103	lipopolysaccharide biosynthesis	biological_process
50591861	GO:0046380	N-acetylneuraminate biosynthesis	biological_process

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gi	acc	name	term_type
50591868	GO:0009650	UV protection	biological_process
50591869	GO:0006113	fermentation	biological_process
50591869	GO:0015942	formate metabolism	biological_process
50591876	GO:0009395	phospholipid catabolism	biological_process
50591877	GO:0006098	pentose-phosphate shunt	biological_process
50591877	GO:0008615	pyridoxine biosynthesis	biological_process
50591877	GO:0009228	thiamin biosynthesis	biological_process
50591877	GO:0009240	isopentenyl diphosphate biosynthesis	biological_process
50591877	GO:0040008	regulation of growth	biological_process
50591878	GO:0006098	pentose-phosphate shunt	biological_process
50591878	GO:0040008	regulation of growth	biological_process
50591881	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591884	GO:0005978	glycogen biosynthesis	biological_process
50591885	GO:0005978	glycogen biosynthesis	biological_process
50591886	GO:0005978	glycogen biosynthesis	biological_process
50591887	GO:0005978	glycogen biosynthesis	biological_process
50591888	GO:0006865	amino acid transport	biological_process
50591890	GO:0006865	amino acid transport	biological_process
50591894	GO:0006289	nucleotide-excision repair	biological_process
50591896	GO:0006868	L-glutamine transport	biological_process
50591897	GO:0006865	amino acid transport	biological_process
50591899	GO:0006810	transport	biological_process
50591900	GO:0009086	methionine biosynthesis	biological_process
50591900	GO:0019344	cysteine biosynthesis	biological_process
50591909	GO:0006313	DNA transposition	biological_process
50591910	GO:0006313	DNA transposition	biological_process
50591911	GO:0006081	aldehyde metabolism	biological_process
50591911	GO:0006113	fermentation	biological_process
50591911	GO:0051144	propanediol catabolism	biological_process
50591914	GO:0006113	fermentation	biological_process
50591919	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591919	GO:0015761	mannose transport	biological_process
50591920	GO:0008645	hexose transport	biological_process
50591920	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591921	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591923	GO:0008643	carbohydrate transport	biological_process
50591925	GO:0006098	pentose-phosphate shunt	biological_process
50591926	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591927	GO:0006313	DNA transposition	biological_process
50591928	GO:0006313	DNA transposition	biological_process
50591929	GO:0006313	DNA transposition	biological_process
50591932	GO:0006012	galactose metabolism	biological_process
50591933	GO:0030245	cellulose catabolism	biological_process
50591933	GO:0045045	secretory pathway	biological_process
50591934	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591934	GO:0015759	beta-glucoside transport	biological_process

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gi	acc	name	term_type
50591934	GO:0019533	cellobiose transport	biological_process
50591935	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
50591935	GO:0015759	beta-glucoside transport	biological_process
50591936	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591937	GO:0019512	lactose catabolism via tagatose-6-phosphate	biological_process
50591938	GO:0006096	glycolysis	biological_process
50591939	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50591940	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50591941	GO:0006355	regulation of transcription, DNA-dependent	biological_process
50591947	GO:0005975	carbohydrate metabolism	biological_process
50591947	GO:0006284	base-excision repair	biological_process
50591947	GO:0006298	mismatch repair	biological_process
50591947	GO:0045786	negative regulation of progression through cell cycle	biological_process
50591949	GO:0006810	transport	biological_process
50591950	GO:0006810	transport	biological_process
50591951	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
50591951	GO:0006108	malate metabolism	biological_process
50591951	GO:0006113	fermentation	biological_process
50591952	GO:0000154	rRNA modification	biological_process
50591953	GO:0019363	pyridine nucleotide biosynthesis	biological_process
50591956	GO:0009116	nucleoside metabolism	biological_process
50591956	GO:0009152	purine ribonucleotide biosynthesis	biological_process
50591956	GO:0009156	ribonucleoside monophosphate biosynthesis	biological_process
50591957	GO:0016226	iron-sulfur cluster assembly	biological_process
50591957	GO:0016259	selenocysteine metabolism	biological_process
50591962	GO:0006281	DNA repair	biological_process
50591964	GO:0006260	DNA replication	biological_process
50591964	GO:0006265	DNA topological change	biological_process
50591965	GO:0006100	tricarboxylic acid cycle intermediate metabolism	biological_process
50591965	GO:0019246	L(+)-lactate biosynthesis from pyruvate	biological_process
50591965	GO:0019642	anaerobic glycolysis	biological_process
50591967	GO:0006313	DNA transposition	biological_process
50591968	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
50589914	GO:0005739	mitochondrion	cellular_component
50589914	GO:0045282	succinate dehydrogenase complex (sensu Bacteria)	cellular_component
50589927	GO:0009360	DNA polymerase III complex	cellular_component
50589931	GO:0009898	internal side of plasma membrane	cellular_component
50589931	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50589933	GO:0009507	chloroplast	cellular_component
50589939	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50589940	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50589944	GO:0009898	internal side of plasma membrane	cellular_component
50589944	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50589946	GO:0005625	soluble fraction	cellular_component
50589949	GO:0005624	membrane fraction	cellular_component
50589949	GO:0016021	integral to membrane	cellular_component

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gi	acc	name	term_type
50589949	GO:0046581	intercellular canaliculus	cellular_component
50589952	GO:0009331	glycerol-3-phosphate dehydrogenase complex	cellular_component
50589962	GO:0005624	membrane fraction	cellular_component
50589966	GO:0005887	integral to plasma membrane	cellular_component
50589966	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50589967	GO:0005887	integral to plasma membrane	cellular_component
50589967	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50589971	GO:0008372	cellular component unknown	cellular_component
50589980	GO:0005737	cytoplasm	cellular_component
50590000	GO:0009898	internal side of plasma membrane	cellular_component
50590000	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590001	GO:0009898	internal side of plasma membrane	cellular_component
50590001	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590019	GO:0012505	endomembrane system	cellular_component
50590020	GO:0012505	endomembrane system	cellular_component
50590025	GO:0005829	cytosol	cellular_component
50590033	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50590064	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590065	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590083	GO:0009345	glycine-tRNA ligase complex	cellular_component
50590084	GO:0009345	glycine-tRNA ligase complex	cellular_component
50590105	GO:0009380	excinuclease ABC complex	cellular_component
50590115	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590145	GO:0005794	Golgi apparatus	cellular_component
50590145	GO:0005887	integral to plasma membrane	cellular_component
50590145	GO:0030659	cytoplasmic vesicle membrane	cellular_component
50590181	GO:0005625	soluble fraction	cellular_component
50590187	GO:0005948	acetolactate synthase complex	cellular_component
50590190	GO:0005739	mitochondrion	cellular_component
50590193	GO:0016469	proton-transporting two-sector ATPase complex	cellular_component
50590204	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590205	GO:0009897	external side of plasma membrane	cellular_component
50590205	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50590205	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590211	GO:0012505	endomembrane system	cellular_component
50590217	GO:0005759	mitochondrial matrix	cellular_component
50590253	GO:0009507	chloroplast	cellular_component
50590254	GO:0009379	Holliday junction helicase complex	cellular_component
50590259	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50590259	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590260	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590261	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590262	GO:0009898	internal side of plasma membrane	cellular_component
50590262	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590286	GO:0000786	nucleosome	cellular_component
50590286	GO:0005859	muscle myosin	cellular_component

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gi	acc	name	term_type
50590286	GO:0005883	neurofilament	cellular_component
50590286	GO:0030018	Z disc	cellular_component
50590286	GO:0030424	axon	cellular_component
50590286	GO:0031430	M line	cellular_component
50590297	GO:0005840	ribosome	cellular_component
50590303	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590316	GO:0009360	DNA polymerase III complex	cellular_component
50590329	GO:0005615	extracellular space	cellular_component
50590329	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
50590329	GO:0042645	mitochondrial nucleoid	cellular_component
50590330	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
50590330	GO:0042645	mitochondrial nucleoid	cellular_component
50590331	GO:0045248	oxoglutarate dehydrogenase complex (sensu Bacteria)	cellular_component
50590332	GO:0005947	alpha-ketoglutarate dehydrogenase complex (sensu Eukaryota)	cellular_component
50590332	GO:0005960	glycine cleavage complex	cellular_component
50590332	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
50590332	GO:0009353	oxoglutarate dehydrogenase complex (sensu Eukaryota)	cellular_component
50590332	GO:0042645	mitochondrial nucleoid	cellular_component
50590345	GO:0005829	cytosol	cellular_component
50590347	GO:0005625	soluble fraction	cellular_component
50590347	GO:0005667	transcription factor complex	cellular_component
50590347	GO:0005737	cytoplasm	cellular_component
50590352	GO:0012505	endomembrane system	cellular_component
50590358	GO:0005634	nucleus	cellular_component
50590361	GO:0005829	cytosol	cellular_component
50590408	GO:0005951	carbamoyl-phosphate synthase complex	cellular_component
50590409	GO:0005951	carbamoyl-phosphate synthase complex	cellular_component
50590410	GO:0009347	aspartate carbamoyltransferase complex	cellular_component
50590415	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50590417	GO:0005758	mitochondrial intermembrane space	cellular_component
50590418	GO:0015627	type II protein secretion system complex	cellular_component
50590419	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590421	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50590422	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590423	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590424	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50590425	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590426	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590427	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590429	GO:0012505	endomembrane system	cellular_component
50590432	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component
50590440	GO:0005741	mitochondrial outer membrane	cellular_component
50590440	GO:0005887	integral to plasma membrane	cellular_component
50590440	GO:0016323	basolateral plasma membrane	cellular_component
50590463	GO:0009360	DNA polymerase III complex	cellular_component
50590466	GO:0009507	chloroplast	cellular_component

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gi	acc	name	term_type
50590479	GO:0020011	apicoplast	cellular_component
50590492	GO:0009536	plastid	cellular_component
50590494	GO:0030428	cell septum	cellular_component
50590495	GO:0005615	extracellular space	cellular_component
50590495	GO:0005624	membrane fraction	cellular_component
50590496	GO:0005615	extracellular space	cellular_component
50590496	GO:0005624	membrane fraction	cellular_component
50590504	GO:0005624	membrane fraction	cellular_component
50590504	GO:0016020	membrane	cellular_component
50590535	GO:0009507	chloroplast	cellular_component
50590571	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590574	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50590587	GO:0005964	phosphorylase kinase complex	cellular_component
50590596	GO:0005829	cytosol	cellular_component
50590604	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590605	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50590609	GO:0012505	endomembrane system	cellular_component
50590612	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590617	GO:0005782	peroxisomal matrix	cellular_component
50590617	GO:0005829	cytosol	cellular_component
50590624	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590630	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50590630	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590631	GO:0009898	internal side of plasma membrane	cellular_component
50590631	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590639	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50590689	GO:0005625	soluble fraction	cellular_component
50590689	GO:0005737	cytoplasm	cellular_component
50590716	GO:0005624	membrane fraction	cellular_component
50590716	GO:0016020	membrane	cellular_component
50590724	GO:0020011	apicoplast	cellular_component
50590737	GO:0009507	chloroplast	cellular_component
50590756	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
50590757	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
50590758	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
50590759	GO:0009507	chloroplast	cellular_component
50590760	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
50590762	GO:0020011	apicoplast	cellular_component
50590776	GO:0008623	chromatin accessibility complex	cellular_component
50590776	GO:0016363	nuclear matrix	cellular_component
50590776	GO:0016589	NURF complex	cellular_component
50590776	GO:0016590	ACF complex	cellular_component
50590776	GO:0035060	brahma complex	cellular_component
50590777	GO:0005694	chromosome	cellular_component
50590777	GO:0008623	chromatin accessibility complex	cellular_component
50590777	GO:0016587	ISW1 complex	cellular_component

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gi	acc	name	term_type
50590777	GO:0031213	RSF complex	cellular_component
50590798	GO:0009360	DNA polymerase III complex	cellular_component
50590811	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
50590815	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
50590831	GO:0009507	chloroplast	cellular_component
50590834	GO:0009898	internal side of plasma membrane	cellular_component
50590834	GO:0015627	type II protein secretion system complex	cellular_component
50590846	GO:0009360	DNA polymerase III complex	cellular_component
50590855	GO:0005764	lysosome	cellular_component
50590855	GO:0009341	beta-galactosidase complex	cellular_component
50590855	GO:0012505	endomembrane system	cellular_component
50590855	GO:0016023	cytoplasmic membrane-bound vesicle	cellular_component
50590891	GO:0005739	mitochondrion	cellular_component
50590893	GO:0008372	cellular component unknown	cellular_component
50590951	GO:0016021	integral to membrane	cellular_component
50590951	GO:0016600	flotillin complex	cellular_component
50590951	GO:0045121	lipid raft	cellular_component
50590971	GO:0016021	integral to membrane	cellular_component
50590980	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50590999	GO:0009316	3-isopropylmalate dehydratase complex	cellular_component
50591000	GO:0009316	3-isopropylmalate dehydratase complex	cellular_component
50591003	GO:0009507	chloroplast	cellular_component
50591014	GO:0005615	extracellular space	cellular_component
50591014	GO:0008372	cellular component unknown	cellular_component
50591014	GO:0009706	chloroplast inner membrane	cellular_component
50591016	GO:0008021	synaptic vesicle	cellular_component
50591025	GO:0005945	6-phosphofructokinase complex	cellular_component
50591026	GO:0009360	DNA polymerase III complex	cellular_component
50591036	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
50591049	GO:0009507	chloroplast	cellular_component
50591087	GO:0012505	endomembrane system	cellular_component
50591090	GO:0005794	Golgi apparatus	cellular_component
50591090	GO:0005887	integral to plasma membrane	cellular_component
50591090	GO:0030659	cytoplasmic vesicle membrane	cellular_component
50591097	GO:0005737	cytoplasm	cellular_component
50591100	GO:0005971	ribonucleoside-diphosphate reductase complex	cellular_component
50591117	GO:0009898	internal side of plasma membrane	cellular_component
50591117	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50591118	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50591122	GO:0008372	cellular component unknown	cellular_component
50591125	GO:0005790	smooth endoplasmic reticulum	cellular_component
50591125	GO:0016021	integral to membrane	cellular_component
50591125	GO:0016529	sarcoplasmic reticulum	cellular_component
50591132	GO:0012505	endomembrane system	cellular_component
50591140	GO:0005829	cytosol	cellular_component
50591146	GO:0005739	mitochondrion	cellular_component

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gi	acc	name	term_type
50591172	GO:0005615	extracellular space	cellular_component
50591172	GO:0005788	endoplasmic reticulum lumen	cellular_component
50591172	GO:0005792	microsome	cellular_component
50591177	GO:0005887	integral to plasma membrane	cellular_component
50591180	GO:0005840	ribosome	cellular_component
50591180	GO:0009507	chloroplast	cellular_component
50591181	GO:0009507	chloroplast	cellular_component
50591189	GO:0009507	chloroplast	cellular_component
50591216	GO:0009368	endopeptidase Clp complex	cellular_component
50591218	GO:0005625	soluble fraction	cellular_component
50591218	GO:0005758	mitochondrial intermembrane space	cellular_component
50591218	GO:0005792	microsome	cellular_component
50591232	GO:0005759	mitochondrial matrix	cellular_component
50591232	GO:0009289	fimbrium	cellular_component
50591232	GO:0009348	ornithine carbamoyltransferase complex	cellular_component
50591249	GO:0009328	phenylalanine-tRNA ligase complex	cellular_component
50591251	GO:0009328	phenylalanine-tRNA ligase complex	cellular_component
50591256	GO:0020011	apicoplast	cellular_component
50591261	GO:0005764	lysosome	cellular_component
50591272	GO:0005625	soluble fraction	cellular_component
50591288	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
50591290	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
50591302	GO:0009507	chloroplast	cellular_component
50591315	GO:0015627	type II protein secretion system complex	cellular_component
50591321	GO:0005739	mitochondrion	cellular_component
50591372	GO:0005625	soluble fraction	cellular_component
50591372	GO:0005754	proton-transporting ATP synthase, catalytic core (sensu Eukaryota)	cellular_component
50591372	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
50591373	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
50591374	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
50591376	GO:0045264	proton-transporting ATP synthase complex, coupling factor F(o) (sensu Bacteria)	cellular_component
50591379	GO:0008372	cellular component unknown	cellular_component
50591385	GO:0008372	cellular component unknown	cellular_component
50591389	GO:0005634	nucleus	cellular_component
50591389	GO:0005694	chromosome	cellular_component
50591396	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
50591396	GO:0009340	DNA topoisomerase IV complex	cellular_component
50591400	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
50591400	GO:0009340	DNA topoisomerase IV complex	cellular_component
50591408	GO:0009380	excinuclease ABC complex	cellular_component
50591425	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
50591428	GO:0016020	membrane	cellular_component
50591436	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
50591442	GO:0005770	late endosome	cellular_component
50591457	GO:0020011	apicoplast	cellular_component
50591459	GO:0000506	glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex	cellular_component

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gi	acc	name	term_type
50591494	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
50591504	GO:0009507	chloroplast	cellular_component
50591509	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
50591511	GO:0009507	chloroplast	cellular_component
50591513	GO:0005737	cytoplasm	cellular_component
50591514	GO:0009536	plastid	cellular_component
50591519	GO:0005737	cytoplasm	cellular_component
50591520	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
50591521	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
50591524	GO:0009898	internal side of plasma membrane	cellular_component
50591524	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50591532	GO:0009379	Holliday junction helicase complex	cellular_component
50591559	GO:0009507	chloroplast	cellular_component
50591561	GO:0009507	chloroplast	cellular_component
50591576	GO:0000785	chromatin	cellular_component
50591611	GO:0030287	periplasmic space (sensu Fungi)	cellular_component
50591617	GO:0005737	cytoplasm	cellular_component
50591623	GO:0009536	plastid	cellular_component
50591628	GO:0016020	membrane	cellular_component
50591647	GO:0005960	glycine cleavage complex	cellular_component
50591647	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
50591647	GO:0009353	oxoglutarate dehydrogenase complex (sensu Eukaryota)	cellular_component
50591647	GO:0042645	mitochondrial nucleoid	cellular_component
50591672	GO:0045298	tubulin	cellular_component
50591693	GO:0005786	signal recognition particle (sensu Eukaryota)	cellular_component
50591693	GO:0048501	signal recognition particle (sensu Bacteria and Archaea)	cellular_component
50591759	GO:0005694	chromosome	cellular_component
50591766	GO:0005739	mitochondrion	cellular_component
50591766	GO:0009507	chloroplast	cellular_component
50591768	GO:0009318	exodeoxyribonuclease VII complex	cellular_component
50591781	GO:0009507	chloroplast	cellular_component
50591788	GO:0008372	cellular component unknown	cellular_component
50591808	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
50591815	GO:0009898	internal side of plasma membrane	cellular_component
50591815	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
50591827	GO:0005783	endoplasmic reticulum	cellular_component
50591835	GO:0008372	cellular component unknown	cellular_component
50591838	GO:0009507	chloroplast	cellular_component
50591848	GO:0009338	exodeoxyribonuclease V complex	cellular_component
50591850	GO:0005770	late endosome	cellular_component
50591850	GO:0005795	Golgi stack	cellular_component
50591850	GO:0005889	hydrogen:potassium-exchanging ATPase complex	cellular_component
50591850	GO:0030140	trans-Golgi network transport vesicle	cellular_component
50591884	GO:0009536	plastid	cellular_component
50591886	GO:0009507	chloroplast	cellular_component
50591888	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component

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gi	acc	name	term_type
50591894	GO:0009380	excinuclease ABC complex	cellular_component
50591899	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component
50591933	GO:0012505	endomembrane system	cellular_component
50591956	GO:0009507	chloroplast	cellular_component
50591957	GO:0005759	mitochondrial matrix	cellular_component
50591964	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
50591965	GO:0005737	cytoplasm	cellular_component
50589875	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
50589882	GO:0004176	ATP-dependent peptidase activity	molecular_function
50589884	GO:0015655	alanine:sodium symporter activity	molecular_function
50589886	GO:0008094	DNA-dependent ATPase activity	molecular_function
50589891	GO:0004056	argininosuccinate lyase activity	molecular_function
50589892	GO:0004055	argininosuccinate synthase activity	molecular_function
50589906	GO:0015579	glucose permease activity	molecular_function
50589907	GO:0005529	sugar binding	molecular_function
50589909	GO:0004803	transposase activity	molecular_function
50589914	GO:0000104	succinate dehydrogenase activity	molecular_function
50589914	GO:0004106	chorismate mutase activity	molecular_function
50589914	GO:0008177	succinate dehydrogenase (ubiquinone) activity	molecular_function
50589914	GO:0008734	L-aspartate oxidase activity	molecular_function
50589914	GO:0009055	electron carrier activity	molecular_function
50589914	GO:0015036	disulfide oxidoreductase activity	molecular_function
50589914	GO:0016156	fumarate reductase (NADH) activity	molecular_function
50589914	GO:0050660	FAD binding	molecular_function
50589917	GO:0004527	exonuclease activity	molecular_function
50589918	GO:0008808	cardiolipin synthase activity	molecular_function
50589927	GO:0003887	DNA-directed DNA polymerase activity	molecular_function
50589930	GO:0015197	peptide transporter activity	molecular_function
50589933	GO:0004134	4-alpha-glucanotransferase activity	molecular_function
50589939	GO:0015415	phosphate-transporting ATPase activity	molecular_function
50589939	GO:0042301	phosphate binding	molecular_function
50589940	GO:0015415	phosphate-transporting ATPase activity	molecular_function
50589944	GO:0043212	carbohydrate-exporting ATPase activity	molecular_function
50589946	GO:0003714	transcription corepressor activity	molecular_function
50589946	GO:0004364	glutathione transferase activity	molecular_function
50589947	GO:0005199	structural constituent of cell wall	molecular_function
50589947	GO:0015159	polysaccharide transporter activity	molecular_function
50589949	GO:0005524	ATP binding	molecular_function
50589949	GO:0015646	permease activity	molecular_function
50589949	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50589950	GO:0005524	ATP binding	molecular_function
50589950	GO:0015646	permease activity	molecular_function
50589950	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50589952	GO:0004367	glycerol-3-phosphate dehydrogenase (NAD+) activity	molecular_function
50589954	GO:0000179	rRNA (adenine-N6,N6-)-dimethyltransferase activity	molecular_function
50589962	GO:0008198	ferrous iron binding	molecular_function

续表 1

gi	acc	name	term_type
50589962	GO:0008253	5'-nucleotidase activity	molecular_function
50589962	GO:0008663	2',3'-cyclic-nucleotide 2'-phosphodiesterase activity	molecular_function
50589966	GO:0015646	permease activity	molecular_function
50589966	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50589967	GO:0005524	ATP binding	molecular_function
50589967	GO:0015646	permease activity	molecular_function
50589967	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50589970	GO:0004731	purine-nucleoside phosphorylase activity	molecular_function
50589970	GO:0004850	uridine phosphorylase activity	molecular_function
50589971	GO:0004645	phosphorylase activity	molecular_function
50589971	GO:0004731	purine-nucleoside phosphorylase activity	molecular_function
50589971	GO:0017061	S-methyl-5-thioadenosine phosphorylase activity	molecular_function
50589973	GO:0008973	phosphopentomutase activity	molecular_function
50589975	GO:0008675	2-dehydro-3-deoxy-phosphogluconate aldolase activity	molecular_function
50589975	GO:0008700	4-hydroxy-2-oxoglutarate aldolase activity	molecular_function
50589978	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
50589980	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
50589981	GO:0004821	histidine-tRNA ligase activity	molecular_function
50589984	GO:0005554	molecular function unknown	molecular_function
50589989	GO:0005524	ATP binding	molecular_function
50589989	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50589998	GO:0004803	transposase activity	molecular_function
50589999	GO:0030528	transcription regulator activity	molecular_function
50590000	GO:0015415	phosphate-transporting ATPase activity	molecular_function
50590001	GO:0015415	phosphate-transporting ATPase activity	molecular_function
50590002	GO:0015415	phosphate-transporting ATPase activity	molecular_function
50590004	GO:0005055	laminin receptor activity	molecular_function
50590004	GO:0030145	manganese ion binding	molecular_function
50590007	GO:0003883	CTP synthase activity	molecular_function
50590016	GO:0000287	magnesium ion binding	molecular_function
50590016	GO:0003869	4-nitrophenylphosphatase activity	molecular_function
50590016	GO:0004035	alkaline phosphatase activity	molecular_function
50590016	GO:0008967	phosphoglycolate phosphatase activity	molecular_function
50590019	GO:0003978	UDP-glucose 4-epimerase activity	molecular_function
50590020	GO:0003978	UDP-glucose 4-epimerase activity	molecular_function
50590023	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590024	GO:0005524	ATP binding	molecular_function
50590024	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590024	GO:0048474	D-methionine transporter activity	molecular_function
50590025	GO:0004180	carboxypeptidase activity	molecular_function
50590025	GO:0008237	metallopeptidase activity	molecular_function
50590025	GO:0042315	cytosol nonspecific dipeptidase activity	molecular_function
50590025	GO:0046983	protein dimerization activity	molecular_function
50590027	GO:0004352	glutamate dehydrogenase activity	molecular_function
50590027	GO:0004354	glutamate dehydrogenase (NADP+) activity	molecular_function
50590033	GO:0003735	structural constituent of ribosome	molecular_function

续表 1

gi	acc	name	term_type
50590034	GO:0003746	translation elongation factor activity	molecular_function
50590044	GO:0030413	competence pheromone activity	molecular_function
50590049	GO:0004818	glutamate-tRNA ligase activity	molecular_function
50590055	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
50590055	GO:0004600	cyclophilin	molecular_function
50590055	GO:0005328	neurotransmitter:sodium symporter activity	molecular_function
50590055	GO:0016018	cyclosporin A binding	molecular_function
50590058	GO:0015646	permease activity	molecular_function
50590058	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590061	GO:0015646	permease activity	molecular_function
50590061	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590064	GO:0003735	structural constituent of ribosome	molecular_function
50590065	GO:0003735	structural constituent of ribosome	molecular_function
50590068	GO:0009008	DNA-methyltransferase activity	molecular_function
50590070	GO:0019213	deacetylase activity	molecular_function
50590071	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
50590072	GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	molecular_function
50590073	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
50590073	GO:0004849	uridine kinase activity	molecular_function
50590073	GO:0005524	ATP binding	molecular_function
50590073	GO:0008974	phosphoribulokinase activity	molecular_function
50590075	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
50590075	GO:0004028	aldehyde dehydrogenase activity	molecular_function
50590075	GO:0005506	iron ion binding	molecular_function
50590076	GO:0004765	shikimate kinase activity	molecular_function
50590076	GO:0004795	threonine synthase activity	molecular_function
50590083	GO:0004820	glycine-tRNA ligase activity	molecular_function
50590084	GO:0004820	glycine-tRNA ligase activity	molecular_function
50590088	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
50590088	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590089	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
50590089	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590090	GO:0015646	permease activity	molecular_function
50590090	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
50590090	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590091	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50590091	GO:0015646	permease activity	molecular_function
50590091	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
50590093	GO:0004089	carbonate dehydratase activity	molecular_function
50590094	GO:0005524	ATP binding	molecular_function
50590096	GO:0004170	dUTP diphosphatase activity	molecular_function
50590097	GO:0005524	ATP binding	molecular_function
50590097	GO:0015646	permease activity	molecular_function
50590097	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590099	GO:0005515	protein binding	molecular_function
50590099	GO:0005524	ATP binding	molecular_function

续表 1

gi	acc	name	term_type
50590099	GO:0016887	ATPase activity	molecular_function
50590101	GO:0016758	transferase activity, transferring hexosyl groups	molecular_function
50590102	GO:0008764	UDP-N-acetylmuramoylalanine-D-glutamate ligase activity	molecular_function
50590104	GO:0004251	X-Pro dipeptidase activity	molecular_function
50590104	GO:0008451	X-Pro aminopeptidase activity	molecular_function
50590105	GO:0009381	excinuclease ABC activity	molecular_function
50590106	GO:0015095	magnesium ion transporter activity	molecular_function
50590108	GO:0004803	transposase activity	molecular_function
50590109	GO:0004803	transposase activity	molecular_function
50590110	GO:0004803	transposase activity	molecular_function
50590115	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function
50590116	GO:0005554	molecular function unknown	molecular_function
50590123	GO:0004647	phosphoserine phosphatase activity	molecular_function
50590124	GO:0008967	phosphoglycolate phosphatase activity	molecular_function
50590125	GO:0008887	glycerate kinase activity	molecular_function
50590140	GO:0003711	transcriptional elongation regulator activity	molecular_function
50590141	GO:0005554	molecular function unknown	molecular_function
50590145	GO:0004245	neprilysin activity	molecular_function
50590145	GO:0008270	zinc ion binding	molecular_function
50590145	GO:0016512	endothelin-converting enzyme 1 activity	molecular_function
50590146	GO:0003746	translation elongation factor activity	molecular_function
50590148	GO:0016857	racemase and epimerase activity, acting on carbohydrates and derivatives	molecular_function
50590151	GO:0005524	ATP binding	molecular_function
50590151	GO:0015646	permease activity	molecular_function
50590151	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590152	GO:0005524	ATP binding	molecular_function
50590152	GO:0015646	permease activity	molecular_function
50590152	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590154	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
50590157	GO:0004160	dihydroxy-acid dehydratase activity	molecular_function
50590169	GO:0003954	NADH dehydrogenase activity	molecular_function
50590169	GO:0015036	disulfide oxidoreductase activity	molecular_function
50590172	GO:0008925	maltose O-acetyltransferase activity	molecular_function
50590173	GO:0005554	molecular function unknown	molecular_function
50590174	GO:0003917	DNA topoisomerase type I activity	molecular_function
50590176	GO:0000179	rRNA (adenine-N6,N6-)-dimethyltransferase activity	molecular_function
50590179	GO:0016563	transcriptional activator activity	molecular_function
50590181	GO:0004814	arginine-tRNA ligase activity	molecular_function
50590181	GO:0005524	ATP binding	molecular_function
50590183	GO:0005524	ATP binding	molecular_function
50590186	GO:0003984	acetolactate synthase activity	molecular_function
50590187	GO:0003984	acetolactate synthase activity	molecular_function
50590187	GO:0016597	amino acid binding	molecular_function
50590188	GO:0004455	ketol-acid reductoisomerase activity	molecular_function
50590189	GO:0004794	threonine ammonia-lyase activity	molecular_function
50590192	GO:0015211	purine nucleoside transporter activity	molecular_function

续表 1

gi	acc	name	term_type
50590193	GO:0004489	methylenetetrahydrofolate reductase (NADPH) activity	molecular_function
50590193	GO:0008702	5,10-methylenetetrahydrofolate reductase (FADH2) activity	molecular_function
50590194	GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	molecular_function
50590201	GO:0015171	amino acid transporter activity	molecular_function
50590203	GO:0015646	permease activity	molecular_function
50590204	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
50590204	GO:0015646	permease activity	molecular_function
50590205	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
50590207	GO:0003746	translation elongation factor activity	molecular_function
50590209	GO:0003715	transcription termination factor activity	molecular_function
50590210	GO:0030528	transcription regulator activity	molecular_function
50590211	GO:0004564	beta-fructofuranosidase activity	molecular_function
50590212	GO:0015582	beta-glucoside permease activity	molecular_function
50590212	GO:0015584	trehalose permease activity	molecular_function
50590214	GO:0004793	threonine aldolase activity	molecular_function
50590217	GO:0004123	cystathionine gamma-lyase activity	molecular_function
50590217	GO:0008483	transaminase activity	molecular_function
50590217	GO:0031071	cysteine desulfurase activity	molecular_function
50590219	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
50590221	GO:0016787	hydrolase activity	molecular_function
50590224	GO:0000309	nicotinamide-nucleotide adenylyltransferase activity	molecular_function
50590224	GO:0004515	nicotinate-nucleotide adenylyltransferase activity	molecular_function
50590232	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50590235	GO:0015589	mannose permease activity	molecular_function
50590240	GO:0005554	molecular function unknown	molecular_function
50590241	GO:0008964	phosphoenolpyruvate carboxylase activity	molecular_function
50590248	GO:0004788	thiamin diphosphokinase activity	molecular_function
50590249	GO:0004750	ribulose-phosphate 3-epimerase activity	molecular_function
50590250	GO:0005554	molecular function unknown	molecular_function
50590253	GO:0008725	DNA-3-methyladenine glycosylase I activity	molecular_function
50590254	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50590254	GO:0009378	Holliday junction helicase activity	molecular_function
50590255	GO:0016887	ATPase activity	molecular_function
50590258	GO:0015108	chloride transporter activity	molecular_function
50590259	GO:0015417	polyamine-transporting ATPase activity	molecular_function
50590259	GO:0019808	polyamine binding	molecular_function
50590260	GO:0015417	polyamine-transporting ATPase activity	molecular_function
50590261	GO:0015417	polyamine-transporting ATPase activity	molecular_function
50590262	GO:0015417	polyamine-transporting ATPase activity	molecular_function
50590263	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity	molecular_function
50590267	GO:0008881	glutamate racemase activity	molecular_function
50590268	GO:0005554	molecular function unknown	molecular_function
50590272	GO:0005488	binding	molecular_function
50590273	GO:0005515	protein binding	molecular_function
50590274	GO:0003723	RNA binding	molecular_function
50590274	GO:0004730	pseudouridylate synthase activity	molecular_function

续表 1

gi	acc	name	term_type
50590274	GO:0009982	pseudouridine synthase activity	molecular_function
50590276	GO:0005381	iron ion transporter activity	molecular_function
50590276	GO:0005524	ATP binding	molecular_function
50590276	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590277	GO:0005506	iron ion binding	molecular_function
50590278	GO:0005381	iron ion transporter activity	molecular_function
50590278	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590279	GO:0005381	iron ion transporter activity	molecular_function
50590279	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590280	GO:0004602	glutathione peroxidase activity	molecular_function
50590280	GO:0009031	thiol peroxidase activity	molecular_function
50590281	GO:0004730	pseudouridylate synthase activity	molecular_function
50590282	GO:0004364	glutathione transferase activity	molecular_function
50590282	GO:0005554	molecular function unknown	molecular_function
50590286	GO:0004601	peroxidase activity	molecular_function
50590286	GO:0005199	structural constituent of cell wall	molecular_function
50590286	GO:0008307	structural constituent of muscle	molecular_function
50590286	GO:0017022	myosin binding	molecular_function
50590299	GO:0008026	ATP-dependent helicase activity	molecular_function
50590300	GO:0005554	molecular function unknown	molecular_function
50590303	GO:0015197	peptide transporter activity	molecular_function
50590303	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590307	GO:0019843	rRNA binding	molecular_function
50590308	GO:0003743	translation initiation factor activity	molecular_function
50590311	GO:0003715	transcription termination factor activity	molecular_function
50590311	GO:0003723	RNA binding	molecular_function
50590315	GO:0004371	glycerone kinase activity	molecular_function
50590316	GO:0003893	epsilon DNA polymerase activity	molecular_function
50590326	GO:0003697	single-stranded DNA binding	molecular_function
50590326	GO:0005524	ATP binding	molecular_function
50590329	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
50590330	GO:0003826	alpha-ketoacid dehydrogenase activity	molecular_function
50590330	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
50590330	GO:0004802	transketolase activity	molecular_function
50590331	GO:0003826	alpha-ketoacid dehydrogenase activity	molecular_function
50590331	GO:0004149	dihydrolipoyllysine-residue succinyltransferase activity	molecular_function
50590331	GO:0004742	dihydrolipoyllysine-residue acetyltransferase activity	molecular_function
50590332	GO:0004148	dihydrolipoyl dehydrogenase activity	molecular_function
50590332	GO:0004375	glycine dehydrogenase (decarboxylating) activity	molecular_function
50590332	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	molecular_function
50590332	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
50590332	GO:0015036	disulfide oxidoreductase activity	molecular_function
50590332	GO:0050660	FAD binding	molecular_function
50590333	GO:0016787	hydrolase activity	molecular_function
50590336	GO:0004808	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase activity	molecular_function
50590337	GO:0003941	L-serine ammonia-lyase activity	molecular_function

续表 1

gi	acc	name	term_type
50590338	GO:0003941	L-serine ammonia-lyase activity	molecular_function
50590340	GO:0015087	cobalt ion transporter activity	molecular_function
50590341	GO:0015087	cobalt ion transporter activity	molecular_function
50590341	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590342	GO:0015087	cobalt ion transporter activity	molecular_function
50590342	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590344	GO:0004462	lactoylglutathione lyase activity	molecular_function
50590345	GO:0004082	bisphosphoglycerate mutase activity	molecular_function
50590345	GO:0004083	bisphosphoglycerate phosphatase activity	molecular_function
50590345	GO:0004619	phosphoglycerate mutase activity	molecular_function
50590345	GO:0042803	protein homodimerization activity	molecular_function
50590346	GO:0003985	acetyl-CoA C-acetyltransferase activity	molecular_function
50590347	GO:0004421	hydroxymethylglutaryl-CoA synthase activity	molecular_function
50590347	GO:0016829	lyase activity	molecular_function
50590348	GO:0004420	hydroxymethylglutaryl-CoA reductase (NADPH) activity	molecular_function
50590352	GO:0004289	subtilase activity	molecular_function
50590353	GO:0005554	molecular function unknown	molecular_function
50590354	GO:0000703	pyrimidine-specific oxidized base lesion DNA N-glycosylase activity	molecular_function
50590358	GO:0008781	N-acylneuraminate cytidylyltransferase activity	molecular_function
50590360	GO:0004396	hexokinase activity	molecular_function
50590360	GO:0005524	ATP binding	molecular_function
50590360	GO:0008761	UDP-N-acetylglucosamine 2-epimerase activity	molecular_function
50590360	GO:0009384	N-acylmannosamine kinase activity	molecular_function
50590361	GO:0008781	N-acylneuraminate cytidylyltransferase activity	molecular_function
50590361	GO:0019007	N-acetylneuraminic acid phosphate synthase activity	molecular_function
50590361	GO:0047444	N-acylneuraminate-9-phosphate synthase activity	molecular_function
50590361	GO:0050462	N-acetylneuraminate synthase activity	molecular_function
50590361	GO:0050825	ice binding	molecular_function
50590375	GO:0008324	cation transporter activity	molecular_function
50590375	GO:0015562	efflux permease activity	molecular_function
50590388	GO:0005524	ATP binding	molecular_function
50590388	GO:0015239	multidrug transporter activity	molecular_function
50590388	GO:0015646	permease activity	molecular_function
50590388	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590389	GO:0005524	ATP binding	molecular_function
50590389	GO:0015646	permease activity	molecular_function
50590389	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590391	GO:0004412	homoserine dehydrogenase activity	molecular_function
50590392	GO:0004413	homoserine kinase activity	molecular_function
50590396	GO:0030188	chaperone regulator activity	molecular_function
50590396	GO:0051087	chaperone binding	molecular_function
50590397	GO:0003697	single-stranded DNA binding	molecular_function
50590399	GO:0000049	tRNA binding	molecular_function
50590399	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
50590401	GO:0030508	thiol-disulfide exchange intermediate activity	molecular_function
50590403	GO:0004177	aminopeptidase activity	molecular_function

续表 1

gi	acc	name	term_type
50590404	GO:0004326	tetrahydrofolylpolyglutamate synthase activity	molecular_function
50590404	GO:0008841	dihydrofolate synthase activity	molecular_function
50590408	GO:0004088	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	molecular_function
50590409	GO:0004049	anthranilate synthase activity	molecular_function
50590409	GO:0004088	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	molecular_function
50590410	GO:0004049	anthranilate synthase activity	molecular_function
50590410	GO:0004070	aspartate carbamoyltransferase activity	molecular_function
50590410	GO:0004087	carbamoyl-phosphate synthase (ammonia) activity	molecular_function
50590410	GO:0004151	dihydroorotase activity	molecular_function
50590410	GO:0016597	amino acid binding	molecular_function
50590411	GO:0003729	mRNA binding	molecular_function
50590411	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
50590415	GO:0003735	structural constituent of ribosome	molecular_function
50590416	GO:0003743	translation initiation factor activity	molecular_function
50590417	GO:0004017	adenylate kinase activity	molecular_function
50590417	GO:0004765	shikimate kinase activity	molecular_function
50590417	GO:0005524	ATP binding	molecular_function
50590417	GO:0046899	nucleoside triphosphate adenylate kinase activity	molecular_function
50590418	GO:0015450	protein translocase activity	molecular_function
50590419	GO:0003735	structural constituent of ribosome	molecular_function
50590421	GO:0003735	structural constituent of ribosome	molecular_function
50590422	GO:0003735	structural constituent of ribosome	molecular_function
50590423	GO:0003735	structural constituent of ribosome	molecular_function
50590424	GO:0003735	structural constituent of ribosome	molecular_function
50590425	GO:0003735	structural constituent of ribosome	molecular_function
50590426	GO:0003735	structural constituent of ribosome	molecular_function
50590427	GO:0003735	structural constituent of ribosome	molecular_function
50590429	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
50590431	GO:0008080	N-acetyltransferase activity	molecular_function
50590432	GO:0005524	ATP binding	molecular_function
50590432	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590436	GO:0005386	carrier activity	molecular_function
50590436	GO:0008834	di-trans,poly-cis-decaprenylcistransferase activity	molecular_function
50590436	GO:0045547	dehydrodolichyl diphosphate synthase activity	molecular_function
50590437	GO:0004605	phosphatidate cytidylyltransferase activity	molecular_function
50590438	GO:0004222	metalloendopeptidase activity	molecular_function
50590439	GO:0004827	proline-tRNA ligase activity	molecular_function
50590440	GO:0005275	amine transporter activity	molecular_function
50590440	GO:0005345	purine transporter activity	molecular_function
50590440	GO:0005350	pyrimidine transporter activity	molecular_function
50590440	GO:0015250	water channel activity	molecular_function
50590440	GO:0015254	glycerol channel activity	molecular_function
50590440	GO:0015288	porin activity	molecular_function
50590440	GO:0046943	carboxylic acid transporter activity	molecular_function
50590442	GO:0004371	glycerone kinase activity	molecular_function
50590443	GO:0004371	glycerone kinase activity	molecular_function

续表 1

gi	acc	name	term_type
50590445	GO:0015423	maltose-transporting ATPase activity	molecular_function
50590448	GO:0004817	cysteine-tRNA ligase activity	molecular_function
50590451	GO:0009001	serine O-acetyltransferase activity	molecular_function
50590452	GO:0003729	mRNA binding	molecular_function
50590452	GO:0004654	polyribonucleotide nucleotidyltransferase activity	molecular_function
50590454	GO:0015036	disulfide oxidoreductase activity	molecular_function
50590455	GO:0004730	pseudouridylate synthase activity	molecular_function
50590458	GO:0008565	protein transporter activity	molecular_function
50590460	GO:0015646	permease activity	molecular_function
50590462	GO:0004798	thymidylate kinase activity	molecular_function
50590463	GO:0003891	delta DNA polymerase activity	molecular_function
50590465	GO:0008168	methyltransferase activity	molecular_function
50590466	GO:0004648	phosphoserine transaminase activity	molecular_function
50590468	GO:0004617	phosphoglycerate dehydrogenase activity	molecular_function
50590468	GO:0016597	amino acid binding	molecular_function
50590468	GO:0016726	oxidoreductase activity, acting on CH2 groups, NAD or NADP as acceptor	molecular_function
50590469	GO:0003908	methylated-DNA-[protein]-cysteine S-methyltransferase activity	molecular_function
50590479	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
50590482	GO:0003977	UDP-N-acetylglucosamine diphosphorylase activity	molecular_function
50590485	GO:0008782	adenosylhomocysteine nucleosidase activity	molecular_function
50590485	GO:0008930	methylthioadenosine nucleosidase activity	molecular_function
50590489	GO:0015249	nonselective channel activity	molecular_function
50590491	GO:0004523	ribonuclease H activity	molecular_function
50590492	GO:0005525	GTP binding	molecular_function
50590494	GO:0005554	molecular function unknown	molecular_function
50590494	GO:0017096	acetylserotonin O-methyltransferase activity	molecular_function
50590495	GO:0008198	ferrous iron binding	molecular_function
50590495	GO:0008253	5'-nucleotidase activity	molecular_function
50590495	GO:0019204	nucleotide phosphatase activity	molecular_function
50590496	GO:0000166	nucleotide binding	molecular_function
50590496	GO:0008198	ferrous iron binding	molecular_function
50590496	GO:0008253	5'-nucleotidase activity	molecular_function
50590497	GO:0004151	dihydroorotase activity	molecular_function
50590501	GO:0004176	ATP-dependent peptidase activity	molecular_function
50590501	GO:0004386	helicase activity	molecular_function
50590501	GO:0005524	ATP binding	molecular_function
50590501	GO:0016887	ATPase activity	molecular_function
50590502	GO:0008998	ribonucleoside-triphosphate reductase activity	molecular_function
50590504	GO:0008081	phosphoric diester hydrolase activity	molecular_function
50590504	GO:0008198	ferrous iron binding	molecular_function
50590504	GO:0008253	5'-nucleotidase activity	molecular_function
50590504	GO:0016827	hydrolase activity, acting on acid carbon-phosphorus bonds	molecular_function
50590504	GO:0019204	nucleotide phosphatase activity	molecular_function
50590505	GO:0008998	ribonucleoside-triphosphate reductase activity	molecular_function
50590518	GO:0017068	glutamyl-tRNA(Gln) amidotransferase activity	molecular_function
50590519	GO:0017068	glutamyl-tRNA(Gln) amidotransferase activity	molecular_function

续表 1

gi	acc	name	term_type
50590521	GO:0030528	transcription regulator activity	molecular_function
50590522	GO:0004335	galactokinase activity	molecular_function
50590522	GO:0004396	hexokinase activity	molecular_function
50590522	GO:0005524	ATP binding	molecular_function
50590526	GO:0008233	peptidase activity	molecular_function
50590527	GO:0008233	peptidase activity	molecular_function
50590529	GO:0030528	transcription regulator activity	molecular_function
50590535	GO:0004329	formate-tetrahydrofolate ligase activity	molecular_function
50590535	GO:0004477	methenyltetrahydrofolate cyclohydrolase activity	molecular_function
50590535	GO:0004488	methylenetetrahydrofolate dehydrogenase (NADP+) activity	molecular_function
50590538	GO:0005375	copper ion transporter activity	molecular_function
50590538	GO:0005524	ATP binding	molecular_function
50590538	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590541	GO:0030528	transcription regulator activity	molecular_function
50590542	GO:0008080	N-acetyltransferase activity	molecular_function
50590543	GO:0005554	molecular function unknown	molecular_function
50590546	GO:0004803	transposase activity	molecular_function
50590552	GO:0005199	structural constituent of cell wall	molecular_function
50590552	GO:0008599	protein phosphatase type 1 regulator activity	molecular_function
50590555	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
50590569	GO:0005554	molecular function unknown	molecular_function
50590572	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50590574	GO:0003735	structural constituent of ribosome	molecular_function
50590577	GO:0005525	GTP binding	molecular_function
50590578	GO:0008534	purine-specific oxidized base lesion DNA N-glycosylase activity	molecular_function
50590579	GO:0004140	dephospho-CoA kinase activity	molecular_function
50590579	GO:0004595	pantetheine-phosphate adenylyltransferase activity	molecular_function
50590579	GO:0004849	uridine kinase activity	molecular_function
50590579	GO:0005524	ATP binding	molecular_function
50590580	GO:0005215	transporter activity	molecular_function
50590582	GO:0008997	ribonuclease R activity	molecular_function
50590583	GO:0003723	RNA binding	molecular_function
50590584	GO:0004327	formaldehyde dehydrogenase (glutathione) activity	molecular_function
50590586	GO:0008943	glyceraldehyde-3-phosphate dehydrogenase activity	molecular_function
50590587	GO:0004618	phosphoglycerate kinase activity	molecular_function
50590587	GO:0004689	phosphorylase kinase activity	molecular_function
50590587	GO:0004807	triose-phosphate isomerase activity	molecular_function
50590590	GO:0004356	glutamate-ammonia ligase activity	molecular_function
50590594	GO:0008999	ribosomal-protein-alanine N-acetyltransferase activity	molecular_function
50590596	GO:0000287	magnesium ion binding	molecular_function
50590596	GO:0004743	pyruvate kinase activity	molecular_function
50590604	GO:0003735	structural constituent of ribosome	molecular_function
50590605	GO:0003735	structural constituent of ribosome	molecular_function
50590608	GO:0005199	structural constituent of cell wall	molecular_function
50590609	GO:0004564	beta-fructofuranosidase activity	molecular_function
50590611	GO:0015646	permease activity	molecular_function

续表 1

gi	acc	name	term_type
50590612	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
50590612	GO:0015646	permease activity	molecular_function
50590614	GO:0005524	ATP binding	molecular_function
50590614	GO:0015646	permease activity	molecular_function
50590614	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590615	GO:0004452	isopentenyl-diphosphate delta-isomerase activity	molecular_function
50590616	GO:0004631	phosphomevalonate kinase activity	molecular_function
50590617	GO:0004163	diphosphomevalonate decarboxylase activity	molecular_function
50590617	GO:0005524	ATP binding	molecular_function
50590617	GO:0016301	kinase activity	molecular_function
50590618	GO:0004496	mevalonate kinase activity	molecular_function
50590619	GO:0015559	multidrug efflux pump activity	molecular_function
50590620	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590624	GO:0005524	ATP binding	molecular_function
50590624	GO:0015646	permease activity	molecular_function
50590624	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590625	GO:0000155	two-component sensor molecule activity	molecular_function
50590625	GO:0000156	two-component response regulator activity	molecular_function
50590626	GO:0000156	two-component response regulator activity	molecular_function
50590628	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
50590628	GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity	molecular_function
50590630	GO:0005275	amine transporter activity	molecular_function
50590630	GO:0015418	quaternary-ammonium-compound-transporting ATPase activity	molecular_function
50590630	GO:0043176	amine binding	molecular_function
50590631	GO:0005524	ATP binding	molecular_function
50590631	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590636	GO:0004019	adenylosuccinate synthase activity	molecular_function
50590637	GO:0004357	glutamate-cysteine ligase activity	molecular_function
50590641	GO:0017150	tRNA dihydrouridine synthase activity	molecular_function
50590649	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50590650	GO:0003954	NADH dehydrogenase activity	molecular_function
50590650	GO:0015036	disulfide oxidoreductase activity	molecular_function
50590652	GO:0004222	metalloendopeptidase activity	molecular_function
50590660	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
50590661	GO:0004815	aspartate-tRNA ligase activity	molecular_function
50590661	GO:0004824	lysine-tRNA ligase activity	molecular_function
50590667	GO:0005215	transporter activity	molecular_function
50590668	GO:0003919	FMN adenylyltransferase activity	molecular_function
50590668	GO:0008531	riboflavin kinase activity	molecular_function
50590669	GO:0004730	pseudouridylate synthase activity	molecular_function
50590676	GO:0016787	hydrolase activity	molecular_function
50590677	GO:0045148	tripeptide aminopeptidase activity	molecular_function
50590680	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
50590688	GO:0004069	aspartate transaminase activity	molecular_function
50590688	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
50590689	GO:0003676	nucleic acid binding	molecular_function

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gi	acc	name	term_type
50590689	GO:0004815	aspartate-tRNA ligase activity	molecular_function
50590689	GO:0004816	asparagine-tRNA ligase activity	molecular_function
50590689	GO:0005524	ATP binding	molecular_function
50590692	GO:0008413	8-oxo-7,8-dihydroguanine triphosphatase activity	molecular_function
50590693	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
50590693	GO:0005524	ATP binding	molecular_function
50590694	GO:0004832	valine-tRNA ligase activity	molecular_function
50590716	GO:0008081	phosphoric diester hydrolase activity	molecular_function
50590716	GO:0008198	ferrous iron binding	molecular_function
50590716	GO:0008253	5'-nucleotidase activity	molecular_function
50590716	GO:0019204	nucleotide phosphatase activity	molecular_function
50590719	GO:0009002	serine-type D-Ala-D-Ala carboxypeptidase activity	molecular_function
50590722	GO:0004123	cystathionine gamma-lyase activity	molecular_function
50590722	GO:0008483	transaminase activity	molecular_function
50590722	GO:0009000	selenocysteine lyase activity	molecular_function
50590724	GO:0004009	ATP-binding cassette (ABC) transporter activity	molecular_function
50590724	GO:0005524	ATP binding	molecular_function
50590724	GO:0016887	ATPase activity	molecular_function
50590725	GO:0008963	phospho-N-acetylmuramoyl-pentapeptide-transferase activity	molecular_function
50590725	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
50590727	GO:0009038	undecaprenol kinase activity	molecular_function
50590730	GO:0005554	molecular function unknown	molecular_function
50590731	GO:0005381	iron ion transporter activity	molecular_function
50590731	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590734	GO:0004516	nicotinate phosphoribosyltransferase activity	molecular_function
50590735	GO:0003952	NAD+ synthase (glutamine-hydrolyzing) activity	molecular_function
50590735	GO:0008795	NAD+ synthase activity	molecular_function
50590737	GO:0005554	molecular function unknown	molecular_function
50590741	GO:0008509	anion transporter activity	molecular_function
50590749	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50590756	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
50590757	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
50590758	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
50590758	GO:0004075	biotin carboxylase activity	molecular_function
50590759	GO:0008693	3-hydroxydecanoyl-[acyl-carrier protein] dehydratase activity	molecular_function
50590760	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
50590760	GO:0009374	biotin binding	molecular_function
50590761	GO:0004315	3-oxoacyl-[acyl-carrier protein] synthase activity	molecular_function
50590762	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
50590763	GO:0004314	[acyl-carrier protein] S-malonyltransferase activity	molecular_function
50590764	GO:0004318	enoyl-[acyl-carrier protein] reductase (NADH) activity	molecular_function
50590766	GO:0004315	3-oxoacyl-[acyl-carrier protein] synthase activity	molecular_function
50590769	GO:0005554	molecular function unknown	molecular_function
50590772	GO:0016657	oxidoreductase activity, acting on NADH or NADPH, nitrogenous group as acceptor	molecular_function
50590773	GO:0005525	GTP binding	molecular_function
50590776	GO:0003677	DNA binding	molecular_function

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gi	acc	name	term_type
50590776	GO:0005524	ATP binding	molecular_function
50590776	GO:0008026	ATP-dependent helicase activity	molecular_function
50590776	GO:0008094	DNA-dependent ATPase activity	molecular_function
50590777	GO:0003677	DNA binding	molecular_function
50590777	GO:0003702	RNA polymerase II transcription factor activity	molecular_function
50590777	GO:0005524	ATP binding	molecular_function
50590777	GO:0008026	ATP-dependent helicase activity	molecular_function
50590777	GO:0042393	histone binding	molecular_function
50590779	GO:0008763	UDP-N-acetylmuramate-L-alanine ligase activity	molecular_function
50590783	GO:0004540	ribonuclease activity	molecular_function
50590784	GO:0004239	methionyl aminopeptidase activity	molecular_function
50590785	GO:0008080	N-acetyltransferase activity	molecular_function
50590786	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
50590788	GO:0000287	magnesium ion binding	molecular_function
50590788	GO:0004478	methionine adenosyltransferase activity	molecular_function
50590788	GO:0030955	potassium ion binding	molecular_function
50590789	GO:0004132	dCMP deaminase activity	molecular_function
50590789	GO:0008270	zinc ion binding	molecular_function
50590792	GO:0004077	biotin-[acetyl-CoA-carboxylase] ligase activity	molecular_function
50590792	GO:0030528	transcription regulator activity	molecular_function
50590798	GO:0003678	DNA helicase activity	molecular_function
50590799	GO:0004349	glutamate 5-kinase activity	molecular_function
50590800	GO:0004350	glutamate-5-semialdehyde dehydrogenase activity	molecular_function
50590801	GO:0004735	pyrroline-5-carboxylate reductase activity	molecular_function
50590804	GO:0008483	transaminase activity	molecular_function
50590804	GO:0030528	transcription regulator activity	molecular_function
50590807	GO:0004803	transposase activity	molecular_function
50590811	GO:0009035	type I site-specific deoxyribonuclease activity	molecular_function
50590815	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
50590816	GO:0004828	serine-tRNA ligase activity	molecular_function
50590821	GO:0003723	RNA binding	molecular_function
50590821	GO:0016788	hydrolase activity, acting on ester bonds	molecular_function
50590825	GO:0004476	mannose-6-phosphate isomerase activity	molecular_function
50590826	GO:0004647	phosphoserine phosphatase activity	molecular_function
50590826	GO:0004672	protein kinase activity	molecular_function
50590827	GO:0008961	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase activity	molecular_function
50590829	GO:0004300	enoyl-CoA hydratase activity	molecular_function
50590829	GO:0016508	long-chain-enoyl-CoA hydratase activity	molecular_function
50590831	GO:0004072	aspartate kinase activity	molecular_function
50590831	GO:0004412	homoserine dehydrogenase activity	molecular_function
50590831	GO:0016597	amino acid binding	molecular_function
50590832	GO:0008784	alanine racemase activity	molecular_function
50590834	GO:0015450	protein translocase activity	molecular_function
50590836	GO:0008865	fructokinase activity	molecular_function
50590839	GO:0005524	ATP binding	molecular_function
50590839	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function

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gi	acc	name	term_type
50590842	GO:0005554	molecular function unknown	molecular_function
50590843	GO:0004252	serine-type endopeptidase activity	molecular_function
50590844	GO:0003677	DNA binding	molecular_function
50590845	GO:0003688	DNA replication origin binding	molecular_function
50590846	GO:0003890	beta DNA polymerase activity	molecular_function
50590850	GO:0003978	UDP-glucose 4-epimerase activity	molecular_function
50590850	GO:0004034	aldose 1-epimerase activity	molecular_function
50590852	GO:0015589	mannose permease activity	molecular_function
50590853	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50590854	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50590855	GO:0004565	beta-galactosidase activity	molecular_function
50590855	GO:0005529	sugar binding	molecular_function
50590856	GO:0030528	transcription regulator activity	molecular_function
50590857	GO:0030528	transcription regulator activity	molecular_function
50590861	GO:0003723	RNA binding	molecular_function
50590861	GO:0008175	tRNA methyltransferase activity	molecular_function
50590861	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function
50590872	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
50590891	GO:0004124	cysteine synthase activity	molecular_function
50590893	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
50590893	GO:0005328	neurotransmitter:sodium symporter activity	molecular_function
50590895	GO:0000155	two-component sensor molecule activity	molecular_function
50590899	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
50590900	GO:0016566	specific transcriptional repressor activity	molecular_function
50590901	GO:0000774	adenyl-nucleotide exchange factor activity	molecular_function
50590901	GO:0005515	protein binding	molecular_function
50590901	GO:0030192	Hsp70/Hsc70 protein regulator activity	molecular_function
50590902	GO:0005515	protein binding	molecular_function
50590903	GO:0005515	protein binding	molecular_function
50590905	GO:0017064	fatty acid amide hydrolase activity	molecular_function
50590906	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50590907	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50590907	GO:0015646	permease activity	molecular_function
50590912	GO:0005375	copper ion transporter activity	molecular_function
50590912	GO:0015434	cadmium-transporting ATPase activity	molecular_function
50590912	GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	molecular_function
50590930	GO:0003954	NADH dehydrogenase activity	molecular_function
50590930	GO:0015036	disulfide oxidoreductase activity	molecular_function
50590931	GO:0004161	dimethylallyltranstransferase activity	molecular_function
50590934	GO:0004659	prenyltransferase activity	molecular_function
50590941	GO:0008168	methyltransferase activity	molecular_function
50590944	GO:0008963	phospho-N-acetylmuramoyl-pentapeptide-transferase activity	molecular_function
50590950	GO:0005554	molecular function unknown	molecular_function
50590951	GO:0005515	protein binding	molecular_function
50590954	GO:0003924	GTPase activity	molecular_function

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gi	acc	name	term_type
50590954	GO:0005525	GTP binding	molecular_function
50590954	GO:0008175	tRNA methyltransferase activity	molecular_function
50590961	GO:0015423	maltose-transporting ATPase activity	molecular_function
50590962	GO:0005351	sugar porter activity	molecular_function
50590962	GO:0015423	maltose-transporting ATPase activity	molecular_function
50590963	GO:0005351	sugar porter activity	molecular_function
50590966	GO:0004133	glycogen debranching enzyme activity	molecular_function
50590966	GO:0004556	alpha-amylase activity	molecular_function
50590968	GO:0005554	molecular function unknown	molecular_function
50590969	GO:0004815	aspartate-tRNA ligase activity	molecular_function
50590970	GO:0008080	N-acetyltransferase activity	molecular_function
50590971	GO:0005249	voltage-gated potassium channel activity	molecular_function
50590971	GO:0015459	potassium channel regulator activity	molecular_function
50590971	GO:0016491	oxidoreductase activity	molecular_function
50590971	GO:0030955	potassium ion binding	molecular_function
50590973	GO:0004722	protein serine/threonine phosphatase activity	molecular_function
50590976	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
50590977	GO:0004558	alpha-glucosidase activity	molecular_function
50590977	GO:0004574	oligo-1,6-glucosidase activity	molecular_function
50590977	GO:0008788	alpha,alpha-phosphotrehalase activity	molecular_function
50590978	GO:0009018	sucrose phosphorylase activity	molecular_function
50590979	GO:0015646	permease activity	molecular_function
50590980	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
50590980	GO:0015646	permease activity	molecular_function
50590983	GO:0030528	transcription regulator activity	molecular_function
50590984	GO:0008483	transaminase activity	molecular_function
50590985	GO:0004121	cystathionine beta-lyase activity	molecular_function
50590985	GO:0004123	cystathionine gamma-lyase activity	molecular_function
50590990	GO:0004073	aspartate-semialdehyde dehydrogenase activity	molecular_function
50590991	GO:0008840	dihydrodipicolinate synthase activity	molecular_function
50590992	GO:0004803	transposase activity	molecular_function
50590994	GO:0004730	pseudouridylate synthase activity	molecular_function
50590997	GO:0008463	formylmethionine deformylase activity	molecular_function
50590997	GO:0042586	peptide deformylase activity	molecular_function
50590999	GO:0003861	3-isopropylmalate dehydratase activity	molecular_function
50591000	GO:0003861	3-isopropylmalate dehydratase activity	molecular_function
50591001	GO:0003862	3-isopropylmalate dehydrogenase activity	molecular_function
50591002	GO:0003862	3-isopropylmalate dehydrogenase activity	molecular_function
50591003	GO:0003852	2-isopropylmalate synthase activity	molecular_function
50591007	GO:0008770	[acyl-carrier protein] phosphodiesterase activity	molecular_function
50591009	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
50591013	GO:0008670	2,4-dienoyl-CoA reductase (NADPH) activity	molecular_function
50591014	GO:0004090	carbonyl reductase (NADPH) activity	molecular_function
50591014	GO:0004745	retinol dehydrogenase activity	molecular_function
50591015	GO:0016298	lipase activity	molecular_function
50591016	GO:0003960	NADPH:quinone reductase activity	molecular_function

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gi	acc	name	term_type
50591016	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
50591016	GO:0008270	zinc ion binding	molecular_function
50591021	GO:0004789	thiamin-phosphate diphosphorylase activity	molecular_function
50591021	GO:0008972	phosphomethylpyrimidine kinase activity	molecular_function
50591022	GO:0004730	pseudouridylate synthase activity	molecular_function
50591022	GO:0016439	tRNA-pseudouridine synthase activity	molecular_function
50591023	GO:0016564	transcriptional repressor activity	molecular_function
50591025	GO:0000287	magnesium ion binding	molecular_function
50591025	GO:0003872	6-phosphofructokinase activity	molecular_function
50591025	GO:0004331	fructose-2,6-bisphosphate 2-phosphatase activity	molecular_function
50591025	GO:0005524	ATP binding	molecular_function
50591026	GO:0003889	alpha DNA polymerase activity	molecular_function
50591027	GO:0030528	transcription regulator activity	molecular_function
50591028	GO:0005524	ATP binding	molecular_function
50591028	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591030	GO:0000034	adenine deaminase activity	molecular_function
50591030	GO:0004000	adenosine deaminase activity	molecular_function
50591032	GO:0004803	transposase activity	molecular_function
50591033	GO:0004803	transposase activity	molecular_function
50591035	GO:0016987	sigma factor activity	molecular_function
50591036	GO:0003896	DNA primase activity	molecular_function
50591039	GO:0004556	alpha-amylase activity	molecular_function
50591042	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591047	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591049	GO:0004802	transketolase activity	molecular_function
50591051	GO:0005525	GTP binding	molecular_function
50591054	GO:0008233	peptidase activity	molecular_function
50591060	GO:0004427	inorganic diphosphatase activity	molecular_function
50591065	GO:0016413	O-acetyltransferase activity	molecular_function
50591065	GO:0042944	D-alanine transporter activity	molecular_function
50591066	GO:0016208	AMP binding	molecular_function
50591073	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
50591074	GO:0005199	structural constituent of cell wall	molecular_function
50591076	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591077	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591078	GO:0015599	glutamine-importing ATPase activity	molecular_function
50591078	GO:0015646	permease activity	molecular_function
50591079	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591079	GO:0016597	amino acid binding	molecular_function
50591081	GO:0015582	beta-glucoside permease activity	molecular_function
50591081	GO:0019190	cellobiose permease activity	molecular_function
50591083	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591084	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591084	GO:0015573	beta-glucoside transporter activity	molecular_function
50591085	GO:0005554	molecular function unknown	molecular_function
50591085	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function

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gi	acc	name	term_type
50591087	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
50591089	GO:0004823	leucine-tRNA ligase activity	molecular_function
50591090	GO:0004245	neprilysin activity	molecular_function
50591090	GO:0008270	zinc ion binding	molecular_function
50591090	GO:0016512	endothelin-converting enzyme 1 activity	molecular_function
50591093	GO:0008965	phosphoenolpyruvate-protein phosphotransferase activity	molecular_function
50591093	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591095	GO:0004450	isocitrate dehydrogenase (NADP+) activity	molecular_function
50591096	GO:0004108	citrate (Si)-synthase activity	molecular_function
50591096	GO:0016833	oxo-acid-lyase activity	molecular_function
50591097	GO:0003994	aconitate hydratase activity	molecular_function
50591097	GO:0005506	iron ion binding	molecular_function
50591097	GO:0030350	iron-responsive element binding	molecular_function
50591099	GO:0004748	ribonucleoside-diphosphate reductase activity	molecular_function
50591100	GO:0004748	ribonucleoside-diphosphate reductase activity	molecular_function
50591101	GO:0030528	transcription regulator activity	molecular_function
50591104	GO:0003743	translation initiation factor activity	molecular_function
50591105	GO:0004127	cytidylate kinase activity	molecular_function
50591111	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
50591117	GO:0005524	ATP binding	molecular_function
50591117	GO:0015162	teichoic acid transporter activity	molecular_function
50591117	GO:0015437	lipopolysaccharide-transporting ATPase activity	molecular_function
50591118	GO:0015162	teichoic acid transporter activity	molecular_function
50591118	GO:0015646	permease activity	molecular_function
50591118	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591122	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	molecular_function
50591122	GO:0004522	pancreatic ribonuclease activity	molecular_function
50591125	GO:0000287	magnesium ion binding	molecular_function
50591125	GO:0005338	nucleotide-sugar transporter activity	molecular_function
50591125	GO:0005388	calcium-transporting ATPase activity	molecular_function
50591125	GO:0005509	calcium ion binding	molecular_function
50591125	GO:0005524	ATP binding	molecular_function
50591125	GO:0015410	manganese-transporting ATPase activity	molecular_function
50591125	GO:0015562	efflux permease activity	molecular_function
50591127	GO:0008767	UDP-galactopyranose mutase activity	molecular_function
50591129	GO:0009009	site-specific recombinase activity	molecular_function
50591131	GO:0004034	aldose 1-epimerase activity	molecular_function
50591132	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
50591133	GO:0015582	beta-glucoside permease activity	molecular_function
50591133	GO:0019190	cellobiose permease activity	molecular_function
50591137	GO:0004813	alanine-tRNA ligase activity	molecular_function
50591139	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
50591140	GO:0008171	O-methyltransferase activity	molecular_function
50591143	GO:0004222	metalloendopeptidase activity	molecular_function
50591146	GO:0004825	methionine-tRNA ligase activity	molecular_function
50591146	GO:0005524	ATP binding	molecular_function

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gi	acc	name	term_type
50591148	GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	molecular_function
50591149	GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	molecular_function
50591150	GO:0004764	shikimate 5-dehydrogenase activity	molecular_function
50591151	GO:0003856	3-dehydroquinate synthase activity	molecular_function
50591152	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591153	GO:0015646	permease activity	molecular_function
50591155	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
50591156	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
50591157	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
50591158	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
50591159	GO:0015582	beta-glucoside permease activity	molecular_function
50591159	GO:0019190	cellobiose permease activity	molecular_function
50591161	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591162	GO:0005554	molecular function unknown	molecular_function
50591162	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591166	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
50591168	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
50591169	GO:0030528	transcription regulator activity	molecular_function
50591172	GO:0004104	cholinesterase activity	molecular_function
50591172	GO:0004759	serine esterase activity	molecular_function
50591172	GO:0016290	palmitoyl-CoA hydrolase activity	molecular_function
50591173	GO:0015582	beta-glucoside permease activity	molecular_function
50591173	GO:0015584	trehalose permease activity	molecular_function
50591173	GO:0019188	sucrose permease (PTS) activity	molecular_function
50591176	GO:0016805	dipeptidase activity	molecular_function
50591177	GO:0015175	neutral amino acid transporter activity	molecular_function
50591177	GO:0015183	L-aspartate transporter activity	molecular_function
50591177	GO:0015295	solute:hydrogen symporter activity	molecular_function
50591177	GO:0017153	sodium:dicarboxylate symporter activity	molecular_function
50591178	GO:0017153	sodium:dicarboxylate symporter activity	molecular_function
50591180	GO:0005524	ATP binding	molecular_function
50591180	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591180	GO:0043023	ribosomal large subunit binding	molecular_function
50591180	GO:0043024	ribosomal small subunit binding	molecular_function
50591181	GO:0005524	ATP binding	molecular_function
50591181	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591182	GO:0004614	phosphoglucomutase activity	molecular_function
50591182	GO:0004615	phosphomannomutase activity	molecular_function
50591182	GO:0008966	phosphoglucosamine mutase activity	molecular_function
50591187	GO:0008989	rRNA (guanine-N1-)-methyltransferase activity	molecular_function
50591189	GO:0005524	ATP binding	molecular_function
50591189	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591196	GO:0004803	transposase activity	molecular_function
50591200	GO:0015559	multidrug efflux pump activity	molecular_function
50591202	GO:0009019	tRNA (guanine-N1-)-methyltransferase activity	molecular_function
50591203	GO:0004400	histidinol-phosphate transaminase activity	molecular_function

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gi	acc	name	term_type
50591204	GO:0030528	transcription regulator activity	molecular_function
50591205	GO:0008662	1-phosphofructokinase activity	molecular_function
50591206	GO:0015585	fructose permease activity	molecular_function
50591209	GO:0008839	dihydrodipicolinate reductase activity	molecular_function
50591210	GO:0000049	tRNA binding	molecular_function
50591210	GO:0004652	polynucleotide adenylyltransferase activity	molecular_function
50591210	GO:0004810	tRNA adenylyltransferase activity	molecular_function
50591211	GO:0005524	ATP binding	molecular_function
50591211	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591213	GO:0004340	glucokinase activity	molecular_function
50591214	GO:0004799	thymidylate synthase activity	molecular_function
50591215	GO:0004146	dihydrofolate reductase activity	molecular_function
50591216	GO:0004176	ATP-dependent peptidase activity	molecular_function
50591216	GO:0005524	ATP binding	molecular_function
50591216	GO:0008462	endopeptidase Clp activity	molecular_function
50591217	GO:0005525	GTP binding	molecular_function
50591218	GO:0000287	magnesium ion binding	molecular_function
50591218	GO:0004536	deoxyribonuclease activity	molecular_function
50591218	GO:0004550	nucleoside diphosphate kinase activity	molecular_function
50591218	GO:0005524	ATP binding	molecular_function
50591219	GO:0003746	translation elongation factor activity	molecular_function
50591219	GO:0005525	GTP binding	molecular_function
50591223	GO:0015559	multidrug efflux pump activity	molecular_function
50591224	GO:0004521	endoribonuclease activity	molecular_function
50591225	GO:0005554	molecular function unknown	molecular_function
50591230	GO:0016990	arginine deiminase activity	molecular_function
50591232	GO:0004070	aspartate carbamoyltransferase activity	molecular_function
50591232	GO:0004585	ornithine carbamoyltransferase activity	molecular_function
50591232	GO:0016597	amino acid binding	molecular_function
50591233	GO:0008804	carbamate kinase activity	molecular_function
50591235	GO:0016805	dipeptidase activity	molecular_function
50591238	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function
50591238	GO:0051075	S-adenosylmethionine:tRNA ribosyltransferase-isomerase activity	molecular_function
50591240	GO:0004342	glucosamine-6-phosphate deaminase activity	molecular_function
50591242	GO:0004156	dihydropteroate synthase activity	molecular_function
50591243	GO:0003934	GTP cyclohydrolase I activity	molecular_function
50591249	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
50591251	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
50591252	GO:0004563	beta-N-acetylhexosaminidase activity	molecular_function
50591254	GO:0004182	carboxypeptidase A activity	molecular_function
50591254	GO:0004563	beta-N-acetylhexosaminidase activity	molecular_function
50591254	GO:0008422	beta-glucosidase activity	molecular_function
50591256	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	molecular_function
50591259	GO:0008675	2-dehydro-3-deoxy-phosphogluconate aldolase activity	molecular_function
50591259	GO:0008700	4-hydroxy-2-oxoglutarate aldolase activity	molecular_function
50591260	GO:0003700	transcription factor activity	molecular_function

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gi	acc	name	term_type
50591261	GO:0004566	beta-glucuronidase activity	molecular_function
50591266	GO:0000156	two-component response regulator activity	molecular_function
50591267	GO:0000155	two-component sensor molecule activity	molecular_function
50591267	GO:0000156	two-component response regulator activity	molecular_function
50591270	GO:0004594	pantothenate kinase activity	molecular_function
50591270	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
50591270	GO:0004849	uridine kinase activity	molecular_function
50591270	GO:0005524	ATP binding	molecular_function
50591272	GO:0004645	phosphorylase activity	molecular_function
50591272	GO:0005161	platelet-derived growth factor receptor binding	molecular_function
50591272	GO:0009032	thymidine phosphorylase activity	molecular_function
50591272	GO:0016154	pyrimidine-nucleoside phosphorylase activity	molecular_function
50591273	GO:0004139	deoxyribose-phosphate aldolase activity	molecular_function
50591274	GO:0004126	cytidine deaminase activity	molecular_function
50591274	GO:0008270	zinc ion binding	molecular_function
50591277	GO:0015646	permease activity	molecular_function
50591278	GO:0015646	permease activity	molecular_function
50591283	GO:0008677	2-dehydropantoate 2-reductase activity	molecular_function
50591285	GO:0008135	translation factor activity, nucleic acid binding	molecular_function
50591286	GO:0009041	uridylate kinase activity	molecular_function
50591288	GO:0003735	structural constituent of ribosome	molecular_function
50591289	GO:0003899	DNA-directed RNA polymerase activity	molecular_function
50591290	GO:0003735	structural constituent of ribosome	molecular_function
50591292	GO:0003746	translation elongation factor activity	molecular_function
50591292	GO:0003747	translation release factor activity	molecular_function
50591292	GO:0005525	GTP binding	molecular_function
50591293	GO:0005388	calcium-transporting ATPase activity	molecular_function
50591293	GO:0008556	potassium-transporting ATPase activity	molecular_function
50591293	GO:0015444	magnesium-importing ATPase activity	molecular_function
50591293	GO:0015562	efflux permease activity	molecular_function
50591295	GO:0008766	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	molecular_function
50591295	GO:0047480	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase activity	molecular_function
50591296	GO:0005524	ATP binding	molecular_function
50591296	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591297	GO:0015646	permease activity	molecular_function
50591299	GO:0008716	D-alanine-D-alanine ligase activity	molecular_function
50591300	GO:0005554	molecular function unknown	molecular_function
50591302	GO:0005524	ATP binding	molecular_function
50591302	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591305	GO:0000155	two-component sensor molecule activity	molecular_function
50591306	GO:0000156	two-component response regulator activity	molecular_function
50591306	GO:0003677	DNA binding	molecular_function
50591314	GO:0008565	protein transporter activity	molecular_function
50591315	GO:0008565	protein transporter activity	molecular_function
50591318	GO:0003899	DNA-directed RNA polymerase activity	molecular_function

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gi	acc	name	term_type
50591320	GO:0008658	penicillin binding	molecular_function
50591321	GO:0004831	tyrosine-tRNA ligase activity	molecular_function
50591321	GO:0005524	ATP binding	molecular_function
50591325	GO:0005055	laminin receptor activity	molecular_function
50591325	GO:0030145	manganese ion binding	molecular_function
50591326	GO:0005384	manganese ion transporter activity	molecular_function
50591326	GO:0005385	zinc ion transporter activity	molecular_function
50591326	GO:0015646	permease activity	molecular_function
50591326	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591327	GO:0005524	ATP binding	molecular_function
50591327	GO:0015410	manganese-transporting ATPase activity	molecular_function
50591362	GO:0003697	single-stranded DNA binding	molecular_function
50591369	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
50591372	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
50591373	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
50591374	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
50591376	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
50591380	GO:0003911	DNA ligase (NAD+) activity	molecular_function
50591381	GO:0015646	permease activity	molecular_function
50591383	GO:0004345	glucose-6-phosphate 1-dehydrogenase activity	molecular_function
50591385	GO:0008080	N-acetyltransferase activity	molecular_function
50591386	GO:0003924	GTPase activity	molecular_function
50591386	GO:0005047	signal recognition particle binding	molecular_function
50591387	GO:0016787	hydrolase activity	molecular_function
50591388	GO:0016787	hydrolase activity	molecular_function
50591389	GO:0005524	ATP binding	molecular_function
50591389	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591390	GO:0004525	ribonuclease III activity	molecular_function
50591394	GO:0004084	branched-chain-amino-acid transaminase activity	molecular_function
50591396	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
50591400	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
50591401	GO:0005554	molecular function unknown	molecular_function
50591402	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50591403	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50591403	GO:0004527	exonuclease activity	molecular_function
50591407	GO:0005525	GTP binding	molecular_function
50591408	GO:0009381	excinuclease ABC activity	molecular_function
50591409	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591412	GO:0004180	carboxypeptidase activity	molecular_function
50591414	GO:0004811	tRNA isopentenyltransferase activity	molecular_function
50591415	GO:0005525	GTP binding	molecular_function
50591417	GO:0004519	endonuclease activity	molecular_function
50591418	GO:0004303	estradiol 17-beta-dehydrogenase activity	molecular_function
50591418	GO:0004745	retinol dehydrogenase activity	molecular_function
50591418	GO:0050327	testosterone 17-beta-dehydrogenase activity	molecular_function
50591420	GO:0008808	cardiolipin synthase activity	molecular_function

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gi	acc	name	term_type
50591421	GO:0008297	single-stranded DNA specific exodeoxyribonuclease activity	molecular_function
50591423	GO:0003999	adenine phosphoribosyltransferase activity	molecular_function
50591424	GO:0008899	homoserine O-succinyltransferase activity	molecular_function
50591427	GO:0005554	molecular function unknown	molecular_function
50591428	GO:0046873	metal ion transporter activity	molecular_function
50591429	GO:0008879	glucose-1-phosphate thymidylyltransferase activity	molecular_function
50591430	GO:0008830	dTDP-4-dehydrorhamnose 3,5-epimerase activity	molecular_function
50591432	GO:0008460	dTDP-glucose 4,6-dehydratase activity	molecular_function
50591433	GO:0008831	dTDP-4-dehydrorhamnose reductase activity	molecular_function
50591435	GO:0008745	N-acetylmuramoyl-L-alanine amidase activity	molecular_function
50591436	GO:0004040	amidase activity	molecular_function
50591436	GO:0008745	N-acetylmuramoyl-L-alanine amidase activity	molecular_function
50591442	GO:0004008	copper-exporting ATPase activity	molecular_function
50591442	GO:0005507	copper ion binding	molecular_function
50591443	GO:0009031	thiol peroxidase activity	molecular_function
50591445	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591446	GO:0015646	permease activity	molecular_function
50591448	GO:0004803	transposase activity	molecular_function
50591450	GO:0003887	DNA-directed DNA polymerase activity	molecular_function
50591450	GO:0008408	3'-5' exonuclease activity	molecular_function
50591450	GO:0008409	5'-3' exonuclease activity	molecular_function
50591454	GO:0008479	queuine tRNA-ribosyltransferase activity	molecular_function
50591455	GO:0004251	X-Pro dipeptidase activity	molecular_function
50591456	GO:0030528	transcription regulator activity	molecular_function
50591457	GO:0005524	ATP binding	molecular_function
50591457	GO:0009982	pseudouridine synthase activity	molecular_function
50591459	GO:0046510	UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity	molecular_function
50591462	GO:0004829	threonine-tRNA ligase activity	molecular_function
50591463	GO:0015599	glutamine-importing ATPase activity	molecular_function
50591465	GO:0004634	phosphopyruvate hydratase activity	molecular_function
50591469	GO:0005554	molecular function unknown	molecular_function
50591469	GO:0015646	permease activity	molecular_function
50591471	GO:0047605	acetolactate decarboxylase activity	molecular_function
50591473	GO:0016563	transcriptional activator activity	molecular_function
50591473	GO:0030401	transcription antiterminator activity	molecular_function
50591474	GO:0015582	beta-glucoside permease activity	molecular_function
50591474	GO:0015584	trehalose permease activity	molecular_function
50591475	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
50591476	GO:0005554	molecular function unknown	molecular_function
50591477	GO:0015646	permease activity	molecular_function
50591478	GO:0015417	polyamine-transporting ATPase activity	molecular_function
50591481	GO:0004803	transposase activity	molecular_function
50591494	GO:0009008	DNA-methyltransferase activity	molecular_function
50591504	GO:0004749	ribose phosphate diphosphokinase activity	molecular_function
50591505	GO:0004069	aspartate transaminase activity	molecular_function
50591505	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function

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gi	acc	name	term_type
50591507	GO:0003824	catalytic activity	molecular_function
50591509	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
50591509	GO:0004639	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	molecular_function
50591510	GO:0004642	phosphoribosylformylglycinamidine synthase activity	molecular_function
50591511	GO:0000287	magnesium ion binding	molecular_function
50591511	GO:0004044	amidophosphoribosyltransferase activity	molecular_function
50591512	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
50591512	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
50591512	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
50591513	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
50591513	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
50591513	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
50591514	GO:0003937	IMP cyclohydrolase activity	molecular_function
50591514	GO:0004643	phosphoribosylaminoimidazolecarboxamide formyltransferase activity	molecular_function
50591515	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
50591519	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
50591519	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
50591519	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
50591520	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
50591521	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
50591523	GO:0004018	adenylosuccinate lyase activity	molecular_function
50591523	GO:0018842	3-carboxymuconate cycloisomerase type II activity	molecular_function
50591524	GO:0005524	ATP binding	molecular_function
50591524	GO:0043212	carbohydrate-exporting ATPase activity	molecular_function
50591529	GO:0005524	ATP binding	molecular_function
50591529	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591531	GO:0005524	ATP binding	molecular_function
50591531	GO:0015646	permease activity	molecular_function
50591531	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591532	GO:0009378	Holliday junction helicase activity	molecular_function
50591538	GO:0003964	RNA-directed DNA polymerase activity	molecular_function
50591538	GO:0004519	endonuclease activity	molecular_function
50591555	GO:0009008	DNA-methyltransferase activity	molecular_function
50591557	GO:0008649	rRNA methyltransferase activity	molecular_function
50591557	GO:0030696	tRNA (m5U54) methyltransferase activity	molecular_function
50591559	GO:0004106	chorismate mutase activity	molecular_function
50591559	GO:0004664	prephenate dehydratase activity	molecular_function
50591560	GO:0004765	shikimate kinase activity	molecular_function
50591561	GO:0003866	3-phosphoshikimate 1-carboxyvinyltransferase activity	molecular_function
50591561	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
50591570	GO:0015646	permease activity	molecular_function
50591576	GO:0003682	chromatin binding	molecular_function
50591576	GO:0008026	ATP-dependent helicase activity	molecular_function
50591591	GO:0030528	transcription regulator activity	molecular_function
50591592	GO:0004340	glucokinase activity	molecular_function
50591593	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function

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gi	acc	name	term_type
50591594	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
50591597	GO:0008484	sulfuric ester hydrolase activity	molecular_function
50591598	GO:0005554	molecular function unknown	molecular_function
50591598	GO:0008168	methyltransferase activity	molecular_function
50591599	GO:0003855	3-dehydroquinate dehydratase activity	molecular_function
50591600	GO:0004107	chorismate synthase activity	molecular_function
50591601	GO:0008977	prephenate dehydrogenase activity	molecular_function
50591607	GO:0004069	aspartate transaminase activity	molecular_function
50591607	GO:0004838	tyrosine transaminase activity	molecular_function
50591607	GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity	molecular_function
50591608	GO:0003677	DNA binding	molecular_function
50591610	GO:0016787	hydrolase activity	molecular_function
50591611	GO:0004067	asparaginase activity	molecular_function
50591613	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50591616	GO:0004176	ATP-dependent peptidase activity	molecular_function
50591616	GO:0004222	metalloendopeptidase activity	molecular_function
50591616	GO:0016887	ATPase activity	molecular_function
50591617	GO:0000287	magnesium ion binding	molecular_function
50591617	GO:0004422	hypoxanthine phosphoribosyltransferase activity	molecular_function
50591618	GO:0004422	hypoxanthine phosphoribosyltransferase activity	molecular_function
50591618	GO:0016879	ligase activity, forming carbon-nitrogen bonds	molecular_function
50591622	GO:0003690	double-stranded DNA binding	molecular_function
50591622	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
50591622	GO:0005515	protein binding	molecular_function
50591622	GO:0005524	ATP binding	molecular_function
50591623	GO:0004045	aminoacyl-tRNA hydrolase activity	molecular_function
50591624	GO:0005525	GTP binding	molecular_function
50591628	GO:0015174	basic amino acid transporter activity	molecular_function
50591628	GO:0015326	cationic amino acid transporter activity	molecular_function
50591628	GO:0015359	amino acid permease activity	molecular_function
50591640	GO:0004614	phosphoglucomutase activity	molecular_function
50591640	GO:0004615	phosphomannomutase activity	molecular_function
50591642	GO:0004632	phosphopantothenate-cysteine ligase activity	molecular_function
50591642	GO:0004633	phosphopantothenoylcysteine decarboxylase activity	molecular_function
50591642	GO:0009055	electron carrier activity	molecular_function
50591643	GO:0004632	phosphopantothenate-cysteine ligase activity	molecular_function
50591643	GO:0004633	phosphopantothenoylcysteine decarboxylase activity	molecular_function
50591643	GO:0009055	electron carrier activity	molecular_function
50591644	GO:0004329	formate-tetrahydrofolate ligase activity	molecular_function
50591647	GO:0004148	dihydrolipoyl dehydrogenase activity	molecular_function
50591647	GO:0004375	glycine dehydrogenase (decarboxylating) activity	molecular_function
50591647	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	molecular_function
50591647	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
50591653	GO:0008862	formate acetyltransferase activating enzyme activity	molecular_function
50591654	GO:0030528	transcription regulator activity	molecular_function
50591655	GO:0016564	transcriptional repressor activity	molecular_function

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gi	acc	name	term_type
50591657	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591657	GO:0015573	beta-glucoside transporter activity	molecular_function
50591658	GO:0015582	beta-glucoside permease activity	molecular_function
50591658	GO:0019190	cellobiose permease activity	molecular_function
50591659	GO:0008861	formate C-acetyltransferase activity	molecular_function
50591660	GO:0004801	transaldolase activity	molecular_function
50591664	GO:0004803	transposase activity	molecular_function
50591665	GO:0004822	isoleucine-tRNA ligase activity	molecular_function
50591671	GO:0008784	alanine racemase activity	molecular_function
50591671	GO:0030170	pyridoxal phosphate binding	molecular_function
50591672	GO:0003924	GTPase activity	molecular_function
50591672	GO:0005198	structural molecule activity	molecular_function
50591674	GO:0004797	thymidine kinase activity	molecular_function
50591675	GO:0003747	translation release factor activity	molecular_function
50591676	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
50591680	GO:0004372	glycine hydroxymethyltransferase activity	molecular_function
50591683	GO:0016491	oxidoreductase activity	molecular_function
50591690	GO:0003922	GMP synthase (glutamine-hydrolyzing) activity	molecular_function
50591691	GO:0016566	specific transcriptional repressor activity	molecular_function
50591693	GO:0003924	GTPase activity	molecular_function
50591693	GO:0005048	signal sequence binding	molecular_function
50591693	GO:0008312	7S RNA binding	molecular_function
50591697	GO:0008907	integrase activity	molecular_function
50591697	GO:0009009	site-specific recombinase activity	molecular_function
50591698	GO:0004614	phosphoglucomutase activity	molecular_function
50591698	GO:0004615	phosphomannomutase activity	molecular_function
50591699	GO:0000155	two-component sensor molecule activity	molecular_function
50591700	GO:0000156	two-component response regulator activity	molecular_function
50591703	GO:0015646	permease activity	molecular_function
50591704	GO:0005524	ATP binding	molecular_function
50591704	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591717	GO:0005524	ATP binding	molecular_function
50591732	GO:0000179	rRNA (adenine-N6,N6-)-dimethyltransferase activity	molecular_function
50591736	GO:0003677	DNA binding	molecular_function
50591742	GO:0003746	translation elongation factor activity	molecular_function
50591742	GO:0005525	GTP binding	molecular_function
50591749	GO:0015639	ferrous iron uptake transporter activity	molecular_function
50591750	GO:0015646	permease activity	molecular_function
50591751	GO:0005524	ATP binding	molecular_function
50591751	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591752	GO:0016149	translation release factor activity, codon specific	molecular_function
50591753	GO:0009055	electron carrier activity	molecular_function
50591759	GO:0003677	DNA binding	molecular_function
50591761	GO:0016298	lipase activity	molecular_function
50591763	GO:0005524	ATP binding	molecular_function
50591766	GO:0004311	farnesyltranstransferase activity	molecular_function

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gi	acc	name	term_type
50591766	GO:0004337	geranyltranstransferase activity	molecular_function
50591768	GO:0008855	exodeoxyribonuclease VII activity	molecular_function
50591773	GO:0000155	two-component sensor molecule activity	molecular_function
50591774	GO:0000156	two-component response regulator activity	molecular_function
50591774	GO:0003677	DNA binding	molecular_function
50591779	GO:0008463	formylmethionine deformylase activity	molecular_function
50591780	GO:0016887	ATPase activity	molecular_function
50591781	GO:0004134	4-alpha-glucanotransferase activity	molecular_function
50591782	GO:0008184	glycogen phosphorylase activity	molecular_function
50591782	GO:0030170	pyridoxal phosphate binding	molecular_function
50591783	GO:0016566	specific transcriptional repressor activity	molecular_function
50591785	GO:0015579	glucose permease activity	molecular_function
50591788	GO:0005554	molecular function unknown	molecular_function
50591792	GO:0005554	molecular function unknown	molecular_function
50591794	GO:0015087	cobalt ion transporter activity	molecular_function
50591794	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591795	GO:0015087	cobalt ion transporter activity	molecular_function
50591796	GO:0003677	DNA binding	molecular_function
50591797	GO:0005554	molecular function unknown	molecular_function
50591798	GO:0008658	penicillin binding	molecular_function
50591804	GO:0009369	quorum sensing signal generator activity	molecular_function
50591804	GO:0009370	quorum sensing response regulator activity	molecular_function
50591806	GO:0004385	guanylate kinase activity	molecular_function
50591808	GO:0003678	DNA helicase activity	molecular_function
50591808	GO:0003688	DNA replication origin binding	molecular_function
50591809	GO:0004479	methionyl-tRNA formyltransferase activity	molecular_function
50591810	GO:0016434	rRNA (cytosine) methyltransferase activity	molecular_function
50591811	GO:0004722	protein serine/threonine phosphatase activity	molecular_function
50591815	GO:0005524	ATP binding	molecular_function
50591815	GO:0015646	permease activity	molecular_function
50591815	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591827	GO:0000318	protein-methionine-R-oxide reductase activity	molecular_function
50591827	GO:0008113	protein-methionine-S-oxide reductase activity	molecular_function
50591828	GO:0004467	long-chain-fatty-acid-CoA ligase activity	molecular_function
50591829	GO:0030508	thiol-disulfide exchange intermediate activity	molecular_function
50591838	GO:0003684	damaged DNA binding	molecular_function
50591838	GO:0005524	ATP binding	molecular_function
50591838	GO:0030983	mismatched DNA binding	molecular_function
50591841	GO:0016566	specific transcriptional repressor activity	molecular_function
50591842	GO:0015582	beta-glucoside permease activity	molecular_function
50591842	GO:0015584	trehalose permease activity	molecular_function
50591843	GO:0004558	alpha-glucosidase activity	molecular_function
50591843	GO:0004574	oligo-1,6-glucosidase activity	molecular_function
50591843	GO:0008788	alpha,alpha-phosphotrehalase activity	molecular_function
50591845	GO:0008746	NAD(P) transhydrogenase activity	molecular_function
50591845	GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	molecular_function

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gi	acc	name	term_type
50591846	GO:0004523	ribonuclease H activity	molecular_function
50591847	GO:0009003	signal peptidase activity	molecular_function
50591848	GO:0008854	exodeoxyribonuclease V activity	molecular_function
50591849	GO:0004008	copper-exporting ATPase activity	molecular_function
50591850	GO:0000287	magnesium ion binding	molecular_function
50591850	GO:0004008	copper-exporting ATPase activity	molecular_function
50591850	GO:0005507	copper ion binding	molecular_function
50591850	GO:0005524	ATP binding	molecular_function
50591850	GO:0008900	hydrogen:potassium-exchanging ATPase activity	molecular_function
50591850	GO:0015097	mercury ion transporter activity	molecular_function
50591853	GO:0004342	glucosamine-6-phosphate deaminase activity	molecular_function
50591860	GO:0015582	beta-glucoside permease activity	molecular_function
50591860	GO:0019190	cellobiose permease activity	molecular_function
50591861	GO:0004340	glucokinase activity	molecular_function
50591861	GO:0004396	hexokinase activity	molecular_function
50591861	GO:0005524	ATP binding	molecular_function
50591861	GO:0008761	UDP-N-acetylglucosamine 2-epimerase activity	molecular_function
50591861	GO:0009384	N-acylmannosamine kinase activity	molecular_function
50591868	GO:0005554	molecular function unknown	molecular_function
50591869	GO:0008861	formate C-acetyltransferase activity	molecular_function
50591876	GO:0008889	glycerophosphodiester phosphodiesterase activity	molecular_function
50591877	GO:0004802	transketolase activity	molecular_function
50591877	GO:0005509	calcium ion binding	molecular_function
50591877	GO:0008661	1-deoxy-D-xylulose-5-phosphate synthase activity	molecular_function
50591878	GO:0004802	transketolase activity	molecular_function
50591878	GO:0005509	calcium ion binding	molecular_function
50591881	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591884	GO:0008878	glucose-1-phosphate adenylyltransferase activity	molecular_function
50591885	GO:0008878	glucose-1-phosphate adenylyltransferase activity	molecular_function
50591886	GO:0004373	glycogen (starch) synthase activity	molecular_function
50591886	GO:0009011	starch synthase activity	molecular_function
50591887	GO:0003844	1,4-alpha-glucan branching enzyme activity	molecular_function
50591887	GO:0004556	alpha-amylase activity	molecular_function
50591888	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591888	GO:0016597	amino acid binding	molecular_function
50591890	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591894	GO:0009381	excinuclease ABC activity	molecular_function
50591896	GO:0015599	glutamine-importing ATPase activity	molecular_function
50591896	GO:0015646	permease activity	molecular_function
50591897	GO:0015424	amino acid-transporting ATPase activity	molecular_function
50591899	GO:0005524	ATP binding	molecular_function
50591899	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591899	GO:0043023	ribosomal large subunit binding	molecular_function
50591899	GO:0043024	ribosomal small subunit binding	molecular_function
50591900	GO:0003961	O-acetylhomoserine aminocarboxypropyltransferase activity	molecular_function
50591900	GO:0004124	cysteine synthase activity	molecular_function
50591909	GO:0004803	transposase activity	molecular_function
50591910	GO:0004803	transposase activity	molecular_function
50591911	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
50591911	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
50591911	GO:0004028	aldehyde dehydrogenase activity	molecular_function

续表 1

gi	acc	name	term_type
50591911	GO:0005506	iron ion binding	molecular_function
50591914	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
50591914	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
50591914	GO:0005506	iron ion binding	molecular_function
50591919	GO:0015589	mannose permease activity	molecular_function
50591920	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591921	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591923	GO:0042806	fucose binding	molecular_function
50591925	GO:0008993	rhamnulokinase activity	molecular_function
50591925	GO:0046316	gluconokinase activity	molecular_function
50591926	GO:0030528	transcription regulator activity	molecular_function
50591927	GO:0004803	transposase activity	molecular_function
50591928	GO:0004803	transposase activity	molecular_function
50591929	GO:0004803	transposase activity	molecular_function
50591932	GO:0004034	aldose 1-epimerase activity	molecular_function
50591933	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
50591934	GO:0015582	beta-glucoside permease activity	molecular_function
50591934	GO:0019190	cellobiose permease activity	molecular_function
50591935	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
50591936	GO:0016563	transcriptional activator activity	molecular_function
50591936	GO:0030401	transcription antiterminator activity	molecular_function
50591937	GO:0009025	tagatose-bisphosphate aldolase activity	molecular_function
50591938	GO:0008662	1-phosphofructokinase activity	molecular_function
50591939	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
50591940	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
50591941	GO:0030528	transcription regulator activity	molecular_function
50591947	GO:0004519	endonuclease activity	molecular_function
50591947	GO:0004844	uracil DNA N-glycosylase activity	molecular_function
50591947	GO:0005506	iron ion binding	molecular_function
50591949	GO:0005524	ATP binding	molecular_function
50591949	GO:0015646	permease activity	molecular_function
50591949	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591950	GO:0005524	ATP binding	molecular_function
50591950	GO:0015646	permease activity	molecular_function
50591950	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
50591951	GO:0008959	phosphate acetyltransferase activity	molecular_function
50591952	GO:0004730	pseudouridylate synthase activity	molecular_function
50591953	GO:0003951	NAD+ kinase activity	molecular_function
50591956	GO:0000287	magnesium ion binding	molecular_function
50591956	GO:0004749	ribose phosphate diphosphokinase activity	molecular_function
50591956	GO:0016978	lipoate-protein ligase B activity	molecular_function
50591957	GO:0004123	cystathionine gamma-lyase activity	molecular_function
50591957	GO:0008483	transaminase activity	molecular_function
50591957	GO:0031071	cysteine desulfurase activity	molecular_function
50591962	GO:0005554	molecular function unknown	molecular_function
50591964	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
50591965	GO:0004459	L-lactate dehydrogenase activity	molecular_function
50591967	GO:0004803	transposase activity	molecular_function
50591968	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function

a) gi, 蛋白序列的 gi 号; acc, Gene Ontology 体系中所预测功能的 accession number; name, 所预测功能的名称; term_type, 所预测功能所属的大类名称

表 2　菌株 P1/7 的蛋白序列 Gene Ontology 功能预测结果列表 [a)]

ssu	acc	name	term_type
1	GO:0006270	DNA replication initiation	biological_process
1	GO:0006275	regulation of DNA replication	biological_process
2	GO:0006260	DNA replication	biological_process
6	GO:0000004	biological process unknown	biological_process
7	GO:0006412	protein biosynthesis	biological_process
8	GO:0006283	transcription-coupled nucleotide-excision repair	biological_process
13	GO:0006166	purine ribonucleoside salvage	biological_process
13	GO:0006400	tRNA modification	biological_process
14	GO:0006164	purine nucleotide biosynthesis	biological_process
14	GO:0006166	purine ribonucleoside salvage	biological_process
14	GO:0007610	behavior	biological_process
14	GO:0019835	cytolysis	biological_process
14	GO:0046651	lymphocyte proliferation	biological_process
15	GO:0000910	cytokinesis	biological_process
21	GO:0009152	purine ribonucleotide biosynthesis	biological_process
22	GO:0006532	aspartate biosynthesis	biological_process
22	GO:0009073	aromatic amino acid family biosynthesis	biological_process
24	GO:0008610	lipid biosynthesis	biological_process
26	GO:0006189	'de novo' IMP biosynthesis	biological_process
26	GO:0009113	purine base biosynthesis	biological_process
27	GO:0006144	purine base metabolism	biological_process
27	GO:0006189	'de novo' IMP biosynthesis	biological_process
27	GO:0006541	glutamine metabolism	biological_process
28	GO:0005996	monosaccharide metabolism	biological_process
28	GO:0006189	'de novo' IMP biosynthesis	biological_process
28	GO:0006541	glutamine metabolism	biological_process
28	GO:0008340	determination of adult life span	biological_process
28	GO:0009113	purine base biosynthesis	biological_process
28	GO:0009116	nucleoside metabolism	biological_process
28	GO:0040016	embryonic cleavage	biological_process
29	GO:0006189	'de novo' IMP biosynthesis	biological_process
29	GO:0009113	purine base biosynthesis	biological_process
30	GO:0006189	'de novo' IMP biosynthesis	biological_process
30	GO:0009113	purine base biosynthesis	biological_process
31	GO:0009152	purine ribonucleotide biosynthesis	biological_process
32	GO:0006189	‘de novo’ IMP biosynthesis	biological_process
32	GO:0009113	purine base biosynthesis	biological_process
33	GO:0006189	‘de novo’ IMP biosynthesis	biological_process
34	GO:0006144	purine base metabolism	biological_process
34	GO:0006189	‘de novo’ IMP biosynthesis	biological_process
37	GO:0006144	purine base metabolism	biological_process
37	GO:0006189	‘de novo’ IMP biosynthesis	biological_process
37	GO:0009712	catechol metabolism	biological_process
42	GO:0006810	transport	biological_process
44	GO:0006810	transport	biological_process
46	GO:0006310	DNA recombination	biological_process

续表 2

ssu	acc	name	term_type
54	GO:0006730	one-carbon compound metabolism	biological_process
54	GO:0046654	tetrahydrofolate biosynthesis	biological_process
54	GO:0046901	tetrahydrofolylpolyglutamate biosynthesis	biological_process
57	GO:0006298	mismatch repair	biological_process
58	GO:0006310	DNA recombination	biological_process
60	GO:0006281	DNA repair	biological_process
62	GO:0009432	SOS response	biological_process
69	GO:0006412	protein biosynthesis	biological_process
69	GO:0007046	ribosome biogenesis	biological_process
70	GO:0006412	protein biosynthesis	biological_process
70	GO:0007046	ribosome biogenesis	biological_process
71	GO:0006412	protein biosynthesis	biological_process
71	GO:0007046	ribosome biogenesis	biological_process
72	GO:0007046	ribosome biogenesis	biological_process
73	GO:0006412	protein biosynthesis	biological_process
73	GO:0007046	ribosome biogenesis	biological_process
74	GO:0006412	protein biosynthesis	biological_process
74	GO:0007046	ribosome biogenesis	biological_process
75	GO:0006412	protein biosynthesis	biological_process
75	GO:0007046	ribosome biogenesis	biological_process
76	GO:0006412	protein biosynthesis	biological_process
76	GO:0007046	ribosome biogenesis	biological_process
77	GO:0006412	protein biosynthesis	biological_process
79	GO:0006412	protein biosynthesis	biological_process
79	GO:0007046	ribosome biogenesis	biological_process
80	GO:0006412	protein biosynthesis	biological_process
80	GO:0007046	ribosome biogenesis	biological_process
81	GO:0006412	protein biosynthesis	biological_process
82	GO:0006412	protein biosynthesis	biological_process
82	GO:0007046	ribosome biogenesis	biological_process
83	GO:0007046	ribosome biogenesis	biological_process
85	GO:0006412	protein biosynthesis	biological_process
85	GO:0007046	ribosome biogenesis	biological_process
88	GO:0006412	protein biosynthesis	biological_process
88	GO:0007046	ribosome biogenesis	biological_process
89	GO:0006412	protein biosynthesis	biological_process
89	GO:0007046	ribosome biogenesis	biological_process
90	GO:0006412	protein biosynthesis	biological_process
92	GO:0006412	protein biosynthesis	biological_process
93	GO:0006886	intracellular protein transport	biological_process
93	GO:0015628	type II protein secretion system	biological_process
94	GO:0006172	ADP biosynthesis	biological_process
94	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
94	GO:0046083	adenine metabolism	biological_process
95	GO:0006413	translational initiation	biological_process

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ssu	acc	name	term_type
97	GO:0006412	protein biosynthesis	biological_process
97	GO:0007046	ribosome biogenesis	biological_process
98	GO:0006412	protein biosynthesis	biological_process
98	GO:0007046	ribosome biogenesis	biological_process
99	GO:0006350	transcription	biological_process
100	GO:0000002	mitochondrial genome maintenance	biological_process
100	GO:0006412	protein biosynthesis	biological_process
100	GO:0007046	ribosome biogenesis	biological_process
113	GO:0006826	iron ion transport	biological_process
113	GO:0006828	manganese ion transport	biological_process
113	GO:0006829	zinc ion transport	biological_process
114	GO:0006828	manganese ion transport	biological_process
114	GO:0006829	zinc ion transport	biological_process
115	GO:0006828	manganese ion transport	biological_process
115	GO:0006829	zinc ion transport	biological_process
115	GO:0007155	cell adhesion	biological_process
115	GO:0009405	pathogenesis	biological_process
120	GO:0006437	tyrosyl-tRNA aminoacylation	biological_process
121	GO:0009252	peptidoglycan biosynthesis	biological_process
123	GO:0006350	transcription	biological_process
126	GO:0009297	fimbriae biogenesis	biological_process
126	GO:0009405	pathogenesis	biological_process
126	GO:0015628	type II protein secretion system	biological_process
127	GO:0009306	protein secretion	biological_process
134	GO:0006083	acetate metabolism	biological_process
134	GO:0006113	fermentation	biological_process
134	GO:0051144	propanediol catabolism	biological_process
136	GO:0046654	tetrahydrofolate biosynthesis	biological_process
137	GO:0006508	proteolysis and peptidolysis	biological_process
142	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
144	GO:0006260	DNA replication	biological_process
144	GO:0006281	DNA repair	biological_process
144	GO:0006310	DNA recombination	biological_process
146	GO:0006457	protein folding	biological_process
147	GO:0006457	protein folding	biological_process
148	GO:0006412	protein biosynthesis	biological_process
149	GO:0006412	protein biosynthesis	biological_process
149	GO:0007046	ribosome biogenesis	biological_process
151	GO:0006414	translational elongation	biological_process
152	GO:0006508	proteolysis and peptidolysis	biological_process
152	GO:0007218	neuropeptide signaling pathway	biological_process
152	GO:0007267	cell-cell signaling	biological_process
152	GO:0010002	cardioblast differentiation	biological_process
152	GO:0016486	peptide hormone processing	biological_process
152	GO:0042310	vasoconstriction	biological_process
153	GO:0006094	gluconeogenesis	biological_process

续表 2

ssu	acc	name	term_type
153	GO:0006096	glycolysis	biological_process
154	GO:0006096	glycolysis	biological_process
157	GO:0006542	glutamine biosynthesis	biological_process
161	GO:0006464	protein modification	biological_process
161	GO:0042254	ribosome biogenesis and assembly	biological_process
162	GO:0006508	proteolysis and peptidolysis	biological_process
163	GO:0006355	regulation of transcription, DNA-dependent	biological_process
163	GO:0009236	cobalamin biosynthesis	biological_process
164	GO:0008643	carbohydrate transport	biological_process
165	GO:0008643	carbohydrate transport	biological_process
166	GO:0008643	carbohydrate transport	biological_process
168	GO:0006865	amino acid transport	biological_process
174	GO:0051189	prosthetic group metabolism	biological_process
176	GO:0030245	cellulose catabolism	biological_process
178	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
181	GO:0006098	pentose-phosphate shunt	biological_process
181	GO:0040008	regulation of growth	biological_process
182	GO:0006098	pentose-phosphate shunt	biological_process
182	GO:0008615	pyridoxine biosynthesis	biological_process
182	GO:0009228	thiamin biosynthesis	biological_process
182	GO:0009240	isopentenyl diphosphate biosynthesis	biological_process
182	GO:0040008	regulation of growth	biological_process
183	GO:0009395	phospholipid catabolism	biological_process
191	GO:0006113	fermentation	biological_process
191	GO:0015942	formate metabolism	biological_process
192	GO:0009650	UV protection	biological_process
195	GO:0006096	glycolysis	biological_process
198	GO:0006047	UDP-N-acetylglucosamine metabolism	biological_process
198	GO:0007155	cell adhesion	biological_process
198	GO:0009103	lipopolysaccharide biosynthesis	biological_process
198	GO:0046380	N-acetylneuraminate biosynthesis	biological_process
199	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
199	GO:0015759	beta-glucoside transport	biological_process
199	GO:0019533	cellobiose transport	biological_process
206	GO:0006002	fructose 6-phosphate metabolism	biological_process
206	GO:0006043	glucosamine catabolism	biological_process
206	GO:0006044	N-acetylglucosamine metabolism	biological_process
206	GO:0007340	acrosome reaction	biological_process
206	GO:0046370	fructose biosynthesis	biological_process
208	GO:0006825	copper ion transport	biological_process
209	GO:0006825	copper ion transport	biological_process
209	GO:0006878	copper ion homeostasis	biological_process
209	GO:0007622	rhythmic behavior	biological_process
209	GO:0015694	mercury ion transport	biological_process
210	GO:0006825	copper ion transport	biological_process
210	GO:0009873	ethylene mediated signaling pathway	biological_process

续表 2

ssu	acc	name	term_type
211	GO:0006281	DNA repair	biological_process
211	GO:0006310	DNA recombination	biological_process
212	GO:0006508	proteolysis and peptidolysis	biological_process
212	GO:0009306	protein secretion	biological_process
213	GO:0006401	RNA catabolism	biological_process
214	GO:0006118	electron transport	biological_process
216	GO:0000025	maltose catabolism	biological_process
216	GO:0005993	trehalose catabolism	biological_process
217	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
217	GO:0015759	beta-glucoside transport	biological_process
217	GO:0015771	trehalose transport	biological_process
218	GO:0006355	regulation of transcription, DNA-dependent	biological_process
218	GO:0015771	trehalose transport	biological_process
221	GO:0006298	mismatch repair	biological_process
223	GO:0006118	electron transport	biological_process
224	GO:0006631	fatty acid metabolism	biological_process
225	GO:0006979	response to oxidative stress	biological_process
225	GO:0030091	protein repair	biological_process
229	GO:0042891	antibiotic transport	biological_process
229	GO:0046677	response to antibiotic	biological_process
230	GO:0015808	L-alanine transport	biological_process
234	GO:0006537	glutamate biosynthesis	biological_process
234	GO:0009083	branched chain family amino acid catabolism	biological_process
235	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
235	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
248	GO:0006820	anion transport	biological_process
248	GO:0015724	formate transport	biological_process
249	GO:0006833	water transport	biological_process
249	GO:0006863	purine transport	biological_process
249	GO:0006970	response to osmotic stress	biological_process
249	GO:0007588	excretion	biological_process
249	GO:0009247	glycolipid biosynthesis	biological_process
249	GO:0009935	nutrient import	biological_process
249	GO:0010033	response to organic substance	biological_process
249	GO:0015793	glycerol transport	biological_process
249	GO:0015855	pyrimidine transport	biological_process
249	GO:0030104	water homeostasis	biological_process
249	GO:0046689	response to mercury ion	biological_process
253	GO:0006125	thioredoxin pathway	biological_process
253	GO:0006334	nucleosome assembly	biological_process
253	GO:0006821	chloride transport	biological_process
253	GO:0006938	sarcomere alignment	biological_process
253	GO:0006942	regulation of striated muscle contraction	biological_process
253	GO:0007214	gamma-aminobutyric acid signaling pathway	biological_process
253	GO:0007638	mechanosensory behavior	biological_process
253	GO:0008366	nerve ensheathment	biological_process

续表 2

ssu	acc	name	term_type
253	GO:0016080	synaptic vesicle targeting	biological_process
253	GO:0030073	insulin secretion	biological_process
253	GO:0045104	intermediate filament cytoskeleton organization and biogenesis	biological_process
253	GO:0045214	sarcomere organization	biological_process
259	GO:0006427	histidyl-tRNA aminoacylation	biological_process
260	GO:0006067	ethanol metabolism	biological_process
260	GO:0006113	fermentation	biological_process
261	GO:0006081	aldehyde metabolism	biological_process
261	GO:0006113	fermentation	biological_process
261	GO:0051144	propanediol catabolism	biological_process
262	GO:0009088	threonine biosynthesis	biological_process
263	GO:0006858	extracellular transport	biological_process
263	GO:0009636	response to toxin	biological_process
264	GO:0006810	transport	biological_process
267	GO:0015833	peptide transport	biological_process
268	GO:0006855	multidrug transport	biological_process
269	GO:0008299	isoprenoid biosynthesis	biological_process
270	GO:0006695	cholesterol biosynthesis	biological_process
270	GO:0006696	ergosterol biosynthesis	biological_process
270	GO:0016310	phosphorylation	biological_process
270	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
271	GO:0016126	sterol biosynthesis	biological_process
271	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
272	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
273	GO:0006810	transport	biological_process
274	GO:0006810	transport	biological_process
278	GO:0009408	response to heat	biological_process
279	GO:0006457	protein folding	biological_process
279	GO:0006950	response to stress	biological_process
280	GO:0006950	response to stress	biological_process
281	GO:0006457	protein folding	biological_process
281	GO:0009408	response to heat	biological_process
284	GO:0006865	amino acid transport	biological_process
285	GO:0006865	amino acid transport	biological_process
288	GO:0006825	copper ion transport	biological_process
288	GO:0015691	cadmium ion transport	biological_process
289	GO:0006355	regulation of transcription, DNA-dependent	biological_process
289	GO:0015682	ferric iron transport	biological_process
290	GO:0006400	tRNA modification	biological_process
291	GO:0009228	thiamin biosynthesis	biological_process
298	GO:0006113	fermentation	biological_process
298	GO:0008631	induction of apoptosis by oxidative stress	biological_process
298	GO:0016049	cell growth	biological_process
299	GO:0016042	lipid catabolism	biological_process
300	GO:0042572	retinol metabolism	biological_process
300	GO:0045494	photoreceptor maintenance	biological_process

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ssu	acc	name	term_type
301	GO:0009062	fatty acid catabolism	biological_process
301	GO:0009395	phospholipid catabolism	biological_process
306	GO:0006457	protein folding	biological_process
307	GO:0000271	polysaccharide biosynthesis	biological_process
308	GO:0006828	manganese ion transport	biological_process
308	GO:0006829	zinc ion transport	biological_process
308	GO:0007155	cell adhesion	biological_process
308	GO:0009405	pathogenesis	biological_process
311	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
312	GO:0006096	glycolysis	biological_process
314	GO:0006268	DNA unwinding	biological_process
314	GO:0006310	DNA recombination	biological_process
315	GO:0006530	asparagine catabolism	biological_process
315	GO:0006995	cellular response to nitrogen starvation	biological_process
318	GO:0006950	response to stress	biological_process
319	GO:0006532	aspartate biosynthesis	biological_process
322	GO:0006412	protein biosynthesis	biological_process
322	GO:0007046	ribosome biogenesis	biological_process
325	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
326	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
327	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
328	GO:0006355	regulation of transcription, DNA-dependent	biological_process
329	GO:0006012	galactose metabolism	biological_process
329	GO:0046835	carbohydrate phosphorylation	biological_process
332	GO:0006878	copper ion homeostasis	biological_process
335	GO:0000004	biological process unknown	biological_process
337	GO:0009435	NAD biosynthesis	biological_process
352	GO:0006289	nucleotide-excision repair	biological_process
353	GO:0005980	glycogen catabolism	biological_process
354	GO:0005980	glycogen catabolism	biological_process
355	GO:0006355	regulation of transcription, DNA-dependent	biological_process
355	GO:0015771	trehalose transport	biological_process
357	GO:0015758	glucose transport	biological_process
360	GO:0000004	biological process unknown	biological_process
364	GO:0000004	biological process unknown	biological_process
366	GO:0006824	cobalt ion transport	biological_process
366	GO:0015675	nickel ion transport	biological_process
367	GO:0006824	cobalt ion transport	biological_process
368	GO:0006355	regulation of transcription, DNA-dependent	biological_process
368	GO:0009409	response to cold	biological_process
369	GO:0000004	biological process unknown	biological_process
370	GO:0009252	peptidoglycan biosynthesis	biological_process
376	GO:0009372	quorum sensing	biological_process
378	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
380	GO:0006260	DNA replication	biological_process
381	GO:0006431	methionyl-tRNA aminoacylation	biological_process

续表 2

ssu	acc	name	term_type
382	GO:0000154	rRNA modification	biological_process
382	GO:0001510	RNA methylation	biological_process
387	GO:0007165	signal transduction	biological_process
389	GO:0006457	protein folding	biological_process
389	GO:0006836	neurotransmitter transport	biological_process
391	GO:0006535	cysteine biosynthesis from serine	biological_process
392	GO:0000004	biological process unknown	biological_process
396	GO:0000154	rRNA modification	biological_process
396	GO:0001510	RNA methylation	biological_process
396	GO:0006400	tRNA modification	biological_process
400	GO:0006355	regulation of transcription, DNA-dependent	biological_process
401	GO:0006355	regulation of transcription, DNA-dependent	biological_process
402	GO:0005975	carbohydrate metabolism	biological_process
402	GO:0035071	salivary gland cell death	biological_process
402	GO:0045045	secretory pathway	biological_process
403	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
404	GO:0008645	hexose transport	biological_process
404	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
405	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
405	GO:0015761	mannose transport	biological_process
407	GO:0006012	galactose metabolism	biological_process
412	GO:0006438	valyl-tRNA aminoacylation	biological_process
421	GO:0009405	pathogenesis	biological_process
424	GO:0006508	proteolysis and peptidolysis	biological_process
430	GO:0009252	peptidoglycan biosynthesis	biological_process
431	GO:0009252	peptidoglycan biosynthesis	biological_process
432	GO:0000910	cytokinesis	biological_process
433	GO:0000910	cytokinesis	biological_process
433	GO:0043093	binary fission	biological_process
434	GO:0000910	cytokinesis	biological_process
434	GO:0046785	microtubule polymerization	biological_process
435	GO:0000004	biological process unknown	biological_process
435	GO:0006522	alanine metabolism	biological_process
441	GO:0006428	isoleucyl-tRNA aminoacylation	biological_process
444	GO:0006289	nucleotide-excision repair	biological_process
446	GO:0006868	L-glutamine transport	biological_process
447	GO:0006865	amino acid transport	biological_process
448	GO:0000105	histidine biosynthesis	biological_process
448	GO:0009086	methionine biosynthesis	biological_process
448	GO:0009113	purine base biosynthesis	biological_process
448	GO:0009257	10-formyltetrahydrofolate biosynthesis	biological_process
448	GO:0015940	pantothenate biosynthesis	biological_process
455	GO:0006355	regulation of transcription, DNA-dependent	biological_process
457	GO:0006508	proteolysis and peptidolysis	biological_process
458	GO:0006508	proteolysis and peptidolysis	biological_process
464	GO:0000305	response to oxygen radicals	biological_process

续表 2

ssu	acc	name	term_type
464	GO:0006118	electron transport	biological_process
464	GO:0006128	oxidized glutathione reduction	biological_process
464	GO:0006750	glutathione biosynthesis	biological_process
464	GO:0030503	regulation of cell redox homeostasis	biological_process
466	GO:0042891	antibiotic transport	biological_process
466	GO:0046677	response to antibiotic	biological_process
467	GO:0042891	antibiotic transport	biological_process
467	GO:0046677	response to antibiotic	biological_process
470	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
470	GO:0006430	lysyl-tRNA aminoacylation	biological_process
478	GO:0000910	cytokinesis	biological_process
478	GO:0009252	peptidoglycan biosynthesis	biological_process
479	GO:0006099	tricarboxylic acid cycle	biological_process
482	GO:0006414	translational elongation	biological_process
483	GO:0006096	glycolysis	biological_process
484	GO:0008152	metabolism	biological_process
485	GO:0006955	immune response	biological_process
489	GO:0006144	purine base metabolism	biological_process
489	GO:0006155	adenosine deaminase reaction	biological_process
489	GO:0009168	purine ribonucleoside monophosphate biosynthesis	biological_process
489	GO:0019735	antimicrobial humoral response (sensu Vertebrata)	biological_process
489	GO:0045187	regulation of circadian sleep/wake cycle, sleep	biological_process
489	GO:0046085	adenosine metabolism	biological_process
491	GO:0006810	transport	biological_process
492	GO:0006355	regulation of transcription, DNA-dependent	biological_process
493	GO:0006260	DNA replication	biological_process
494	GO:0001678	cell glucose homeostasis	biological_process
494	GO:0005977	glycogen metabolism	biological_process
494	GO:0006002	fructose 6-phosphate metabolism	biological_process
494	GO:0006110	regulation of glycolysis	biological_process
495	GO:0006090	pyruvate metabolism	biological_process
495	GO:0006096	glycolysis	biological_process
496	GO:0001403	invasive growth (sensu Saccharomyces)	biological_process
496	GO:0007124	pseudohyphal growth	biological_process
500	GO:0006040	amino sugar metabolism	biological_process
501	GO:0006868	L-glutamine transport	biological_process
502	GO:0006865	amino acid transport	biological_process
503	GO:0006865	amino acid transport	biological_process
507	GO:0006281	DNA repair	biological_process
508	GO:0006561	proline biosynthesis	biological_process
509	GO:0006561	proline biosynthesis	biological_process
510	GO:0006118	electron transport	biological_process
510	GO:0006561	proline biosynthesis	biological_process
510	GO:0008652	amino acid biosynthesis	biological_process
513	GO:0006355	regulation of transcription, DNA-dependent	biological_process
518	GO:0045227	capsule polysaccharide biosynthesis	biological_process

续表 2

ssu	acc	name	term_type
519	GO:0000271	polysaccharide biosynthesis	biological_process
521	GO:0009103	lipopolysaccharide biosynthesis	biological_process
525	GO:0000271	polysaccharide biosynthesis	biological_process
526	GO:0000271	polysaccharide biosynthesis	biological_process
535	GO:0009103	lipopolysaccharide biosynthesis	biological_process
535	GO:0009631	cold acclimation	biological_process
535	GO:0042309	homoiothermy	biological_process
535	GO:0050826	response to freezing	biological_process
536	GO:0006047	UDP-N-acetylglucosamine metabolism	biological_process
536	GO:0007155	cell adhesion	biological_process
536	GO:0009103	lipopolysaccharide biosynthesis	biological_process
536	GO:0046380	N-acetylneuraminate biosynthesis	biological_process
538	GO:0006055	CMP-N-acetylneuraminate biosynthesis	biological_process
538	GO:0009103	lipopolysaccharide biosynthesis	biological_process
546	GO:0006313	DNA transposition	biological_process
547	GO:0006313	DNA transposition	biological_process
549	GO:0006313	DNA transposition	biological_process
552	GO:0006310	DNA recombination	biological_process
552	GO:0015074	DNA integration	biological_process
557	GO:0009423	chorismate biosynthesis	biological_process
557	GO:0018920	glyphosate metabolism	biological_process
558	GO:0009423	chorismate biosynthesis	biological_process
559	GO:0019274	phenylalanine biosynthesis, prephenate pathway	biological_process
561	GO:0000154	rRNA modification	biological_process
561	GO:0001510	RNA methylation	biological_process
561	GO:0006400	tRNA modification	biological_process
563	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
569	GO:0006532	aspartate biosynthesis	biological_process
570	GO:0006421	asparaginyl-tRNA aminoacylation	biological_process
570	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
573	GO:0006855	multidrug transport	biological_process
574	GO:0000002	mitochondrial genome maintenance	biological_process
574	GO:0000294	mRNA catabolism, endonucleolytic cleavage-dependent decay	biological_process
574	GO:0006449	regulation of translational termination	biological_process
574	GO:0009097	isoleucine biosynthesis	biological_process
574	GO:0017148	negative regulation of protein biosynthesis	biological_process
575	GO:0000004	biological process unknown	biological_process
580	GO:0019546	arginine deiminase pathway	biological_process
582	GO:0000050	urea cycle	biological_process
582	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
582	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
582	GO:0006526	arginine biosynthesis	biological_process
583	GO:0019546	arginine deiminase pathway	biological_process
585	GO:0006508	proteolysis and peptidolysis	biological_process
589	GO:0008616	queuosine biosynthesis	biological_process
591	GO:0006002	fructose 6-phosphate metabolism	biological_process

续表 2

ssu	acc	name	term_type
591	GO:0006046	N-acetylglucosamine catabolism	biological_process
591	GO:0007340	acrosome reaction	biological_process
591	GO:0046370	fructose biosynthesis	biological_process
596	GO:0009252	peptidoglycan biosynthesis	biological_process
596	GO:0019290	siderophore biosynthesis	biological_process
597	GO:0000271	polysaccharide biosynthesis	biological_process
597	GO:0042941	D-alanine transport	biological_process
597	GO:0046374	teichoic acid metabolism	biological_process
599	GO:0019350	teichoic acid biosynthesis	biological_process
602	GO:0000154	rRNA modification	biological_process
603	GO:0006750	glutathione biosynthesis	biological_process
603	GO:0006982	response to lipid hydroperoxide	biological_process
603	GO:0009636	response to toxin	biological_process
604	GO:0006826	iron ion transport	biological_process
605	GO:0006826	iron ion transport	biological_process
606	GO:0006826	iron ion transport	biological_process
607	GO:0006826	iron ion transport	biological_process
608	GO:0009252	peptidoglycan biosynthesis	biological_process
611	GO:0009290	cellular DNA import	biological_process
611	GO:0030420	establishment of competence for transformation	biological_process
616	GO:0000004	biological process unknown	biological_process
617	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
618	GO:0006260	DNA replication	biological_process
621	GO:0006564	L-serine biosynthesis	biological_process
621	GO:0008615	pyridoxine biosynthesis	biological_process
621	GO:0009113	purine base biosynthesis	biological_process
623	GO:0006564	L-serine biosynthesis	biological_process
623	GO:0007420	brain development	biological_process
623	GO:0031102	neurite regeneration	biological_process
624	GO:0006281	DNA repair	biological_process
627	GO:0006284	base-excision repair	biological_process
627	GO:0030503	regulation of cell redox homeostasis	biological_process
627	GO:0051101	regulation of DNA binding	biological_process
629	GO:0006520	amino acid metabolism	biological_process
629	GO:0006865	amino acid transport	biological_process
643	GO:0006313	DNA transposition	biological_process
644	GO:0005996	monosaccharide metabolism	biological_process
646	GO:0009651	response to salt stress	biological_process
646	GO:0015937	coenzyme A biosynthesis	biological_process
646	GO:0015939	pantothenate metabolism	biological_process
647	GO:0015937	coenzyme A biosynthesis	biological_process
647	GO:0015939	pantothenate metabolism	biological_process
648	GO:0000105	histidine biosynthesis	biological_process
648	GO:0006730	one-carbon compound metabolism	biological_process
648	GO:0009086	methionine biosynthesis	biological_process
648	GO:0009113	purine base biosynthesis	biological_process

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ssu	acc	name	term_type
648	GO:0009257	10-formyltetrahydrofolate biosynthesis	biological_process
648	GO:0015940	pantothenate biosynthesis	biological_process
650	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
650	GO:0009083	branched chain family amino acid catabolism	biological_process
651	GO:0009307	DNA restriction-modification system	biological_process
652	GO:0006304	DNA modification	biological_process
661	GO:0006113	fermentation	biological_process
661	GO:0006800	oxygen and reactive oxygen species metabolism	biological_process
662	GO:0006355	regulation of transcription, DNA-dependent	biological_process
663	GO:0006355	regulation of transcription, DNA-dependent	biological_process
663	GO:0009204	deoxyribonucleoside triphosphate catabolism	biological_process
665	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
665	GO:0015759	beta-glucoside transport	biological_process
665	GO:0019533	cellobiose transport	biological_process
666	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
666	GO:0015759	beta-glucoside transport	biological_process
666	GO:0019533	cellobiose transport	biological_process
667	GO:0006113	fermentation	biological_process
667	GO:0015942	formate metabolism	biological_process
668	GO:0006098	pentose-phosphate shunt	biological_process
671	GO:0009086	methionine biosynthesis	biological_process
671	GO:0009088	threonine biosynthesis	biological_process
671	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
671	GO:0009097	isoleucine biosynthesis	biological_process
672	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
675	GO:0006071	glycerol metabolism	biological_process
676	GO:0006007	glucose catabolism	biological_process
676	GO:0006072	glycerol-3-phosphate metabolism	biological_process
676	GO:0006094	gluconeogenesis	biological_process
676	GO:0006116	NADH oxidation	biological_process
676	GO:0006118	electron transport	biological_process
677	GO:0006833	water transport	biological_process
677	GO:0006863	purine transport	biological_process
677	GO:0006970	response to osmotic stress	biological_process
677	GO:0007588	excretion	biological_process
677	GO:0009247	glycolipid biosynthesis	biological_process
677	GO:0009935	nutrient import	biological_process
677	GO:0010033	response to organic substance	biological_process
677	GO:0015722	canalicular bile acid transport	biological_process
677	GO:0015791	polyol transport	biological_process
677	GO:0015837	amine transport	biological_process
677	GO:0015855	pyrimidine transport	biological_process
677	GO:0030104	water homeostasis	biological_process
677	GO:0046689	response to mercury ion	biological_process
680	GO:0006508	proteolysis and peptidolysis	biological_process
683	GO:0006281	DNA repair	biological_process

续表 2

ssu	acc	name	term_type
683	GO:0006310	DNA recombination	biological_process
685	GO:0009228	thiamin biosynthesis	biological_process
686	GO:0009228	thiamin biosynthesis	biological_process
687	GO:0009228	thiamin biosynthesis	biological_process
689	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	biological_process
692	GO:0006824	cobalt ion transport	biological_process
693	GO:0006824	cobalt ion transport	biological_process
698	GO:0009252	peptidoglycan biosynthesis	biological_process
702	GO:0006289	nucleotide-excision repair	biological_process
704	GO:0000004	biological process unknown	biological_process
708	GO:0006310	DNA recombination	biological_process
709	GO:0000004	biological process unknown	biological_process
710	GO:0006260	DNA replication	biological_process
710	GO:0006265	DNA topological change	biological_process
717	GO:0006260	DNA replication	biological_process
717	GO:0006265	DNA topological change	biological_process
719	GO:0007595	lactation	biological_process
719	GO:0009082	branched chain family amino acid biosynthesis	biological_process
719	GO:0009083	branched chain family amino acid catabolism	biological_process
721	GO:0006412	protein biosynthesis	biological_process
721	GO:0007046	ribosome biogenesis	biological_process
722	GO:0006567	threonine catabolism	biological_process
725	GO:0016226	iron-sulfur cluster assembly	biological_process
725	GO:0016259	selenocysteine metabolism	biological_process
726	GO:0009228	thiamin biosynthesis	biological_process
727	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
728	GO:0006412	protein biosynthesis	biological_process
728	GO:0007046	ribosome biogenesis	biological_process
729	GO:0006412	protein biosynthesis	biological_process
730	GO:0006355	regulation of transcription, DNA-dependent	biological_process
730	GO:0019344	cysteine biosynthesis	biological_process
731	GO:0006508	proteolysis and peptidolysis	biological_process
731	GO:0009306	protein secretion	biological_process
732	GO:0000154	rRNA modification	biological_process
733	GO:0019636	phosphonoacetate metabolism	biological_process
735	GO:0006353	transcription termination	biological_process
735	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
736	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
737	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
738	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
742	GO:0006412	protein biosynthesis	biological_process
742	GO:0007046	ribosome biogenesis	biological_process
744	GO:0006810	transport	biological_process
745	GO:0006810	transport	biological_process
747	GO:0009086	methionine biosynthesis	biological_process
747	GO:0009088	threonine biosynthesis	biological_process

续表 2

ssu	acc	name	term_type
747	GO:0009097	isoleucine biosynthesis	biological_process
748	GO:0006549	isoleucine metabolism	biological_process
748	GO:0006555	methionine metabolism	biological_process
748	GO:0009088	threonine biosynthesis	biological_process
748	GO:0009092	homoserine metabolism	biological_process
750	GO:0009252	peptidoglycan biosynthesis	biological_process
751	GO:0015847	putrescine transport	biological_process
751	GO:0015848	spermidine transport	biological_process
752	GO:0015847	putrescine transport	biological_process
752	GO:0015848	spermidine transport	biological_process
753	GO:0015847	putrescine transport	biological_process
753	GO:0015848	spermidine transport	biological_process
754	GO:0015847	putrescine transport	biological_process
754	GO:0015848	spermidine transport	biological_process
755	GO:0006821	chloride transport	biological_process
757	GO:0006508	proteolysis and peptidolysis	biological_process
758	GO:0000004	biological process unknown	biological_process
759	GO:0006281	DNA repair	biological_process
760	GO:0009152	purine ribonucleotide biosynthesis	biological_process
760	GO:0009409	response to cold	biological_process
760	GO:0030224	monocyte differentiation	biological_process
760	GO:0046038	GMP catabolism	biological_process
761	GO:0006855	multidrug transport	biological_process
762	GO:0006855	multidrug transport	biological_process
764	GO:0030488	tRNA methylation	biological_process
765	GO:0000105	histidine biosynthesis	biological_process
766	GO:0006355	regulation of transcription, DNA-dependent	biological_process
767	GO:0006096	glycolysis	biological_process
768	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
768	GO:0015755	fructose transport	biological_process
771	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
772	GO:0006396	RNA processing	biological_process
773	GO:0006810	transport	biological_process
778	GO:0006206	pyrimidine base metabolism	biological_process
778	GO:0006231	dTMP biosynthesis	biological_process
778	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
779	GO:0046654	tetrahydrofolate biosynthesis	biological_process
781	GO:0006510	ATP-dependent proteolysis	biological_process
782	GO:0000004	biological process unknown	biological_process
783	GO:0006165	nucleoside diphosphate phosphorylation	biological_process
783	GO:0006183	GTP biosynthesis	biological_process
783	GO:0006228	UTP biosynthesis	biological_process
783	GO:0006241	CTP biosynthesis	biological_process
783	GO:0006917	induction of apoptosis	biological_process
783	GO:0007427	tracheal epithelial cell migration (sensu Insecta)	biological_process
783	GO:0008285	negative regulation of cell proliferation	biological_process

续表 2

ssu	acc	name	term_type
783	GO:0018105	peptidyl-serine phosphorylation	biological_process
783	GO:0045786	negative regulation of progression through cell cycle	biological_process
785	GO:0000004	biological process unknown	biological_process
789	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
790	GO:0006415	translational termination	biological_process
791	GO:0006306	DNA methylation	biological_process
794	GO:0006730	one-carbon compound metabolism	biological_process
794	GO:0009396	folic acid and derivative biosynthesis	biological_process
794	GO:0019264	glycine biosynthesis from serine	biological_process
797	GO:0008152	metabolism	biological_process
816	GO:0009152	purine ribonucleotide biosynthesis	biological_process
816	GO:0046037	GMP metabolism	biological_process
817	GO:0006355	regulation of transcription, DNA-dependent	biological_process
817	GO:0015771	trehalose transport	biological_process
819	GO:0006617	SRP-dependent cotranslational protein-membrane targeting, signal sequence recognition	biological_process
819	GO:0009306	protein secretion	biological_process
825	GO:0006310	DNA recombination	biological_process
825	GO:0015074	DNA integration	biological_process
826	GO:0005975	carbohydrate metabolism	biological_process
827	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
828	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
828	GO:0006817	phosphate transport	biological_process
845	GO:0006412	protein biosynthesis	biological_process
845	GO:0007046	ribosome biogenesis	biological_process
846	GO:0006412	protein biosynthesis	biological_process
846	GO:0007046	ribosome biogenesis	biological_process
847	GO:0006265	DNA topological change	biological_process
847	GO:0006268	DNA unwinding	biological_process
848	GO:0009294	DNA mediated transformation	biological_process
854	GO:0009405	pathogenesis	biological_process
854	GO:0019835	cytolysis	biological_process
856	GO:0006401	RNA catabolism	biological_process
859	GO:0000917	barrier septum formation	biological_process
859	GO:0030187	melatonin biosynthesis	biological_process
860	GO:0009166	nucleotide catabolism	biological_process
861	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
862	GO:0005975	carbohydrate metabolism	biological_process
862	GO:0006284	base-excision repair	biological_process
863	GO:0000271	polysaccharide biosynthesis	biological_process
864	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
864	GO:0006222	UMP biosynthesis	biological_process
864	GO:0009116	nucleoside metabolism	biological_process
866	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
867	GO:0006118	electron transport	biological_process
867	GO:0006207	'de novo' pyrimidine base biosynthesis	biological_process
867	GO:0006212	uracil catabolism	biological_process

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ssu	acc	name	term_type
867	GO:0006214	thymidine catabolism	biological_process
867	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
868	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process
869	GO:0006355	regulation of transcription, DNA-dependent	biological_process
870	GO:0005978	glycogen biosynthesis	biological_process
872	GO:0005978	glycogen biosynthesis	biological_process
873	GO:0005978	glycogen biosynthesis	biological_process
874	GO:0005978	glycogen biosynthesis	biological_process
875	GO:0006865	amino acid transport	biological_process
876	GO:0006865	amino acid transport	biological_process
882	GO:0006289	nucleotide-excision repair	biological_process
883	GO:0006868	L-glutamine transport	biological_process
884	GO:0006865	amino acid transport	biological_process
886	GO:0006448	regulation of translational elongation	biological_process
886	GO:0006810	transport	biological_process
887	GO:0009086	methionine biosynthesis	biological_process
887	GO:0019344	cysteine biosynthesis	biological_process
890	GO:0006012	galactose metabolism	biological_process
891	GO:0030245	cellulose catabolism	biological_process
892	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
892	GO:0015759	beta-glucoside transport	biological_process
892	GO:0019533	cellobiose transport	biological_process
893	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
893	GO:0015759	beta-glucoside transport	biological_process
894	GO:0006355	regulation of transcription, DNA-dependent	biological_process
895	GO:0019512	lactose catabolism via tagatose-6-phosphate	biological_process
896	GO:0006096	glycolysis	biological_process
898	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
899	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
901	GO:0006355	regulation of transcription, DNA-dependent	biological_process
909	GO:0005975	carbohydrate metabolism	biological_process
909	GO:0006284	base-excision repair	biological_process
909	GO:0006298	mismatch repair	biological_process
909	GO:0045786	negative regulation of progression through cell cycle	biological_process
911	GO:0006810	transport	biological_process
912	GO:0006810	transport	biological_process
913	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
913	GO:0006108	malate metabolism	biological_process
913	GO:0006113	fermentation	biological_process
914	GO:0000154	rRNA modification	biological_process
915	GO:0019363	pyridine nucleotide biosynthesis	biological_process
918	GO:0009116	nucleoside metabolism	biological_process
918	GO:0009152	purine ribonucleotide biosynthesis	biological_process
918	GO:0009156	ribonucleoside monophosphate biosynthesis	biological_process
919	GO:0016226	iron-sulfur cluster assembly	biological_process
919	GO:0016259	selenocysteine metabolism	biological_process

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ssu	acc	name	term_type
924	GO:0006281	DNA repair	biological_process
926	GO:0006260	DNA replication	biological_process
926	GO:0006265	DNA topological change	biological_process
927	GO:0006100	tricarboxylic acid cycle intermediate metabolism	biological_process
927	GO:0019246	L(+)-lactate biosynthesis from pyruvate	biological_process
927	GO:0019642	anaerobic glycolysis	biological_process
935	GO:0006206	pyrimidine base metabolism	biological_process
935	GO:0006216	cytidine catabolism	biological_process
935	GO:0006217	deoxycytidine catabolism	biological_process
936	GO:0009264	deoxyribonucleotide catabolism	biological_process
937	GO:0000002	mitochondrial genome maintenance	biological_process
937	GO:0001525	angiogenesis	biological_process
937	GO:0006206	pyrimidine base metabolism	biological_process
937	GO:0006220	pyrimidine nucleotide metabolism	biological_process
937	GO:0006935	chemotaxis	biological_process
937	GO:0009103	lipopolysaccharide biosynthesis	biological_process
939	GO:0015937	coenzyme A biosynthesis	biological_process
941	GO:0006313	DNA transposition	biological_process
943	GO:0007528	neuromuscular junction development	biological_process
944	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
944	GO:0006817	phosphate transport	biological_process
945	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
945	GO:0006355	regulation of transcription, DNA-dependent	biological_process
948	GO:0006796	phosphate metabolism	biological_process
948	GO:0006817	phosphate transport	biological_process
949	GO:0006817	phosphate transport	biological_process
950	GO:0006817	phosphate transport	biological_process
951	GO:0006817	phosphate transport	biological_process
952	GO:0006817	phosphate transport	biological_process
953	GO:0006817	phosphate transport	biological_process
954	GO:0000074	regulation of progression through cell cycle	biological_process
954	GO:0000154	rRNA modification	biological_process
954	GO:0001510	RNA methylation	biological_process
954	GO:0006364	rRNA processing	biological_process
954	GO:0008284	positive regulation of cell proliferation	biological_process
955	GO:0006020	myo-inositol metabolism	biological_process
955	GO:0006661	phosphatidylinositol biosynthesis	biological_process
955	GO:0007165	signal transduction	biological_process
955	GO:0016311	dephosphorylation	biological_process
959	GO:0006747	FAD biosynthesis	biological_process
959	GO:0009231	riboflavin biosynthesis	biological_process
959	GO:0009398	FMN biosynthesis	biological_process
960	GO:0006400	tRNA modification	biological_process
984	GO:0006812	cation transport	biological_process
986	GO:0009396	folic acid and derivative biosynthesis	biological_process
987	GO:0006760	folic acid and derivative metabolism	biological_process

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ssu	acc	name	term_type
988	GO:0009396	folic acid and derivative biosynthesis	biological_process
989	GO:0006559	L-phenylalanine catabolism	biological_process
989	GO:0006727	ommochrome biosynthesis	biological_process
989	GO:0006729	tetrahydrobiopterin biosynthesis	biological_process
989	GO:0006809	nitric oxide biosynthesis	biological_process
989	GO:0042133	neurotransmitter metabolism	biological_process
989	GO:0046654	tetrahydrofolate biosynthesis	biological_process
995	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
997	GO:0006432	phenylalanyl-tRNA aminoacylation	biological_process
998	GO:0009254	peptidoglycan turnover	biological_process
998	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
999	GO:0009254	peptidoglycan turnover	biological_process
1001	GO:0008152	metabolism	biological_process
1004	GO:0009255	Entner-Doudoroff pathway	biological_process
1005	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1006	GO:0006027	glycosaminoglycan catabolism	biological_process
1011	GO:0009252	peptidoglycan biosynthesis	biological_process
1014	GO:0001321	age-dependent general metabolic decline during replicative cell aging	biological_process
1014	GO:0015986	ATP synthesis coupled proton transport	biological_process
1015	GO:0015986	ATP synthesis coupled proton transport	biological_process
1016	GO:0015986	ATP synthesis coupled proton transport	biological_process
1018	GO:0015986	ATP synthesis coupled proton transport	biological_process
1021	GO:0007205	protein kinase C activation	biological_process
1022	GO:0006260	DNA replication	biological_process
1022	GO:0006281	DNA repair	biological_process
1022	GO:0006310	DNA recombination	biological_process
1025	GO:0006010	glucose 6-phosphate utilization	biological_process
1025	GO:0006098	pentose-phosphate shunt	biological_process
1025	GO:0006749	glutathione metabolism	biological_process
1025	GO:0045767	regulation of anti-apoptosis	biological_process
1028	GO:0009306	protein secretion	biological_process
1031	GO:0000067	DNA replication and chromosome cycle	biological_process
1031	GO:0000910	cytokinesis	biological_process
1031	GO:0006302	double-strand break repair	biological_process
1031	GO:0007001	chromosome organization and biogenesis (sensu Eukaryota)	biological_process
1031	GO:0007064	mitotic sister chromatid cohesion	biological_process
1031	GO:0007076	mitotic chromosome condensation	biological_process
1032	GO:0006396	RNA processing	biological_process
1038	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1040	GO:0006099	tricarboxylic acid cycle	biological_process
1041	GO:0006099	tricarboxylic acid cycle	biological_process
1041	GO:0006113	fermentation	biological_process
1041	GO:0019629	propionate catabolism, 2-methylcitrate cycle	biological_process
1042	GO:0006447	regulation of translational initiation by iron	biological_process
1042	GO:0006879	iron ion homeostasis	biological_process
1042	GO:0008652	amino acid biosynthesis	biological_process

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ssu	acc	name	term_type
1042	GO:0016478	negative regulation of translation	biological_process
1042	GO:0019643	reductive tricarboxylic acid cycle	biological_process
1044	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
1046	GO:0008340	determination of adult life span	biological_process
1046	GO:0009186	deoxyribonucleoside diphosphate metabolism	biological_process
1046	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
1046	GO:0040035	hermaphrodite genital morphogenesis	biological_process
1047	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1055	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1055	GO:0015761	mannose transport	biological_process
1056	GO:0008645	hexose transport	biological_process
1056	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1057	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1059	GO:0008645	hexose transport	biological_process
1059	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1061	GO:0009255	Entner-Doudoroff pathway	biological_process
1064	GO:0006633	fatty acid biosynthesis	biological_process
1065	GO:0006313	DNA transposition	biological_process
1076	GO:0006419	alanyl-tRNA aminoacylation	biological_process
1082	GO:0006508	proteolysis and peptidolysis	biological_process
1084	GO:0006431	methionyl-tRNA aminoacylation	biological_process
1086	GO:0009423	chorismate biosynthesis	biological_process
1087	GO:0009423	chorismate biosynthesis	biological_process
1088	GO:0009423	chorismate biosynthesis	biological_process
1089	GO:0009423	chorismate biosynthesis	biological_process
1095	GO:0019512	lactose catabolism via tagatose-6-phosphate	biological_process
1096	GO:0006044	N-acetylglucosamine metabolism	biological_process
1098	GO:0019274	phenylalanine biosynthesis, prephenate pathway	biological_process
1099	GO:0009073	aromatic amino acid family biosynthesis	biological_process
1100	GO:0009423	chorismate biosynthesis	biological_process
1101	GO:0000004	biological process unknown	biological_process
1104	GO:0007046	ribosome biogenesis	biological_process
1106	GO:0006413	translational initiation	biological_process
1107	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
1113	GO:0000271	polysaccharide biosynthesis	biological_process
1116	GO:0000271	polysaccharide biosynthesis	biological_process
1121	GO:0015777	teichoic acid transport	biological_process
1121	GO:0015920	lipopolysaccharide transport	biological_process
1122	GO:0015777	teichoic acid transport	biological_process
1123	GO:0000271	polysaccharide biosynthesis	biological_process
1126	GO:0009253	peptidoglycan catabolism	biological_process
1126	GO:0016998	cell wall catabolism	biological_process
1127	GO:0009253	peptidoglycan catabolism	biological_process
1127	GO:0016998	cell wall catabolism	biological_process
1129	GO:0009243	O antigen biosynthesis	biological_process
1129	GO:0019305	dTDP-rhamnose biosynthesis	biological_process

续表 2

ssu	acc	name	term_type
1130	GO:0009103	lipopolysaccharide biosynthesis	biological_process
1130	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
1132	GO:0009243	O antigen biosynthesis	biological_process
1132	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
1133	GO:0009103	lipopolysaccharide biosynthesis	biological_process
1133	GO:0019305	dTDP-rhamnose biosynthesis	biological_process
1134	GO:0030001	metal ion transport	biological_process
1135	GO:0000004	biological process unknown	biological_process
1137	GO:0006269	DNA replication, synthesis of RNA primer	biological_process
1138	GO:0009086	methionine biosynthesis	biological_process
1139	GO:0006166	purine ribonucleoside salvage	biological_process
1139	GO:0006168	adenine salvage	biological_process
1141	GO:0006310	DNA recombination	biological_process
1142	GO:0008654	phospholipid biosynthesis	biological_process
1144	GO:0006703	estrogen biosynthesis	biological_process
1145	GO:0008033	tRNA processing	biological_process
1147	GO:0000004	biological process unknown	biological_process
1148	GO:0006400	tRNA modification	biological_process
1148	GO:0008033	tRNA processing	biological_process
1153	GO:0000004	biological process unknown	biological_process
1157	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
1157	GO:0015940	pantothenate biosynthesis	biological_process
1159	GO:0006412	protein biosynthesis	biological_process
1160	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process
1160	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
1161	GO:0000271	polysaccharide biosynthesis	biological_process
1161	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
1162	GO:0006805	xenobiotic metabolism	biological_process
1162	GO:0006808	regulation of nitrogen utilization	biological_process
1162	GO:0010044	response to aluminum ion	biological_process
1164	GO:0006412	protein biosynthesis	biological_process
1164	GO:0007046	ribosome biogenesis	biological_process
1165	GO:0006412	protein biosynthesis	biological_process
1168	GO:0000910	cytokinesis	biological_process
1169	GO:0005987	sucrose catabolism	biological_process
1172	GO:0008643	carbohydrate transport	biological_process
1173	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1177	GO:0006457	protein folding	biological_process
1177	GO:0006605	protein targeting	biological_process
1177	GO:0006836	neurotransmitter transport	biological_process
1179	GO:0006414	translational elongation	biological_process
1179	GO:0006415	translational termination	biological_process
1180	GO:0015672	monovalent inorganic cation transport	biological_process
1180	GO:0015693	magnesium ion transport	biological_process
1182	GO:0009252	peptidoglycan biosynthesis	biological_process
1184	GO:0009252	peptidoglycan biosynthesis	biological_process

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ssu	acc	name	term_type
1185	GO:0006281	DNA repair	biological_process
1185	GO:0006310	DNA recombination	biological_process
1186	GO:0009252	peptidoglycan biosynthesis	biological_process
1187	GO:0006810	transport	biological_process
1188	GO:0006810	transport	biological_process
1190	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1191	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1191	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1192	GO:0006865	amino acid transport	biological_process
1193	GO:0006865	amino acid transport	biological_process
1194	GO:0006865	amino acid transport	biological_process
1195	GO:0006868	L-glutamine transport	biological_process
1196	GO:0006435	threonyl-tRNA aminoacylation	biological_process
1199	GO:0006506	GPI anchor biosynthesis	biological_process
1199	GO:0016036	cellular response to phosphate starvation	biological_process
1199	GO:0046506	sulfolipid biosynthesis	biological_process
1200	GO:0000271	polysaccharide biosynthesis	biological_process
1200	GO:0042493	response to drug	biological_process
1202	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1203	GO:0006508	proteolysis and peptidolysis	biological_process
1204	GO:0008033	tRNA processing	biological_process
1204	GO:0008616	queuosine biosynthesis	biological_process
1208	GO:0006260	DNA replication	biological_process
1208	GO:0006308	DNA catabolism	biological_process
1211	GO:0006810	transport	biological_process
1213	GO:0006979	response to oxidative stress	biological_process
1214	GO:0006825	copper ion transport	biological_process
1214	GO:0009873	ethylene mediated signaling pathway	biological_process
1218	GO:0006450	regulation of translational fidelity	biological_process
1219	GO:0006396	RNA processing	biological_process
1219	GO:0006401	RNA catabolism	biological_process
1223	GO:0015937	coenzyme A biosynthesis	biological_process
1224	GO:0006281	DNA repair	biological_process
1225	GO:0016049	cell growth	biological_process
1226	GO:0008654	phospholipid biosynthesis	biological_process
1229	GO:0015758	glucose transport	biological_process
1230	GO:0006040	amino sugar metabolism	biological_process
1231	GO:0009405	pathogenesis	biological_process
1231	GO:0019836	hemolysis	biological_process
1233	GO:0006810	transport	biological_process
1234	GO:0006810	transport	biological_process
1237	GO:0015684	ferrous iron transport	biological_process
1238	GO:0000910	cytokinesis	biological_process
1239	GO:0000910	cytokinesis	biological_process
1239	GO:0006810	transport	biological_process
1240	GO:0006415	translational termination	biological_process

续表 2

ssu	acc	name	term_type
1241	GO:0006118	electron transport	biological_process
1246	GO:0006816	calcium ion transport	biological_process
1246	GO:0006828	manganese ion transport	biological_process
1246	GO:0006874	calcium ion homeostasis	biological_process
1246	GO:0006942	regulation of striated muscle contraction	biological_process
1246	GO:0015992	proton transport	biological_process
1246	GO:0018987	osmoregulation	biological_process
1250	GO:0006313	DNA transposition	biological_process
1251	GO:0006313	DNA transposition	biological_process
1255	GO:0006352	transcription initiation	biological_process
1256	GO:0006269	DNA replication, synthesis of RNA primer	biological_process
1258	GO:0009225	nucleotide-sugar metabolism	biological_process
1258	GO:0046369	galactose biosynthesis	biological_process
1261	GO:0016576	histone dephosphorylation	biological_process
1263	GO:0006633	fatty acid biosynthesis	biological_process
1264	GO:0006779	porphyrin biosynthesis	biological_process
1265	GO:0005980	glycogen catabolism	biological_process
1266	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	biological_process
1267	GO:0006144	purine base metabolism	biological_process
1267	GO:0006152	purine nucleoside catabolism	biological_process
1267	GO:0006166	purine ribonucleoside salvage	biological_process
1270	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
1273	GO:0006306	DNA methylation	biological_process
1274	GO:0009307	DNA restriction-modification system	biological_process
1275	GO:0006400	tRNA modification	biological_process
1275	GO:0009636	response to toxin	biological_process
1278	GO:0007155	cell adhesion	biological_process
1278	GO:0008544	epidermis development	biological_process
1279	GO:0000004	biological process unknown	biological_process
1283	GO:0006508	proteolysis and peptidolysis	biological_process
1284	GO:0006835	dicarboxylic acid transport	biological_process
1284	GO:0007268	synaptic transmission	biological_process
1284	GO:0015804	neutral amino acid transport	biological_process
1284	GO:0015810	L-aspartate transport	biological_process
1284	GO:0015813	L-glutamate transport	biological_process
1289	GO:0006810	transport	biological_process
1290	GO:0009103	lipopolysaccharide biosynthesis	biological_process
1290	GO:0009252	peptidoglycan biosynthesis	biological_process
1295	GO:0000154	rRNA modification	biological_process
1298	GO:0006810	transport	biological_process
1301	GO:0006644	phospholipid metabolism	biological_process
1305	GO:0015847	putrescine transport	biological_process
1305	GO:0015848	spermidine transport	biological_process
1307	GO:0000004	biological process unknown	biological_process
1308	GO:0030245	cellulose catabolism	biological_process
1309	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process

续表 2

ssu	acc	name	term_type
1309	GO:0015759	beta-glucoside transport	biological_process
1309	GO:0015771	trehalose transport	biological_process
1310	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1311	GO:0009405	pathogenesis	biological_process
1312	GO:0019660	glycolytic fermentation	biological_process
1320	GO:0006096	glycolysis	biological_process
1322	GO:0009436	glyoxylate catabolism	biological_process
1323	GO:0005975	carbohydrate metabolism	biological_process
1325	GO:0006545	glycine biosynthesis	biological_process
1325	GO:0006564	L-serine biosynthesis	biological_process
1326	GO:0000918	selection of site for barrier septum formation	biological_process
1327	GO:0006260	DNA replication	biological_process
1327	GO:0006265	DNA topological change	biological_process
1328	GO:0006457	protein folding	biological_process
1328	GO:0006732	coenzyme metabolism	biological_process
1328	GO:0007265	Ras protein signal transduction	biological_process
1328	GO:0009110	vitamin biosynthesis	biological_process
1328	GO:0051189	prosthetic group metabolism	biological_process
1329	GO:0000910	cytokinesis	biological_process
1329	GO:0008360	regulation of cell shape	biological_process
1348	GO:0007046	ribosome biogenesis	biological_process
1349	GO:0009228	thiamin biosynthesis	biological_process
1352	GO:0006412	protein biosynthesis	biological_process
1355	GO:0009166	nucleotide catabolism	biological_process
1355	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
1356	GO:0006801	superoxide metabolism	biological_process
1360	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
1361	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
1362	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
1363	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
1364	GO:0015803	branched-chain aliphatic amino acid transport	biological_process
1366	GO:0006510	ATP-dependent proteolysis	biological_process
1367	GO:0008655	pyrimidine salvage	biological_process
1367	GO:0009116	nucleoside metabolism	biological_process
1368	GO:0000025	maltose catabolism	biological_process
1368	GO:0005993	trehalose catabolism	biological_process
1369	GO:0005987	sucrose catabolism	biological_process
1370	GO:0008643	carbohydrate transport	biological_process
1371	GO:0008643	carbohydrate transport	biological_process
1374	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1375	GO:0009073	aromatic amino acid family biosynthesis	biological_process
1376	GO:0009086	methionine biosynthesis	biological_process
1376	GO:0019344	cysteine biosynthesis	biological_process
1376	GO:0019346	transsulfuration	biological_process
1383	GO:0009108	coenzyme biosynthesis	biological_process
1387	GO:0006401	RNA catabolism	biological_process

续表 2

ssu	acc	name	term_type
1387	GO:0009631	cold acclimation	biological_process
1390	GO:0006961	antibacterial humoral response (sensu Protostomia)	biological_process
1390	GO:0009405	pathogenesis	biological_process
1390	GO:0016203	muscle attachment	biological_process
1390	GO:0030260	entry into host cell	biological_process
1397	GO:0009103	lipopolysaccharide biosynthesis	biological_process
1397	GO:0009252	peptidoglycan biosynthesis	biological_process
1405	GO:0006313	DNA transposition	biological_process
1408	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1409	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1409	GO:0006817	phosphate transport	biological_process
1411	GO:0009073	aromatic amino acid family biosynthesis	biological_process
1413	GO:0015697	quaternary ammonium group transport	biological_process
1413	GO:0018987	osmoregulation	biological_process
1414	GO:0015697	quaternary ammonium group transport	biological_process
1414	GO:0018987	osmoregulation	biological_process
1418	GO:0009249	protein-lipoylation	biological_process
1419	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1419	GO:0045013	negative regulation of transcription by carbon catabolites	biological_process
1426	GO:0006325	establishment and/or maintenance of chromatin architecture	biological_process
1426	GO:0007242	intracellular signaling cascade	biological_process
1426	GO:0009299	mRNA transcription	biological_process
1427	GO:0009651	response to salt stress	biological_process
1427	GO:0019568	arabinose catabolism	biological_process
1427	GO:0042843	D-xylose catabolism	biological_process
1431	GO:0006464	protein modification	biological_process
1433	GO:0009252	peptidoglycan biosynthesis	biological_process
1434	GO:0006118	electron transport	biological_process
1434	GO:0006805	xenobiotic metabolism	biological_process
1434	GO:0006809	nitric oxide biosynthesis	biological_process
1434	GO:0007271	synaptic transmission, cholinergic	biological_process
1434	GO:0009636	response to toxin	biological_process
1435	GO:0006555	methionine metabolism	biological_process
1435	GO:0006556	S-adenosylmethionine biosynthesis	biological_process
1436	GO:0006206	pyrimidine base metabolism	biological_process
1436	GO:0006220	pyrimidine nucleotide metabolism	biological_process
1436	GO:0009165	nucleotide biosynthesis	biological_process
1439	GO:0009102	biotin biosynthesis	biological_process
1439	GO:0018054	peptidyl-lysine biotinylation	biological_process
1441	GO:0006260	DNA replication	biological_process
1445	GO:0005975	carbohydrate metabolism	biological_process
1445	GO:0008655	pyrimidine salvage	biological_process
1445	GO:0009058	biosynthesis	biological_process
1445	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process
1445	GO:0046108	uridine metabolism	biological_process
1446	GO:0006118	electron transport	biological_process

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ssu	acc	name	term_type
1447	GO:0009631	cold acclimation	biological_process
1448	GO:0005975	carbohydrate metabolism	biological_process
1449	GO:0005975	carbohydrate metabolism	biological_process
1449	GO:0009438	methylglyoxal metabolism	biological_process
1450	GO:0006313	DNA transposition	biological_process
1451	GO:0006096	glycolysis	biological_process
1451	GO:0006941	striated muscle contraction	biological_process
1452	GO:0006629	lipid metabolism	biological_process
1453	GO:0006554	lysine catabolism	biological_process
1453	GO:0006695	cholesterol biosynthesis	biological_process
1453	GO:0006696	ergosterol biosynthesis	biological_process
1453	GO:0006700	C21-steroid hormone biosynthesis	biological_process
1453	GO:0007548	sex differentiation	biological_process
1453	GO:0019287	isopentenyl diphosphate biosynthesis, mevalonate pathway	biological_process
1453	GO:0046951	ketone body biosynthesis	biological_process
1455	GO:0006313	DNA transposition	biological_process
1457	GO:0006313	DNA transposition	biological_process
1458	GO:0006323	DNA packaging	biological_process
1462	GO:0006281	DNA repair	biological_process
1462	GO:0006310	DNA recombination	biological_process
1464	GO:0009405	pathogenesis	biological_process
1464	GO:0019836	hemolysis	biological_process
1465	GO:0016114	terpenoid biosynthesis	biological_process
1465	GO:0045337	farnesyl diphosphate biosynthesis	biological_process
1467	GO:0006308	DNA catabolism	biological_process
1472	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1472	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1478	GO:0006793	phosphorus metabolism	biological_process
1480	GO:0006113	fermentation	biological_process
1480	GO:0006800	oxygen and reactive oxygen species metabolism	biological_process
1481	GO:0000004	biological process unknown	biological_process
1482	GO:0006826	iron ion transport	biological_process
1484	GO:0009306	protein secretion	biological_process
1484	GO:0009405	pathogenesis	biological_process
1485	GO:0019358	nicotinate nucleotide salvage	biological_process
1485	GO:0019363	pyridine nucleotide biosynthesis	biological_process
1486	GO:0009435	NAD biosynthesis	biological_process
1488	GO:0000004	biological process unknown	biological_process
1491	GO:0015937	coenzyme A biosynthesis	biological_process
1496	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1497	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1499	GO:0008643	carbohydrate transport	biological_process
1502	GO:0006470	protein amino acid dephosphorylation	biological_process
1507	GO:0000154	rRNA modification	biological_process
1507	GO:0001510	RNA methylation	biological_process
1507	GO:0006396	RNA processing	biological_process

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ssu	acc	name	term_type
1510	GO:0000154	rRNA modification	biological_process
1511	GO:0007059	chromosome segregation	biological_process
1511	GO:0030261	chromosome condensation	biological_process
1512	GO:0007059	chromosome segregation	biological_process
1512	GO:0030261	chromosome condensation	biological_process
1516	GO:0000004	biological process unknown	biological_process
1517	GO:0009252	peptidoglycan biosynthesis	biological_process
1519	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
1520	GO:0006508	proteolysis and peptidolysis	biological_process
1520	GO:0009407	toxin catabolism	biological_process
1520	GO:0046677	response to antibiotic	biological_process
1523	GO:0001510	RNA methylation	biological_process
1523	GO:0006396	RNA processing	biological_process
1526	GO:0006354	RNA elongation	biological_process
1527	GO:0000004	biological process unknown	biological_process
1529	GO:0009252	peptidoglycan biosynthesis	biological_process
1531	GO:0006348	chromatin silencing at telomere	biological_process
1531	GO:0016584	nucleosome spacing	biological_process
1531	GO:0046020	negative regulation of transcription from RNA polymerase II promoter by pheromones	biological_process
1534	GO:0000004	biological process unknown	biological_process
1538	GO:0000004	biological process unknown	biological_process
1540	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1541	GO:0006098	pentose-phosphate shunt	biological_process
1543	GO:0006739	NADP metabolism	biological_process
1543	GO:0030503	regulation of cell redox homeostasis	biological_process
1545	GO:0006364	rRNA processing	biological_process
1545	GO:0042255	ribosome assembly	biological_process
1547	GO:0009252	peptidoglycan biosynthesis	biological_process
1548	GO:0009252	peptidoglycan biosynthesis	biological_process
1550	GO:0000004	biological process unknown	biological_process
1559	GO:0009228	thiamin biosynthesis	biological_process
1561	GO:0006744	ubiquinone biosynthesis	biological_process
1561	GO:0009234	menaquinone biosynthesis	biological_process
1562	GO:0006118	electron transport	biological_process
1565	GO:0006813	potassium ion transport	biological_process
1566	GO:0006813	potassium ion transport	biological_process
1567	GO:0006855	multidrug transport	biological_process
1570	GO:0006426	glycyl-tRNA aminoacylation	biological_process
1571	GO:0006426	glycyl-tRNA aminoacylation	biological_process
1574	GO:0006810	transport	biological_process
1575	GO:0048473	D-methionine transport	biological_process
1576	GO:0006508	proteolysis and peptidolysis	biological_process
1577	GO:0048473	D-methionine transport	biological_process
1579	GO:0009086	methionine biosynthesis	biological_process
1580	GO:0008015	circulation	biological_process
1580	GO:0009086	methionine biosynthesis	biological_process

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ssu	acc	name	term_type
1581	GO:0015860	purine nucleoside transport	biological_process
1583	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1584	GO:0008645	hexose transport	biological_process
1584	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1585	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1585	GO:0015761	mannose transport	biological_process
1587	GO:0006434	seryl-tRNA aminoacylation	biological_process
1588	GO:0006304	DNA modification	biological_process
1590	GO:0009307	DNA restriction-modification system	biological_process
1597	GO:0006633	fatty acid biosynthesis	biological_process
1598	GO:0006633	fatty acid biosynthesis	biological_process
1599	GO:0006633	fatty acid biosynthesis	biological_process
1600	GO:0006633	fatty acid biosynthesis	biological_process
1601	GO:0006633	fatty acid biosynthesis	biological_process
1602	GO:0006633	fatty acid biosynthesis	biological_process
1603	GO:0006633	fatty acid biosynthesis	biological_process
1604	GO:0006633	fatty acid biosynthesis	biological_process
1605	GO:0008654	phospholipid biosynthesis	biological_process
1607	GO:0006633	fatty acid biosynthesis	biological_process
1611	GO:0006532	aspartate biosynthesis	biological_process
1611	GO:0009088	threonine biosynthesis	biological_process
1611	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
1613	GO:0009252	peptidoglycan biosynthesis	biological_process
1615	GO:0015628	type II protein secretion system	biological_process
1616	GO:0001403	invasive growth (sensu Saccharomyces)	biological_process
1616	GO:0007124	pseudohyphal growth	biological_process
1616	GO:0016337	cell-cell adhesion	biological_process
1617	GO:0005985	sucrose metabolism	biological_process
1618	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1618	GO:0015759	beta-glucoside transport	biological_process
1618	GO:0015771	trehalose transport	biological_process
1619	GO:0005976	polysaccharide metabolism	biological_process
1620	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1621	GO:0006353	transcription termination	biological_process
1623	GO:0006414	translational elongation	biological_process
1624	GO:0006508	proteolysis and peptidolysis	biological_process
1625	GO:0006289	nucleotide-excision repair	biological_process
1626	GO:0015693	magnesium ion transport	biological_process
1629	GO:0006260	DNA replication	biological_process
1629	GO:0006281	DNA repair	biological_process
1629	GO:0006310	DNA recombination	biological_process
1632	GO:0006464	protein modification	biological_process
1632	GO:0006629	lipid metabolism	biological_process
1632	GO:0009108	coenzyme biosynthesis	biological_process
1634	GO:0006086	acetyl-CoA biosynthesis from pyruvate	biological_process
1634	GO:0006118	electron transport	biological_process

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ssu	acc	name	term_type
1634	GO:0006546	glycine catabolism	biological_process
1634	GO:0006550	isoleucine catabolism	biological_process
1634	GO:0006552	leucine catabolism	biological_process
1634	GO:0006564	L-serine biosynthesis	biological_process
1634	GO:0006574	valine catabolism	biological_process
1634	GO:0006748	lipoamide metabolism	biological_process
1635	GO:0006090	pyruvate metabolism	biological_process
1635	GO:0006554	lysine catabolism	biological_process
1636	GO:0006090	pyruvate metabolism	biological_process
1636	GO:0006096	glycolysis	biological_process
1636	GO:0006099	tricarboxylic acid cycle	biological_process
1637	GO:0006084	acetyl-CoA metabolism	biological_process
1637	GO:0006090	pyruvate metabolism	biological_process
1637	GO:0006096	glycolysis	biological_process
1641	GO:0006396	RNA processing	biological_process
1642	GO:0006413	translational initiation	biological_process
1645	GO:0006353	transcription termination	biological_process
1646	GO:0000004	biological process unknown	biological_process
1647	GO:0006400	tRNA modification	biological_process
1650	GO:0006825	copper ion transport	biological_process
1653	GO:0045449	regulation of transcription	biological_process
1655	GO:0000004	biological process unknown	biological_process
1659	GO:0006313	DNA transposition	biological_process
1660	GO:0015833	peptide transport	biological_process
1661	GO:0006857	oligopeptide transport	biological_process
1663	GO:0015833	peptide transport	biological_process
1664	GO:0006857	oligopeptide transport	biological_process
1665	GO:0009252	peptidoglycan biosynthesis	biological_process
1666	GO:0016226	iron-sulfur cluster assembly	biological_process
1669	GO:0016226	iron-sulfur cluster assembly	biological_process
1669	GO:0016261	selenocysteine catabolism	biological_process
1670	GO:0016226	iron-sulfur cluster assembly	biological_process
1671	GO:0016226	iron-sulfur cluster assembly	biological_process
1672	GO:0009243	O antigen biosynthesis	biological_process
1672	GO:0009252	peptidoglycan biosynthesis	biological_process
1674	GO:0046677	response to antibiotic	biological_process
1675	GO:0006868	L-glutamine transport	biological_process
1676	GO:0006865	amino acid transport	biological_process
1679	GO:0006566	threonine metabolism	biological_process
1679	GO:0009097	isoleucine biosynthesis	biological_process
1680	GO:0009097	isoleucine biosynthesis	biological_process
1680	GO:0009099	valine biosynthesis	biological_process
1681	GO:0009097	isoleucine biosynthesis	biological_process
1681	GO:0009099	valine biosynthesis	biological_process
1682	GO:0009097	isoleucine biosynthesis	biological_process
1682	GO:0009099	valine biosynthesis	biological_process

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ssu	acc	name	term_type
1683	GO:0000271	polysaccharide biosynthesis	biological_process
1686	GO:0009097	isoleucine biosynthesis	biological_process
1686	GO:0009099	valine biosynthesis	biological_process
1691	GO:0006412	protein biosynthesis	biological_process
1691	GO:0007046	ribosome biogenesis	biological_process
1692	GO:0006412	protein biosynthesis	biological_process
1696	GO:0000154	rRNA modification	biological_process
1696	GO:0001510	RNA methylation	biological_process
1701	GO:0015768	maltose transport	biological_process
1703	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1703	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1703	GO:0009236	cobalamin biosynthesis	biological_process
1704	GO:0000160	two-component signal transduction system (phosphorelay)	biological_process
1708	GO:0008643	carbohydrate transport	biological_process
1709	GO:0006810	transport	biological_process
1712	GO:0005975	carbohydrate metabolism	biological_process
1717	GO:0006423	cysteinyl-tRNA aminoacylation	biological_process
1720	GO:0006535	cysteine biosynthesis from serine	biological_process
1721	GO:0006402	mRNA catabolism	biological_process
1725	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1725	GO:0015759	beta-glucoside transport	biological_process
1725	GO:0015770	sucrose transport	biological_process
1725	GO:0015771	trehalose transport	biological_process
1727	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1728	GO:0006412	protein biosynthesis	biological_process
1728	GO:0007046	ribosome biogenesis	biological_process
1729	GO:0015857	uracil transport	biological_process
1732	GO:0000154	rRNA modification	biological_process
1736	GO:0006464	protein modification	biological_process
1738	GO:0009098	leucine biosynthesis	biological_process
1739	GO:0009098	leucine biosynthesis	biological_process
1740	GO:0009098	leucine biosynthesis	biological_process
1741	GO:0009098	leucine biosynthesis	biological_process
1744	GO:0045922	negative regulation of fatty acid metabolism	biological_process
1746	GO:0006260	DNA replication	biological_process
1747	GO:0019563	glycerol catabolism	biological_process
1749	GO:0019563	glycerol catabolism	biological_process
1750	GO:0019563	glycerol catabolism	biological_process
1752	GO:0006833	water transport	biological_process
1752	GO:0006863	purine transport	biological_process
1752	GO:0006970	response to osmotic stress	biological_process
1752	GO:0007588	excretion	biological_process
1752	GO:0009935	nutrient import	biological_process
1752	GO:0010033	response to organic substance	biological_process
1752	GO:0015722	canalicular bile acid transport	biological_process
1752	GO:0015793	glycerol transport	biological_process

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ssu	acc	name	term_type
1752	GO:0015837	amine transport	biological_process
1752	GO:0015855	pyrimidine transport	biological_process
1752	GO:0030104	water homeostasis	biological_process
1752	GO:0046689	response to mercury ion	biological_process
1753	GO:0006433	prolyl-tRNA aminoacylation	biological_process
1754	GO:0006508	proteolysis and peptidolysis	biological_process
1755	GO:0008654	phospholipid biosynthesis	biological_process
1756	GO:0009252	peptidoglycan biosynthesis	biological_process
1756	GO:0019408	dolichol biosynthesis	biological_process
1758	GO:0009152	purine ribonucleotide biosynthesis	biological_process
1759	GO:0006750	glutathione biosynthesis	biological_process
1761	GO:0006457	protein folding	biological_process
1761	GO:0006979	response to oxidative stress	biological_process
1761	GO:0050821	protein stabilization	biological_process
1762	GO:0006400	tRNA modification	biological_process
1766	GO:0006289	nucleotide-excision repair	biological_process
1766	GO:0006510	ATP-dependent proteolysis	biological_process
1770	GO:0006414	translational elongation	biological_process
1771	GO:0006412	protein biosynthesis	biological_process
1774	GO:0006353	transcription termination	biological_process
1777	GO:0009252	peptidoglycan biosynthesis	biological_process
1779	GO:0000154	rRNA modification	biological_process
1784	GO:0006772	thiamin metabolism	biological_process
1785	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process
1786	GO:0000004	biological process unknown	biological_process
1787	GO:0006810	transport	biological_process
1789	GO:0045941	positive regulation of transcription	biological_process
1793	GO:0000154	rRNA modification	biological_process
1793	GO:0046677	response to antibiotic	biological_process
1802	GO:0006308	DNA catabolism	biological_process
1805	GO:0000004	biological process unknown	biological_process
1807	GO:0000050	urea cycle	biological_process
1807	GO:0006526	arginine biosynthesis	biological_process
1807	GO:0006527	arginine catabolism	biological_process
1808	GO:0000050	urea cycle	biological_process
1808	GO:0000053	argininosuccinate metabolism	biological_process
1808	GO:0006526	arginine biosynthesis	biological_process
1813	GO:0009086	methionine biosynthesis	biological_process
1813	GO:0009396	folic acid and derivative biosynthesis	biological_process
1814	GO:0015819	L-lysine transport	biological_process
1815	GO:0006424	glutamyl-tRNA aminoacylation	biological_process
1820	GO:0006730	one-carbon compound metabolism	biological_process
1821	GO:0006281	DNA repair	biological_process
1823	GO:0009394	2'-deoxyribonucleotide metabolism	biological_process
1824	GO:0006810	transport	biological_process
1825	GO:0006858	extracellular transport	biological_process

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ssu	acc	name	term_type
1827	GO:0006072	glycerol-3-phosphate metabolism	biological_process
1827	GO:0008654	phospholipid biosynthesis	biological_process
1828	GO:0005976	polysaccharide metabolism	biological_process
1828	GO:0006012	galactose metabolism	biological_process
1828	GO:0009225	nucleotide-sugar metabolism	biological_process
1828	GO:0019255	glucose 1-phosphate metabolism	biological_process
1830	GO:0015942	formate metabolism	biological_process
1830	GO:0045978	negative regulation of nucleoside metabolism	biological_process
1831	GO:0006508	proteolysis and peptidolysis	biological_process
1832	GO:0009089	lysine biosynthesis via diaminopimelate	biological_process
1835	GO:0006470	protein amino acid dephosphorylation	biological_process
1836	GO:0006094	gluconeogenesis	biological_process
1836	GO:0006096	glycolysis	biological_process
1836	GO:0006098	pentose-phosphate shunt	biological_process
1838	GO:0000004	biological process unknown	biological_process
1839	GO:0006098	pentose-phosphate shunt	biological_process
1841	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1846	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1850	GO:0006355	regulation of transcription, DNA-dependent	biological_process
1851	GO:0006865	amino acid transport	biological_process
1852	GO:0006868	L-glutamine transport	biological_process
1853	GO:0006865	amino acid transport	biological_process
1855	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1855	GO:0015759	beta-glucoside transport	biological_process
1855	GO:0019533	cellobiose transport	biological_process
1857	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1857	GO:0015759	beta-glucoside transport	biological_process
1858	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process
1858	GO:0015759	beta-glucoside transport	biological_process
1858	GO:0019533	cellobiose transport	biological_process
1859	GO:0000004	biological process unknown	biological_process
1861	GO:0030245	cellulose catabolism	biological_process
1863	GO:0006429	leucyl-tRNA aminoacylation	biological_process
1864	GO:0006508	proteolysis and peptidolysis	biological_process
1864	GO:0007218	neuropeptide signaling pathway	biological_process
1864	GO:0007267	cell-cell signaling	biological_process
1864	GO:0010002	cardioblast differentiation	biological_process
1864	GO:0016486	peptide hormone processing	biological_process
1864	GO:0042310	vasoconstriction	biological_process
1866	GO:0006828	manganese ion transport	biological_process
1866	GO:0006829	zinc ion transport	biological_process
1867	GO:0006826	iron ion transport	biological_process
1867	GO:0006828	manganese ion transport	biological_process
1867	GO:0006829	zinc ion transport	biological_process
1869	GO:0006828	manganese ion transport	biological_process
1869	GO:0006829	zinc ion transport	biological_process

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ssu	acc	name	term_type
1877	GO:0006412	protein biosynthesis	biological_process
1877	GO:0019478	D-amino acid catabolism	biological_process
1878	GO:0015968	stringent response	biological_process
1879	GO:0006259	DNA metabolism	biological_process
1879	GO:0009166	nucleotide catabolism	biological_process
1888	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process
1893	GO:0000004	biological process unknown	biological_process
1894	GO:0006464	protein modification	biological_process
1894	GO:0042254	ribosome biogenesis and assembly	biological_process
1898	GO:0000731	DNA synthesis during DNA repair	biological_process
1898	GO:0030174	regulation of DNA replication initiation	biological_process
1899	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
1901	GO:0009166	nucleotide catabolism	biological_process
1903	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process
1908	GO:0006298	mismatch repair	biological_process
1910	GO:0006420	arginyl-tRNA aminoacylation	biological_process
1910	GO:0040019	positive regulation of embryonic development	biological_process
1914	GO:0005980	glycogen catabolism	biological_process
1915	GO:0008643	carbohydrate transport	biological_process
1916	GO:0015768	maltose transport	biological_process
1917	GO:0008643	carbohydrate transport	biological_process
1920	GO:0005980	glycogen catabolism	biological_process
1922	GO:0000004	biological process unknown	biological_process
1923	GO:0006422	aspartyl-tRNA aminoacylation	biological_process
1925	GO:0006813	potassium ion transport	biological_process
1927	GO:0005976	polysaccharide metabolism	biological_process
1933	GO:0006099	tricarboxylic acid cycle	biological_process
1933	GO:0006118	electron transport	biological_process
1933	GO:0009061	anaerobic respiration	biological_process
1933	GO:0009094	L-phenylalanine biosynthesis	biological_process
1935	GO:0006412	protein biosynthesis	biological_process
1938	GO:0006270	DNA replication initiation	biological_process
1938	GO:0006271	DNA strand elongation	biological_process
1939	GO:0007046	ribosome biogenesis	biological_process
1941	GO:0000004	biological process unknown	biological_process
1947	GO:0008033	tRNA processing	biological_process
1948	GO:0006094	gluconeogenesis	biological_process
1948	GO:0006565	L-serine catabolism	biological_process
1949	GO:0006094	gluconeogenesis	biological_process
1949	GO:0006565	L-serine catabolism	biological_process
1951	GO:0006824	cobalt ion transport	biological_process
1952	GO:0006824	cobalt ion transport	biological_process
1953	GO:0006824	cobalt ion transport	biological_process
1954	GO:0008654	phospholipid biosynthesis	biological_process
1959	GO:0006260	DNA replication	biological_process
1959	GO:0006281	DNA repair	biological_process

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ssu	acc	name	term_type
1959	GO:0006310	DNA recombination	biological_process
1959	GO:0009432	SOS response	biological_process
1960	GO:0009152	purine ribonucleotide biosynthesis	biological_process
1961	GO:0006436	tryptophanyl-tRNA aminoacylation	biological_process
1962	GO:0000004	biological process unknown	biological_process
1963	GO:0006810	transport	biological_process
1967	GO:0000004	biological process unknown	biological_process
1968	GO:0006508	proteolysis and peptidolysis	biological_process
1969	GO:0000910	cytokinesis	biological_process
2	GO:0009360	DNA polymerase III complex	cellular_component
7	GO:0009536	plastid	cellular_component
14	GO:0005737	cytoplasm	cellular_component
21	GO:0009507	chloroplast	cellular_component
26	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
28	GO:0009507	chloroplast	cellular_component
30	GO:0005737	cytoplasm	cellular_component
31	GO:0009536	plastid	cellular_component
32	GO:0005737	cytoplasm	cellular_component
33	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
34	GO:0009320	phosphoribosylaminoimidazole carboxylase complex	cellular_component
44	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component
46	GO:0009379	Holliday junction helicase complex	cellular_component
54	GO:0005739	mitochondrion	cellular_component
54	GO:0009570	chloroplast stroma	cellular_component
58	GO:0009379	Holliday junction helicase complex	cellular_component
60	GO:0009507	chloroplast	cellular_component
69	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
70	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
71	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
72	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
73	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
74	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
75	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
76	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
77	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
79	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
80	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
81	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
82	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
83	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
85	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
88	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
89	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
90	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
92	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
93	GO:0015627	type II protein secretion system complex	cellular_component

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ssu	acc	name	term_type
94	GO:0005758	mitochondrial intermembrane space	cellular_component
97	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
98	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
100	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
120	GO:0005739	mitochondrion	cellular_component
126	GO:0015627	type II protein secretion system complex	cellular_component
148	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
149	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
152	GO:0005794	Golgi apparatus	cellular_component
152	GO:0005887	integral to plasma membrane	cellular_component
152	GO:0030659	cytoplasmic vesicle membrane	cellular_component
154	GO:0005964	phosphorylase kinase complex	cellular_component
164	GO:0009897	external side of plasma membrane	cellular_component
164	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
164	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
165	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
174	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component
176	GO:0012505	endomembrane system	cellular_component
209	GO:0005770	late endosome	cellular_component
209	GO:0005795	Golgi stack	cellular_component
209	GO:0005889	hydrogen:potassium-exchanging ATPase complex	cellular_component
209	GO:0030140	trans-Golgi network transport vesicle	cellular_component
211	GO:0009338	exodeoxyribonuclease V complex	cellular_component
221	GO:0009507	chloroplast	cellular_component
225	GO:0005783	endoplasmic reticulum	cellular_component
229	GO:0009898	internal side of plasma membrane	cellular_component
229	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
249	GO:0005887	integral to plasma membrane	cellular_component
249	GO:0016323	basolateral plasma membrane	cellular_component
253	GO:0000786	nucleosome	cellular_component
253	GO:0005615	extracellular space	cellular_component
253	GO:0005859	muscle myosin	cellular_component
253	GO:0005883	neurofilament	cellular_component
253	GO:0030018	Z disc	cellular_component
253	GO:0030424	axon	cellular_component
253	GO:0031430	M line	cellular_component
253	GO:0045202	synapse	cellular_component
260	GO:0005737	cytoplasm	cellular_component
263	GO:0005743	mitochondrial inner membrane	cellular_component
267	GO:0009898	internal side of plasma membrane	cellular_component
267	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
270	GO:0005782	peroxisomal matrix	cellular_component
270	GO:0005829	cytosol	cellular_component
298	GO:0008021	synaptic vesicle	cellular_component
300	GO:0005615	extracellular space	cellular_component
300	GO:0008372	cellular component unknown	cellular_component

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ssu	acc	name	term_type
300	GO:0009706	chloroplast inner membrane	cellular_component
315	GO:0030287	periplasmic space (sensu Fungi)	cellular_component
322	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
353	GO:0009507	chloroplast	cellular_component
360	GO:0008372	cellular component unknown	cellular_component
380	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
389	GO:0008372	cellular component unknown	cellular_component
391	GO:0005739	mitochondrion	cellular_component
395	GO:0005840	ribosome	cellular_component
402	GO:0005764	lysosome	cellular_component
402	GO:0009341	beta-galactosidase complex	cellular_component
402	GO:0012505	endomembrane system	cellular_component
402	GO:0016023	cytoplasmic membrane-bound vesicle	cellular_component
434	GO:0045298	tubulin	cellular_component
464	GO:0005739	mitochondrion	cellular_component
466	GO:0005887	integral to plasma membrane	cellular_component
466	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
467	GO:0005887	integral to plasma membrane	cellular_component
467	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
485	GO:0008372	cellular component unknown	cellular_component
493	GO:0009360	DNA polymerase III complex	cellular_component
494	GO:0005945	6-phosphofructokinase complex	cellular_component
495	GO:0005829	cytosol	cellular_component
503	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
507	GO:0009360	DNA polymerase III complex	cellular_component
535	GO:0005829	cytosol	cellular_component
538	GO:0005634	nucleus	cellular_component
557	GO:0009507	chloroplast	cellular_component
559	GO:0009507	chloroplast	cellular_component
570	GO:0005625	soluble fraction	cellular_component
570	GO:0005737	cytoplasm	cellular_component
582	GO:0005759	mitochondrial matrix	cellular_component
582	GO:0009289	fimbrium	cellular_component
582	GO:0009348	ornithine carbamoyltransferase complex	cellular_component
606	GO:0009897	external side of plasma membrane	cellular_component
618	GO:0009360	DNA polymerase III complex	cellular_component
621	GO:0009507	chloroplast	cellular_component
627	GO:0005634	nucleus	cellular_component
627	GO:0005783	endoplasmic reticulum	cellular_component
627	GO:0005840	ribosome	cellular_component
627	GO:0048471	perinuclear region	cellular_component
629	GO:0016020	membrane	cellular_component
651	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
652	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
676	GO:0005739	mitochondrion	cellular_component
676	GO:0009331	glycerol-3-phosphate dehydrogenase complex	cellular_component

续表 2

ssu	acc	name	term_type
677	GO:0005741	mitochondrial outer membrane	cellular_component
677	GO:0005887	integral to plasma membrane	cellular_component
677	GO:0016323	basolateral plasma membrane	cellular_component
702	GO:0009380	excinuclease ABC complex	cellular_component
710	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
710	GO:0009340	DNA topoisomerase IV complex	cellular_component
717	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
717	GO:0009340	DNA topoisomerase IV complex	cellular_component
719	GO:0005739	mitochondrion	cellular_component
719	GO:0005829	cytosol	cellular_component
721	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
725	GO:0005759	mitochondrial matrix	cellular_component
728	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
729	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
737	GO:0005951	carbamoyl-phosphate synthase complex	cellular_component
738	GO:0005951	carbamoyl-phosphate synthase complex	cellular_component
742	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
751	GO:0009898	internal side of plasma membrane	cellular_component
751	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
752	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
753	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
754	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
754	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
757	GO:0012505	endomembrane system	cellular_component
781	GO:0009368	endopeptidase Clp complex	cellular_component
783	GO:0005625	soluble fraction	cellular_component
783	GO:0005758	mitochondrial intermembrane space	cellular_component
783	GO:0005792	microsome	cellular_component
819	GO:0005786	signal recognition particle (sensu Eukaryota)	cellular_component
819	GO:0048501	signal recognition particle (sensu Bacteria and Archaea)	cellular_component
845	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
846	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
857	GO:0009536	plastid	cellular_component
859	GO:0030428	cell septum	cellular_component
860	GO:0005624	membrane fraction	cellular_component
860	GO:0016020	membrane	cellular_component
867	GO:0005737	cytoplasm	cellular_component
870	GO:0009536	plastid	cellular_component
873	GO:0009507	chloroplast	cellular_component
875	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
876	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
882	GO:0009380	excinuclease ABC complex	cellular_component
886	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component
891	GO:0012505	endomembrane system	cellular_component
918	GO:0009507	chloroplast	cellular_component
919	GO:0005759	mitochondrial matrix	cellular_component

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ssu	acc	name	term_type
926	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
927	GO:0005737	cytoplasm	cellular_component
937	GO:0005625	soluble fraction	cellular_component
949	GO:0009898	internal side of plasma membrane	cellular_component
949	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
950	GO:0009898	internal side of plasma membrane	cellular_component
950	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
951	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
952	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
953	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
954	GO:0005730	nucleolus	cellular_component
955	GO:0008372	cellular component unknown	cellular_component
995	GO:0009328	phenylalanine-tRNA ligase complex	cellular_component
997	GO:0009328	phenylalanine-tRNA ligase complex	cellular_component
1001	GO:0020011	apicoplast	cellular_component
1006	GO:0005764	lysosome	cellular_component
1014	GO:0005625	soluble fraction	cellular_component
1014	GO:0005754	proton-transporting ATP synthase, catalytic core (sensu Eukaryota)	cellular_component
1014	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
1015	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
1016	GO:0045262	proton-transporting ATP synthase complex, catalytic core F(1) (sensu Bacteria)	cellular_component
1018	GO:0045264	proton-transporting ATP synthase complex, coupling factor F(o) (sensu Bacteria)	cellular_component
1027	GO:0008372	cellular component unknown	cellular_component
1031	GO:0000798	nuclear cohesin complex	cellular_component
1042	GO:0005737	cytoplasm	cellular_component
1044	GO:0005971	ribonucleoside-diphosphate reductase complex	cellular_component
1046	GO:0005971	ribonucleoside-diphosphate reductase complex	cellular_component
1079	GO:0005829	cytosol	cellular_component
1084	GO:0005739	mitochondrion	cellular_component
1104	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1121	GO:0009898	internal side of plasma membrane	cellular_component
1121	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1122	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1126	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
1134	GO:0016020	membrane	cellular_component
1137	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
1148	GO:0005634	nucleus	cellular_component
1162	GO:0005625	soluble fraction	cellular_component
1164	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1165	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1169	GO:0012505	endomembrane system	cellular_component
1172	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1187	GO:0009507	chloroplast	cellular_component
1199	GO:0000506	glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex	cellular_component
1221	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1246	GO:0005790	smooth endoplasmic reticulum	cellular_component

续表 2

ssu	acc	name	term_type
1246	GO:0016021	integral to membrane	cellular_component
1246	GO:0016529	sarcoplasmic reticulum	cellular_component
1256	GO:0005658	alpha DNA polymerase:primase complex	cellular_component
1258	GO:0012505	endomembrane system	cellular_component
1267	GO:0008372	cellular component unknown	cellular_component
1273	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
1274	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
1278	GO:0016021	integral to membrane	cellular_component
1278	GO:0016600	flotillin complex	cellular_component
1278	GO:0045121	lipid raft	cellular_component
1284	GO:0005624	membrane fraction	cellular_component
1284	GO:0005887	integral to plasma membrane	cellular_component
1289	GO:0009507	chloroplast	cellular_component
1298	GO:0009507	chloroplast	cellular_component
1327	GO:0009330	DNA topoisomerase complex (ATP-hydrolyzing)	cellular_component
1327	GO:0009340	DNA topoisomerase IV complex	cellular_component
1348	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1352	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
1355	GO:0005624	membrane fraction	cellular_component
1355	GO:0016020	membrane	cellular_component
1357	GO:0009360	DNA polymerase III complex	cellular_component
1366	GO:0009368	endopeptidase Clp complex	cellular_component
1371	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1372	GO:0009897	external side of plasma membrane	cellular_component
1400	GO:0020011	apicoplast	cellular_component
1413	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
1413	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1414	GO:0009898	internal side of plasma membrane	cellular_component
1414	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1441	GO:0009360	DNA polymerase III complex	cellular_component
1445	GO:0009507	chloroplast	cellular_component
1451	GO:0005829	cytosol	cellular_component
1453	GO:0005625	soluble fraction	cellular_component
1453	GO:0005667	transcription factor complex	cellular_component
1453	GO:0005737	cytoplasm	cellular_component
1458	GO:0005694	chromosome	cellular_component
1465	GO:0005739	mitochondrion	cellular_component
1465	GO:0009507	chloroplast	cellular_component
1467	GO:0009318	exodeoxyribonuclease VII complex	cellular_component
1488	GO:0009507	chloroplast	cellular_component
1499	GO:0009898	internal side of plasma membrane	cellular_component
1499	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1502	GO:0005625	soluble fraction	cellular_component
1502	GO:0019717	synaptosome	cellular_component
1519	GO:0009507	chloroplast	cellular_component
1520	GO:0005625	soluble fraction	cellular_component

续表 2

ssu	acc	name	term_type
1531	GO:0005694	chromosome	cellular_component
1531	GO:0008623	chromatin accessibility complex	cellular_component
1531	GO:0016587	ISW1 complex	cellular_component
1531	GO:0031213	RSF complex	cellular_component
1570	GO:0009345	glycine-tRNA ligase complex	cellular_component
1571	GO:0009345	glycine-tRNA ligase complex	cellular_component
1576	GO:0005829	cytosol	cellular_component
1577	GO:0009897	external side of plasma membrane	cellular_component
1580	GO:0016469	proton-transporting two-sector ATPase complex	cellular_component
1588	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
1590	GO:0019812	type I site-specific deoxyribonuclease complex	cellular_component
1597	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
1598	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
1599	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
1600	GO:0009507	chloroplast	cellular_component
1601	GO:0009317	acetyl-CoA carboxylase complex	cellular_component
1602	GO:0009536	plastid	cellular_component
1603	GO:0020011	apicoplast	cellular_component
1611	GO:0009507	chloroplast	cellular_component
1615	GO:0009898	internal side of plasma membrane	cellular_component
1615	GO:0015627	type II protein secretion system complex	cellular_component
1619	GO:0012505	endomembrane system	cellular_component
1625	GO:0009380	excinuclease ABC complex	cellular_component
1628	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
1634	GO:0005947	alpha-ketoglutarate dehydrogenase complex (sensu Eukaryota)	cellular_component
1634	GO:0005960	glycine cleavage complex	cellular_component
1634	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
1634	GO:0009353	oxoglutarate dehydrogenase complex (sensu Eukaryota)	cellular_component
1634	GO:0042645	mitochondrial nucleoid	cellular_component
1635	GO:0045248	oxoglutarate dehydrogenase complex (sensu Bacteria)	cellular_component
1636	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
1636	GO:0042645	mitochondrial nucleoid	cellular_component
1637	GO:0005615	extracellular space	cellular_component
1637	GO:0005967	pyruvate dehydrogenase complex (sensu Eukaryota)	cellular_component
1637	GO:0042645	mitochondrial nucleoid	cellular_component
1662	GO:0009898	internal side of plasma membrane	cellular_component
1662	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1664	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
1671	GO:0020011	apicoplast	cellular_component
1678	GO:0005739	mitochondrion	cellular_component
1681	GO:0005948	acetolactate synthase complex	cellular_component
1691	GO:0005843	cytosolic small ribosomal subunit (sensu Eukaryota)	cellular_component
1691	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
1692	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1709	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component
1728	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component

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ssu	acc	name	term_type
1738	GO:0009316	3-isopropylmalate dehydratase complex	cellular_component
1739	GO:0009316	3-isopropylmalate dehydratase complex	cellular_component
1741	GO:0009507	chloroplast	cellular_component
1746	GO:0009360	DNA polymerase III complex	cellular_component
1752	GO:0005741	mitochondrial outer membrane	cellular_component
1752	GO:0005887	integral to plasma membrane	cellular_component
1752	GO:0016323	basolateral plasma membrane	cellular_component
1760	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component
1766	GO:0009570	chloroplast stroma	cellular_component
1771	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
1825	GO:0005743	mitochondrial inner membrane	cellular_component
1827	GO:0009331	glycerol-3-phosphate dehydrogenase complex	cellular_component
1830	GO:0005829	cytosol	cellular_component
1835	GO:0008287	protein serine/threonine phosphatase complex	cellular_component
1839	GO:0009507	chloroplast	cellular_component
1861	GO:0012505	endomembrane system	cellular_component
1864	GO:0005794	Golgi apparatus	cellular_component
1864	GO:0005887	integral to plasma membrane	cellular_component
1864	GO:0030659	cytoplasmic vesicle membrane	cellular_component
1877	GO:0005737	cytoplasm	cellular_component
1879	GO:0005624	membrane fraction	cellular_component
1894	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1901	GO:0005624	membrane fraction	cellular_component
1901	GO:0016020	membrane	cellular_component
1910	GO:0005625	soluble fraction	cellular_component
1914	GO:0009507	chloroplast	cellular_component
1925	GO:0016021	integral to membrane	cellular_component
1933	GO:0005739	mitochondrion	cellular_component
1933	GO:0045282	succinate dehydrogenase complex (sensu Bacteria)	cellular_component
1935	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component
1939	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component
1	GO:0003688	DNA replication origin binding	molecular_function
2	GO:0003890	beta DNA polymerase activity	molecular_function
6	GO:0005525	GTP binding	molecular_function
7	GO:0004045	aminoacyl-tRNA hydrolase activity	molecular_function
8	GO:0003690	double-stranded DNA binding	molecular_function
8	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
8	GO:0005515	protein binding	molecular_function
8	GO:0005524	ATP binding	molecular_function
13	GO:0004422	hypoxanthine phosphoribosyltransferase activity	molecular_function
13	GO:0016879	ligase activity, forming carbon-nitrogen bonds	molecular_function
14	GO:0000287	magnesium ion binding	molecular_function
14	GO:0004422	hypoxanthine phosphoribosyltransferase activity	molecular_function
15	GO:0004222	metalloendopeptidase activity	molecular_function
15	GO:0016887	ATPase activity	molecular_function
21	GO:0004749	ribose phosphate diphosphokinase activity	molecular_function

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ssu	acc	name	term_type
22	GO:0004069	aspartate transaminase activity	molecular_function
22	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
24	GO:0003824	catalytic activity	molecular_function
26	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
26	GO:0004639	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	molecular_function
27	GO:0004642	phosphoribosylformylglycinamidine synthase activity	molecular_function
28	GO:0000287	magnesium ion binding	molecular_function
28	GO:0004044	amidophosphoribosyltransferase activity	molecular_function
29	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
29	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
29	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
30	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
30	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
30	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
31	GO:0003937	IMP cyclohydrolase activity	molecular_function
31	GO:0004643	phosphoribosylaminoimidazolecarboxamide formyltransferase activity	molecular_function
32	GO:0004637	phosphoribosylamine-glycine ligase activity	molecular_function
32	GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	molecular_function
32	GO:0004644	phosphoribosylglycinamide formyltransferase activity	molecular_function
33	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
34	GO:0004638	phosphoribosylaminoimidazole carboxylase activity	molecular_function
37	GO:0004018	adenylosuccinate lyase activity	molecular_function
37	GO:0018842	3-carboxymuconate cycloisomerase type II activity	molecular_function
42	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
44	GO:0005524	ATP binding	molecular_function
44	GO:0015646	permease activity	molecular_function
44	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
46	GO:0009378	Holliday junction helicase activity	molecular_function
54	GO:0004326	tetrahydrofolylpolyglutamate synthase activity	molecular_function
54	GO:0005524	ATP binding	molecular_function
54	GO:0008841	dihydrofolate synthase activity	molecular_function
57	GO:0016887	ATPase activity	molecular_function
58	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
58	GO:0009378	Holliday junction helicase activity	molecular_function
60	GO:0008725	DNA-3-methyladenine glycosylase I activity	molecular_function
62	GO:0008094	DNA-dependent ATPase activity	molecular_function
69	GO:0003735	structural constituent of ribosome	molecular_function
70	GO:0003735	structural constituent of ribosome	molecular_function
71	GO:0003735	structural constituent of ribosome	molecular_function
71	GO:0004623	phospholipase A2 activity	molecular_function
73	GO:0003735	structural constituent of ribosome	molecular_function
74	GO:0003735	structural constituent of ribosome	molecular_function
75	GO:0003735	structural constituent of ribosome	molecular_function
76	GO:0003735	structural constituent of ribosome	molecular_function
77	GO:0003735	structural constituent of ribosome	molecular_function
79	GO:0003735	structural constituent of ribosome	molecular_function

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ssu	acc	name	term_type
80	GO:0003735	structural constituent of ribosome	molecular_function
81	GO:0003735	structural constituent of ribosome	molecular_function
82	GO:0003735	structural constituent of ribosome	molecular_function
85	GO:0003735	structural constituent of ribosome	molecular_function
88	GO:0003735	structural constituent of ribosome	molecular_function
89	GO:0003735	structural constituent of ribosome	molecular_function
90	GO:0003735	structural constituent of ribosome	molecular_function
92	GO:0003735	structural constituent of ribosome	molecular_function
93	GO:0015450	protein translocase activity	molecular_function
94	GO:0004017	adenylate kinase activity	molecular_function
94	GO:0005524	ATP binding	molecular_function
95	GO:0003743	translation initiation factor activity	molecular_function
97	GO:0003735	structural constituent of ribosome	molecular_function
98	GO:0003735	structural constituent of ribosome	molecular_function
99	GO:0003899	DNA-directed RNA polymerase activity	molecular_function
100	GO:0003735	structural constituent of ribosome	molecular_function
113	GO:0005524	ATP binding	molecular_function
113	GO:0015410	manganese-transporting ATPase activity	molecular_function
114	GO:0005384	manganese ion transporter activity	molecular_function
114	GO:0005385	zinc ion transporter activity	molecular_function
114	GO:0015646	permease activity	molecular_function
114	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
115	GO:0005055	laminin receptor activity	molecular_function
115	GO:0030145	manganese ion binding	molecular_function
120	GO:0004831	tyrosine-tRNA ligase activity	molecular_function
120	GO:0005524	ATP binding	molecular_function
121	GO:0008658	penicillin binding	molecular_function
123	GO:0003899	DNA-directed RNA polymerase activity	molecular_function
126	GO:0008565	protein transporter activity	molecular_function
127	GO:0008565	protein transporter activity	molecular_function
134	GO:0008776	acetate kinase activity	molecular_function
134	GO:0008980	propionate kinase activity	molecular_function
136	GO:0004326	tetrahydrofolylpolyglutamate synthase activity	molecular_function
136	GO:0008841	dihydrofolate synthase activity	molecular_function
137	GO:0004177	aminopeptidase activity	molecular_function
140	GO:0030508	thiol-disulfide exchange intermediate activity	molecular_function
142	GO:0000049	tRNA binding	molecular_function
142	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
144	GO:0003697	single-stranded DNA binding	molecular_function
146	GO:0030188	chaperone regulator activity	molecular_function
146	GO:0051087	chaperone binding	molecular_function
147	GO:0016887	ATPase activity	molecular_function
148	GO:0003735	structural constituent of ribosome	molecular_function
149	GO:0003735	structural constituent of ribosome	molecular_function
151	GO:0003746	translation elongation factor activity	molecular_function
152	GO:0004245	neprilysin activity	molecular_function

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ssu	acc	name	term_type
152	GO:0008270	zinc ion binding	molecular_function
152	GO:0016512	endothelin-converting enzyme 1 activity	molecular_function
153	GO:0008943	glyceraldehyde-3-phosphate dehydrogenase activity	molecular_function
154	GO:0004618	phosphoglycerate kinase activity	molecular_function
154	GO:0004689	phosphorylase kinase activity	molecular_function
157	GO:0004356	glutamate-ammonia ligase activity	molecular_function
161	GO:0008999	ribosomal-protein-alanine N-acetyltransferase activity	molecular_function
162	GO:0008450	O-sialoglycoprotein endopeptidase activity	molecular_function
163	GO:0030528	transcription regulator activity	molecular_function
164	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
165	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
165	GO:0015646	permease activity	molecular_function
166	GO:0015646	permease activity	molecular_function
168	GO:0015171	amino acid transporter activity	molecular_function
174	GO:0005524	ATP binding	molecular_function
174	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
176	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
178	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
181	GO:0004802	transketolase activity	molecular_function
181	GO:0005509	calcium ion binding	molecular_function
182	GO:0004802	transketolase activity	molecular_function
182	GO:0005509	calcium ion binding	molecular_function
182	GO:0008661	1-deoxy-D-xylulose-5-phosphate synthase activity	molecular_function
183	GO:0008889	glycerophosphodiester phosphodiesterase activity	molecular_function
191	GO:0008861	formate C-acetyltransferase activity	molecular_function
192	GO:0005554	molecular function unknown	molecular_function
195	GO:0008662	1-phosphofructokinase activity	molecular_function
198	GO:0004396	hexokinase activity	molecular_function
198	GO:0005524	ATP binding	molecular_function
198	GO:0008761	UDP-N-acetylglucosamine 2-epimerase activity	molecular_function
198	GO:0009384	N-acylmannosamine kinase activity	molecular_function
199	GO:0015582	beta-glucoside permease activity	molecular_function
199	GO:0019190	cellobiose permease activity	molecular_function
206	GO:0004342	glucosamine-6-phosphate deaminase activity	molecular_function
208	GO:0005375	copper ion transporter activity	molecular_function
208	GO:0015662	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	molecular_function
209	GO:0000287	magnesium ion binding	molecular_function
209	GO:0004008	copper-exporting ATPase activity	molecular_function
209	GO:0005507	copper ion binding	molecular_function
209	GO:0005524	ATP binding	molecular_function
209	GO:0008900	hydrogen:potassium-exchanging ATPase activity	molecular_function
209	GO:0015097	mercury ion transporter activity	molecular_function
210	GO:0004008	copper-exporting ATPase activity	molecular_function
211	GO:0008854	exodeoxyribonuclease V activity	molecular_function
212	GO:0009003	signal peptidase activity	molecular_function
213	GO:0004523	ribonuclease H activity	molecular_function

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ssu	acc	name	term_type
214	GO:0008746	NAD(P) transhydrogenase activity	molecular_function
214	GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	molecular_function
216	GO:0004558	alpha-glucosidase activity	molecular_function
216	GO:0004574	oligo-1,6-glucosidase activity	molecular_function
216	GO:0008788	alpha,alpha-phosphotrehalase activity	molecular_function
217	GO:0015582	beta-glucoside permease activity	molecular_function
217	GO:0015584	trehalose permease activity	molecular_function
218	GO:0016566	specific transcriptional repressor activity	molecular_function
221	GO:0003684	damaged DNA binding	molecular_function
221	GO:0005524	ATP binding	molecular_function
221	GO:0030983	mismatched DNA binding	molecular_function
223	GO:0030508	thiol-disulfide exchange intermediate activity	molecular_function
224	GO:0004467	long-chain-fatty-acid-CoA ligase activity	molecular_function
225	GO:0000318	protein-methionine-R-oxide reductase activity	molecular_function
225	GO:0008113	protein-methionine-S-oxide reductase activity	molecular_function
229	GO:0005524	ATP binding	molecular_function
229	GO:0015646	permease activity	molecular_function
229	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
230	GO:0015655	alanine:sodium symporter activity	molecular_function
234	GO:0004352	glutamate dehydrogenase activity	molecular_function
234	GO:0004354	glutamate dehydrogenase (NADP+) activity	molecular_function
235	GO:0004152	dihydroorotate dehydrogenase activity	molecular_function
235	GO:0004158	dihydroorotate oxidase activity	molecular_function
237	GO:0016787	hydrolase activity	molecular_function
240	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
248	GO:0008509	anion transporter activity	molecular_function
248	GO:0015499	formate transporter activity	molecular_function
249	GO:0005345	purine transporter activity	molecular_function
249	GO:0005350	pyrimidine transporter activity	molecular_function
249	GO:0015168	glycerol transporter activity	molecular_function
249	GO:0015250	water channel activity	molecular_function
249	GO:0015288	porin activity	molecular_function
253	GO:0004601	peroxidase activity	molecular_function
253	GO:0004791	thioredoxin-disulfide reductase activity	molecular_function
253	GO:0004890	GABA-A receptor activity	molecular_function
253	GO:0005199	structural constituent of cell wall	molecular_function
253	GO:0005230	extracellular ligand-gated ion channel activity	molecular_function
253	GO:0005522	profilin binding	molecular_function
253	GO:0008307	structural constituent of muscle	molecular_function
253	GO:0017022	myosin binding	molecular_function
259	GO:0004821	histidine-tRNA ligase activity	molecular_function
260	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
261	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
261	GO:0004028	aldehyde dehydrogenase activity	molecular_function
261	GO:0005506	iron ion binding	molecular_function
262	GO:0004765	shikimate kinase activity	molecular_function

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ssu	acc	name	term_type
262	GO:0004795	threonine synthase activity	molecular_function
263	GO:0005319	lipid transporter activity	molecular_function
263	GO:0015646	permease activity	molecular_function
263	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
264	GO:0005524	ATP binding	molecular_function
264	GO:0015646	permease activity	molecular_function
264	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
267	GO:0015440	peptide-transporting ATPase activity	molecular_function
268	GO:0015559	multidrug efflux pump activity	molecular_function
269	GO:0004496	mevalonate kinase activity	molecular_function
269	GO:0004631	phosphomevalonate kinase activity	molecular_function
270	GO:0004163	diphosphomevalonate decarboxylase activity	molecular_function
270	GO:0005524	ATP binding	molecular_function
270	GO:0016301	kinase activity	molecular_function
271	GO:0004631	phosphomevalonate kinase activity	molecular_function
272	GO:0004452	isopentenyl-diphosphate delta-isomerase activity	molecular_function
273	GO:0005524	ATP binding	molecular_function
273	GO:0015646	permease activity	molecular_function
273	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
274	GO:0005524	ATP binding	molecular_function
274	GO:0015646	permease activity	molecular_function
274	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
277	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
278	GO:0016566	specific transcriptional repressor activity	molecular_function
279	GO:0000774	adenyl-nucleotide exchange factor activity	molecular_function
279	GO:0005515	protein binding	molecular_function
279	GO:0030192	Hsp70/Hsc70 protein regulator activity	molecular_function
280	GO:0005515	protein binding	molecular_function
281	GO:0005515	protein binding	molecular_function
284	GO:0015424	amino acid-transporting ATPase activity	molecular_function
285	GO:0015424	amino acid-transporting ATPase activity	molecular_function
285	GO:0015646	permease activity	molecular_function
288	GO:0005375	copper ion transporter activity	molecular_function
288	GO:0015434	cadmium-transporting ATPase activity	molecular_function
288	GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	molecular_function
289	GO:0016564	transcriptional repressor activity	molecular_function
290	GO:0004730	pseudouridylate synthase activity	molecular_function
290	GO:0016439	tRNA-pseudouridine synthase activity	molecular_function
291	GO:0004789	thiamin-phosphate diphosphorylase activity	molecular_function
291	GO:0008972	phosphomethylpyrimidine kinase activity	molecular_function
298	GO:0003960	NADPH:quinone reductase activity	molecular_function
298	GO:0004024	alcohol dehydrogenase activity, zinc-dependent	molecular_function
298	GO:0008270	zinc ion binding	molecular_function
299	GO:0016298	lipase activity	molecular_function
300	GO:0004090	carbonyl reductase (NADPH) activity	molecular_function

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ssu	acc	name	term_type
300	GO:0004745	retinol dehydrogenase activity	molecular_function
301	GO:0008670	2,4-dienoyl-CoA reductase (NADPH) activity	molecular_function
306	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
308	GO:0005055	laminin receptor activity	molecular_function
308	GO:0030145	manganese ion binding	molecular_function
311	GO:0003883	CTP synthase activity	molecular_function
312	GO:0004332	fructose-bisphosphate aldolase activity	molecular_function
314	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
315	GO:0004067	asparaginase activity	molecular_function
316	GO:0016787	hydrolase activity	molecular_function
318	GO:0003677	DNA binding	molecular_function
319	GO:0004069	aspartate transaminase activity	molecular_function
319	GO:0004838	tyrosine transaminase activity	molecular_function
319	GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity	molecular_function
322	GO:0003735	structural constituent of ribosome	molecular_function
325	GO:0017068	glutamyl-tRNA(Gln) amidotransferase activity	molecular_function
326	GO:0017068	glutamyl-tRNA(Gln) amidotransferase activity	molecular_function
327	GO:0008832	dGTPase activity	molecular_function
328	GO:0030528	transcription regulator activity	molecular_function
329	GO:0004335	galactokinase activity	molecular_function
329	GO:0004396	hexokinase activity	molecular_function
329	GO:0005524	ATP binding	molecular_function
337	GO:0000309	nicotinamide-nucleotide adenylyltransferase activity	molecular_function
337	GO:0004515	nicotinate-nucleotide adenylyltransferase activity	molecular_function
351	GO:0008463	formylmethionine deformylase activity	molecular_function
352	GO:0016787	hydrolase activity	molecular_function
353	GO:0004134	4-alpha-glucanotransferase activity	molecular_function
354	GO:0008184	glycogen phosphorylase activity	molecular_function
354	GO:0030170	pyridoxal phosphate binding	molecular_function
355	GO:0016566	specific transcriptional repressor activity	molecular_function
357	GO:0015579	glucose permease activity	molecular_function
360	GO:0005554	molecular function unknown	molecular_function
364	GO:0005554	molecular function unknown	molecular_function
366	GO:0015087	cobalt ion transporter activity	molecular_function
366	GO:0015099	nickel ion transporter activity	molecular_function
366	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
367	GO:0015087	cobalt ion transporter activity	molecular_function
368	GO:0003677	DNA binding	molecular_function
369	GO:0005554	molecular function unknown	molecular_function
370	GO:0008658	penicillin binding	molecular_function
376	GO:0009369	quorum sensing signal generator activity	molecular_function
376	GO:0009370	quorum sensing response regulator activity	molecular_function
378	GO:0004385	guanylate kinase activity	molecular_function
380	GO:0003678	DNA helicase activity	molecular_function
380	GO:0003688	DNA replication origin binding	molecular_function
381	GO:0004479	methionyl-tRNA formyltransferase activity	molecular_function

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ssu	acc	name	term_type
382	GO:0016434	rRNA (cytosine) methyltransferase activity	molecular_function
383	GO:0004722	protein serine/threonine phosphatase activity	molecular_function
387	GO:0000155	two-component sensor molecule activity	molecular_function
389	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
389	GO:0005328	neurotransmitter:sodium symporter activity	molecular_function
391	GO:0004124	cysteine synthase activity	molecular_function
392	GO:0005554	molecular function unknown	molecular_function
393	GO:0008026	ATP-dependent helicase activity	molecular_function
396	GO:0003723	RNA binding	molecular_function
396	GO:0008175	tRNA methyltransferase activity	molecular_function
396	GO:0008649	rRNA methyltransferase activity	molecular_function
400	GO:0030528	transcription regulator activity	molecular_function
401	GO:0030528	transcription regulator activity	molecular_function
402	GO:0004565	beta-galactosidase activity	molecular_function
402	GO:0005529	sugar binding	molecular_function
403	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
404	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
405	GO:0015589	mannose permease activity	molecular_function
407	GO:0003978	UDP-glucose 4-epimerase activity	molecular_function
407	GO:0004034	aldose 1-epimerase activity	molecular_function
412	GO:0004832	valine-tRNA ligase activity	molecular_function
421	GO:0005525	GTP binding	molecular_function
424	GO:0008233	peptidase activity	molecular_function
430	GO:0008764	UDP-N-acetylmuramoylalanine-D-glutamate ligase activity	molecular_function
431	GO:0016758	transferase activity, transferring hexosyl groups	molecular_function
433	GO:0005515	protein binding	molecular_function
433	GO:0005524	ATP binding	molecular_function
433	GO:0016887	ATPase activity	molecular_function
434	GO:0003924	GTPase activity	molecular_function
434	GO:0005198	structural molecule activity	molecular_function
435	GO:0008784	alanine racemase activity	molecular_function
435	GO:0030170	pyridoxal phosphate binding	molecular_function
441	GO:0004822	isoleucine-tRNA ligase activity	molecular_function
444	GO:0016787	hydrolase activity	molecular_function
446	GO:0015599	glutamine-importing ATPase activity	molecular_function
446	GO:0015646	permease activity	molecular_function
447	GO:0015424	amino acid-transporting ATPase activity	molecular_function
448	GO:0004477	methenyltetrahydrofolate cyclohydrolase activity	molecular_function
448	GO:0004486	methylenetetrahydrofolate dehydrogenase activity	molecular_function
455	GO:0030528	transcription regulator activity	molecular_function
457	GO:0008233	peptidase activity	molecular_function
458	GO:0008233	peptidase activity	molecular_function
464	GO:0004362	glutathione-disulfide reductase activity	molecular_function
464	GO:0004791	thioredoxin-disulfide reductase activity	molecular_function
464	GO:0016654	oxidoreductase activity, acting on NADH or NADPH, disulfide as acceptor	molecular_function
464	GO:0050660	FAD binding	molecular_function

续表 2

ssu	acc	name	term_type
466	GO:0005524	ATP binding	molecular_function
466	GO:0015646	permease activity	molecular_function
466	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
467	GO:0015646	permease activity	molecular_function
467	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
470	GO:0004815	aspartate-tRNA ligase activity	molecular_function
470	GO:0004824	lysine-tRNA ligase activity	molecular_function
471	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function
478	GO:0005554	molecular function unknown	molecular_function
479	GO:0008964	phosphoenolpyruvate carboxylase activity	molecular_function
482	GO:0003746	translation elongation factor activity	molecular_function
482	GO:0005525	GTP binding	molecular_function
483	GO:0004618	phosphoglycerate kinase activity	molecular_function
483	GO:0004807	triose-phosphate isomerase activity	molecular_function
484	GO:0016787	hydrolase activity	molecular_function
485	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	molecular_function
485	GO:0004522	pancreatic ribonuclease activity	molecular_function
489	GO:0004000	adenosine deaminase activity	molecular_function
491	GO:0005524	ATP binding	molecular_function
491	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
492	GO:0030528	transcription regulator activity	molecular_function
493	GO:0003889	alpha DNA polymerase activity	molecular_function
494	GO:0000287	magnesium ion binding	molecular_function
494	GO:0003872	6-phosphofructokinase activity	molecular_function
494	GO:0004331	fructose-2,6-bisphosphate 2-phosphatase activity	molecular_function
494	GO:0005524	ATP binding	molecular_function
495	GO:0000287	magnesium ion binding	molecular_function
495	GO:0004743	pyruvate kinase activity	molecular_function
500	GO:0004360	glutamine-fructose-6-phosphate transaminase (isomerizing) activity	molecular_function
501	GO:0015359	amino acid permease activity	molecular_function
501	GO:0015599	glutamine-importing ATPase activity	molecular_function
501	GO:0015646	permease activity	molecular_function
502	GO:0015424	amino acid-transporting ATPase activity	molecular_function
503	GO:0015424	amino acid-transporting ATPase activity	molecular_function
503	GO:0016597	amino acid binding	molecular_function
507	GO:0003678	DNA helicase activity	molecular_function
508	GO:0004349	glutamate 5-kinase activity	molecular_function
509	GO:0004350	glutamate-5-semialdehyde dehydrogenase activity	molecular_function
510	GO:0004735	pyrroline-5-carboxylate reductase activity	molecular_function
513	GO:0003700	transcription factor activity	molecular_function
513	GO:0008483	transaminase activity	molecular_function
521	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
525	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
535	GO:0008781	N-acylneuraminate cytidylyltransferase activity	molecular_function
535	GO:0019007	N-acetylneuraminic acid phosphate synthase activity	molecular_function
535	GO:0047444	N-acylneuraminate-9-phosphate synthase activity	molecular_function

续表 2

ssu	acc	name	term_type
535	GO:0050462	N-acetylneuraminate synthase activity	molecular_function
535	GO:0050825	ice binding	molecular_function
536	GO:0004396	hexokinase activity	molecular_function
536	GO:0005524	ATP binding	molecular_function
536	GO:0008761	UDP-N-acetylglucosamine 2-epimerase activity	molecular_function
536	GO:0009384	N-acylmannosamine kinase activity	molecular_function
538	GO:0008781	N-acylneuraminate cytidylyltransferase activity	molecular_function
546	GO:0004803	transposase activity	molecular_function
547	GO:0004803	transposase activity	molecular_function
549	GO:0004803	transposase activity	molecular_function
552	GO:0008907	integrase activity	molecular_function
552	GO:0009009	site-specific recombinase activity	molecular_function
557	GO:0003866	3-phosphoshikimate 1-carboxyvinyltransferase activity	molecular_function
557	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
558	GO:0004765	shikimate kinase activity	molecular_function
559	GO:0004106	chorismate mutase activity	molecular_function
559	GO:0004664	prephenate dehydratase activity	molecular_function
561	GO:0008175	tRNA methyltransferase activity	molecular_function
561	GO:0008649	rRNA methyltransferase activity	molecular_function
563	GO:0008767	UDP-galactopyranose mutase activity	molecular_function
569	GO:0004069	aspartate transaminase activity	molecular_function
569	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
570	GO:0003676	nucleic acid binding	molecular_function
570	GO:0004815	aspartate-tRNA ligase activity	molecular_function
570	GO:0004816	asparagine-tRNA ligase activity	molecular_function
570	GO:0005524	ATP binding	molecular_function
573	GO:0015559	multidrug efflux pump activity	molecular_function
574	GO:0004521	endoribonuclease activity	molecular_function
575	GO:0005554	molecular function unknown	molecular_function
580	GO:0016990	arginine deiminase activity	molecular_function
582	GO:0004070	aspartate carbamoyltransferase activity	molecular_function
582	GO:0004585	ornithine carbamoyltransferase activity	molecular_function
582	GO:0016597	amino acid binding	molecular_function
583	GO:0008804	carbamate kinase activity	molecular_function
585	GO:0016805	dipeptidase activity	molecular_function
589	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function
589	GO:0051075	S-adenosylmethionine:tRNA ribosyltransferase-isomerase activity	molecular_function
591	GO:0004342	glucosamine-6-phosphate deaminase activity	molecular_function
596	GO:0016208	AMP binding	molecular_function
597	GO:0016413	O-acetyltransferase activity	molecular_function
597	GO:0042944	D-alanine transporter activity	molecular_function
601	GO:0004364	glutathione transferase activity	molecular_function
601	GO:0005554	molecular function unknown	molecular_function
602	GO:0004730	pseudouridylate synthase activity	molecular_function
603	GO:0004602	glutathione peroxidase activity	molecular_function
603	GO:0009031	thiol peroxidase activity	molecular_function

续表 2

ssu	acc	name	term_type
604	GO:0005381	iron ion transporter activity	molecular_function
604	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
605	GO:0005381	iron ion transporter activity	molecular_function
605	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
606	GO:0005506	iron ion binding	molecular_function
606	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
607	GO:0005381	iron ion transporter activity	molecular_function
607	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
608	GO:0008764	UDP-N-acetylmuramoylalanine-D-glutamate ligase activity	molecular_function
608	GO:0008765	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase activity	molecular_function
611	GO:0030413	competence pheromone activity	molecular_function
616	GO:0005554	molecular function unknown	molecular_function
617	GO:0004798	thymidylate kinase activity	molecular_function
618	GO:0003891	delta DNA polymerase activity	molecular_function
620	GO:0008168	methyltransferase activity	molecular_function
621	GO:0004648	phosphoserine transaminase activity	molecular_function
623	GO:0004617	phosphoglycerate dehydrogenase activity	molecular_function
623	GO:0016597	amino acid binding	molecular_function
623	GO:0016726	oxidoreductase activity, acting on CH2 groups, NAD or NADP as acceptor	molecular_function
624	GO:0003908	methylated-DNA-[protein]-cysteine S-methyltransferase activity	molecular_function
627	GO:0000287	magnesium ion binding	molecular_function
627	GO:0000703	pyrimidine-specific oxidized base lesion DNA N-glycosylase activity	molecular_function
627	GO:0003713	transcription coactivator activity	molecular_function
627	GO:0004523	ribonuclease H activity	molecular_function
627	GO:0004528	phosphodiesterase I activity	molecular_function
627	GO:0004844	uracil DNA N-glycosylase activity	molecular_function
627	GO:0008311	double-stranded DNA specific 3'-5' exodeoxyribonuclease activity	molecular_function
627	GO:0008853	exodeoxyribonuclease III activity	molecular_function
629	GO:0015174	basic amino acid transporter activity	molecular_function
629	GO:0015326	cationic amino acid transporter activity	molecular_function
629	GO:0015359	amino acid permease activity	molecular_function
643	GO:0004803	transposase activity	molecular_function
644	GO:0004614	phosphoglucomutase activity	molecular_function
644	GO:0004615	phosphomannomutase activity	molecular_function
646	GO:0004632	phosphopantothenate-cysteine ligase activity	molecular_function
646	GO:0004633	phosphopantothenoylcysteine decarboxylase activity	molecular_function
646	GO:0009055	electron carrier activity	molecular_function
647	GO:0004632	phosphopantothenate-cysteine ligase activity	molecular_function
647	GO:0004633	phosphopantothenoylcysteine decarboxylase activity	molecular_function
647	GO:0009055	electron carrier activity	molecular_function
648	GO:0004329	formate-tetrahydrofolate ligase activity	molecular_function
650	GO:0004148	dihydrolipoyl dehydrogenase activity	molecular_function
651	GO:0009035	type I site-specific deoxyribonuclease activity	molecular_function
652	GO:0009008	DNA-methyltransferase activity	molecular_function
661	GO:0008862	formate acetyltransferase activating enzyme activity	molecular_function
662	GO:0030528	transcription regulator activity	molecular_function

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ssu	acc	name	term_type
663	GO:0016564	transcriptional repressor activity	molecular_function
665	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
665	GO:0015573	beta-glucoside transporter activity	molecular_function
666	GO:0015582	beta-glucoside permease activity	molecular_function
666	GO:0019190	cellobiose permease activity	molecular_function
667	GO:0008861	formate C-acetyltransferase activity	molecular_function
668	GO:0004801	transaldolase activity	molecular_function
670	GO:0004025	alcohol dehydrogenase activity, iron-dependent	molecular_function
671	GO:0004073	aspartate-semialdehyde dehydrogenase activity	molecular_function
672	GO:0008840	dihydrodipicolinate synthase activity	molecular_function
673	GO:0003954	NADH dehydrogenase activity	molecular_function
673	GO:0015036	disulfide oxidoreductase activity	molecular_function
675	GO:0004370	glycerol kinase activity	molecular_function
676	GO:0004368	glycerol-3-phosphate dehydrogenase activity	molecular_function
676	GO:0005509	calcium ion binding	molecular_function
677	GO:0005275	amine transporter activity	molecular_function
677	GO:0005345	purine transporter activity	molecular_function
677	GO:0005350	pyrimidine transporter activity	molecular_function
677	GO:0015166	polyol transporter activity	molecular_function
677	GO:0015250	water channel activity	molecular_function
677	GO:0015288	porin activity	molecular_function
677	GO:0046943	carboxylic acid transporter activity	molecular_function
680	GO:0004222	metalloendopeptidase activity	molecular_function
682	GO:0003954	NADH dehydrogenase activity	molecular_function
682	GO:0015036	disulfide oxidoreductase activity	molecular_function
683	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
685	GO:0004789	thiamin-phosphate diphosphorylase activity	molecular_function
685	GO:0008972	phosphomethylpyrimidine kinase activity	molecular_function
686	GO:0004417	hydroxyethylthiazole kinase activity	molecular_function
686	GO:0004789	thiamin-phosphate diphosphorylase activity	molecular_function
687	GO:0004417	hydroxyethylthiazole kinase activity	molecular_function
687	GO:0004789	thiamin-phosphate diphosphorylase activity	molecular_function
687	GO:0008972	phosphomethylpyrimidine kinase activity	molecular_function
689	GO:0004645	phosphorylase activity	molecular_function
689	GO:0004731	purine-nucleoside phosphorylase activity	molecular_function
689	GO:0004850	uridine phosphorylase activity	molecular_function
692	GO:0005524	ATP binding	molecular_function
692	GO:0015087	cobalt ion transporter activity	molecular_function
692	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
693	GO:0015087	cobalt ion transporter activity	molecular_function
693	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
698	GO:0004180	carboxypeptidase activity	molecular_function
701	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
702	GO:0009381	excinuclease ABC activity	molecular_function
704	GO:0005525	GTP binding	molecular_function
707	GO:0004003	ATP-dependent DNA helicase activity	molecular_function

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ssu	acc	name	term_type
707	GO:0004527	exonuclease activity	molecular_function
708	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
709	GO:0005554	molecular function unknown	molecular_function
710	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
717	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
719	GO:0004084	branched-chain-amino-acid transaminase activity	molecular_function
721	GO:0003735	structural constituent of ribosome	molecular_function
722	GO:0004793	threonine aldolase activity	molecular_function
725	GO:0004123	cystathionine gamma-lyase activity	molecular_function
725	GO:0008483	transaminase activity	molecular_function
725	GO:0031071	cysteine desulfurase activity	molecular_function
727	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
728	GO:0003735	structural constituent of ribosome	molecular_function
729	GO:0003735	structural constituent of ribosome	molecular_function
730	GO:0030528	transcription regulator activity	molecular_function
731	GO:0009005	signal peptidase II activity	molecular_function
732	GO:0004730	pseudouridylate synthase activity	molecular_function
735	GO:0003729	mRNA binding	molecular_function
735	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
736	GO:0004070	aspartate carbamoyltransferase activity	molecular_function
737	GO:0004049	anthranilate synthase activity	molecular_function
737	GO:0004088	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	molecular_function
738	GO:0004088	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	molecular_function
742	GO:0003735	structural constituent of ribosome	molecular_function
744	GO:0005524	ATP binding	molecular_function
744	GO:0015646	permease activity	molecular_function
744	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
745	GO:0005524	ATP binding	molecular_function
745	GO:0015646	permease activity	molecular_function
745	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
747	GO:0004412	homoserine dehydrogenase activity	molecular_function
748	GO:0004413	homoserine kinase activity	molecular_function
750	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity	molecular_function
751	GO:0015417	polyamine-transporting ATPase activity	molecular_function
752	GO:0015417	polyamine-transporting ATPase activity	molecular_function
753	GO:0015417	polyamine-transporting ATPase activity	molecular_function
754	GO:0015417	polyamine-transporting ATPase activity	molecular_function
754	GO:0019808	polyamine binding	molecular_function
755	GO:0005247	voltage-gated chloride channel activity	molecular_function
755	GO:0015108	chloride transporter activity	molecular_function
757	GO:0004289	subtilase activity	molecular_function
758	GO:0005554	molecular function unknown	molecular_function
759	GO:0000703	pyrimidine-specific oxidized base lesion DNA N-glycosylase activity	molecular_function
760	GO:0003920	GMP reductase activity	molecular_function
760	GO:0003938	IMP dehydrogenase activity	molecular_function
760	GO:0030955	potassium ion binding	molecular_function

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ssu	acc	name	term_type
761	GO:0015559	multidrug efflux pump activity	molecular_function
762	GO:0015559	multidrug efflux pump activity	molecular_function
764	GO:0009019	tRNA (guanine-N1-)-methyltransferase activity	molecular_function
765	GO:0004400	histidinol-phosphate transaminase activity	molecular_function
766	GO:0030528	transcription regulator activity	molecular_function
767	GO:0008662	1-phosphofructokinase activity	molecular_function
768	GO:0015585	fructose permease activity	molecular_function
771	GO:0008839	dihydrodipicolinate reductase activity	molecular_function
772	GO:0004652	polynucleotide adenylyltransferase activity	molecular_function
773	GO:0005524	ATP binding	molecular_function
773	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
775	GO:0004340	glucokinase activity	molecular_function
778	GO:0004799	thymidylate synthase activity	molecular_function
779	GO:0004146	dihydrofolate reductase activity	molecular_function
781	GO:0004176	ATP-dependent peptidase activity	molecular_function
781	GO:0005524	ATP binding	molecular_function
781	GO:0008462	endopeptidase Clp activity	molecular_function
782	GO:0005525	GTP binding	molecular_function
783	GO:0000287	magnesium ion binding	molecular_function
783	GO:0004536	deoxyribonuclease activity	molecular_function
783	GO:0004550	nucleoside diphosphate kinase activity	molecular_function
783	GO:0005524	ATP binding	molecular_function
785	GO:0003746	translation elongation factor activity	molecular_function
785	GO:0005525	GTP binding	molecular_function
789	GO:0004797	thymidine kinase activity	molecular_function
790	GO:0003747	translation release factor activity	molecular_function
791	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
794	GO:0004372	glycine hydroxymethyltransferase activity	molecular_function
797	GO:0016491	oxidoreductase activity	molecular_function
816	GO:0003922	GMP synthase (glutamine-hydrolyzing) activity	molecular_function
817	GO:0016566	specific transcriptional repressor activity	molecular_function
819	GO:0003924	GTPase activity	molecular_function
819	GO:0005048	signal sequence binding	molecular_function
819	GO:0008312	7S RNA binding	molecular_function
825	GO:0008907	integrase activity	molecular_function
825	GO:0009009	site-specific recombinase activity	molecular_function
826	GO:0004614	phosphoglucomutase activity	molecular_function
826	GO:0004615	phosphomannomutase activity	molecular_function
827	GO:0000155	two-component sensor molecule activity	molecular_function
828	GO:0000156	two-component response regulator activity	molecular_function
831	GO:0015646	permease activity	molecular_function
832	GO:0005524	ATP binding	molecular_function
832	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
835	GO:0005524	ATP binding	molecular_function
845	GO:0003735	structural constituent of ribosome	molecular_function
846	GO:0003735	structural constituent of ribosome	molecular_function

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ssu	acc	name	term_type
847	GO:0003917	DNA topoisomerase type I activity	molecular_function
848	GO:0005554	molecular function unknown	molecular_function
849	GO:0008925	maltose O-acetyltransferase activity	molecular_function
852	GO:0003954	NADH dehydrogenase activity	molecular_function
852	GO:0015036	disulfide oxidoreductase activity	molecular_function
854	GO:0015249	nonselective channel activity	molecular_function
856	GO:0004523	ribonuclease H activity	molecular_function
857	GO:0003924	GTPase activity	molecular_function
857	GO:0005525	GTP binding	molecular_function
859	GO:0005554	molecular function unknown	molecular_function
859	GO:0017096	acetylserotonin O-methyltransferase activity	molecular_function
860	GO:0008081	phosphoric diester hydrolase activity	molecular_function
860	GO:0008198	ferrous iron binding	molecular_function
860	GO:0008253	5'-nucleotidase activity	molecular_function
860	GO:0019204	nucleotide phosphatase activity	molecular_function
861	GO:0004151	dihydroorotase activity	molecular_function
862	GO:0004844	uracil DNA N-glycosylase activity	molecular_function
862	GO:0045437	uridine nucleosidase activity	molecular_function
863	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
864	GO:0004588	orotate phosphoribosyltransferase activity	molecular_function
864	GO:0004590	orotidine-5'-phosphate decarboxylase activity	molecular_function
866	GO:0004590	orotidine-5'-phosphate decarboxylase activity	molecular_function
867	GO:0004152	dihydroorotate dehydrogenase activity	molecular_function
867	GO:0004158	dihydroorotate oxidase activity	molecular_function
867	GO:0005489	electron transporter activity	molecular_function
867	GO:0005506	iron ion binding	molecular_function
867	GO:0015036	disulfide oxidoreductase activity	molecular_function
867	GO:0017113	dihydropyrimidine dehydrogenase (NADP+) activity	molecular_function
868	GO:0004152	dihydroorotate dehydrogenase activity	molecular_function
868	GO:0004158	dihydroorotate oxidase activity	molecular_function
869	GO:0030528	transcription regulator activity	molecular_function
870	GO:0008878	glucose-1-phosphate adenylyltransferase activity	molecular_function
872	GO:0008878	glucose-1-phosphate adenylyltransferase activity	molecular_function
873	GO:0004373	glycogen (starch) synthase activity	molecular_function
873	GO:0009011	starch synthase activity	molecular_function
874	GO:0003844	1,4-alpha-glucan branching enzyme activity	molecular_function
874	GO:0004556	alpha-amylase activity	molecular_function
875	GO:0015424	amino acid-transporting ATPase activity	molecular_function
875	GO:0016597	amino acid binding	molecular_function
876	GO:0015424	amino acid-transporting ATPase activity	molecular_function
876	GO:0016597	amino acid binding	molecular_function
882	GO:0009381	excinuclease ABC activity	molecular_function
883	GO:0015599	glutamine-importing ATPase activity	molecular_function
883	GO:0015646	permease activity	molecular_function
884	GO:0015424	amino acid-transporting ATPase activity	molecular_function
886	GO:0005524	ATP binding	molecular_function

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ssu	acc	name	term_type
886	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
887	GO:0003961	O-acetylhomoserine aminocarboxypropyltransferase activity	molecular_function
887	GO:0004124	cysteine synthase activity	molecular_function
890	GO:0004034	aldose 1-epimerase activity	molecular_function
891	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
892	GO:0015582	beta-glucoside permease activity	molecular_function
892	GO:0019190	cellobiose permease activity	molecular_function
893	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
894	GO:0016563	transcriptional activator activity	molecular_function
894	GO:0030401	transcription antiterminator activity	molecular_function
895	GO:0009025	tagatose-bisphosphate aldolase activity	molecular_function
896	GO:0008662	1-phosphofructokinase activity	molecular_function
898	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
899	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
901	GO:0030528	transcription regulator activity	molecular_function
909	GO:0004519	endonuclease activity	molecular_function
909	GO:0004844	uracil DNA N-glycosylase activity	molecular_function
909	GO:0005506	iron ion binding	molecular_function
911	GO:0005524	ATP binding	molecular_function
911	GO:0015646	permease activity	molecular_function
911	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
912	GO:0005524	ATP binding	molecular_function
912	GO:0015646	permease activity	molecular_function
912	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
913	GO:0008959	phosphate acetyltransferase activity	molecular_function
914	GO:0004730	pseudouridylate synthase activity	molecular_function
915	GO:0003951	NAD+ kinase activity	molecular_function
918	GO:0000287	magnesium ion binding	molecular_function
918	GO:0004749	ribose phosphate diphosphokinase activity	molecular_function
918	GO:0016978	lipoate-protein ligase B activity	molecular_function
919	GO:0004123	cystathionine gamma-lyase activity	molecular_function
919	GO:0008483	transaminase activity	molecular_function
919	GO:0031071	cysteine desulfurase activity	molecular_function
924	GO:0005554	molecular function unknown	molecular_function
926	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
927	GO:0004459	L-lactate dehydrogenase activity	molecular_function
931	GO:0015646	permease activity	molecular_function
935	GO:0004126	cytidine deaminase activity	molecular_function
935	GO:0008270	zinc ion binding	molecular_function
936	GO:0004139	deoxyribose-phosphate aldolase activity	molecular_function
937	GO:0004645	phosphorylase activity	molecular_function
937	GO:0005161	platelet-derived growth factor receptor binding	molecular_function
937	GO:0009032	thymidine phosphorylase activity	molecular_function
937	GO:0016154	pyrimidine-nucleoside phosphorylase activity	molecular_function
939	GO:0004594	pantothenate kinase activity	molecular_function
939	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function

续表 2

ssu	acc	name	term_type
939	GO:0004849	uridine kinase activity	molecular_function
941	GO:0004803	transposase activity	molecular_function
944	GO:0000155	two-component sensor molecule activity	molecular_function
944	GO:0000156	two-component response regulator activity	molecular_function
945	GO:0000156	two-component response regulator activity	molecular_function
948	GO:0030528	transcription regulator activity	molecular_function
949	GO:0015415	phosphate-transporting ATPase activity	molecular_function
950	GO:0015415	phosphate-transporting ATPase activity	molecular_function
951	GO:0015415	phosphate-transporting ATPase activity	molecular_function
952	GO:0015415	phosphate-transporting ATPase activity	molecular_function
953	GO:0015415	phosphate-transporting ATPase activity	molecular_function
953	GO:0042301	phosphate binding	molecular_function
954	GO:0016434	rRNA (cytosine) methyltransferase activity	molecular_function
955	GO:0000287	magnesium ion binding	molecular_function
955	GO:0008934	inositol-1(or 4)-monophosphatase activity	molecular_function
958	GO:0005215	transporter activity	molecular_function
959	GO:0003919	FMN adenylyltransferase activity	molecular_function
959	GO:0008531	riboflavin kinase activity	molecular_function
960	GO:0004730	pseudouridylate synthase activity	molecular_function
972	GO:0016787	hydrolase activity	molecular_function
973	GO:0045148	tripeptide aminopeptidase activity	molecular_function
984	GO:0008324	cation transporter activity	molecular_function
984	GO:0015562	efflux permease activity	molecular_function
986	GO:0003848	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase activity	molecular_function
986	GO:0004150	dihydroneopterin aldolase activity	molecular_function
986	GO:0004156	dihydropteroate synthase activity	molecular_function
987	GO:0004150	dihydroneopterin aldolase activity	molecular_function
988	GO:0004156	dihydropteroate synthase activity	molecular_function
989	GO:0003934	GTP cyclohydrolase I activity	molecular_function
995	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
997	GO:0004826	phenylalanine-tRNA ligase activity	molecular_function
998	GO:0004563	beta-N-acetylhexosaminidase activity	molecular_function
999	GO:0004182	carboxypeptidase A activity	molecular_function
999	GO:0004563	beta-N-acetylhexosaminidase activity	molecular_function
999	GO:0008422	beta-glucosidase activity	molecular_function
1001	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	molecular_function
1004	GO:0008675	2-dehydro-3-deoxy-phosphogluconate aldolase activity	molecular_function
1004	GO:0008700	4-hydroxy-2-oxoglutarate aldolase activity	molecular_function
1005	GO:0003700	transcription factor activity	molecular_function
1006	GO:0004566	beta-glucuronidase activity	molecular_function
1011	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
1014	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
1015	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
1016	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
1018	GO:0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	molecular_function
1021	GO:0004143	diacylglycerol kinase activity	molecular_function

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ssu	acc	name	term_type
1021	GO:0017050	D-erythro-sphingosine kinase activity	molecular_function
1022	GO:0003911	DNA ligase (NAD+) activity	molecular_function
1023	GO:0015646	permease activity	molecular_function
1025	GO:0004345	glucose-6-phosphate 1-dehydrogenase activity	molecular_function
1027	GO:0008080	N-acetyltransferase activity	molecular_function
1028	GO:0003924	GTPase activity	molecular_function
1028	GO:0005047	signal recognition particle binding	molecular_function
1029	GO:0016787	hydrolase activity	molecular_function
1030	GO:0016787	hydrolase activity	molecular_function
1031	GO:0000217	DNA secondary structure binding	molecular_function
1031	GO:0003680	AT DNA binding	molecular_function
1031	GO:0003690	double-stranded DNA binding	molecular_function
1031	GO:0005524	ATP binding	molecular_function
1031	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1032	GO:0004525	ribonuclease III activity	molecular_function
1038	GO:0008965	phosphoenolpyruvate-protein phosphotransferase activity	molecular_function
1038	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1040	GO:0004450	isocitrate dehydrogenase (NADP+) activity	molecular_function
1041	GO:0004108	citrate (Si)-synthase activity	molecular_function
1041	GO:0016833	oxo-acid-lyase activity	molecular_function
1042	GO:0003994	aconitate hydratase activity	molecular_function
1042	GO:0005506	iron ion binding	molecular_function
1042	GO:0030350	iron-responsive element binding	molecular_function
1044	GO:0004748	ribonucleoside-diphosphate reductase activity	molecular_function
1046	GO:0004748	ribonucleoside-diphosphate reductase activity	molecular_function
1047	GO:0030528	transcription regulator activity	molecular_function
1055	GO:0015589	mannose permease activity	molecular_function
1056	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1057	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1059	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1061	GO:0008675	2-dehydro-3-deoxy-phosphogluconate aldolase activity	molecular_function
1061	GO:0008700	4-hydroxy-2-oxoglutarate aldolase activity	molecular_function
1064	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
1065	GO:0004803	transposase activity	molecular_function
1076	GO:0004813	alanine-tRNA ligase activity	molecular_function
1078	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
1079	GO:0008171	O-methyltransferase activity	molecular_function
1082	GO:0004222	metalloendopeptidase activity	molecular_function
1084	GO:0004825	methionine-tRNA ligase activity	molecular_function
1084	GO:0005524	ATP binding	molecular_function
1086	GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	molecular_function
1087	GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	molecular_function
1088	GO:0004764	shikimate 5-dehydrogenase activity	molecular_function
1089	GO:0003855	3-dehydroquinate dehydratase activity	molecular_function
1089	GO:0003856	3-dehydroquinate synthase activity	molecular_function
1089	GO:0003866	3-phosphoshikimate 1-carboxyvinyltransferase activity	molecular_function

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ssu	acc	name	term_type
1089	GO:0004764	shikimate 5-dehydrogenase activity	molecular_function
1089	GO:0004765	shikimate kinase activity	molecular_function
1090	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1091	GO:0015646	permease activity	molecular_function
1095	GO:0009025	tagatose-bisphosphate aldolase activity	molecular_function
1096	GO:0008448	N-acetylglucosamine-6-phosphate deacetylase activity	molecular_function
1098	GO:0008977	prephenate dehydrogenase activity	molecular_function
1099	GO:0004107	chorismate synthase activity	molecular_function
1100	GO:0003855	3-dehydroquinate dehydratase activity	molecular_function
1101	GO:0005554	molecular function unknown	molecular_function
1101	GO:0008168	methyltransferase activity	molecular_function
1102	GO:0008484	sulfuric ester hydrolase activity	molecular_function
1104	GO:0003735	structural constituent of ribosome	molecular_function
1106	GO:0003743	translation initiation factor activity	molecular_function
1107	GO:0004127	cytidylate kinase activity	molecular_function
1113	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
1121	GO:0005524	ATP binding	molecular_function
1121	GO:0015162	teichoic acid transporter activity	molecular_function
1121	GO:0015437	lipopolysaccharide-transporting ATPase activity	molecular_function
1122	GO:0015162	teichoic acid transporter activity	molecular_function
1122	GO:0015646	permease activity	molecular_function
1122	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1123	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
1126	GO:0004040	amidase activity	molecular_function
1126	GO:0008745	N-acetylmuramoyl-L-alanine amidase activity	molecular_function
1127	GO:0008745	N-acetylmuramoyl-L-alanine amidase activity	molecular_function
1129	GO:0008831	dTDP-4-dehydrorhamnose reductase activity	molecular_function
1130	GO:0008460	dTDP-glucose 4,6-dehydratase activity	molecular_function
1132	GO:0008830	dTDP-4-dehydrorhamnose 3,5-epimerase activity	molecular_function
1133	GO:0008879	glucose-1-phosphate thymidylyltransferase activity	molecular_function
1134	GO:0046873	metal ion transporter activity	molecular_function
1135	GO:0005554	molecular function unknown	molecular_function
1138	GO:0008899	homoserine O-succinyltransferase activity	molecular_function
1139	GO:0003999	adenine phosphoribosyltransferase activity	molecular_function
1141	GO:0008297	single-stranded DNA specific exodeoxyribonuclease activity	molecular_function
1142	GO:0008808	cardiolipin synthase activity	molecular_function
1144	GO:0004022	alcohol dehydrogenase activity	molecular_function
1144	GO:0004303	estradiol 17-beta-dehydrogenase activity	molecular_function
1144	GO:0004745	retinol dehydrogenase activity	molecular_function
1144	GO:0050327	testosterone 17-beta-dehydrogenase activity	molecular_function
1145	GO:0004519	endonuclease activity	molecular_function
1147	GO:0005525	GTP binding	molecular_function
1148	GO:0004811	tRNA isopentenyltransferase activity	molecular_function
1148	GO:0008270	zinc ion binding	molecular_function
1157	GO:0008677	2-dehydropantoate 2-reductase activity	molecular_function
1159	GO:0008135	translation factor activity, nucleic acid binding	molecular_function

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ssu	acc	name	term_type
1160	GO:0009041	uridylate kinase activity	molecular_function
1161	GO:0005199	structural constituent of cell wall	molecular_function
1161	GO:0015159	polysaccharide transporter activity	molecular_function
1162	GO:0003714	transcription corepressor activity	molecular_function
1162	GO:0004364	glutathione transferase activity	molecular_function
1164	GO:0003735	structural constituent of ribosome	molecular_function
1165	GO:0003735	structural constituent of ribosome	molecular_function
1168	GO:0005199	structural constituent of cell wall	molecular_function
1169	GO:0004564	beta-fructofuranosidase activity	molecular_function
1171	GO:0015646	permease activity	molecular_function
1172	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
1172	GO:0015646	permease activity	molecular_function
1173	GO:0030528	transcription regulator activity	molecular_function
1177	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular_function
1177	GO:0004600	cyclophilin	molecular_function
1177	GO:0005328	neurotransmitter:sodium symporter activity	molecular_function
1177	GO:0016018	cyclosporin A binding	molecular_function
1179	GO:0003746	translation elongation factor activity	molecular_function
1179	GO:0003747	translation release factor activity	molecular_function
1179	GO:0005525	GTP binding	molecular_function
1180	GO:0008556	potassium-transporting ATPase activity	molecular_function
1180	GO:0015444	magnesium-importing ATPase activity	molecular_function
1180	GO:0015562	efflux permease activity	molecular_function
1180	GO:0019829	cation-transporting ATPase activity	molecular_function
1182	GO:0008766	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	molecular_function
1182	GO:0047480	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase activity	molecular_function
1184	GO:0008716	D-alanine-D-alanine ligase activity	molecular_function
1185	GO:0005554	molecular function unknown	molecular_function
1187	GO:0005524	ATP binding	molecular_function
1187	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1188	GO:0005524	ATP binding	molecular_function
1188	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1190	GO:0000155	two-component sensor molecule activity	molecular_function
1191	GO:0000156	two-component response regulator activity	molecular_function
1191	GO:0003677	DNA binding	molecular_function
1192	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1193	GO:0016597	amino acid binding	molecular_function
1194	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1194	GO:0015646	permease activity	molecular_function
1195	GO:0015599	glutamine-importing ATPase activity	molecular_function
1196	GO:0004829	threonine-tRNA ligase activity	molecular_function
1199	GO:0046510	UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity	molecular_function
1202	GO:0030528	transcription regulator activity	molecular_function
1203	GO:0004251	X-Pro dipeptidase activity	molecular_function
1204	GO:0008479	queuine tRNA-ribosyltransferase activity	molecular_function

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ssu	acc	name	term_type
1208	GO:0003887	DNA-directed DNA polymerase activity	molecular_function
1208	GO:0008408	3'-5' exonuclease activity	molecular_function
1208	GO:0008409	5'-3' exonuclease activity	molecular_function
1210	GO:0015646	permease activity	molecular_function
1211	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1213	GO:0009031	thiol peroxidase activity	molecular_function
1214	GO:0004008	copper-exporting ATPase activity	molecular_function
1217	GO:0004327	formaldehyde dehydrogenase (glutathione) activity	molecular_function
1218	GO:0003723	RNA binding	molecular_function
1219	GO:0008997	ribonuclease R activity	molecular_function
1222	GO:0005215	transporter activity	molecular_function
1223	GO:0004140	dephospho-CoA kinase activity	molecular_function
1223	GO:0004595	pantetheine-phosphate adenylyltransferase activity	molecular_function
1223	GO:0005524	ATP binding	molecular_function
1224	GO:0008534	purine-specific oxidized base lesion DNA N-glycosylase activity	molecular_function
1225	GO:0005525	GTP binding	molecular_function
1226	GO:0004143	diacylglycerol kinase activity	molecular_function
1228	GO:0005529	sugar binding	molecular_function
1229	GO:0015579	glucose permease activity	molecular_function
1230	GO:0016857	racemase and epimerase activity, acting on carbohydrates and derivatives	molecular_function
1231	GO:0015485	cholesterol binding	molecular_function
1233	GO:0005524	ATP binding	molecular_function
1233	GO:0015646	permease activity	molecular_function
1233	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1234	GO:0005524	ATP binding	molecular_function
1234	GO:0015646	permease activity	molecular_function
1234	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1237	GO:0015639	ferrous iron uptake transporter activity	molecular_function
1238	GO:0015646	permease activity	molecular_function
1239	GO:0005524	ATP binding	molecular_function
1239	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1240	GO:0016149	translation release factor activity, codon specific	molecular_function
1241	GO:0009055	electron carrier activity	molecular_function
1246	GO:0000287	magnesium ion binding	molecular_function
1246	GO:0005338	nucleotide-sugar transporter activity	molecular_function
1246	GO:0005388	calcium-transporting ATPase activity	molecular_function
1246	GO:0005509	calcium ion binding	molecular_function
1246	GO:0005524	ATP binding	molecular_function
1246	GO:0015410	manganese-transporting ATPase activity	molecular_function
1246	GO:0015562	efflux permease activity	molecular_function
1250	GO:0004803	transposase activity	molecular_function
1251	GO:0004803	transposase activity	molecular_function
1255	GO:0016987	sigma factor activity	molecular_function
1256	GO:0003896	DNA primase activity	molecular_function
1258	GO:0003978	UDP-glucose 4-epimerase activity	molecular_function
1258	GO:0051287	NAD binding	molecular_function

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ssu	acc	name	term_type
1261	GO:0000287	magnesium ion binding	molecular_function
1261	GO:0003869	4-nitrophenylphosphatase activity	molecular_function
1261	GO:0004035	alkaline phosphatase activity	molecular_function
1261	GO:0008967	phosphoglycolate phosphatase activity	molecular_function
1263	GO:0000036	acyl carrier activity	molecular_function
1264	GO:0004109	coproporphyrinogen oxidase activity	molecular_function
1265	GO:0008184	glycogen phosphorylase activity	molecular_function
1265	GO:0030170	pyridoxal phosphate binding	molecular_function
1266	GO:0004731	purine-nucleoside phosphorylase activity	molecular_function
1266	GO:0004850	uridine phosphorylase activity	molecular_function
1267	GO:0004645	phosphorylase activity	molecular_function
1267	GO:0004731	purine-nucleoside phosphorylase activity	molecular_function
1267	GO:0017061	S-methyl-5-thioadenosine phosphorylase activity	molecular_function
1269	GO:0008973	phosphopentomutase activity	molecular_function
1270	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function
1273	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
1274	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
1274	GO:0009035	type I site-specific deoxyribonuclease activity	molecular_function
1275	GO:0003924	GTPase activity	molecular_function
1275	GO:0005525	GTP binding	molecular_function
1275	GO:0008175	tRNA methyltransferase activity	molecular_function
1278	GO:0005515	protein binding	molecular_function
1279	GO:0005554	molecular function unknown	molecular_function
1283	GO:0016805	dipeptidase activity	molecular_function
1284	GO:0005313	L-glutamate transporter activity	molecular_function
1284	GO:0015175	neutral amino acid transporter activity	molecular_function
1284	GO:0015183	L-aspartate transporter activity	molecular_function
1284	GO:0015295	solute:hydrogen symporter activity	molecular_function
1284	GO:0017153	sodium:dicarboxylate symporter activity	molecular_function
1289	GO:0005524	ATP binding	molecular_function
1289	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1290	GO:0004614	phosphoglucomutase activity	molecular_function
1290	GO:0004615	phosphomannomutase activity	molecular_function
1290	GO:0008966	phosphoglucosamine mutase activity	molecular_function
1295	GO:0008989	rRNA (guanine-N1-)-methyltransferase activity	molecular_function
1298	GO:0005524	ATP binding	molecular_function
1298	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1305	GO:0015417	polyamine-transporting ATPase activity	molecular_function
1306	GO:0015646	permease activity	molecular_function
1307	GO:0005554	molecular function unknown	molecular_function
1308	GO:0008706	6-phospho-beta-glucosidase activity	molecular_function
1309	GO:0015582	beta-glucoside permease activity	molecular_function
1309	GO:0015584	trehalose permease activity	molecular_function
1310	GO:0016563	transcriptional activator activity	molecular_function
1310	GO:0030401	transcription antiterminator activity	molecular_function
1312	GO:0047605	acetolactate decarboxylase activity	molecular_function

续表 2

ssu	acc	name	term_type
1314	GO:0015646	permease activity	molecular_function
1320	GO:0004634	phosphopyruvate hydratase activity	molecular_function
1322	GO:0008887	glycerate kinase activity	molecular_function
1323	GO:0008967	phosphoglycolate phosphatase activity	molecular_function
1325	GO:0004647	phosphoserine phosphatase activity	molecular_function
1327	GO:0003918	DNA topoisomerase (ATP-hydrolyzing) activity	molecular_function
1328	GO:0003729	mRNA binding	molecular_function
1328	GO:0051082	unfolded protein binding	molecular_function
1329	GO:0005554	molecular function unknown	molecular_function
1330	GO:0009009	site-specific recombinase activity	molecular_function
1351	GO:0009055	electron carrier activity	molecular_function
1352	GO:0003735	structural constituent of ribosome	molecular_function
1354	GO:0005247	voltage-gated chloride channel activity	molecular_function
1355	GO:0008081	phosphoric diester hydrolase activity	molecular_function
1355	GO:0008198	ferrous iron binding	molecular_function
1355	GO:0008253	5'-nucleotidase activity	molecular_function
1355	GO:0019204	nucleotide phosphatase activity	molecular_function
1356	GO:0008383	manganese superoxide dismutase activity	molecular_function
1357	GO:0003887	DNA-directed DNA polymerase activity	molecular_function
1360	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
1360	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1361	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
1361	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1362	GO:0015646	permease activity	molecular_function
1362	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
1362	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1363	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1363	GO:0015646	permease activity	molecular_function
1363	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
1364	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function
1364	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1366	GO:0008462	endopeptidase Clp activity	molecular_function
1367	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
1368	GO:0004558	alpha-glucosidase activity	molecular_function
1368	GO:0004574	oligo-1,6-glucosidase activity	molecular_function
1368	GO:0008788	alpha,alpha-phosphotrehalase activity	molecular_function
1369	GO:0009018	sucrose phosphorylase activity	molecular_function
1370	GO:0015646	permease activity	molecular_function
1371	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
1371	GO:0015646	permease activity	molecular_function
1374	GO:0030528	transcription regulator activity	molecular_function
1375	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
1376	GO:0004121	cystathionine beta-lyase activity	molecular_function
1376	GO:0004123	cystathionine gamma-lyase activity	molecular_function
1383	GO:0008770	[acyl-carrier protein] phosphodiesterase activity	molecular_function
1387	GO:0004004	ATP-dependent RNA helicase activity	molecular_function

续表 2

ssu	acc	name	term_type
1390	GO:0005199	structural constituent of cell wall	molecular_function
1390	GO:0005554	molecular function unknown	molecular_function
1390	GO:0008599	protein phosphatase type 1 regulator activity	molecular_function
1394	GO:0008782	adenosylhomocysteine nucleosidase activity	molecular_function
1394	GO:0008930	methylthioadenosine nucleosidase activity	molecular_function
1397	GO:0003977	UDP-N-acetylglucosamine diphosphorylase activity	molecular_function
1400	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
1405	GO:0004803	transposase activity	molecular_function
1406	GO:0015646	permease activity	molecular_function
1407	GO:0005524	ATP binding	molecular_function
1407	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1408	GO:0000155	two-component sensor molecule activity	molecular_function
1408	GO:0000156	two-component response regulator activity	molecular_function
1409	GO:0000156	two-component response regulator activity	molecular_function
1411	GO:0008793	aromatic-amino-acid transaminase activity	molecular_function
1411	GO:0016847	1-aminocyclopropane-1-carboxylate synthase activity	molecular_function
1413	GO:0005275	amine transporter activity	molecular_function
1413	GO:0015418	quaternary-ammonium-compound-transporting ATPase activity	molecular_function
1413	GO:0043176	amine binding	molecular_function
1414	GO:0005524	ATP binding	molecular_function
1414	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1418	GO:0008961	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase activity	molecular_function
1419	GO:0004647	phosphoserine phosphatase activity	molecular_function
1419	GO:0004672	protein kinase activity	molecular_function
1420	GO:0004476	mannose-6-phosphate isomerase activity	molecular_function
1426	GO:0003723	RNA binding	molecular_function
1426	GO:0016788	hydrolase activity, acting on ester bonds	molecular_function
1427	GO:0004032	aldehyde reductase activity	molecular_function
1427	GO:0008106	alcohol dehydrogenase (NADP+) activity	molecular_function
1430	GO:0004540	ribonuclease activity	molecular_function
1431	GO:0004239	methionyl aminopeptidase activity	molecular_function
1432	GO:0008080	N-acetyltransferase activity	molecular_function
1433	GO:0008760	UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity	molecular_function
1434	GO:0003955	NAD(P)H dehydrogenase (quinone) activity	molecular_function
1434	GO:0004128	cytochrome-b5 reductase activity	molecular_function
1434	GO:0008753	NADPH dehydrogenase (quinone) activity	molecular_function
1435	GO:0000287	magnesium ion binding	molecular_function
1435	GO:0004478	methionine adenosyltransferase activity	molecular_function
1435	GO:0030955	potassium ion binding	molecular_function
1436	GO:0004132	dCMP deaminase activity	molecular_function
1436	GO:0008270	zinc ion binding	molecular_function
1439	GO:0004077	biotin-[acetyl-CoA-carboxylase] ligase activity	molecular_function
1439	GO:0030528	transcription regulator activity	molecular_function
1441	GO:0003887	DNA-directed DNA polymerase activity	molecular_function
1445	GO:0004845	uracil phosphoribosyltransferase activity	molecular_function
1445	GO:0004849	uridine kinase activity	molecular_function

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ssu	acc	name	term_type
1445	GO:0005524	ATP binding	molecular_function
1445	GO:0008974	phosphoribulokinase activity	molecular_function
1446	GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	molecular_function
1447	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
1448	GO:0019213	deacetylase activity	molecular_function
1449	GO:0004462	lactoylglutathione lyase activity	molecular_function
1450	GO:0004803	transposase activity	molecular_function
1451	GO:0004082	bisphosphoglycerate mutase activity	molecular_function
1451	GO:0004083	bisphosphoglycerate phosphatase activity	molecular_function
1451	GO:0004619	phosphoglycerate mutase activity	molecular_function
1451	GO:0042803	protein homodimerization activity	molecular_function
1452	GO:0003985	acetyl-CoA C-acetyltransferase activity	molecular_function
1453	GO:0004421	hydroxymethylglutaryl-CoA synthase activity	molecular_function
1453	GO:0016829	lyase activity	molecular_function
1454	GO:0004420	hydroxymethylglutaryl-CoA reductase (NADPH) activity	molecular_function
1455	GO:0004803	transposase activity	molecular_function
1457	GO:0004803	transposase activity	molecular_function
1458	GO:0003677	DNA binding	molecular_function
1460	GO:0016298	lipase activity	molecular_function
1462	GO:0005524	ATP binding	molecular_function
1465	GO:0004311	farnesyltranstransferase activity	molecular_function
1465	GO:0004337	geranyltranstransferase activity	molecular_function
1467	GO:0008855	exodeoxyribonuclease VII activity	molecular_function
1471	GO:0000155	two-component sensor molecule activity	molecular_function
1472	GO:0000156	two-component response regulator activity	molecular_function
1472	GO:0003677	DNA binding	molecular_function
1478	GO:0004427	inorganic diphosphatase activity	molecular_function
1480	GO:0008862	formate acetyltransferase activating enzyme activity	molecular_function
1481	GO:0005554	molecular function unknown	molecular_function
1482	GO:0005381	iron ion transporter activity	molecular_function
1482	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1485	GO:0004516	nicotinate phosphoribosyltransferase activity	molecular_function
1486	GO:0003952	NAD+ synthase (glutamine-hydrolyzing) activity	molecular_function
1486	GO:0008795	NAD+ synthase activity	molecular_function
1488	GO:0005554	molecular function unknown	molecular_function
1491	GO:0004595	pantetheine-phosphate adenylyltransferase activity	molecular_function
1492	GO:0008168	methyltransferase activity	molecular_function
1496	GO:0000156	two-component response regulator activity	molecular_function
1497	GO:0000155	two-component sensor molecule activity	molecular_function
1499	GO:0043212	carbohydrate-exporting ATPase activity	molecular_function
1502	GO:0003993	acid phosphatase activity	molecular_function
1502	GO:0004726	non-membrane spanning protein tyrosine phosphatase activity	molecular_function
1502	GO:0004727	prenylated protein tyrosine phosphatase activity	molecular_function
1507	GO:0008649	rRNA methyltransferase activity	molecular_function
1510	GO:0004730	pseudouridylate synthase activity	molecular_function
1511	GO:0005515	protein binding	molecular_function

续表 2

ssu	acc	name	term_type
1512	GO:0005488	binding	molecular_function
1516	GO:0005554	molecular function unknown	molecular_function
1517	GO:0008881	glutamate racemase activity	molecular_function
1519	GO:0008836	diaminopimelate decarboxylase activity	molecular_function
1520	GO:0004177	aminopeptidase activity	molecular_function
1520	GO:0004180	carboxypeptidase activity	molecular_function
1520	GO:0008423	bleomycin hydrolase activity	molecular_function
1523	GO:0003723	RNA binding	molecular_function
1523	GO:0008173	RNA methyltransferase activity	molecular_function
1526	GO:0003711	transcriptional elongation regulator activity	molecular_function
1527	GO:0005554	molecular function unknown	molecular_function
1529	GO:0008763	UDP-N-acetylmuramate-L-alanine ligase activity	molecular_function
1531	GO:0003677	DNA binding	molecular_function
1531	GO:0003702	RNA polymerase II transcription factor activity	molecular_function
1531	GO:0005524	ATP binding	molecular_function
1531	GO:0008026	ATP-dependent helicase activity	molecular_function
1531	GO:0042393	histone binding	molecular_function
1534	GO:0005525	GTP binding	molecular_function
1535	GO:0016657	oxidoreductase activity, acting on NADH or NADPH, nitrogenous group as acceptor	molecular_function
1538	GO:0005554	molecular function unknown	molecular_function
1539	GO:0005554	molecular function unknown	molecular_function
1540	GO:0000156	two-component response regulator activity	molecular_function
1541	GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	molecular_function
1543	GO:0004791	thioredoxin-disulfide reductase activity	molecular_function
1545	GO:0004004	ATP-dependent RNA helicase activity	molecular_function
1547	GO:0008963	phospho-N-acetylmuramoyl-pentapeptide-transferase activity	molecular_function
1550	GO:0008168	methyltransferase activity	molecular_function
1558	GO:0004659	prenyltransferase activity	molecular_function
1561	GO:0004161	dimethylallyltranstransferase activity	molecular_function
1562	GO:0003954	NADH dehydrogenase activity	molecular_function
1562	GO:0015036	disulfide oxidoreductase activity	molecular_function
1565	GO:0015079	potassium ion transporter activity	molecular_function
1566	GO:0015079	potassium ion transporter activity	molecular_function
1567	GO:0015559	multidrug efflux pump activity	molecular_function
1570	GO:0004820	glycine-tRNA ligase activity	molecular_function
1571	GO:0004820	glycine-tRNA ligase activity	molecular_function
1574	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1575	GO:0005524	ATP binding	molecular_function
1575	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1575	GO:0048474	D-methionine transporter activity	molecular_function
1576	GO:0004180	carboxypeptidase activity	molecular_function
1576	GO:0008237	metallopeptidase activity	molecular_function
1576	GO:0042315	cytosol nonspecific dipeptidase activity	molecular_function
1576	GO:0046983	protein dimerization activity	molecular_function
1577	GO:0048474	D-methionine transporter activity	molecular_function
1579	GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	molecular_function

续表 2

ssu	acc	name	term_type
1580	GO:0004489	methylenetetrahydrofolate reductase (NADPH) activity	molecular_function
1580	GO:0008702	5,10-methylenetetrahydrofolate reductase (FADH2) activity	molecular_function
1581	GO:0015211	purine nucleoside transporter activity	molecular_function
1583	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1584	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1585	GO:0015589	mannose permease activity	molecular_function
1587	GO:0004828	serine-tRNA ligase activity	molecular_function
1588	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity	molecular_function
1590	GO:0009035	type I site-specific deoxyribonuclease activity	molecular_function
1597	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
1598	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
1599	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
1599	GO:0004075	biotin carboxylase activity	molecular_function
1600	GO:0008693	3-hydroxydecanoyl-[acyl-carrier protein] dehydratase activity	molecular_function
1601	GO:0003989	acetyl-CoA carboxylase activity	molecular_function
1602	GO:0004315	3-oxoacyl-[acyl-carrier protein] synthase activity	molecular_function
1603	GO:0004316	3-oxoacyl-[acyl-carrier protein] reductase activity	molecular_function
1604	GO:0004314	[acyl-carrier protein] S-malonyltransferase activity	molecular_function
1605	GO:0004318	enoyl-[acyl-carrier protein] reductase (NADH) activity	molecular_function
1607	GO:0004315	3-oxoacyl-[acyl-carrier protein] synthase activity	molecular_function
1611	GO:0004072	aspartate kinase activity	molecular_function
1611	GO:0004412	homoserine dehydrogenase activity	molecular_function
1611	GO:0016597	amino acid binding	molecular_function
1613	GO:0008784	alanine racemase activity	molecular_function
1614	GO:0008897	phosphopantetheinyltransferase activity	molecular_function
1615	GO:0015450	protein translocase activity	molecular_function
1617	GO:0008865	fructokinase activity	molecular_function
1618	GO:0015582	beta-glucoside permease activity	molecular_function
1618	GO:0015584	trehalose permease activity	molecular_function
1619	GO:0004564	beta-fructofuranosidase activity	molecular_function
1620	GO:0030528	transcription regulator activity	molecular_function
1621	GO:0003715	transcription termination factor activity	molecular_function
1623	GO:0003746	translation elongation factor activity	molecular_function
1624	GO:0004251	X-Pro dipeptidase activity	molecular_function
1624	GO:0008451	X-Pro aminopeptidase activity	molecular_function
1625	GO:0009381	excinuclease ABC activity	molecular_function
1626	GO:0015095	magnesium ion transporter activity	molecular_function
1629	GO:0003697	single-stranded DNA binding	molecular_function
1632	GO:0016979	lipoate-protein ligase activity	molecular_function
1632	GO:0017118	lipoyltransferase activity	molecular_function
1634	GO:0004148	dihydrolipoyl dehydrogenase activity	molecular_function
1634	GO:0004375	glycine dehydrogenase (decarboxylating) activity	molecular_function
1634	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	molecular_function
1634	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
1634	GO:0015036	disulfide oxidoreductase activity	molecular_function
1634	GO:0050660	FAD binding	molecular_function

续表 2

ssu	acc	name	term_type
1635	GO:0003826	alpha-ketoacid dehydrogenase activity	molecular_function
1635	GO:0004149	dihydrolipoyllysine-residue succinyltransferase activity	molecular_function
1635	GO:0004742	dihydrolipoyllysine-residue acetyltransferase activity	molecular_function
1636	GO:0003826	alpha-ketoacid dehydrogenase activity	molecular_function
1636	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
1636	GO:0004802	transketolase activity	molecular_function
1637	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	molecular_function
1641	GO:0019843	rRNA binding	molecular_function
1642	GO:0003743	translation initiation factor activity	molecular_function
1645	GO:0003715	transcription termination factor activity	molecular_function
1645	GO:0003723	RNA binding	molecular_function
1646	GO:0005554	molecular function unknown	molecular_function
1647	GO:0008176	tRNA (guanine-N7-)-methyltransferase activity	molecular_function
1649	GO:0015646	permease activity	molecular_function
1650	GO:0005375	copper ion transporter activity	molecular_function
1650	GO:0005524	ATP binding	molecular_function
1650	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1653	GO:0030528	transcription regulator activity	molecular_function
1654	GO:0008080	N-acetyltransferase activity	molecular_function
1655	GO:0005554	molecular function unknown	molecular_function
1659	GO:0004803	transposase activity	molecular_function
1660	GO:0015197	peptide transporter activity	molecular_function
1660	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1661	GO:0015421	oligopeptide-transporting ATPase activity	molecular_function
1661	GO:0015646	permease activity	molecular_function
1663	GO:0015197	peptide transporter activity	molecular_function
1664	GO:0015421	oligopeptide-transporting ATPase activity	molecular_function
1665	GO:0009002	serine-type D-Ala-D-Ala carboxypeptidase activity	molecular_function
1669	GO:0004123	cystathionine gamma-lyase activity	molecular_function
1669	GO:0008483	transaminase activity	molecular_function
1669	GO:0009000	selenocysteine lyase activity	molecular_function
1671	GO:0004009	ATP-binding cassette (ABC) transporter activity	molecular_function
1671	GO:0005524	ATP binding	molecular_function
1671	GO:0016887	ATPase activity	molecular_function
1672	GO:0008963	phospho-N-acetylmuramoyl-pentapeptide-transferase activity	molecular_function
1672	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
1674	GO:0009038	undecaprenol kinase activity	molecular_function
1675	GO:0015359	amino acid permease activity	molecular_function
1675	GO:0015599	glutamine-importing ATPase activity	molecular_function
1675	GO:0015646	permease activity	molecular_function
1676	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1679	GO:0004794	threonine ammonia-lyase activity	molecular_function
1680	GO:0004455	ketol-acid reductoisomerase activity	molecular_function
1681	GO:0003984	acetolactate synthase activity	molecular_function
1681	GO:0016597	amino acid binding	molecular_function
1682	GO:0003984	acetolactate synthase activity	molecular_function

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ssu	acc	name	term_type
1683	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function
1686	GO:0004160	dihydroxy-acid dehydratase activity	molecular_function
1691	GO:0003735	structural constituent of ribosome	molecular_function
1692	GO:0003735	structural constituent of ribosome	molecular_function
1696	GO:0008649	rRNA methyltransferase activity	molecular_function
1701	GO:0015423	maltose-transporting ATPase activity	molecular_function
1703	GO:0000156	two-component response regulator activity	molecular_function
1704	GO:0000155	two-component sensor molecule activity	molecular_function
1708	GO:0015646	permease activity	molecular_function
1709	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
1709	GO:0015646	permease activity	molecular_function
1711	GO:0004340	glucokinase activity	molecular_function
1712	GO:0004559	alpha-mannosidase activity	molecular_function
1715	GO:0016798	hydrolase activity, acting on glycosyl bonds	molecular_function
1717	GO:0004817	cysteine-tRNA ligase activity	molecular_function
1720	GO:0009001	serine O-acetyltransferase activity	molecular_function
1721	GO:0003729	mRNA binding	molecular_function
1721	GO:0004654	polyribonucleotide nucleotidyltransferase activity	molecular_function
1725	GO:0015582	beta-glucoside permease activity	molecular_function
1725	GO:0015584	trehalose permease activity	molecular_function
1725	GO:0019188	sucrose permease (PTS) activity	molecular_function
1726	GO:0005529	sugar binding	molecular_function
1727	GO:0005529	sugar binding	molecular_function
1727	GO:0016564	transcriptional repressor activity	molecular_function
1728	GO:0003735	structural constituent of ribosome	molecular_function
1729	GO:0015505	uracil permease activity	molecular_function
1729	GO:0015646	permease activity	molecular_function
1732	GO:0004730	pseudouridylate synthase activity	molecular_function
1736	GO:0008463	formylmethionine deformylase activity	molecular_function
1736	GO:0042586	peptide deformylase activity	molecular_function
1738	GO:0003861	3-isopropylmalate dehydratase activity	molecular_function
1739	GO:0003861	3-isopropylmalate dehydratase activity	molecular_function
1740	GO:0003862	3-isopropylmalate dehydrogenase activity	molecular_function
1741	GO:0003852	2-isopropylmalate synthase activity	molecular_function
1746	GO:0003893	epsilon DNA polymerase activity	molecular_function
1747	GO:0004371	glycerone kinase activity	molecular_function
1749	GO:0004371	glycerone kinase activity	molecular_function
1750	GO:0004371	glycerone kinase activity	molecular_function
1752	GO:0005275	amine transporter activity	molecular_function
1752	GO:0005345	purine transporter activity	molecular_function
1752	GO:0005350	pyrimidine transporter activity	molecular_function
1752	GO:0015250	water channel activity	molecular_function
1752	GO:0015254	glycerol channel activity	molecular_function
1752	GO:0015288	porin activity	molecular_function
1752	GO:0046943	carboxylic acid transporter activity	molecular_function
1753	GO:0004827	proline-tRNA ligase activity	molecular_function

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ssu	acc	name	term_type
1754	GO:0004222	metalloendopeptidase activity	molecular_function
1755	GO:0004605	phosphatidate cytidylyltransferase activity	molecular_function
1756	GO:0005386	carrier activity	molecular_function
1756	GO:0008834	di-trans,poly-cis-decaprenylcistransferase activity	molecular_function
1756	GO:0045547	dehydrodolichyl diphosphate synthase activity	molecular_function
1758	GO:0004019	adenylosuccinate synthase activity	molecular_function
1759	GO:0004357	glutamate-cysteine ligase activity	molecular_function
1762	GO:0017150	tRNA dihydrouridine synthase activity	molecular_function
1766	GO:0005524	ATP binding	molecular_function
1766	GO:0016887	ATPase activity	molecular_function
1767	GO:0016564	transcriptional repressor activity	molecular_function
1770	GO:0003746	translation elongation factor activity	molecular_function
1771	GO:0003735	structural constituent of ribosome	molecular_function
1774	GO:0003715	transcription termination factor activity	molecular_function
1777	GO:0008658	penicillin binding	molecular_function
1778	GO:0015036	disulfide oxidoreductase activity	molecular_function
1779	GO:0004730	pseudouridylate synthase activity	molecular_function
1784	GO:0004788	thiamin diphosphokinase activity	molecular_function
1785	GO:0004750	ribulose-phosphate 3-epimerase activity	molecular_function
1786	GO:0005554	molecular function unknown	molecular_function
1787	GO:0005319	lipid transporter activity	molecular_function
1787	GO:0015646	permease activity	molecular_function
1787	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1789	GO:0016563	transcriptional activator activity	molecular_function
1793	GO:0000179	rRNA (adenine-N6,N6-)-dimethyltransferase activity	molecular_function
1802	GO:0004536	deoxyribonuclease activity	molecular_function
1805	GO:0005554	molecular function unknown	molecular_function
1807	GO:0004056	argininosuccinate lyase activity	molecular_function
1808	GO:0004055	argininosuccinate synthase activity	molecular_function
1808	GO:0005524	ATP binding	molecular_function
1813	GO:0004156	dihydropteroate synthase activity	molecular_function
1813	GO:0008705	methionine synthase activity	molecular_function
1813	GO:0008898	homocysteine S-methyltransferase activity	molecular_function
1813	GO:0016205	selenocysteine methyltransferase activity	molecular_function
1813	GO:0050897	cobalt ion binding	molecular_function
1814	GO:0005293	lysine permease activity	molecular_function
1815	GO:0004818	glutamate-tRNA ligase activity	molecular_function
1820	GO:0004089	carbonate dehydratase activity	molecular_function
1821	GO:0005524	ATP binding	molecular_function
1823	GO:0004170	dUTP diphosphatase activity	molecular_function
1824	GO:0005524	ATP binding	molecular_function
1824	GO:0015646	permease activity	molecular_function
1824	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1825	GO:0005524	ATP binding	molecular_function
1825	GO:0015646	permease activity	molecular_function
1825	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function

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ssu	acc	name	term_type
1827	GO:0004367	glycerol-3-phosphate dehydrogenase (NAD+) activity	molecular_function
1828	GO:0003983	UTP-glucose-1-phosphate uridylyltransferase activity	molecular_function
1830	GO:0000287	magnesium ion binding	molecular_function
1830	GO:0005542	folic acid binding	molecular_function
1830	GO:0030272	5-formyltetrahydrofolate cyclo-ligase activity	molecular_function
1831	GO:0004181	metallocarboxypeptidase activity	molecular_function
1832	GO:0008666	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase activity	molecular_function
1832	GO:0009001	serine O-acetyltransferase activity	molecular_function
1835	GO:0004722	protein serine/threonine phosphatase activity	molecular_function
1836	GO:0004347	glucose-6-phosphate isomerase activity	molecular_function
1838	GO:0008270	zinc ion binding	molecular_function
1839	GO:0004802	transketolase activity	molecular_function
1841	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1846	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1849	GO:0004556	alpha-amylase activity	molecular_function
1850	GO:0030528	transcription regulator activity	molecular_function
1851	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1852	GO:0015599	glutamine-importing ATPase activity	molecular_function
1852	GO:0015646	permease activity	molecular_function
1853	GO:0015424	amino acid-transporting ATPase activity	molecular_function
1853	GO:0016597	amino acid binding	molecular_function
1855	GO:0015582	beta-glucoside permease activity	molecular_function
1855	GO:0019190	cellobiose permease activity	molecular_function
1857	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1858	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1858	GO:0015573	beta-glucoside transporter activity	molecular_function
1859	GO:0005554	molecular function unknown	molecular_function
1859	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function
1861	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function
1863	GO:0004823	leucine-tRNA ligase activity	molecular_function
1864	GO:0004245	neprilysin activity	molecular_function
1864	GO:0008270	zinc ion binding	molecular_function
1864	GO:0016512	endothelin-converting enzyme 1 activity	molecular_function
1866	GO:0005384	manganese ion transporter activity	molecular_function
1866	GO:0005385	zinc ion transporter activity	molecular_function
1866	GO:0015646	permease activity	molecular_function
1866	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1867	GO:0005524	ATP binding	molecular_function
1867	GO:0015410	manganese-transporting ATPase activity	molecular_function
1869	GO:0005055	laminin receptor activity	molecular_function
1869	GO:0030145	manganese ion binding	molecular_function
1877	GO:0004045	aminoacyl-tRNA hydrolase activity	molecular_function
1878	GO:0008728	GTP diphosphokinase activity	molecular_function
1878	GO:0008893	guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity	molecular_function
1879	GO:0008198	ferrous iron binding	molecular_function
1879	GO:0008253	5'-nucleotidase activity	molecular_function

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ssu	acc	name	term_type
1879	GO:0008663	2',3'-cyclic-nucleotide 2'-phosphodiesterase activity	molecular_function
1888	GO:0005199	structural constituent of cell wall	molecular_function
1893	GO:0005554	molecular function unknown	molecular_function
1894	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function
1898	GO:0004176	ATP-dependent peptidase activity	molecular_function
1898	GO:0004386	helicase activity	molecular_function
1898	GO:0005524	ATP binding	molecular_function
1898	GO:0016887	ATPase activity	molecular_function
1899	GO:0008998	ribonucleoside-triphosphate reductase activity	molecular_function
1901	GO:0008081	phosphoric diester hydrolase activity	molecular_function
1901	GO:0008198	ferrous iron binding	molecular_function
1901	GO:0008253	5'-nucleotidase activity	molecular_function
1901	GO:0016827	hydrolase activity, acting on acid carbon-phosphorus bonds	molecular_function
1901	GO:0019204	nucleotide phosphatase activity	molecular_function
1903	GO:0008998	ribonucleoside-triphosphate reductase activity	molecular_function
1908	GO:0005524	ATP binding	molecular_function
1910	GO:0004814	arginine-tRNA ligase activity	molecular_function
1910	GO:0005524	ATP binding	molecular_function
1914	GO:0004134	4-alpha-glucanotransferase activity	molecular_function
1915	GO:0015608	carbohydrate-importing ATPase activity	molecular_function
1916	GO:0015423	maltose-transporting ATPase activity	molecular_function
1916	GO:0015646	permease activity	molecular_function
1917	GO:0005351	sugar porter activity	molecular_function
1920	GO:0004133	glycogen debranching enzyme activity	molecular_function
1920	GO:0004556	alpha-amylase activity	molecular_function
1922	GO:0005554	molecular function unknown	molecular_function
1923	GO:0004815	aspartate-tRNA ligase activity	molecular_function
1924	GO:0008080	N-acetyltransferase activity	molecular_function
1925	GO:0004033	aldo-keto reductase activity	molecular_function
1925	GO:0005249	voltage-gated potassium channel activity	molecular_function
1925	GO:0015459	potassium channel regulator activity	molecular_function
1925	GO:0030955	potassium ion binding	molecular_function
1927	GO:0008422	beta-glucosidase activity	molecular_function
1929	GO:0008422	beta-glucosidase activity	molecular_function
1932	GO:0004722	protein serine/threonine phosphatase activity	molecular_function
1933	GO:0000104	succinate dehydrogenase activity	molecular_function
1933	GO:0004106	chorismate mutase activity	molecular_function
1933	GO:0008177	succinate dehydrogenase (ubiquinone) activity	molecular_function
1933	GO:0009055	electron carrier activity	molecular_function
1933	GO:0015036	disulfide oxidoreductase activity	molecular_function
1933	GO:0016156	fumarate reductase (NADH) activity	molecular_function
1933	GO:0050660	FAD binding	molecular_function
1935	GO:0003735	structural constituent of ribosome	molecular_function
1938	GO:0004003	ATP-dependent DNA helicase activity	molecular_function
1941	GO:0005554	molecular function unknown	molecular_function
1947	GO:0004808	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase activity	molecular_function

续表 2

ssu	acc	name	term_type
1948	GO:0003941	L-serine ammonia-lyase activity	molecular_function
1949	GO:0003941	L-serine ammonia-lyase activity	molecular_function
1951	GO:0015087	cobalt ion transporter activity	molecular_function
1952	GO:0015087	cobalt ion transporter activity	molecular_function
1952	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1953	GO:0015087	cobalt ion transporter activity	molecular_function
1953	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1954	GO:0008444	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity	molecular_function
1959	GO:0003697	single-stranded DNA binding	molecular_function
1959	GO:0005524	ATP binding	molecular_function
1960	GO:0003938	IMP dehydrogenase activity	molecular_function
1961	GO:0004830	tryptophan-tRNA ligase activity	molecular_function
1962	GO:0005554	molecular function unknown	molecular_function
1963	GO:0005524	ATP binding	molecular_function
1963	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function
1967	GO:0005554	molecular function unknown	molecular_function
1968	GO:0008233	peptidase activity	molecular_function
1969	GO:0003677	DNA binding	molecular_function

a) ssu，蛋白序列的 Id; acc, Gene Ontology 体系中所预测功能的 accession number; name，所预测功能的名称; term_type，所预测功能所属的大类名称

表 3 和其他物种相比，菌株 89-1591 的蛋白序列显著的注释较多、较集中的 Gene Ontology 功能结点

goid	acc	name	term_type	p	depth
6571	GO:0009987	cellular process	biological_process	0	2
4612	GO:0007582	physiological process	biological_process	0	2
4806	GO:0008152	metabolism	biological_process	0	3
18611	GO:0050875	cellular physiological process	biological_process	0	3
14190	GO:0044419	interaction between organisms	biological_process	0.0000452	3
18914	GO:0051179	localization	biological_process	0.0000727	3
14130	GO:0044237	cellular metabolism	biological_process	0	4
5660	GO:0009056	catabolism	biological_process	0	4
13964	GO:0043283	biopolymer metabolism	biological_process	0	4
3878	GO:0006807	nitrogen compound metabolism	biological_process	0	4
14131	GO:0044238	primary metabolism	biological_process	0	4
5662	GO:0009058	biosynthesis	biological_process	0	4
13851	GO:0043170	macromolecule metabolism	biological_process	1.57E-10	4
6306	GO:0009719	response to endogenous stimulus	biological_process	0.0000124	4
14174	GO:0044403	symbiosis, mutualism through parasitism	biological_process	0.000018	4
18969	GO:0051234	establishment of localization	biological_process	0.0000443	4
10564	GO:0019748	secondary metabolism	biological_process	0.00271	4
19035	GO:0051301	cell division	biological_process	0.00301	4
4008	GO:0006950	response to stress	biological_process	0.00986	4
14414	GO:0045229	external encapsulating structure organization and biogenesis	biological_process	0	5
5905	GO:0009308	amine metabolism	biological_process	0	5
3186	GO:0006082	organic acid metabolism	biological_process	0	5
14142	GO:0044249	cellular biosynthesis	biological_process	0	5
3600	GO:0006519	amino acid and derivative metabolism	biological_process	0	5

续表 3

goid	acc	name	term_type	p	depth
13965	GO:0043284	biopolymer biosynthesis	biological_process	0	5
3802	GO:0006725	aromatic compound metabolism	biological_process	0	5
3170	GO:0006066	alcohol metabolism	biological_process	0	5
15651	GO:0046483	heterocycle metabolism	biological_process	0	5
18921	GO:0051186	cofactor metabolism	biological_process	0	5
3839	GO:0006766	vitamin metabolism	biological_process	0	5
3241	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	biological_process	0	5
3079	GO:0005975	carbohydrate metabolism	biological_process	0	5
14141	GO:0044248	cellular catabolism	biological_process	0	5
14153	GO:0044260	cellular macromolecule metabolism	biological_process	3.71E-10	5
3861	GO:0006790	sulfur metabolism	biological_process	3.32E-09	5
15658	GO:0046490	isopentenyl diphosphate metabolism	biological_process	0.00000139	5
5661	GO:0009057	macromolecule catabolism	biological_process	0.00000162	5
4031	GO:0006974	response to DNA damage stimulus	biological_process	0.00000288	5
526	GO:0000910	cytokinesis	biological_process	0.0000101	5
13775	GO:0043094	metabolic compound salvage	biological_process	0.0000126	5
3195	GO:0006091	generation of precursor metabolites and energy	biological_process	0.0000175	5
14175	GO:0044404	symbiotic interaction between host and other organism	biological_process	0.000018	5
3709	GO:0006629	lipid metabolism	biological_process	0.0000422	5
3881	GO:0006810	transport	biological_process	0.000205	5
54	GO:0000051	urea cycle intermediate metabolism	biological_process	0.00049	5
4084	GO:0007028	cytoplasm organization and biogenesis	biological_process	0.00248	5
6575	GO:0009991	response to extracellular stimulus	biological_process	0.00374	5
13131	GO:0042445	hormone metabolism	biological_process	0.00826	5
3807	GO:0006730	one-carbon compound metabolism	biological_process	0.0095	5
7857	GO:0016052	carbohydrate catabolism	biological_process	0	6
3809	GO:0006732	coenzyme metabolism	biological_process	0	6
5663	GO:0009059	macromolecule biosynthesis	biological_process	0	6
3840	GO:0006767	water-soluble vitamin metabolism	biological_process	0	6
7651	GO:0015837	amine transport	biological_process	0	6
5721	GO:0009117	nucleotide metabolism	biological_process	0	6
3080	GO:0005976	polysaccharide metabolism	biological_process	0	6
5716	GO:0009112	nucleobase metabolism	biological_process	0	6
7662	GO:0015849	organic acid transport	biological_process	0	6
15333	GO:0046164	alcohol catabolism	biological_process	0	6
14164	GO:0044271	nitrogen compound biosynthesis	biological_process	0	6
7790	GO:0015980	energy derivation by oxidation of organic compounds	biological_process	0	6
4103	GO:0007047	cell wall organization and biogenesis	biological_process	0	6
5262	GO:0008643	carbohydrate transport	biological_process	0	6
3360	GO:0006259	DNA metabolism	biological_process	0	6
7874	GO:0016070	RNA metabolism	biological_process	0	6
10568	GO:0019752	carboxylic acid metabolism	biological_process	0	6
14155	GO:0044262	cellular carbohydrate metabolism	biological_process	3.45E-11	6
14165	GO:0044272	sulfur compound biosynthesis	biological_process	3.71E-10	6
7759	GO:0015949	nucleobase, nucleoside and nucleotide interconversion	biological_process	8.86E-10	6
7858	GO:0016053	organic acid biosynthesis	biological_process	3.76E-09	6
5826	GO:0009225	nucleotide-sugar metabolism	biological_process	3.93E-08	6
5720	GO:0009116	nucleoside metabolism	biological_process	6.91E-08	6

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goid	acc	name	term_type	p	depth
11948	GO:0031163	metallo-sulfur cluster assembly	biological_process	7.39E-08	6
10263	GO:0019438	aromatic compound biosynthesis	biological_process	0.000000137	6
14148	GO:0044255	cellular lipid metabolism	biological_process	0.000000978	6
14158	GO:0044265	cellular macromolecule catabolism	biological_process	0.00000138	6
5997	GO:0009405	pathogenesis	biological_process	0.00000185	6
18923	GO:0051188	cofactor biosynthesis	biological_process	0.00000385	6
14163	GO:0044270	nitrogen compound catabolism	biological_process	0.000005	6
15334	GO:0046165	alcohol biosynthesis	biological_process	0.0000159	6
5714	GO:0009110	vitamin biosynthesis	biological_process	0.0000271	6
10567	GO:0019751	polyol metabolism	biological_process	0.000164	6
5903	GO:0009306	protein secretion	biological_process	0.00066	6
12946	GO:0042254	ribosome biogenesis and assembly	biological_process	0.00105	6
12914	GO:0042221	response to chemical substance	biological_process	0.00252	6
3882	GO:0006811	ion transport	biological_process	0.00299	6
14095	GO:0043414	biopolymer methylation	biological_process	0.00456	6
13627	GO:0042946	glucoside transport	biological_process	0	7
3100	GO:0005996	monosaccharide metabolism	biological_process	0	7
5860	GO:0009259	ribonucleotide metabolism	biological_process	0	7
3246	GO:0006144	purine base metabolism	biological_process	0	7
5766	GO:0009165	nucleotide biosynthesis	biological_process	0	7
12288	GO:0031504	cell wall organization and biogenesis (sensu Bacteria)	biological_process	0	7
263	GO:0000272	polysaccharide catabolism	biological_process	0	7
7582	GO:0015766	disaccharide transport	biological_process	0	7
16101	GO:0046942	carboxylic acid transport	biological_process	0	7
13229	GO:0042546	cell wall biosynthesis	biological_process	0	7
3196	GO:0006092	main pathways of carbohydrate metabolism	biological_process	0	7
5906	GO:0009309	amine biosynthesis	biological_process	0	7
14157	GO:0044264	cellular polysaccharide metabolism	biological_process	0	7
261	GO:0000270	peptidoglycan metabolism	biological_process	0	7
3601	GO:0006520	amino acid metabolism	biological_process	0	7
7856	GO:0016051	carbohydrate biosynthesis	biological_process	0	7
15281	GO:0046112	nucleobase biosynthesis	biological_process	0	7
5725	GO:0009123	nucleoside monophosphate metabolism	biological_process	0	7
6042	GO:0009451	RNA modification	biological_process	0	7
3493	GO:0006399	tRNA metabolism	biological_process	0	7
5993	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	biological_process	0	7
14168	GO:0044275	cellular carbohydrate catabolism	biological_process	0	7
5230	GO:0008610	lipid biosynthesis	biological_process	2.96E-12	7
3215	GO:0006113	fermentation	biological_process	1.34E-10	7
3810	GO:0006733	oxidoreduction coenzyme metabolism	biological_process	2.11E-10	7
3409	GO:0006310	DNA recombination	biological_process	5.65E-10	7
3321	GO:0006220	pyrimidine nucleotide metabolism	biological_process	1.21E-09	7
15563	GO:0046394	carboxylic acid biosynthesis	biological_process	1.85E-08	7
3265	GO:0006163	purine nucleotide metabolism	biological_process	0.000000025	7
8019	GO:0016226	iron-sulfur cluster assembly	biological_process	7.39E-08	7
5712	GO:0009108	coenzyme biosynthesis	biological_process	9.36E-08	7
5723	GO:0009119	ribonucleoside metabolism	biological_process	0.000000179	7
15586	GO:0046417	chorismate metabolism	biological_process	0.000000228	7

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goid	acc	name	term_type	p	depth
3380	GO:0006281	DNA repair	biological_process	0.000000563	7
3214	GO:0006112	energy reserve metabolism	biological_process	0.00000073	7
3188	GO:0006084	acetyl-CoA metabolism	biological_process	0.000000808	7
5863	GO:0009262	deoxyribonucleotide metabolism	biological_process	0.000000812	7
3194	GO:0006090	pyruvate metabolism	biological_process	0.00000132	7
5767	GO:0009166	nucleotide catabolism	biological_process	0.00000144	7
7659	GO:0015846	polyamine transport	biological_process	0.00000349	7
15343	GO:0046174	polyol catabolism	biological_process	0.00000349	7
5907	GO:0009310	amine catabolism	biological_process	0.00000448	7
12967	GO:0042278	purine nucleoside metabolism	biological_process	0.00000634	7
7565	GO:0015749	monosaccharide transport	biological_process	0.00000777	7
3361	GO:0006260	DNA replication	biological_process	0.0000104	7
13176	GO:0042493	response to drug	biological_process	0.0000104	7
6285	GO:0009698	phenylpropanoid metabolism	biological_process	0.0000155	7
3826	GO:0006752	group transfer coenzyme metabolism	biological_process	0.0000164	7
3505	GO:0006412	protein biosynthesis	biological_process	0.0000271	7
3088	GO:0005984	disaccharide metabolism	biological_process	0.0000316	7
13050	GO:0042364	water-soluble vitamin biosynthesis	biological_process	0.0000337	7
3308	GO:0006206	pyrimidine base metabolism	biological_process	0.0000339	7
7876	GO:0016072	rRNA metabolism	biological_process	0.000104	7
3798	GO:0006720	isoprenoid metabolism	biological_process	0.000205	7
3403	GO:0006304	DNA modification	biological_process	0.00091	7
13404	GO:0042723	thiamin and derivative metabolism	biological_process	0.000964	7
3144	GO:0006040	amino sugar metabolism	biological_process	0.00298	7
3883	GO:0006812	cation transport	biological_process	0.00389	7
3495	GO:0006401	RNA catabolism	biological_process	0.00457	7
4102	GO:0007046	ribosome biogenesis	biological_process	0.00751	7
5685	GO:0009081	branched chain family amino acid metabolism	biological_process	0	8
147	GO:0000154	rRNA modification	biological_process	0	8
10358	GO:0019533	cellobiose transport	biological_process	0	8
5726	GO:0009124	nucleoside monophosphate biosynthesis	biological_process	0	8
3494	GO:0006400	tRNA modification	biological_process	0	8
13718	GO:0043037	translation	biological_process	0	8
5270	GO:0008652	amino acid biosynthesis	biological_process	0	8
5861	GO:0009260	ribonucleotide biosynthesis	biological_process	0	8
94	GO:0000096	sulfur amino acid metabolism	biological_process	0	8
5673	GO:0009069	serine family amino acid metabolism	biological_process	0	8
10145	GO:0019318	hexose metabolism	biological_process	0	8
5717	GO:0009113	purine base biosynthesis	biological_process	0	8
13719	GO:0043038	amino acid activation	biological_process	0	8
5874	GO:0009273	cell wall biosynthesis (sensu Bacteria)	biological_process	0	8
14140	GO:0044247	cellular polysaccharide catabolism	biological_process	0	8
3177	GO:0006073	glucan metabolism	biological_process	0	8
262	GO:0000271	polysaccharide biosynthesis	biological_process	0	8
7575	GO:0015759	beta-glucoside transport	biological_process	0	8
5670	GO:0009066	aspartate family amino acid metabolism	biological_process	0	8
3931	GO:0006865	amino acid transport	biological_process	0	8
5762	GO:0009161	ribonucleoside monophosphate metabolism	biological_process	6.11E-11	8

续表 3

goid	acc	name	term_type	p	depth
15534	GO:0046365	monosaccharide catabolism	biological_process	7.97E-11	8
5728	GO:0009126	purine nucleoside monophosphate metabolism	biological_process	2.15E-10	8
5271	GO:0008653	lipopolysaccharide metabolism	biological_process	4.41E-10	8
10189	GO:0019362	pyridine nucleotide metabolism	biological_process	4.71E-10	8
7491	GO:0015674	di-, tri-valent inorganic cation transport	biological_process	2.23E-09	8
3266	GO:0006164	purine nucleotide biosynthesis	biological_process	1.27E-08	8
5752	GO:0009150	purine ribonucleotide metabolism	biological_process	4.34E-08	8
3322	GO:0006221	pyrimidine nucleotide biosynthesis	biological_process	4.41E-08	8
7661	GO:0015848	spermidine transport	biological_process	0.000000068	8
15521	GO:0046352	disaccharide catabolism	biological_process	9.82E-08	8
3412	GO:0006313	DNA transposition	biological_process	0.00000011	8
7660	GO:0015847	putrescine transport	biological_process	0.000000191	8
5676	GO:0009072	aromatic amino acid family metabolism	biological_process	0.000000211	8
5668	GO:0009064	glutamine family amino acid metabolism	biological_process	0.000000255	8
5986	GO:0009394	2'-deoxyribonucleotide metabolism	biological_process	0.000000291	8
5667	GO:0009063	amino acid catabolism	biological_process	0.00000168	8
15840	GO:0046677	response to antibiotic	biological_process	0.00000275	8
5263	GO:0008645	hexose transport	biological_process	0.00000336	8
15297	GO:0046128	purine ribonucleoside metabolism	biological_process	0.00000589	8
15533	GO:0046364	monosaccharide biosynthesis	biological_process	0.0000146	8
7704	GO:0015893	drug transport	biological_process	0.0000316	8
5864	GO:0009263	deoxyribonucleotide biosynthesis	biological_process	0.000035	8
5819	GO:0009218	pyrimidine ribonucleotide metabolism	biological_process	0.0000386	8
7749	GO:0015939	pantothenate metabolism	biological_process	0.0000426	8
3833	GO:0006760	folic acid and derivative metabolism	biological_process	0.0000778	8
4943	GO:0008299	isoprenoid biosynthesis	biological_process	0.000337	8
3362	GO:0006261	DNA-dependent DNA replication	biological_process	0.000554	8
3388	GO:0006289	nucleotide-excision repair	biological_process	0.000597	8
3844	GO:0006772	thiamin metabolism	biological_process	0.000839	8
10822	GO:0030001	metal ion transport	biological_process	0.000849	8
3712	GO:0006633	fatty acid biosynthesis	biological_process	0.00116	8
5671	GO:0009067	aspartate family amino acid biosynthesis	biological_process	0	9
3630	GO:0006549	isoleucine metabolism	biological_process	0	9
5686	GO:0009082	branched chain family amino acid biosynthesis	biological_process	0	9
5852	GO:0009251	glucan catabolism	biological_process	0	9
11055	GO:0030243	cellulose metabolism	biological_process	0	9
44	GO:0000041	transition metal ion transport	biological_process	0	9
13720	GO:0043039	tRNA aminoacylation	biological_process	0	9
5768	GO:0009167	purine ribonucleoside monophosphate metabolism	biological_process	4.24E-11	9
10147	GO:0019320	hexose catabolism	biological_process	9.44E-11	9
5853	GO:0009252	peptidoglycan biosynthesis	biological_process	1.6E-10	9
3110	GO:0006006	glucose metabolism	biological_process	3.76E-10	9
5707	GO:0009103	lipopolysaccharide biosynthesis	biological_process	4.41E-10	9
5758	GO:0009156	ribonucleoside monophosphate biosynthesis	biological_process	9.57E-10	9
95	GO:0000097	sulfur amino acid biosynthesis	biological_process	1.02E-09	9
5677	GO:0009073	aromatic amino acid family biosynthesis	biological_process	2.28E-09	9
5729	GO:0009127	purine nucleoside monophosphate biosynthesis	biological_process	3.2E-09	9
3842	GO:0006769	nicotinamide metabolism	biological_process	5.09E-09	9

续表 3

goid	acc	name	term_type	p	depth
3636	GO:0006555	methionine metabolism	biological_process	6.01E-09	9
5754	GO:0009152	purine ribonucleotide biosynthesis	biological_process	2.73E-08	9
3644	GO:0006563	L-serine metabolism	biological_process	3.12E-08	9
3632	GO:0006551	leucine metabolism	biological_process	4.76E-08	9
3647	GO:0006566	threonine metabolism	biological_process	5.62E-08	9
5674	GO:0009070	serine family amino acid biosynthesis	biological_process	0.00000011	9
5988	GO:0009396	folic acid and derivative biosynthesis	biological_process	0.000000416	9
5841	GO:0009240	isopentenyl diphosphate biosynthesis	biological_process	0.00000139	9
5866	GO:0009265	2'-deoxyribonucleotide biosynthesis	biological_process	0.0000017	9
3081	GO:0005977	glycogen metabolism	biological_process	0.00000207	9
7619	GO:0015803	branched-chain aliphatic amino acid transport	biological_process	0.00000411	9
3654	GO:0006573	valine metabolism	biological_process	0.00000427	9
10146	GO:0019319	hexose biosynthesis	biological_process	0.0000146	9
3116	GO:0006012	galactose metabolism	biological_process	0.0000253	9
5821	GO:0009220	pyrimidine ribonucleotide biosynthesis	biological_process	0.0000347	9
3634	GO:0006553	lysine metabolism	biological_process	0.0000659	9
5675	GO:0009071	serine family amino acid catabolism	biological_process	0.000324	9
3606	GO:0006525	arginine metabolism	biological_process	0.000451	9
7623	GO:0015807	L-amino acid transport	biological_process	0.000626	9
5688	GO:0009084	glutamine family amino acid biosynthesis	biological_process	0.00139	9
3888	GO:0006817	phosphate transport	biological_process	0.0051	9
3510	GO:0006418	tRNA aminoacylation for protein translation	biological_process	0	10
15209	GO:0046040	IMP metabolism	biological_process	0	10
3111	GO:0006007	glucose catabolism	biological_process	0	10
5699	GO:0009095	aromatic amino acid family biosynthesis, prephenate pathway	biological_process	1.88E-09	10
5769	GO:0009168	purine ribonucleoside monophosphate biosynthesis	biological_process	2.73E-09	10
5701	GO:0009097	isoleucine biosynthesis	biological_process	3.3E-09	10
3814	GO:0006739	NADP metabolism	biological_process	4.58E-09	10
5690	GO:0009086	methionine biosynthesis	biological_process	1.19E-08	10
3897	GO:0006828	manganese ion transport	biological_process	4.55E-08	10
7893	GO:0016089	aromatic amino acid family biosynthesis, shikimate pathway	biological_process	0.000000882	10
5692	GO:0009088	threonine biosynthesis	biological_process	0.00000206	10
5702	GO:0009098	leucine biosynthesis	biological_process	0.00000411	10
3893	GO:0006824	cobalt ion transport	biological_process	0.00000481	10
3645	GO:0006564	L-serine biosynthesis	biological_process	0.000159	10
3895	GO:0006826	iron ion transport	biological_process	0.000375	10
3894	GO:0006825	copper ion transport	biological_process	0.000386	10
3290	GO:0006188	IMP biosynthesis	biological_process	0	11
3815	GO:0006740	NADPH regeneration	biological_process	1.9E-09	11
6015	GO:0009423	chorismate biosynthesis	biological_process	0.000000228	11
3198	GO:0006096	glycolysis	biological_process	0.000222	11
3291	GO:0006189	'de novo' IMP biosynthesis	biological_process	0	12
3200	GO:0006098	pentose-phosphate shunt	biological_process	1.36E-09	12
5656	GO:0009052	pentose-phosphate shunt, non-oxidative branch	biological_process	1.62E-08	13
13915	GO:0043234	protein complex	cellular_component	0	2
2750	GO:0005623	cell	cellular_component	0.00233	2
13871	GO:0043190	ATP-binding cassette (ABC) transporter complex	cellular_component	2.36E-11	3
3046	GO:0005941	unlocalized protein complex	cellular_component	3.53E-11	3

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goid	acc	name	term_type	p	depth
13279	GO:0042597	periplasmic space	cellular_component	9.64E-11	3
11124	GO:0030312	external encapsulating structure	cellular_component	0.00000769	3
13909	GO:0043228	non-membrane-bound organelle	cellular_component	0.000114	3
258	GO:0000267	cell fraction	cellular_component	0.000244	3
13873	GO:0043192	ATP-binding cassette (ABC) transporter complex (sensu Bacteria and Archaea)	cellular_component	0	4
11125	GO:0030313	cell envelope	cellular_component	2.11E-09	4
13257	GO:0042575	DNA polymerase complex	cellular_component	4.63E-08	4
11324	GO:0030529	ribonucleoprotein complex	cellular_component	0.00000181	4
2752	GO:0005625	soluble fraction	cellular_component	0.0000663	4
2993	GO:0005886	plasma membrane	cellular_component	0.000629	4
2858	GO:0005737	cytoplasm	cellular_component	0.000854	4
2945	GO:0005829	cytosol	cellular_component	0	5
11100	GO:0030288	periplasmic space (sensu Gram-negative Bacteria)	cellular_component	3.4E-11	5
6483	GO:0009898	internal side of plasma membrane	cellular_component	8.25E-11	5
5957	GO:0009360	DNA polymerase III complex	cellular_component	6.7E-10	5
13913	GO:0043232	intracellular non-membrane-bound organelle	cellular_component	0.000114	5
2956	GO:0005840	ribosome	cellular_component	1.24E-08	6
2815	GO:0005694	chromosome	cellular_component	0.0094	6
5882	GO:0009281	cytosolic ribosome (sensu Bacteria)	cellular_component	0	7
7744	GO:0015934	large ribosomal subunit	cellular_component	8.03E-09	7
6096	GO:0009507	chloroplast	cellular_component	0.00000198	7
2877	GO:0005759	mitochondrial matrix	cellular_component	0.000249	7
7745	GO:0015935	small ribosomal subunit	cellular_component	0.00163	7
10797	GO:0020011	apicoplast	cellular_component	0.00532	7
5883	GO:0009282	cytosolic large ribosomal subunit (sensu Bacteria)	cellular_component	1.21E-10	8
5884	GO:0009283	cytosolic small ribosomal subunit (sensu Bacteria)	cellular_component	0.000000754	8
1173	GO:0003824	catalytic activity	molecular_function	0	2
2453	GO:0005215	transporter activity	molecular_function	7.37E-11	2
6977	GO:0015144	carbohydrate transporter activity	molecular_function	0	3
8471	GO:0016740	transferase activity	molecular_function	0	3
8516	GO:0016787	hydrolase activity	molecular_function	0	3
2493	GO:0005275	amine transporter activity	molecular_function	0	3
7278	GO:0015455	group translocator activity	molecular_function	0	3
8580	GO:0016853	isomerase activity	molecular_function	0	3
7464	GO:0015646	permease activity	molecular_function	0	3
8556	GO:0016829	lyase activity	molecular_function	0	3
8601	GO:0016874	ligase activity	molecular_function	1.31E-10	3
2549	GO:0005342	organic acid transporter activity	molecular_function	4.66E-10	3
2068	GO:0004803	transposase activity	molecular_function	0.000000084	3
13857	GO:0043176	amine binding	molecular_function	0.00000104	3
2438	GO:0005199	structural constituent of cell wall	molecular_function	0.00012	3
1686	GO:0004386	helicase activity	molecular_function	0.000205	3
8235	GO:0016491	oxidoreductase activity	molecular_function	0.000614	3
10066	GO:0019239	deaminase activity	molecular_function	0.00496	3
8501	GO:0016772	transferase activity, transferring phosphorus-containing groups	molecular_function	0	4
18854	GO:0051119	sugar transporter activity	molecular_function	0	4
8544	GO:0016817	hydrolase activity, acting on acid anhydrides	molecular_function	1.81E-11	4
8562	GO:0016835	carbon-oxygen lyase activity	molecular_function	1.32E-10	4
16102	GO:0046943	carboxylic acid transporter activity	molecular_function	1.4E-10	4

续表 3

goid	acc	name	term_type	p	depth
8593	GO:0016866	intramolecular transferase activity	molecular_function	1.93E-10	4
8472	GO:0016741	transferase activity, transferring one-carbon groups	molecular_function	3.3E-10	4
8602	GO:0016875	ligase activity, forming carbon-oxygen bonds	molecular_function	1.66E-09	4
8613	GO:0016886	ligase activity, forming phosphoric ester bonds	molecular_function	2.34E-09	4
8581	GO:0016854	racemase and epimerase activity	molecular_function	2.62E-09	4
8352	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	molecular_function	1.97E-08	4
8495	GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups	molecular_function	0.00000042	4
8335	GO:0016597	amino acid binding	molecular_function	0.00000146	4
16033	GO:0046873	metal ion transporter activity	molecular_function	0.00000221	4
8557	GO:0016830	carbon-carbon lyase activity	molecular_function	0.00000263	4
8526	GO:0016798	hydrolase activity, acting on glycosyl bonds	molecular_function	0.00000385	4
8475	GO:0016744	transferase activity, transferring aldehyde or ketonic groups	molecular_function	0.00000477	4
8498	GO:0016769	transferase activity, transferring nitrogenous groups	molecular_function	0.00000536	4
8587	GO:0016860	intramolecular oxidoreductase activity	molecular_function	0.00000838	4
1060	GO:0003678	DNA helicase activity	molecular_function	0.0000137	4
8476	GO:0016746	transferase activity, transferring acyl groups	molecular_function	0.000023	4
8573	GO:0016846	carbon-sulfur lyase activity	molecular_function	0.0000315	4
8457	GO:0016725	oxidoreductase activity, acting on CH2 groups	molecular_function	0.0000569	4
8606	GO:0016879	ligase activity, forming carbon-nitrogen bonds	molecular_function	0.000106	4
8630	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	molecular_function	0.000435	4
8537	GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	molecular_function	0.000512	4
8487	GO:0016757	transferase activity, transferring glycosyl groups	molecular_function	0.000677	4
6871	GO:0015036	disulfide oxidoreductase activity	molecular_function	0.0013	4
8567	GO:0016840	carbon-nitrogen lyase activity	molecular_function	0.00263	4
8779	GO:0017076	purine nucleotide binding	molecular_function	0.00267	4
7004	GO:0015171	amino acid transporter activity	molecular_function	0	5
16074	GO:0046915	transition metal ion transporter activity	molecular_function	0	5
8547	GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	molecular_function	2.71E-11	5
6987	GO:0015154	disaccharide transporter activity	molecular_function	7.12E-11	5
6917	GO:0015082	di-, tri-valent inorganic cation transporter activity	molecular_function	8.75E-11	5
8545	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	molecular_function	1.94E-10	5
4822	GO:0008168	methyltransferase activity	molecular_function	2.1E-10	5
8603	GO:0016876	ligase activity, forming aminoacyl-tRNA and related compounds	molecular_function	1.66E-09	5
5091	GO:0008452	RNA ligase activity	molecular_function	1.93E-09	5
8354	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	molecular_function	2.92E-09	5
8584	GO:0016857	racemase and epimerase activity, acting on carbohydrates and derivatives	molecular_function	1.24E-08	5
8502	GO:0016773	phosphotransferase activity, alcohol group as acceptor	molecular_function	3.12E-08	5
8563	GO:0016836	hydro-lyase activity	molecular_function	0.000000105	5
8595	GO:0016868	intramolecular transferase activity, phosphotransferases	molecular_function	0.000000358	5
8493	GO:0016763	transferase activity, transferring pentosyl groups	molecular_function	0.000000413	5
8588	GO:0016861	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	molecular_function	0.00000058	5
5120	GO:0008483	transaminase activity	molecular_function	0.00000211	5
8366	GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	molecular_function	0.0000105	5
1807	GO:0004518	nuclease activity	molecular_function	0.0000384	5

续表 3

goid	acc	name	term_type	p	depth
1832	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	molecular_function	0.0000469	5
8611	GO:0016884	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	molecular_function	0.0000993	5
8477	GO:0016747	transferase activity, transferring groups other than amino-acyl groups	molecular_function	0.000138	5
8560	GO:0016833	oxo-acid-lyase activity	molecular_function	0.00024	5
6978	GO:0015145	monosaccharide transporter activity	molecular_function	0.000309	5
8508	GO:0016779	nucleotidyltransferase activity	molecular_function	0.000333	5
8559	GO:0016832	aldehyde-lyase activity	molecular_function	0.000699	5
11349	GO:0030554	adenyl nucleotide binding	molecular_function	0.00136	5
8505	GO:0016776	phosphotransferase activity, phosphate group as acceptor	molecular_function	0.00155	5
8541	GO:0016814	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	molecular_function	0.00352	5
8558	GO:0016831	carboxy-lyase activity	molecular_function	0.0039	5
1112	GO:0003746	translation elongation factor activity	molecular_function	0.00569	5
8527	GO:0016799	hydrolase activity, hydrolyzing N-glycosyl compounds	molecular_function	0.00692	5
8207	GO:0016462	pyrophosphatase activity	molecular_function	0	6
5587	GO:0008982	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	molecular_function	0	6
10021	GO:0019191	cellobiose transporter activity	molecular_function	2.83E-10	6
2077	GO:0004812	tRNA ligase activity	molecular_function	1.52E-09	6
10030	GO:0019200	carbohydrate kinase activity	molecular_function	0.000000186	6
2020	GO:0004751	ribose-5-phosphate isomerase activity	molecular_function	0.000000579	6
7736	GO:0015926	glucosidase activity	molecular_function	0.000000705	6
4827	GO:0008173	RNA methyltransferase activity	molecular_function	0.00000133	6
5613	GO:0009008	DNA-methyltransferase activity	molecular_function	0.00000172	6
6922	GO:0015087	cobalt ion transporter activity	molecular_function	0.0000025	6
7475	GO:0015658	branched-chain aliphatic amino acid transporter activity	molecular_function	0.00000353	6
1825	GO:0004536	deoxyribonuclease activity	molecular_function	0.00000375	6
1999	GO:0004730	pseudouridylate synthase activity	molecular_function	0.0000199	6
10035	GO:0019205	nucleobase, nucleoside, nucleotide kinase activity	molecular_function	0.0000493	6
8533	GO:0016805	dipeptidase activity	molecular_function	0.0000519	6
5369	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	molecular_function	0.0000961	6
1672	GO:0004372	glycine hydroxymethyltransferase activity	molecular_function	0.000101	6
5055	GO:0008415	acyltransferase activity	molecular_function	0.000107	6
6982	GO:0015149	hexose transporter activity	molecular_function	0.000141	6
2578	GO:0005375	copper ion transporter activity	molecular_function	0.00016	6
1808	GO:0004519	endonuclease activity	molecular_function	0.000341	6
2581	GO:0005381	iron ion transporter activity	molecular_function	0.000347	6
1357	GO:0004022	alcohol dehydrogenase activity	molecular_function	0.000678	6
2641	GO:0005506	iron ion binding	molecular_function	0.00192	6
6948	GO:0015114	phosphate transporter activity	molecular_function	0.00322	6
2656	GO:0005524	ATP binding	molecular_function	0.00417	6
8812	GO:0017111	nucleoside-triphosphatase activity	molecular_function	1.27E-10	7
10020	GO:0019190	cellobiose permease activity	molecular_function	2.83E-10	7
5062	GO:0008422	beta-glucosidase activity	molecular_function	3.17E-09	7
4848	GO:0008198	ferrous iron binding	molecular_function	1.07E-08	7
5267	GO:0008649	rRNA methyltransferase activity	molecular_function	0.00000532	7
1613	GO:0004312	fatty-acid synthase activity	molecular_function	0.00000856	7
4898	GO:0008252	nucleotidase activity	molecular_function	0.000102	7
4829	GO:0008175	tRNA methyltransferase activity	molecular_function	0.00012	7
8473	GO:0016742	hydroxymethyl-, formyl- and related transferase activity	molecular_function	0.000172	7
8154	GO:0016407	acetyltransferase activity	molecular_function	0.000172	7
1809	GO:0004520	endodeoxyribonuclease activity	molecular_function	0.000817	7
10031	GO:0019201	nucleotide kinase activity	molecular_function	0.00588	7
8614	GO:0016887	ATPase activity	molecular_function	0	8

续表 3

goid	acc	name	term_type	p	depth
4899	GO:0008253	5'-nucleotidase activity	molecular_function	0.00000872	8
13305	GO:0042623	ATPase activity, coupled	molecular_function	2.68E-11	9
13308	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	molecular_function	2.82E-11	10
4753	GO:0008094	DNA-dependent ATPase activity	molecular_function	0.000128	10
4690	GO:0008026	ATP-dependent helicase activity	molecular_function	0.000186	10
12047	GO:0031263	amine-transporting ATPase activity	molecular_function	0	11
13892	GO:0043211	carbohydrate-transporting ATPase activity	molecular_function	1.3E-09	11
7240	GO:0015417	polyamine-transporting ATPase activity	molecular_function	9.96E-08	11
1341	GO:0004003	ATP-dependent DNA helicase activity	molecular_function	0.0000535	11
7247	GO:0015424	amino acid-transporting ATPase activity	molecular_function	0	12
13906	GO:0043225	anion-transporting ATPase activity	molecular_function	0.000197	12
7238	GO:0015415	phosphate-transporting ATPase activity	molecular_function	0.00000172	13

a) goid, Gene Ontology 功能结点的内部编号; acc, Gene Ontology 体系中所预测功能的 accession number; name, 所预测功能的名称; term_type, 所预测功能所属的大类名称

图 1　比较菌株 89-1591 和菌株 P1/7 蛋白序列预测结果

注释蛋白比率有显著不同的功能结点位于 Gene Ontology 层次结构上的图示，用红色椭圆表示

图 2：单 1 中的事件 (0.126) 的重分析发现该事件和事件的相关性在 Dear Desktop 程序的有上的图示

特此在概图解示

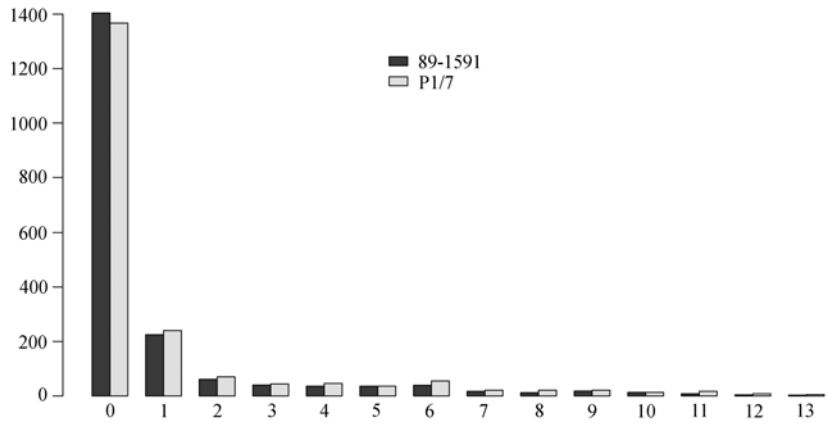

图 3　菌株 89-1591 和 P1/7 的跨膜蛋白分布图

深灰色条带表示菌株 89-1591，浅灰色条带表示菌株 P1/7. 横轴是跨膜区域的个数，纵轴是蛋白的计数

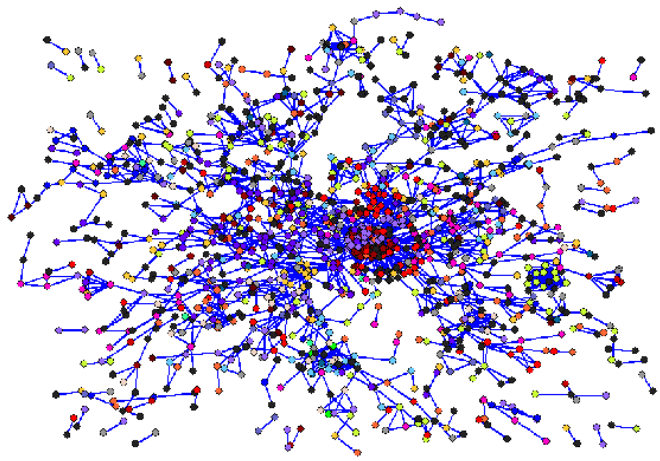

图 4　菌株 P1/7 蛋白质组范围内相互作用图

根据预测结果用 Pajek 绘制，参数默认，不同颜色表示 COG 的不同功能分类

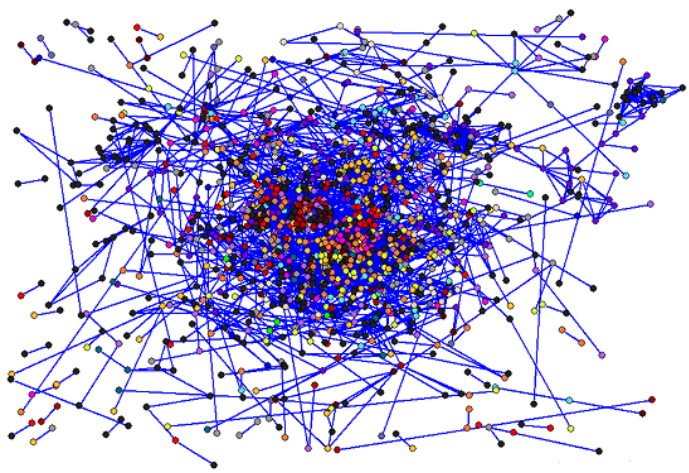

图 5　菌株 89-1581 蛋白质组范围内相互作用图

根据预测结果用 Pajek 绘制，参数默认，不同颜色表示 COG 的不同功能分类