Table 1. Predicted Structures and functions of hypothetical proteins in *Mycobacterium tuberculosis micro variant 12* through comparative genomic approach.

NCBI Protein ID		CDD-Blast	pfam	cello v2.5	ps2 structure			String Database protein protein interaction (Only after templete detection)	Jpred 4				PHYRE2		
					Templete	Identity	E-value		PDB	Chain	Description	Blast E-value	Templet	Templet Information	Confidence
AMC57474		YqgE/AlgH family protein	Uncharacterized ACR, COG1678	Cytoplasmic 4.139 *	2gs5A	0,4407	0	RN08_0047	2haf	A	Putative translation repressor	3e-14	d2gs5a1	**Fold:** VC0467-like	100
									2aj2	A	Hypothetical UPF0301 protein VC0467	0		**Superfamily:** VC0467-like	
									2mui	A	UPF0301 protein AlgH	0		**Family:** VC0467-like	
									2do8	A	UPF0301 protein HD_1794	0,000000002			
									2gzo	A	UPF0301 protein SO3346	0,00000004			
													d2hafa1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
													c2aj2A_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**hypothetical upf0301 protein vc0467	
														PDBTitle: x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.	
													c2muiA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**upf0301 protein algh	
														PDBTitle: solution structure of the algh protein from pseudomonas aeruginosa,2 pa0405, upf0301	

													d2gzoa1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
													d2do8a1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
													d2ew0a1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
AMC57437		RN08_0010 [Mycobacterium tuberculosis variant microti]	No	Extracellular 1.878 *	2ux9C	30,56	6,3	RN08_1680	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	**0**	d1nh2d2	**Fold:** Transcription factor IIA (TFIIA), beta-barrel domain	**19,5**
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	**0**		**Superfamily:** Transcription factor IIA (TFIIA), beta-barrel domain	
														Family: Transcription factor IIA (TFIIA), beta-barrel domain	
AMC57453		AMC57453.1 hypothetical protein RN08_0026 [Mycobacterium tuberculosis variant microti]	No	Extracellular 3.114 *	1odkB	23,23	2,8	No string found					c2zomC_	**PDB header:**unknown function	8,4
														Chain: C: **PDB Molecule:**protein cuta, chloroplast, putative, expressed	
														PDBTitle: crystal structure of cuta1 from oryza sativa	
AMC57454		NAD(P)H-dependent flavin oxidoreductase YrpB, nitropropane dioxygenase family	Nitronate monooxygenase	Extracellular 2.595 *	3bo9A	3bo9A	3bo9A	RN08_3068	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0			

									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2z6jB_	**PDB header:**oxidoreductase	100
									2z6j	B	Trans-2-enoyl-ACP reductase II	0,000004		**Chain:** B: **PDB Molecule:**trans-2-enoyl-acp reductase ii	
									2z6j	A	Trans-2-enoyl-ACP reductase II	0,000004		**PDBTitle:** crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor	
									2z6i	B	Trans-2-enoyl-ACP reductase II	0,000004			
									2z6i	A	Trans-2-enoyl-ACP reductase II	0,000004			
													c3bo9B_	**PDB header:**oxidoreductase	100
														Chain: B: **PDB Molecule:**putative nitroalkan dioxygenase	
														PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution	
													c2gjlA_	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**hypothetical protein pa1024	
														PDBTitle: crystal structure of 2-nitropropane dioxygenase	
													c4iqlB_	**PDB header:**oxidoreductase	100
														Chain: B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase ii	
														PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn	
													c3bw2A_	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**2-nitropropane dioxygenase	
														PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes	
													c5lsmF_	**PDB header:**oxidoreductase	100
														Chain: F: **PDB Molecule:**fmn-dependent nitronate monooxygenase	

														PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1	
													c6bkaA_	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**nitronate monooxygenase	
														PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus	
AMC57461		Domain of unknown function (DUF4226)	Domain of unknown function (DUF4226)	Cytoplasmic 2.269 *	1y0fA	25,7	0,94	No string found	No	No	No	No	c2x43S_	**PDB header:**membrane protein	**0,061**
														Chain: S: **PDB Molecule:**sherp	
														PDBTitle: structural basis of molecular recognition by sherp at membrane2 surfaces	
AMC57462		hypothetical protein RN08_0035	Excreted virulence factor EspC	Cytoplasmic 2.098 *	no	no	no	RN08_0035	No	No	No	No	c4iogD_	**PDB header:**unknown function	89,4
														Chain: D: **PDB Molecule:** Secreted protein esxb	
														PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne	
AMC57464		hypothetical protein RN08_0037	No	Cytoplasmic 1.598 *	NO	NO	NO	RN08_0037	No	No	No	No	d1nmla1		46,8
														Fold: Cytochrome c	
														Superfamily: Cytochrome c	
														Family: Di-heme cytochrome c peroxidase	
AMC57465		Family of unknown function (DUF5632)	Ribosomal protein L5	Cytoplasmic 3.409 *	1iirA	20,14	1,8	RN08_1710	5imu	A	Tat (Twin-arginine translocation)	0	c5imuA_	**PDB header:**signaling protein	100

									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**tat (twin-arginine translocation) pathway signal sequence	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDBTitle:** a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis	
AMC57466		Protein of unknown function (DUF2710)	Protein of unknown function (DUF2710)	Cytoplasmic 3.251 *	1ybxB	17,65	0,2	RN08_4098	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000001	c1ybxA_	**PDB header:**structural genomics, unknown function	91,5
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000001		**Chain:** A: **PDB Molecule:**conserved hypothetical protein	
														PDBTitle: conserved hypothetical protein cth-383 from clostridium thermocellum	
AMC57470		Ketosteroid isomerase-related protein	SnoaL-like domain	Cytoplasmic 2.874 *	1tuhA	32,81	3.2e-10	No	1tuh	A	hypothetical protein EGC068	0	d1tuha_	**Fold:** Cystatin-like	100
									3g8z	A	Protein of unknown function	0,0000002		**Superfamily:** NTF2-like	
														Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette	
													c1tuhA_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**hypothetical protein egc068	
														PDBTitle: structure of bal32a from a soil-derived mobile gene cassette	
AMC57472		TIGR03084 family protein	Mycothiol maleylpyruvate isomerase	Cytoplasmic 2.532 *	2nsfA	17,13	0,066	No	1nth	A	Monomethylamine methyltransferase	0,0000002	c2nsfA_	**PDB header:**isomerase	100
									1l2q	A	monomethylamine methyltransferase	0,0000002		**Chain:** A: **PDB Molecule:**hypothetical protein cgl3021	
														PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase	

													d2nsfa1	**Fold:** DinB/YfiT-like putative metalloenzymes	100
														Superfamily: DinB/YfiT-like putative metalloenzymes	
														Family: Maleylpyruvate isomerase-like	
AMC57473		Macrolide efflux protein A and similar proteins	Major Facilitator Superfamily	Membrane 4.838 *	1pw4A	14,98	0,0000075	No String found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c7nqkA	**PDB header:**membrane protein	99,8
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**solute carrier family 15 member 2	
									1nth	A	Monomethylamine methyltransferase	0,000002		**PDBTitle:** cryo-em structure of the mammalian peptide transporter pept2	
									1l2q	A	monomethylamine methyltransferase	0,000002			
AMC57474		YqgE/AlgH family protein	Uncharacterized ACR, COG1678	Cytoplasmic 4.139 *	2hafA	26,46	0	RN08_0047	2gs5	A	Conserved hypothetical protein	0	d2gs5a1	**Fold:** VC0467-like	100
									2hrx	A	Hypothetical protein	0		**Superfamily:** VC0467-like	
									2aj2	A	Hypothetical UPF0301 protein VC0467	0		**Family:** VC0467-like	
									2haf	A	Putative translation repressor	0			
									2mui	A	UPF0301 protein AlgH	0			
									2do8	A	UPF0301 protein HD_1794	0,000000002	d2hafa1	**Fold:** VC0467-like	100
									2ew0	A	hypothetical protein ACIAD0353	0,00000001		**Superfamily:** VC0467-like	
									2gzo	A	UPF0301 protein SO3346	0,00000004		**Family:** VC0467-like	
													c2aj2A_	**PDB header:**unknown function	100

														Chain: A: **PDB Molecule:**hypothetical upf0301 protein vc0467	
														PDBTitle: x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.	
													c2muiA_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**upf0301 protein algh	
														PDBTitle: solution structure of the algh protein from pseudomonas aeruginosa,2 pa0405, upf0301	
													d2gzoa1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
													d2do8a1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
													d2ew0a1	**Fold:** VC0467-like	100
														Superfamily: VC0467-like	
														Family: VC0467-like	
AMC57483		Transcriptional regulator PadR-like family	Virulence activator alpha C-term		1yg2A	21,79	0,000027	RN08_1321	No	No	No	No	No	No	No
AMC57488		Type 1 glutamine amidotransferase (GATase1)-like domain	DJ-1/PfpI family	Membrane 2.311 *	3ewnA	34,88	0	RN08_2144	7ldb	B	Isonitrile hydratase InhA	0	c3nooB_	**PDB header:**lyase	100
									7ldb	A	Isonitrile hydratase InhA	0		**Chain:** B: **PDB Molecule:**thij/pfpi family protein	

									7ldo	A	Isonitrile hydratase InhA	0		**PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens	
									7ldm	A	Isonitrile hydratase InhA	0			100
									44868	A	ThiJ/PfpI family protein	0			
									3nor	A	ThiJ/PfpI family protein	0	c3ewnA_	**PDB header:**structural genomics, unknown function	
									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**thij/pfpi family protein	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDBTitle:** crystal structure of a thij/pfpi family protein from pseudomonas2 syringae	
									3mgk	B	Intracellular protease/amidase	0			
									3mgk	A	Intracellular protease/amidase	0			100
									5sy4	B	Chaperone YajL	0,000003	c3mgkA_	**PDB header:**structural genomics, unknown function	
									5sy4	A	Chaperone YajL	0,000003		**Chain:** A: **PDB Molecule:**intracellular protease/amidase related enzyme (thij	
									2ab0	B	YajL	0,000003		**PDBTitle:** crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824	
									2ab0	A	YajL	0,000003			
													c3uk7B_	**PDB header:**transferase	100
														Chain: B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing	
														PDBTitle: crystal structure of arabidopsis thaliana dj-1d	
													d2ab0a1	**Fold:** Flavodoxin-like	
														Superfamily: Class I glutamine amidotransferase-like	100

														Family: DJ-1/PfpI	
													c4ge0C_	**PDB header:**unknown function	100
														Chain: C: **PDB Molecule:**uncharacterized protein c22e12.03c	
														PDBTitle: schizosaccharomyces pombe dj-1 t114p mutant	
													c3bhnA_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**thij/pfpi domain protein	
														PDBTitle: crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution	
													d1p5fa_	**Fold:** Flavodoxin-like	100
														Superfamily: Class I glutamine amidotransferase-like	
														Family: DJ-1/PfpI	
													c4k2hG	**PDB header:**unknown function	
														Chain: G: **PDB Molecule:**intracellular protease/amidase	100
														PDBTitle: crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium	
													c4e08B_	**PDB header:**motor protein	100
														Chain: B: **PDB Molecule:**dj-1 beta	
														PDBTitle: crystal structure of drosophila melanogaster dj-1beta	
													c4xllB_	**PDB header:**unknown function	
														Chain: B: **PDB Molecule:**dj-1 family protein	
														PDBTitle: toxoplasma gondii dj-1, oxidized	
													c3fseB	**PDB header:**hydrolase	100

														Chain: B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and	
														PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution	
													c3er6D_	**PDB header:**structural genomics, unknown function	100
														Chain: D: **PDB Molecule:**putative transcriptional regulator protein	
														PDBTitle: crystal structure of a putative transcriptional regulator protein from2 vibrio parahaemolyticus	
													c3ot1B_	**PDB header:**structural genomics	100
														Chain: B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate	
														PDBTitle: crystal structure of vc2308 protein	
													d1sy7a1	**Fold:** Flavodoxin-like	100
														Superfamily: Class I glutamine amidotransferase-like	
														Family: Catalase, C-terminal domain	
AMC57493		hypothetical protein RN08_0066	Repeat of unknown function (DUF5650)	Extracellular 3.524 *	3c48A	13,95	1,8	RN08_0540	No	No	No	No	c6fviA_	**PDB header:**cell cycle	26,3
														Chain: A: **PDB Molecule:**centrosomal protein of 192 kda	
														PDBTitle: ash / papd-like domain of human cep192 (papd-like domain 7)	
AMC57496		O-acetyl-ADP-ribose deacetylase (regulator of RNase III)	Domain of unknown function (DUF1719)	Cytoplasmic 4.457 *	1spvA	18,35	0,000019	RN08_2109	5m3i	D	RNase III inhibitor	0	c5m3iB_	**PDB header:**antitoxin	100
									5m3i	C	RNase III inhibitor	0		**Chain:** B: **PDB Molecule:**rnase iii inhibitor	

									5m3i	B	RNase III inhibitor	0		**PDBTitle:** macrodomain of mycobacterium tuberculosis darg	
									5m3i	A	RNase III inhibitor	0			
									5m3e	A	Appr-1-p processing domain protein	0			
									5m31	A	Appr-1-p processing domain protein	0	c5m31A_	**PDB header:**antitoxin	100
									7omu	BBB	Macro domain-containing protein	0		**Chain:** A: **PDB Molecule:**appr-1-p processing domain protein	
									7omu	AAA	Macro domain-containing protein	0		**PDBTitle:** macrodomain of thermus aquaticus darg	
									1nth	A	Monomethylamine methyltransferase	0,0000006			
									1l2q	A	monomethylamine methyltransferase	0,0000006			
									7b1n	B	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000007	c6lftA_	**PDB header:**hydrolase	100
									7b1n	A	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000007		**Chain:** A: **PDB Molecule:**adp-ribose 1"-phosphate phosphatase	
														PDBTitle: poa1p s30a mutant in complex with adp-ribose	
													c5e3bA_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**macrodomain protein	
														PDBTitle: structure of macrodomain protein from streptomyces coelicolor	
													c2dx6B_	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**hypothetical protein ttha0132	
														PDBTitle: crystal structure of conserved hypothetical protein,	

														ttha0132 from2 thermus thermophilus hb8	
													d2fg1a1	**Fold:** Macro domain-like	100
														Superfamily: Macro domain-like	
														Family: Macro domain	
													c2eeeA_	**PDB header:**gene regulation	100
														Chain: A: **PDB Molecule:**uncharacterized protein c6orf130	
														PDBTitle: solution structure of the a1pp domain from human protein c6orf130	
													c3vfqA_	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**poly [adp-ribose] polymerase 14	
														PDBTitle: human parp14 (artd8, bal2) - macro domains 1 and 2 in complex with2 adenosine-5-diphosphoribose	
													c3q71A_	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**poly [adp-ribose] polymerase 14	
														PDBTitle: human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose	
													c7d3yA_	**PDB header:**dna binding protein	100
														Chain: A: **PDB Molecule:**spx domain-containing protein 2,isoform 1 of core histone	
														PDBTitle: crystal structure of the osphr2-osspx2 complex	
													c5iitC_	**PDB header:**inositol phosphate binding protein	100
														Chain: C: **PDB Molecule:**vacuolar transporter chaperone 4,core histone macro-h2a.1	
														PDBTitle: structure of spx domain of the yeast inorganic polyphophate polymerase2 vtc4 crystallized by carrier-driven crystallization in fusion with3 the macro domain of human histone macroh2a1.1	

AMC57514		Metallo-dependent hydrolases, subgroup A	HMGL-like	Cytoplasmic 3.424 *	3be7A	24,82	0	No String Found	3mtw	A	L-Arginine carboxypeptidase Cc2672	0	c3gnhA	**PDB header:**hydrolase	100
									2qs8	B	Xaa-Pro Dipeptidase	0		**Chain:** A: **PDB Molecule:**l-lysine, l-arginine carboxypeptidase cc2672	
									3dug	H	zn-dependent arginine carboxypeptidase	0		**PDBTitle:** crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.	
									3be7	H	zn-dependent arginine carboxypeptidase	0			
									3mkv	H	putative amidohydrolase	0			
									2p9b	A	Possible prolidase	0	c2r8cB	**PDB header:**structural genomics, unknown function	100
									4c65	H	ochratoxinase	0		**Chain:** B: **PDB Molecule:**putative amidohydrolase	
									3n2c	P	prolidase	0		**PDBTitle:** crystal structure of uncharacterized protein eaj56179	
									3feq	P	putative amidohydrolase	0			
									4whb	H	Phenylurea hydrolase B	0,00000001			
									7b1n	B	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000005	c4c65A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**ochratoxinase	
														PDBTitle: crystal structure of a. niger ochratoxinase	
													c2qs8A_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**xaa-pro dipeptidase	
														PDBTitle: crystal structure of a xaa-pro dipeptidase with bound methionine in2 the active site	

													c2p9bA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**possible prolidase	
														PDBTitle: crystal structure of putative prolidase from bifidobacterium longum	
													c3be7B_	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**zn-dependent arginine carboxypeptidase	
														PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase	
													c3feqB_	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**putative amidohydrolase	
														PDBTitle: crystal structure of uncharacterized protein eah89906	
													c4whbC	**PDB header:**hydrolase	100
														Chain: C: **PDB Molecule:**phenylurea hydrolase b	
														PDBTitle: crystal structure of phenylurea hydrolase b	
													c6sj0B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**amidohydrolase	
														PDBTitle: amidohydrolase, ahs	
													c4dzhA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**amidohydrolase	
														PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn	
													c6i5sA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**bottromycin amidohydrolase	

														PDBTitle: ah, bottromycin amidohydrolase	
													c3gipB_	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**n-acyl-d-glutamate deacylase	
														PDBTitle: crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.	
													c4v1xA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**atrazine chlorohydrolase	
														PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza	
													c4wgxD	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**molinate hydrolase	
														PDBTitle: crystal structure of molinate hydrolase	
													c1rjqA_	**DB header:**hydrolase	100
														Chain: A: **PDB Molecule:**d-aminoacylase	
														PDBTitle: the crystal structure of the d-aminoacylase mutant d366a	
													c4f0rA_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**5-methylthioadenosine/s-adenosylhomocysteine deaminase	
														PDBTitle: crystal structure of an adenosine deaminase homolog from2 chromobacterium violaceum (target nysgrc-019589) bound zn and 5'-3 methylthioadenosine (unproductive complex)	
AMC57523		Pyridoxamine 5'-phosphate oxidase	Pyridoxamine 5'-phosphate oxidase	Cytoplasmic 1.977 *	3cp3A	29,71	0,0000000022	RN08_3449	6eci	T	Pyridoxamine 5'-phosphate oxidase	0,000000007	c3fkhB_	**PDB header:**oxidoreductase	100
									6eci	S	Pyridoxamine 5'-phosphate oxidase	0,000000007		**Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase	

									6bo4	C	Transient receptor potential cation channel	0,0000009		**PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution	
									6bo4	B	Transient receptor potential cation channel	0,0000009			
									3fkh	F	Putative pyridoxamine 5'-phosphate oxidase...	0,000002			
									3fkh	E	Putative pyridoxamine 5'-phosphate oxidase	0,000002	c6eciQ_	**PDB header:**fad-binding protein	100
									3fkh	D	Putative pyridoxamine 5'-phosphate oxidase	0,000002		**Chain:** Q: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-binding	
									3fkh	C	Putative pyridoxamine 5'-phosphate oxidase	0,000002		**PDBTitle:** structure of the fad binding protein msmeg_5243 from mycobacterium2 smegmatis	
													c3cp3A_	**PDB header:**structural genomics, unknown function	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae	
													d2hq9a1	**Fold:** Split barrel-like	
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
													d2vpaa1	**Fold:** Split barrel-like	100
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
													c6rk0A_	**PDB header:**flavoprotein	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii	

													c4ybnB_	**PDB header:**oxidoreductase	100
														Chain: B: **PDB Molecule:**flavin-nucleotide-binding protein	
														PDBTitle: structure of the fad and heme binding protein msmeg_4975 from2 mycobacterium smegmatis	
AMC57567		PPOX class probable F420-dependent enzyme, Rv0121 family	Ribosomal Proteins L2, RNA binding domai	Cytoplasmic 1.773 *	1rfeA	23,33	0,000026	RN08_3300	5jv4	F	Pyridoxamine 5'- phosphate oxidase	0	c4zkyB_	**PDB header:**oxidoreductase	100
									5jv4	E	Pyridoxamine 5'- phosphate oxidase	0		**Chain:** B: **PDB Molecule:**pyridoxamine 5-phosphate oxidase	
									4zky	B	Pyridoxamine 5'- phosphate oxidase	0		**PDBTitle:** structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis	
									4zky	A	Pyridoxamine 5'- phosphate oxidase	0			
													d1rfea_	**Fold:** Split barrel-like	100
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
													d2asfa1	**Fold:** Split barrel-like	100
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
													c2iabB_	**PDB header:**unknown function	100
														Chain: B: **PDB Molecule:**hypothetical protein	
														PDBTitle: crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution	
													c3f7eB_	**PDB header:**unknown function	100
														Chain: B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related	

														PDBTitle: msmeg_3380 f420 reductase	
													c3u0iA_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**probable fad-binding, putative uncharacterized protein	
														PDBTitle: crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis	
													d2hq9a1	**Fold:** Split barrel-like	100
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
													d2fg9a1	**Fold:** Split barrel-like	100
														Superfamily: FMN-binding split barrel	
														Family: PNP-oxidase like	
AMC57588		Uncharacterized conserved protein	Domain of unknown function (DUF427)	Extracellular 2.049 *	3djmB	33,05	0,000000081	RN08_0161	3djm	E	Uncharacterized Protein DUF427	0	c3djmA_	**PDB header:**unknown function	100
									3djm	D	Uncharacterized Protein DUF427	0		**Chain:** A: **PDB Molecule:**uncharacterized protein duf427	
									7b1n	B	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000000008		**PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution	
									7b1n	A	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000000008			
AMC57598		No	No	Membrane 2.024 *	1pq3A	19,79	6,6	No String found	No	No	No	No	c4rhjE_	**PDB header:**unknown function	10,8
														Chain: E: **PDB Molecule:**arginase	
														PDBTitle: crystal structure of wild-type t. brucei arginase-like protein in a2 reduced form	

AMC57614		Ligand-binding SRPBCC domain of an uncharacterized subfamily of proteins	Protein of unknown function (DUF1997)	Cytoplasmic 3.523 *	2d4rA	17,12	0,000024	No String Found	5z8o	B	Cyclase/dehydrase	0	c5z8oA_	**PDB header:**unknown function	99,9
									5z8o	A	Cyclase/dehydrase	0		**Chain:** A: **PDB Molecule:**cyclase/dehydrase	
									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDBTitle:** structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0			
													c2kf2A_	**PDB header:**structural genomics, unknown function	99,9
														Chain: A: **PDB Molecule:**putative polyketide cyclase	
														PDBTitle: solution nmr structure of of streptomyces coelicolor polyketide2 cyclase sco5315. northeast structural genomics consortium target3 rr365	
AMC57637		putative metallohydrolase, TIGR04338 family	No	Cytoplasmic 3.657 *	1budA	11,17	5,7	No String found	No	No	No	No	c6mdxA	**PDB header:**dna binding protein/dna	93,1
														Chain: A: **PDB Molecule:**sprt-like domain-containing protein spartan	
														PDBTitle: mechanism of protease dependent dpc repair	
AMC57646		No	No	Periplasmic 1.497 *	2dw3A	22,64	3,7	No String Found	No	No	No	No	c3ah9D	**PDB header:**structural protein	34,6
														Chain: D: **PDB Molecule:**collagen-like peptide	
														PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution	
AMC57649		No	EAL domain	Cytoplasmic 4.364 *	1we3F	13,28	0,72	No String found	No	No	No	No	c5erlD_	**PDB header:**isomerase	98,9
														Chain: D: **PDB Molecule:**snon,snon	
														PDBTitle: crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro	

AMC57667		No	Transcriptional activator TraM	Membrane 3.420 *	2j69A	14,18	0,39	No String Found	No	No	No	No	c6j73B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**isoniazid inducible gene protein inia	
														PDBTitle: crystal structure of inia from mycobacterium smegmatis	
AMC57682		phosphatidyl-myo-inositol mannosyltransferase	Glycosyl transferases group 1	Cytoplasmic 3.806 *	3c48A	23,51	23,51	RN08_0540	No	No	No	No			
													c6gneB	**PDB header:**transferase	100
														Chain: B: **PDB Molecule:**probable starch synthase 4, chloroplastic/amyloplastic	
														PDBTitle: catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose	
													d2bisa1	**Fold:** UDP-Glycosyltransferase/glycogen phosphorylase	100
														Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase	
														Family: Glycosyl transferases group 1	
													c2qzsA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**glycogen synthase	
														PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)	
													c3c4vB	**PDB header:**transferase	100
														Chain: B: **PDB Molecule:**predicted glycosyltransferases	
														PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.	
													d1rzua_	**Fold:** UDP-Glycosyltransferase/glycogen phosphorylase	100

														Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase	
														Family: Glycosyl transferases group 1	
													c3okaA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol	
														PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)	
													c4rbnD_	**PDB header:**transferase	100
														Chain: D: **PDB Molecule:**sucrose synthase:glycosyl transferases group 1	
														PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes	
													c3nb0A	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**glycogen [starch] synthase isoform 2	
														PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase	
													c2gejA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima)	
														PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man	
													c6kihJ_	**PDB header:**transferase	100
														Chain: J: **PDB Molecule:**tll1590 protein	
														PDBTitle: sucrose-phosphate synthase (tll1590) from thermosynechococcus2 elongatus	
													c2xmpB	**PDB header:**sugar binding protein	100

														Chain: B: **PDB Molecule:**trehalose-synthase tret	
														PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp	
													c2x6rA	**PDB header:**isomerase	100
														Chain: A: **PDB Molecule:**trehalose-synthase tret	
														PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose	
													c2jjmH	**PDB header:**transferase	100
														Chain: H: **PDB Molecule:**glycosyl transferase, group 1 family protein	
														PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.	
													c3vufA	**PDB header:**transferase	
														Chain: A: **PDB Molecule:**granule-bound starch synthase 1,	
														PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp	
													c5zesA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**udp-glucose:tetrahydrobiopterin glucosyltransferase	
														PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex	
													c2r60A	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**glycosyl transferase, group 1	
														PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii	
													c3o3cD_	**PDB header:**transferase	100
														Chain: D: **PDB Molecule:**glycogen [starch] synthase isoform 2	

														PDBTitle: glycogen synthase basal state udp complex	
													c6gngB	**PDB header:**transferase	100
														Chain: B: **PDB Molecule:**granule-bound starch synthase	
														PDBTitle: granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp	
													c6d9tA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**glycosyl transferase	
														PDBTitle: bsha from staphylococcus aureus complexed with udp	
													c6tvpA	**PDB header:**sugar binding protein	100
														Chain: A: **PDB Molecule:**alpha-maltose-1-phosphate synthase	
														PDBTitle: structure of mycobacterium smegmatis alpha-maltose-1-phosphate2 synthase glgm	
AMC57686		VapC-like PIN domain of Mycobacterium tuberculosis VapC3, VapC21 and related proteins	Phosphatase	Cytoplasmic 2.836 *	3dboB	21,6	0,0004	RN08_0700	5sv2	A	Ribonuclease VapC21	0	c5sv2A	**PDB header:**hydrolase	100
									3h87	B	Putative uncharacterized protein	0		**Chain:** A: **PDB Molecule:**ribonuclease vapc21	
									3h87	A	Putative uncharacterized protein	0		**PDBTitle:** toxin vapc21 from mycobacterium tuberculosis	
													c3h87B	**PDB header:**toxin/antitoxin	100
														Chain: B: **PDB Molecule:**putative uncharacterized protein	
														PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis	

AMC57695		Protein of unknown function (DUF2613)	Protein of unknown function (DUF2613)	Extracellular 2.239 *	2k1kA	28,57	6	No String Found	1nth	A	Monomethylamine methyltransferase	0,0000008	c2k1lB	**PDB header:**signaling protein	30,9
									1l2q	A	monomethylamine methyltransferase	0,0000008		**Chain:** B: **PDB Molecule:**ephrin type-a receptor 1	
														PDBTitle: nmr structures of dimeric transmembrane domain of the receptor2 tyrosine kinase epha1 in lipid bicelles at ph 6.3	
AMC57717		Tetracyclin repressor-like, C-terminal domain TetR family regulators	Tetracyclin repressor-like, C-terminal d	Membrane 2.969 *	2np3A	21,64	0,000057	No String Found	No	No	No	No	c2np3A	**PDB header:**transcription	100
														Chain: A: **PDB Molecule:**putative tetr-family regulator	
														PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.	
													d2np3a2	**Fold:** Tetracyclin repressor-like, C-terminal domain	100
														Superfamily: Tetracyclin repressor-like, C-terminal domain	
														Family: Tetracyclin repressor-like, C-terminal domain	
AMC57718		Sirohydrochlorin ferrochelatase	CbiX	Membrane 3.577 *	2jh3A	20,07	0,0066	No String Found	No	No	No	No	c2jh3C	**PDB header:**ribosomal protein	100
														Chain: C: **PDB Molecule:**ribosomal protein s2-related protein	
														PDBTitle: the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains	
													c4ccsA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**cbix	
														PDBTitle: the structure of cbix, the terminal enzyme for biosynthesis2 of siroheme in denitrifying bacteria	

													c2xvzA	**PDB header:**metal binding protein	100
														Chain: A: **PDB Molecule:**chelatase, putative	
														PDBTitle: cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)	
													c5zt7A	**PDB header:**biosynthetic protein	100
														Chain: A: **PDB Molecule:**sirohydrochlorin ferrochelatase	
														PDBTitle: sirb from bacillus subtilis with co2+	
													d1qgoa	**Fold:** Chelatase-like	100
														Superfamily: Chelatase	
														Family: Cobalt chelatase CbiK	
AMC57723		Allophanate hydrolase subunit 1 [Amino acid transport and metabolism]	Carboxyltransferase domain, subdomain C	Extracellular 1.765 *	2phcB	25,24	0	RN08_0296	3mml	H	Allophanate hydrolase subunit 1	0	c3mmlD	**PDB header:**hydrolase	100
									3mml	F	Allophanate hydrolase subunit 1	0		**Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1	
									3ore	B	Putative uncharacterized protein	0		**PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436	
									3ore	A	Putative uncharacterized protein	0			
									5dud	B	YbgJ	0	c3oepA	**PDB header:**structural genomics, unknown function	100
									2zp2	B	Kinase A inhibitor	0		**Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988	
									2zp2	A	Kinase A inhibitor	0		**PDBTitle:** crystal structure of ttha0988 in space group p43212	
													c5dudB	**PDB header:**unknown function	100

														Chain: B: **PDB Molecule:**ybgj	
														PDBTitle: crystal structure of e. coli ybgjk	
													c2phcB	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**uncharacterized protein ph0987	
														PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii	
													c2zp2B_	**PDB header:**transferase inhibitor	100
														Chain: B: **PDB Molecule:**kinase a inhibitor	
														PDBTitle: c-terminal domain of kipi from bacillus subtilis	
													d2phcb1	**Fold:** Cyclophilin-like	100
														Superfamily: Cyclophilin-like	
														Family: PH0987 C-terminal domain-like	
													c3va7A	**PDB header:**ligase	100
														Chain: A: **PDB Molecule:**klla0e08119p	
														PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase	
													c5i8iD	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**urea amidolyase	
														PDBTitle: crystal structure of the k. lactis urea amidolyase	
AMC57733		Serine aminopeptidase, S33	Serine aminopeptidase, S33	Extracellular 1.651 *	1brtA	15,06	0,000099	RN08_2458	7b1n	B	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000006	c6eicA	**PDB header:**hydrolase	100
									7b1n	A	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000006		**Chain:** A: **PDB Molecule:**mycobacterium tuberculosis monoglyceride lipase	

														PDBTitle: crystal structure of rv0183, a monoglyceride lipase from mycobacterium2 tuberculosis	
													c5xksB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**thermostable monoacylglycerol lipase	
														PDBTitle: crystal structure of monoacylglycerol lipase from thermophilic2 geobacillus sp. 12amor	
													c2ecfA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**dipeptidyl peptidase iv	
														PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia	
													c3i28A_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**epoxide hydrolase 2	
														PDBTitle: crystal structure of soluble epoxide hydrolase	
													d1zd3a2	**Fold:** alpha/beta-Hydrolases	100
														Superfamily: alpha/beta-Hydrolases	
														Family: Epoxide hydrolase	
													c3om8A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**probable hydrolase	
														PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01	
													c6qe2A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**monoacylglycerol lipase	
														PDBTitle: crystal structure of paleococcus ferrophilus monoacylglycerol lipase.	
													d1l7aa	**Fold:** alpha/beta-Hydrolases	100

														Superfamily: alpha/beta-Hydrolases	
														Family: Acetyl xylan esterase-like	
													d1a88a	**Fold:** alpha/beta-Hydrolases	100
														Superfamily: alpha/beta-Hydrolases	
														Family: Haloperoxidase	
AMC57735		Glyoxalase/ Bleomycin resistance protein/Dioxygenase superfamily	Glyoxalase/Bleomycin resistance protein/	Cytoplasmic 3.491 *	1npbA	22,91	0,000027	No String Found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c3l7tB	**PDB header:**metal binding protein	99,9
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** B: **PDB Molecule:**putative uncharacterized protein	
									6bo4	C	Transient Receptor Potential (TRP) channels	0,0000007		**PDBTitle:** crystal structure of smu.1112c	
									6bo4	B	Transient Receptor Potential (TRP) channels	0,0000007			
AMC57739		No	No	Extracellular 3.303 *	1y0fB	41,51	0,000000069	No String Found	7jjv	B	GrAFP antifreeze protein	0,0000000001	c7jjvB	**PDB header:**antifreeze protein	97,8
									7jjv	A	GrAFP antifreeze protein	0,0000000001		**Chain:** B: **PDB Molecule:**grafp antifreeze protein	
									3boi	B	6.5 kda glycine-rich antifreeze protection	0,0000000003		**PDBTitle:** crystal waters on the nine polyproline type ii helical bundle2 springtail antifreeze protein from granisotoma rainieri match the ice3 lattice	
									3boi	A	6.5 kda glycine-rich antifreeze protection	0,0000000003			
									7mqa	SD	rRNA 2'-O-methyltransferase fibr...	0,0000002			
									7mqa	SC	rRNA 2'-O-methyltransferase fibr...	0,0000002			
									5yvg	Y	RNA-binding protein FUS	0,0000002			
									5yvg	X	RNA-binding protein FUS	0,0000002			

									7d63	3C	rRNA 2'-O-methyltransferase fibr...	0,0000003			
									7d63	3B	rRNA 2'-O-methyltransferase fibr...	0,0000003			
									6nd4	D	Bud21	0,0000003			
									6nd4	c	Nop1.1	0,0000003			
									5wlc	SD	Nop1	0,0000003			
									5wlc	SC	Nop1	0,0000003			
									3hr2	B	Collagen alpha-2(I) chain	0,000004			
									3hqv	B	Collagen alpha-2(I) chain	0,000004			
AMC57741		No	No	Extracellular 3.246 *	1y0fB	37,8	0	No string Found	7jjv	B	GrAFP antifreeze protein	0	c7jjvB_	**PDB header:**antifreeze protein	98,8
									7jjv	A	GrAFP antifreeze protein	0		**Chain:** B: **PDB Molecule:**grafp antifreeze protein	
									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDBTitle:** crystal waters on the nine polyproline type ii helical bundle2 springtail antifreeze protein from granisotoma rainieri match the ice3 lattice	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0			
									5yvg	Y	RNA-binding protein FUS	0,0000000004			
									5yvg	X	RNA-binding protein FUS	0,0000000004			
									3hr2	B	Collagen alpha-2(I) chain	0,000000004			

									3hqv	B	Collagen alpha-2(I) chain	0,000000004			
									6f45	D	Receptor recognition protein	0,000000005			
									5aor	B	DOSAGE COMPENSATION REGULATOR	0,000000006			
									5aor	A	DOSAGE COMPENSATION REGULATOR	0,000000006			
									6wqk	E	MCherry fluorescent protein	0,000000008			
									6wqk	D	MCherry fluorescent protein	0,000000008			
									7mqa	SD	rRNA 2'-O-methyltransferase fibrillarin	0,00000001			
									7mqa	SC	rRNA 2'-O-methyltransferase fibrillarin	0,00000001			
									3boi	B	6.5 kda glycine-rich antifreeze protection	0,00000002			
									3boi	A	6.5 kda glycine-rich antifreeze protection	0,00000002			
									3eiv	D	Single-stranded DNA-binding protein	0,00000009			
									3eiv	C	Single-stranded DNA-binding protein	0,00000009			
									7d63	3C	rRNA 2'-O-methyltransferase fibrillarin.	0,0000001			
									7d63	3B	rRNA 2'-O-methyltransferase fibrillarin.	0,0000001			
AMC57744		No	No	Extracellular 2.506 *	1y0fB	37,81	0	No String Found	No	No	No	No	c7nx4A_	**PDB header:**protein binding	38,2
														Chain: A: **PDB Molecule:**alk tyrosine kinase receptor	
														PDBTitle: crystal structure of the tg and egf-like domains of alk	

AMC57748		No	No	Extracellular 2.710 *	1bh6A	20,99	4,6	RN08_3811	1nth	A	Monomethylamine methyltransferase	0,000007	c5d88A	**PDB header:**hydrolase	22,6
									1l2q	A	monomethylamine methyltransferase	0,000007		**Chain:** A: **PDB Molecule:**predicted protease of the collagenase family	
														PDBTitle: the structure of the u32 peptidase mk0906	
AMC57762		No	alpha/beta hydrolase fold	Membrane 2.855 *	1l7aA	15,81	0,0000027	No String Found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c6fkxD	**PDB header:**hydrolase	100
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** D: **PDB Molecule:**acetyl xylan esterase	
														PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome	
													c4d9jI	**PDB header:**de novo protein	100
														Chain: I: **PDB Molecule:**designed 16nm tetrahedral protein cage containing non-haem	
														PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains	
													c2y6vB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**peroxisomal membrane protein lpx1	
														PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)	
													c6lzhA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**grgf	
														PDBTitle: crystal structure of alpha/beta hydrolase grgf from penicillium sp.2 sh18	
													c7d78D	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**dltd domain-containing protein	
														PDBTitle: the structure of thioesterase dcsb	

													c2wtmC	**PDB header:**hydrolase	100
														Chain: C: **PDB Molecule:**est1e	
														PDBTitle: est1e from butyrivibrio proteoclasticus	
													c3fcyB	**PDB header:**hydrolase	
														Chain: B: **PDB Molecule:**xylan esterase 1	
														PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485	
													c5yznA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**acyl-peptide hydrolase, putative	
														PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1	
													c1yr2A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**prolyl oligopeptidase	
														PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity	
													c6eosB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**dipeptidyl peptidase 8	
														PDBTitle: dpp8 - apo, space group 19	
													c3azqA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**aminopeptidase	
														PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg	
AMC57764		LPS sulfotransferase NodH [Cell wall/membrane/envelope biogenesis]	Sulfotransferase family	Cytoplasmic 3.005 *	1texD	66,67	0		No	No	No	No	No	No	No

AMC57776		PPE-repeat protein [Function unknown]	PPE family	Extracellular 2.386 *	2g38B	43,24	1,4	RN08_2696	No	No	No	No	c5xfsB	**PDB header:**protein transport	99,1
														Chain: B: **PDB Molecule:**ppe family protein ppe15	
														PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis	
AMC57781		SnoaL-like domain This family contains a large number of proteins that share the SnoaL fold.	SnoaL-like domain	Cytoplasmic 3.545 *	3b8lA	22,45	0,0000093	no String Found	4leh	C	Bile acid 7-alpha dehydratase, BaiE	0	c4lehA_	**PDB header:**lyase	99,9
									4leh	B	Bile acid 7-alpha dehydratase, BaiE	0		**Chain:** A: **PDB Molecule:**bile acid 7-alpha dehydratase, baie	
									4leh	A	Bile acid 7-alpha dehydratase, BaiE	0		**PDBTitle:** crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution	
									4n3v	B	Bile acid 7-alpha dehydratase, BaiE	0			
									4n3v	A	Bile acid 7-alpha dehydratase, BaiE	0			
									4l8p	A	Bile acid 7a-dehydratase, BaiE	0			
									4l8o	A	Bile acid 7a-dehydratase, BaiE	0			
AMC57782		No	No	Cytoplasmic 4.194 *	1z47A	14,29	2,7	RN08_2660	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2is9A	**PDB header:**transcription	38,8
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1	
									7b1n	B	cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000004		**PDBTitle:** structure of yeast dcn-1	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000004			
AMC57784		No	No	Cytoplasmic 2.933 *	1tmxA	16,13	3,8	No string Found	6b	C	Transient receptor potential cation channel	0,000002	c1f7uA_	**PDB header:**ligase/rna	45,7

									o4						
									6bo4	B	Transient receptor potential cation channel	0,000002		**Chain:** A: **PDB Molecule:**arginyl-trna synthetase	
									6bo4	D	Transient receptor potential cation channel	0,000002		**PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg	
									6bo4	A	Transient receptor potential cation channel	0,000002			
AMC57795		Methyltransferase domain This family appears to be a methyltransferase domain.	Methyltransferase domain	Cytoplasmic 4.845 *	3e23A	22,54	0,00000045	No String found	2i6g	B	Putative methyltransferase	0,000005	c4pneA_	**PDB header:**biosynthetic protein	99,9
									2i6g	A	Putative methyltransferase	0,000005		**Chain:** A: **PDB Molecule:**methyltransferase-like protein	
									3mer	B	Slr1183 protein	0,000006		**PDBTitle:** crystal structure of the [4+2]-cyclase spnf	
									3mer	A	Slr1183 protein	0,000006			
									2n47	A	Slr1183 protein	0,000006			
									2kw5	A	Slr1183 protein	0,000006			
AMC57798		Methyltransferase domain Members of this family are SAM dependent methyltransferases.	Methyltransferase domain	Cytoplasmic 2.387 *	3busA	21,02	0,000023	RN08_1569	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2gs9A_	**PDB header:**transferase	99,8
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**hypothetical protein tt1324	
									3bus	B	Methyltransferase	0,000000003		**PDBTitle:** crystal structure of tt1324 from thermus thermophilis hb8	
									3bus	A	Methyltransferase	0,000000003			

									6uwd	A	D-glucose O-methyltransferase	0,000000007			
									6uvq	B	D-glucose O-methyltransferase	0,000000007			
									6uvq	A	D-glucose O-methyltransferase	0,000000007			
									6uv6	C	D-glucose O-methyltransferase	0,000000007			
									6uv6	B	D-glucose O-methyltransferase	0,000000007			
									6uv6	A	D-glucose O-methyltransferase	0,000000007			
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			
AMC57802		SnoaL-like domain This family contains a large number of proteins that share the SnoaL fold.	SnoaL-like domain	Cytoplasmic 3.220 *	1nwwB	20,39	2,2	No String Found	No	No	No	No	c3ff2A	**PDB header:**unknown function	95,9
														Chain: A: PDB Molecule:uncharacterized cystatin fold protein (yp_497570.1) from	
														PDBTitle: crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution	
AMC57805		Domain of unknown function (DUF222)	HNH endonuclease	Extracellular 2.056 *	2vsyA	14,46	1	no string found	1nth	A	Monomethylamine methyltransferase	0,000003	c5zmmD	**PDB header:**dna binding protein	97,8
									1l2q	A	monomethylamine methyltransferase	0,000003		**Chain: D: PDB Molecule:**uncharacterized protein mcra	

									6bo4	C	Transient receptor potential cation channel	0,000006		**PDBTitle:** structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra	
									6bo4	B	Transient receptor potential cation channel	0,000006			
									6bo4	D	Transient receptor potential cation channel	0,000006			
									6bo4	A	Transient receptor potential cation channel	0,000006			
AMC57821		No	No	Cytoplasmic 3.166 *	1rssA	15,56	1,4	RN08_0762	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,00000005	c1sfeA	**PDB header:**dna-binding protein	23,6
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,00000005		**Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase	
														PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli	
AMC57828		No	Thioesterase superfamily	Cytoplasmic 3.820 *	2ov9C	24,76	0	No String Found	1nth	A	Monomethylamine methyltransferase	0,0000005	d2ov9a1	**Fold:** Thioesterase/thiol ester dehydrase-isomerase	100
									1l2q	A	monomethylamine methyltransferase	0,0000005		**Superfamily:** Thioesterase/thiol ester dehydrase-isomerase	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002		**Family:** PaaI/YdiI-like	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			
									4gah	B	Thioesterase superfamily member 4	0,000006			
									4gah	A	Thioesterase superfamily member 4	0,000006	c4ae8D_	**PDB header:**hydrolase	100
									4ae8	D	Thioesterase superfamily member 4	0,000006		**Chain:** D: **PDB Molecule:**thioesterase superfamily member 4	
									4ae8	C	Thioesterase superfamily member 4	0,000006		**PDBTitle:** crystal structure of human them4	

									4ae8	B	Thioesterase superfamily member 4	0,000006			
									4ae8	A	Thioesterase superfamily member 4	0,000006			
													c4ae7A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**thioesterase superfamily member 5	
														PDBTitle: crystal structure of human them5	
AMC57830		No	Type III secretion chaperone domain	Cytoplasmic 4.247 *	2eq6A	23,08	7,3	RN08_0515	No	No	No	No	c2an1D	**PDB header:**transferase	97,2
														Chain: D: **PDB Molecule:**putative kinase	
														PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2	
AMC57832		No	Protein of unknown function (DUF3151)	Cytoplasmic 2.427 *	2q24B	24	4,3	RN08_0079	No	No	No	No	d1bxca_	**Fold:** TIM beta/alpha-barrel	75,3
														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
AMC57837		Predicted alpha-1,6-mannanase, GH76 family [Carbohydrate transport and metabolism]	Fungalysin/Thermolysin Propeptide Motif	Cytoplasmic 3.629 *	2ahfA	16,41	0,002	No String Found	6shd	C	Alpha-1,6-mannanase	0	c6shdC_	**PDB header:**hydrolase	100
									6shd	B	Alpha-1,6-mannanase	0		**Chain:** C: **PDB Molecule:**alpha-1,6-mannanase	
									6shd	A	Alpha-1,6-mannanase	0		**PDBTitle:** structure of the gh76a alpha-1,6-mannanase from salegentibacter sp.2 hel1_6	
									6y8f	A	Mutant alpha-1,6-mannanase GH76A	0			

									6shm	A	Mutant alpha-1,6-mannanase GH76A	0			
									3k7x	A	Lin0763 protein	0	c3k7xA	**PDB header:**structural genomics, unknown function	100
														Chain: A: **PDB Molecule:**lin0763 protein	
														PDBTitle: crystal structure of the lin0763 protein from listeria innocua.2 northeast structural genomics consortium target lkr23.	
													c4bojC_	**PDB header:**hydrolase	100
														Chain: C: **PDB Molecule:**alpha-1,6-mannanase	
														PDBTitle: crystal structure of bacillus circulans tn-31 aman6 in complex with2 mannobiose	
													c6ry5A_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**mannan endo-1,6-alpha-mannosidase	
														PDBTitle: crystal structure of dfg5 from chaetomium thermophilum in complex with2 alpha-1,6-mannobiose	
													c4c1sA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**glycoside hydrolase family 76 mannosidase	
														PDBTitle: glycoside hydrolase family 76 (mannosidase) bt3792 from2 bacteroides thetaiotaomicron vpi-5482	
													c4mu9B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**glycoside hydrolase family 73	
														PDBTitle: crystal structure of a putative glycosylhydrolase (bt_3782) from2 bacteroides thetaiotaomicron vpi-5482 at 1.89 a resolution	
													c6u4zA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**alpha-1,6-mannanase	
														PDBTitle: crystal structure of a family 76 glycoside hydrolase from a	

														bovine2 bacteroides thetaiotaomicron strain	
													c4v1sA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**alpha-1,6-mannanase	
														PDBTitle: structure of the gh76 alpha-mannanase bt2949 from2 bacteroides thetaiotaomicron	
AMC57838		Predicted ABC-type ATPase	Zeta toxin	Cytoplasmic 3.629 *	2p5tD	16,58	0,0038	No String Found	1nth	A	Monomethylamine methyltransferase	0,000002	c6gveG_	**PDB header:**photosynthesis	98,5
									1l2q	A	monomethylamine methyltransferase	0,000002		**Chain:** G: **PDB Molecule:**phosphoribulokinase	
														PDBTitle: gapdh-cp12-prk complex	
AMC57851		No	Collagen triple helix repeat (20 copies)	Extracellular 3.311 *	1y0fA	40,7	0,000000016	No String Found	3hr2	B	Collagen alpha-2(I) chain	0,000000005	c3bogB	**PDB header:**antifreeze protein	99,1
									3hqv	B	Collagen alpha-2(I) chain	0,000000005		**Chain:** B: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein	
									3boi	B	6.5 kda glycine-rich antifreeze protection	0,00000003		**PDBTitle:** snow flea antifreeze protein quasi-racemate	
									3boi	A	6.5 kda glycine-rich antifreeze protection	0,00000003			
									3hr2	C	Collagen alpha-1(I) chain	0,00000007			
									3hr2	A	Collagen alpha-1(I) chain	0,00000007			
									7jjv	B	GrAFP antifreeze protein	0,00000009			
									7jjv	A	GrAFP antifreeze protein	0,00000009			
									5kca	A	Cerebellin-1	0,000009			
AMC57854		No	No	zszc	2jjiA	18,8	2,2	No String Found	No	No	No	No	d3c0na2	**Fold:** Aerolisin/ETX pore-forming domain	46,1

														Superfamily: Aerolisin/ETX pore-forming domain	
														Family: (Pro)aerolysin, pore-forming lobe	
AMC57864		Member of the Rhodanese Homology Domain superfamily	Rhodanese-like domain	Cytoplasmic 4.386 *	2fsxA	94,44	0	RN08_0437	NO	No	No	No	c2fsxA_	**PDB header:**structural genomics, unknown function	100
														Chain: A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase	
														PDBTitle: crystal structure of rv0390 from m. tuberculosis	
AMC57869		HNH nucleases HNH endonuclease signature which is found in viral, prokaryotic, and eukaryotic proteins	HNH endonuclease	Membrane 1.650 *	2ogaA	17,59	0,22	RN08_1684	1nth	A	Monomethylamine methyltransferase	0,0000001	c5zmmD_	**PDB header:**dna binding protein	97,9
									1l2q	A	monomethylamine methyltransferase	0,0000001		**Chain:** D: **PDB Molecule:**uncharacterized protein mcra	
														PDBTitle: structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra	
AMC57871		No	No	Cytoplasmic 1.990 *	3fapB	28,3	6,9	No String found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2f7lA_	**PDB header:**isomerase	68
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase	
														PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase	
AMC57873		No	No	Extracellular 3.411 *	1mdyA	21,28	0,79	No string Found	6bo4	C	Transient receptor potential cation channel	0,000001	d2ysca1	**Fold:** WW domain-like	79,2
									6bo4	B	Transient receptor potential cation channel	0,000001		**Superfamily:** WW domain	
									6bo4	D	Transient receptor potential cation channel	0,000001		**Family:** WW domain	

									6bo4	A	Transient receptor potential cation channel	0,000001			
AMC57874		No	No	Extracellular 3.217 *	1iw4A	25	3,5	No String Found	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000004	c1xrzA	**PDB header:**transcription	20,6
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000004		**Chain:** A: **PDB Molecule:**zinc finger y-chromosomal protein	
														PDBTitle: nmr structure of a zinc finger with cyclohexanylalanine substituted2 for the central aromatic residue	
AMC57875		No	No	Extracellular 4.167 *	3evtA	20,83	3,8	RN08_0809	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000002	d1xrua1	**Fold:** Double-stranded beta-helix	14,6
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000002		**Superfamily:** RmlC-like cupins	
														Family: KduI-like	
AMC57920		No	No	Cytoplasmic 2.306 *	2aq6A	22,22	7,2	RN08_1295	No	No	No	No	c4zkyB		95,9
														PDB header:oxidoreductase	
														Chain: B: **PDB Molecule:**pyridoxamine 5-phosphate oxidase	
														PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis	
AMC57921		PPE-repeat protein [Function unknown]	Pentapeptide repeats (8 copies)	Extracellular 3.720 *	2g38B	29,81	0,00000032	RN08_2696	5xfs	B	PPE family protein PPE15	0	c5xfsB_	**PDB header:**protein transport	100
									6vhr	B	PPE family protein PPE4	0		**Chain:** B: **PDB Molecule:**ppe family protein ppe15	
									6uuj	K	PPE family protein PPE4	0		**PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis	
									6vj5	B	PPE family protein PPE41	0			
									4w4l	B	PPE family protein PPE41	0			

									4kxr	B	PPE41	0	c6uujE_	**PDB header:**protein transport	100
									2g38	D	PPE FAMILY PROTEIN	0		**Chain:** E: **PDB Molecule:**ppe family protein ppe4	
									2g38	B	PPE FAMILY PROTEIN	0		**PDBTitle:** structure of pe5-ppe4-espg3 complex from the type vii (esx-3)2 secretion system, space group p212121	
									6wqk	E	MCherry fluorescent protein	0,00000007			
									6wqk	D	MCherry fluorescent protein	0,00000007			
									7wot	W	Nucleoporin NUP57	0,0000001	c2g38B	**PDB header:**structural genomics, unknown function	100
									7wot	T	Nucleoporin NUP57	0,0000001		**Chain:** B: **PDB Molecule:**ppe family protein	
									7n9f	k	Protein transport protein SEC13	0,0000001		**PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis	
									7n9f	h	Nucleoporin NUP120	0,0000001			
									7n9f	e	Nucleoporin SEH1	0,0000001			
									7n9f	b	Nucleoporin NUP85	0,0000001	d2g38b1	**Fold:** Ferritin-like	100
									1nth	A	Monomethylamine methyltransferase	0,0000001		**Superfamily:** PE/PPE dimer-like	
									1l2q	A	monomethylamine methyltransferase	0,0000001		**Family:** PPE	
									7wot	X	Nucleoporin NSP1	0,0000002			
									7wot	U	Nucleoporin NSP1	0,0000002			
									7n9f	Z	Nucleoporin NUP157	0,0000002	c7p0zF	**PDB header:**protein transport	100

									7n9f	Y	Nucleoporin NUP170	0,0000002		**Chain:** F: **PDB Molecule:**esx-1 secretion-associated protein espb	
									7n9f	j	Nucleoporin 145c	0,0000002		**PDBTitle:** 2.43 a mycobacterium marinum espb.	
									7n9f	g	Nucleoporin NUP133	0,0000002			
									7n9f	d	Protein transport protein SEC13	0,0000002			
									7bx7	F	Heterogeneous nuclear ribonucleoproteins (hnRNPs)	0,0000003	c4xy3A		100
									7bx7	E	Heterogeneous nuclear ribonucleoproteins (hnRNPs)	0,0000003		**PDB header:**protein transport	
									7vop	e	Nucleoporin CAN	0,0000006		**Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb	
									7vop	A	Nuclear pore complex protein Nup85	0,0000006		**PDBTitle:** structure of esx-1 secreted protein espb	
									7nrc	A	GCN1	0,000005			
									3ghg	J	Fibrinogen alpha chain	0,000006			
									3ghg	G	Fibrinogen alpha chain	0,000006			
AMC57922		Protein of unknown function (DUF664) This family is commonly found in Streptomyces coelicolor	Protein of unknown function (DUF664)	Cytoplasmic 4.534 *	3cexA	36,42	0	No String Found	3cex	B	Uncharacterized protein	0	c3cexB_	**PDB header:**structural genomics, unknown function	100
									3cex	A	Uncharacterized protein	0		**Chain:** B: **PDB Molecule:**uncharacterized protein	
														PDBTitle: crystal structure of the conserved protein of locus ef_3021 from2 enterococcus faecalis	

													d2ou6a1	**Fold:** DinB/YfiT-like putative metalloenzymes	100
														Superfamily: DinB/YfiT-like putative metalloenzymes	
														Family: DinB-like	
													c3e4xB	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**apc36150	
														PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150	
													c3dkaA_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**dinb-like protein	
														PDBTitle: crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution	
													d2p1aa1	**Fold:** DinB/YfiT-like putative metalloenzymes	100
														Superfamily: DinB/YfiT-like putative metalloenzymes	
														Family: DinB-like	
													d1rxqa	**Fold:** DinB/YfiT-like putative metalloenzymes	100
														Superfamily: DinB/YfiT-like putative metalloenzymes	
														Family: YfiT-like putative metal-dependent hydrolases	
AMC57933		No	No	Cytoplasmic 3.257 *	1ve5A	23,33	3,6	RN08_1748	1nth	A	Monomethylamine methyltransferase	0,0000005	d1xqaa_	**Fold:** Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	41,1
									1l2q	A	monomethylamine methyltransferase	0,0000005		**Superfamily:** Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002		**Family:** Antibiotic resistance proteins	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			

AMC57940		Putative holin This is a family of putative holins from Actinobacteria with three TM regions.	Domain of unknown function (DUF543)	Membrane 4.412 *	1q16C	20.51	2,1	No string found	No	No	No	No	d1o82a_	**Fold:** Saposin-like	45,8
														Superfamily: Bacteriocin AS-48	
														Family: Bacteriocin AS-48	
AMC57944		Alkylhydroperoxidase family enzyme, contains CxxC motif [Inorganic ion transport and metabolism]	Carboxymuconolactone decarboxylase family	Cytoplasmic 3.100 *	2prrD	16,58	0,000005	No String found	No	No	No	No	d2oyoa1	**Fold:** AhpD-like	100
														Superfamily: AhpD-like	
														Family: Atu0492-like	
													c3c1lB_	**PDB header:**oxidoreductase	
														Chain: B: **PDB Molecule:**putative antioxidant defense protein mlr4105	100
														PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution	
													d2prra1	**Fold:** AhpD-like	
														Superfamily: AhpD-like	100
														Family: Atu0492-like	
													d2pfxa1	**Fold:** AhpD-like	
														Superfamily: AhpD-like	
														Family: Atu0492-like	
															100
													d2o4da1	**Fold:** AhpD-like	100

														Superfamily: AhpD-like	
														Family: Atu0492-like	
													c6ohiA	**Fold:** AhpD-like	100
														Superfamily: AhpD-like	
														Family: Atu0492-like	
													d2gmya1	**Fold:** AhpD-like	100
														Superfamily: AhpD-like	
														Family: Atu0492-like	
													c3lvyB_	**PDB header:**lyase	100
														Chain: B: **PDB Molecule:**carboxymuconolactone decarboxylase family	
														PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans	
AMC57946		Acyl-ACP thioesterase [Lipid transport and metabolism]	Acyl-ACP thioesterase	Cytoplasmic 4.848 *	2ownB	18,01	0	No String Found	No	No	No	No	c5x04B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**dodecanoyl-[acyl-carrier-protein] hydrolase, chloroplastic	
														PDBTitle: 12:0-acp thioesterase from umbellularia californica	
													c2ownA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**putative oleoyl-[acyl-carrier protein] thioesterase	
														PDBTitle: crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution	
													c4gakA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**acyl-acp thioesterase	

														PDBTitle: crystal structure of acyl-acp thioesterase from spirosoma linguale	
													c2essA_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**acyl-acp thioesterase	
														PDBTitle: crystal structure of an acyl-acp thioesterase (np_810988.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.90 a resolution	
AMC57962		Protein of unknown function (DUF2505) Members of this family are all Actinobacteria.	Protein of unknown function (DUF2505)	Cytoplasmic 4.068 *	2ns9A	17,18	0,056	No string found	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000009	c4xrtB	**PDB header:**lyase	98
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000009		**Chain:** B: **PDB Molecule:**stfq aromatase/cyclase	
														PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway	
AMC57968		Putative bacterial sensory transduction regulator YbjN is a putative sensory transduction regulator	Putative bacterial sensory transduction regulation	Cytoplasmic 3.459 *	2plgA	16,55	0,092	No string found	No	No	No	No	d2plga1	**Fold:** Secretion chaperone-like	98,7
														Superfamily: Type III secretory system chaperone-like	
														Family: Tll0839-like	
AMC57972		No	No	Cytoplasmic 2.340 *	2cpyA	28,57	4,4	No string found	No	No	No	No	c3t4xA_	**PDB header:**oxidoreductase	14,1
														Chain: A: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family	
														PDBTitle: short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor	
AMC57975		No	No	Cytoplasmic 1.839 *	2ei4A	22,12	2,4	No string found	No	No	No	No	c2xg8D	**PDB header:**transcription	46,7
														Chain: D: **PDB Molecule:**pipx	

														PDBTitle: structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942	
AMC57976		No	No	Cytoplasmic 3.023 *	2ichB	13,94	1,1	RN08_1103	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	d2icha1	**Fold:** AttH-like	100
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Superfamily:** AttH-like	
									1nth	A	Monomethylamine methyltransferase	0,00000002		**Family:** AttH-like	
									1l2q	A	monomethylamine methyltransferase	0,00000002			
													c7a0qA_	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**crtc domain-containing protein	
														PDBTitle: crystal structure of kievitone hydratase from nectria haematococca (c22 sg)	
AMC57978		No	No	Cytoplasmic 4.717 *	2nn6F	15,09	3,2	No String found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c4rg6S	**PDB header:**protein binding	34,7
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** S: **PDB Molecule:**anaphase-promoting complex subunit 16	
									1nth	A	Monomethylamine methyltransferase	0,00000006		**PDBTitle:** crystal structure of apc3-apc16 complex	
									1l2q	A	monomethylamine methyltransferase	0,00000006			
AMC57982		Sugar phosphate isomerase/epimerase [Carbohydrate transport and metabolism]	Xylose isomerase-like TIM barrel	Cytoplasmic 3.564 *	2qulA	16,67	0,000074	No String Found	3wqo	B	Uncharacterized protein MJ1311	0,00000001	c3wqoB	**PDB header:**unknown function	100
									3wqo	A	Uncharacterized protein MJ1311	0,00000001		**Chain:** B: **PDB Molecule:**uncharacterized protein mj1311	
														PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein	
													c3aamA_	**PDB header:**hydrolase	100

														Chain: A: **PDB Molecule:**endonuclease iv	
														PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8	
													c6n98A	**PDB header:**isomerase	100
														Chain: A: **PDB Molecule:**xylose isomerase	
														PDBTitle: xylose isomerase 1f1 variant from streptomyces sp. f-1	
													c2ou4C_	**PDB header:**isomerase	100
														Chain: C: **PDB Molecule:**d-tagatose 3-epimerase	
														PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii	
													c3vniC	**PDB header:**isomerase	100
														Chain: C: **PDB Molecule:**xylose isomerase domain protein tim barrel	
														PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars	
													d1muwa	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
													d1qt1a	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
													d1bxba	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
													d1xima	**Fold:** TIM beta/alpha-barrel	100

														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
													c2hk1D	**PDB header:**isomerase	100
														Chain: D: **PDB Molecule:**d-psicose 3-epimerase	
														PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose	
													c6wn6C	**PDB header:**isomerase	100
														Chain: C: **PDB Molecule:**3-keto-d-glucoside 4-epimerase	
														PDBTitle: crystal structure of 3-keto-d-glucoside 4-epimerase, ycjr, from e.2 coli, apo form	
													d1bxca	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Xylose isomerase-like	
														Family: Xylose isomerase	
													c2zdsB	**PDB header:**dna binding protein	100
														Chain: B: **PDB Molecule:**putative dna-binding protein	
														PDBTitle: crystal structure of sco6571 from streptomyces coelicolor a3(2)	
													d1qtwa	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Xylose isomerase-like	
														Family: Endonuclease IV	
													c5zfsA	**PDB header:**isomerase	100
														Chain: A: **PDB Molecule:**d-allulose-3-epimerase	
														PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose	
													d1xp3a1	**Fold:** TIM beta/alpha-barrel	100

														Superfamily: Xylose isomerase-like	
														Family: Endonuclease IV	
													c5hmqE	**PDB header:**lyase	100
														Chain: E: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase	
														PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein	
													c4k3zA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**d-erythrulose 4-phosphate dehydrogenase	
														PDBTitle: crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad	
													c5zhzA	**PDB header:**dna binding protein	100
														Chain: A: **PDB Molecule:**probable endonuclease 4	
														PDBTitle: crystal structure of the apurinic/apyrimidinic endonuclease iv from2 mycobacterium tuberculosis	
AMC57983		Thioesterase-like superfamily	Thioesterase-like superfamily	Membrane 2.065 *	3bbjA	23,99	0	No String Found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c3bbjA	**PDB header:**hydrolase	100
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**putative thioesterase ii	
									3bbj	B	Putative thioesterase II	0		**PDBTitle:** crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution	
									3bbj	A	Putative thioesterase II	0			
													c1c8uA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**acyl-coa thioesterase ii	

														PDBTitle: crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme	
													c3rqbB	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**uncharacterized protein	
														PDBTitle: crystal structure of conserved protein of unknown function with hot2 dog fold from alicyclobacillus acidocaldarius	
													c3cjyA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**putative thioesterase	
														PDBTitle: crystal structure of putative thioesterase (yp_496845.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.70 a resolution	
													c3rd7A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**acyl-coa thioesterase	
														PDBTitle: crystal structure of acyl-coa thioesterase from mycobacterium avium	
													c4r9zB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**uncharacterized protein	
														PDBTitle: mycobacterium avium subs paratuberculosis tesb protein map1729c	
AMC57988		Lysophospholipid Acyltransferases (LPLATs) of Glycerophospholipid Biosynthesis	Acyltransferase	Cytoplasmic 3.302 *	1iuqA	13,42	0,064	No string found	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000007	c5kymA	**PDB header:**transferase	100
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000007		**Chain:** A: **PDB Molecule:**1-acyl-sn-glycerol-3-phosphate acyltransferase	
														PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima	

AMC57990		The hotdog fold was initially identified in the E. coli FabA (Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase)	N-terminal half of MaoC dehydratase	Cytoplasmic 4.470 *	3exzB	17,22	0,000063	No string found	4rlw	A	(3R)-hydroxyacyl-ACP dehydratase	0	c4rltA_	**PDB header:**lyase/lyase inhibitor	100
									4rlu	A	(3R)-hydroxyacyl-ACP dehydratase	0		**Chain:** A: **PDB Molecule:**(3r)-hydroxyacyl-acp dehydratase subunit hada	
									5zy8	C	UPF0336 protein Rv0637	0		**PDBTitle:** crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium tuberculosis complexed with fisetin	
									5zy8	A	UPF0336 protein Rv0637	0			
									4rv2	A	UPF0336 PROTEIN MSMEG_1340/MSMEI_1302 MAOC FAMILY PROTEIN	0			
									4v12	A	MAOC LIKE DOMAIN PROTEIN	0	c5zy8A_	**PDB header:**lyase	100
									5i7n	A	MaoC-like dehydratase	0		**Chain:** A: **PDB Molecule:**upf0336 protein rv0637	
									1nth	A	Monomethylamine methyltransferase	0,0000003		**PDBTitle:** crystal structure of c terminal truncated hadbc (3r-hydroxyacyl-acp2 dehydratase) complex from mycobacterium tuberculosis	
													c4rv2A	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**upf0336 protein msmeg_1340/msmei_1302	
														PDBTitle: crystal structure of (3r)-hydroxyacyl-acp dehydratase hadab hetero-2 dimer from mycobacterium smegmatis	
													c4v12A_	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**maoc like domain protein	
														PDBTitle: crystal structure of the msmeg_6754 dehydratase from mycobacterium2 smegmatis	
													c4w7bG_	**PDB header:**lyase	100

														Chain: G: **PDB Molecule:**hydratase chsh1	
														PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis	
													d1q6wa	**Fold:** Thioesterase/thiol ester dehydrase-isomerase	
														Superfamily: Thioesterase/thiol ester dehydrase-isomerase	
														Family: MaoC-like	
													c3exzA	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**maoc-like dehydratase	
														PDBTitle: crystal structure of the maoc-like dehydratase from rhodospirillum2 rubrum. northeast structural genomics consortium target rrr103a.	
AMC57995		Glutaredoxin-like domain (DUF836) These proteins are related to the pfam00462 family.	Glutaredoxin-like domain (DUF836)	Cytoplasmic 4.245 *	1ttzA	27,71	0,00014	No String found	No	No	No	No	c2znmA	**PDB header:**oxidoreductase	95,2
														Chain: A: **PDB Molecule:**thiol:disulfide interchange protein dsba	
														PDBTitle: oxidoreductase nmdsba3 from neisseria meningitidis	
AMC58003		Domain of unknown function (DUF222)	HNH endonuclease	Membrane 1.439 *	2vsyA	14,51	0,52	NO String found	1nth	A	Monomethylamine methyltransferase	0,000003	c5zmmD	**PDB header:**dna binding protein	97,8
									1l2q	A	monomethylamine methyltransferase	0,000003		**Chain:** D: **PDB Molecule:**uncharacterized protein mcra	
									6bo4	C	Transient receptor potential cation channel	0,000006		**PDBTitle:** structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra	
									6bo4	B	Transient receptor potential cation channel	0,000006			

AMC58006		SGNH_hydrolase, or GDSL_hydrolase, is a diverse family of lipases and esterases.	GDSL-like Lipase/Acylhydrolase family	Cytoplasmic 3.897 *	1ivnA	16,84	0,000077	No String found	No	No	No	No	c4jggB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**esterase tesa	
														PDBTitle: crystal structure of tesa	
													c4xvhA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**carbohydrate esterase family 2 (ce2)	
														PDBTitle: crystal structure of a corynascus thermopiles (myceliophthora2 fergusii) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd)	
													c2waoA_	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**endoglucanase e	
														PDBTitle: structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose	
AMC58014		Histidine phosphatase superfamily (branch 1) The histidine phosphatase superfamily	Histidine phosphatase superfamily	Cytoplasmic 3.965 *	1h2eA	22,39	0	RN08_2682	6s2r	B	Glucosyl-3-phosphoglycerate phosphatase	0,000002	c4pz9B	**PDB header:**hydrolase	100
									6s2r	A	Glucosyl-3-phosphoglycerate phosphatase	0,000002		**Chain:** B: **PDB Molecule:**glucosyl-3-phosphoglycerate phosphatase	
									6s2q	D	Glucosyl-3-phosphoglycerate phosphatase	0,000002		**PDBTitle:** the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c	
									6s2q	C	Glucosyl-3-phosphoglycerate phosphatase	0,000002			
													c4ij5B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**phosphoserine phosphatase 1	

														PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from2 *hydrogenobacter thermophilus* tk-6	
													c3e9eB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**zgc:56074	
														PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio	
													d1h2ea	**Fold:** Phosphoglycerate mutase-like	100
														Superfamily: Phosphoglycerate mutase-like	
														Family: Cofactor-dependent phosphoglycerate mutase	
													c3dcyA	**PDB header:**apoptosis regulator	100
														Chain: A: **PDB Molecule:**regulator protein	
														PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.	
													d1fzta	**Fold:** Phosphoglycerate mutase-like	100
														Superfamily: Phosphoglycerate mutase-like	
														Family: Cofactor-dependent phosphoglycerate mutase	
													c2a6pA	**PDB header:**structural genomics, unknown function	100
														Chain: A: **PDB Molecule:**possible phosphoglycerate mutase gpm2	
														PDBTitle: structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis	
													c2yn0A	**PDB header:**transcription	100
														Chain: A: **PDB Molecule:**transcription factor tau 55 kda subunit	
														PDBTitle: tau55 histidine phosphatase domain	

													c6e4bC	**PDB header:**hydrolase	100
														Chain: C: **PDB Molecule:**adenosylcobalamin/alpha-ribazole phosphatase	
														PDBTitle: the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from escherichia coli str. k-12 substr. mg1655	
													c3d4iD	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**sts-2 protein	
														PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2	
													c5zkkA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**phosphoglycerate mutase family protein, putative	
														PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica	
													c3r7aA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**phosphoglycerate mutase, putative	
														PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne	
													c3c7tB	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**ecdysteroid-phosphate phosphatase	
														PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate	
														PDB Entry: PDBe RCSB PDB	
													d1xq9a	**Fold:** Phosphoglycerate mutase-like	100
														Superfamily: Phosphoglycerate mutase-like	
														Family: Cofactor-dependent phosphoglycerate mutase	

													d3pgma	**Fold:** Phosphoglycerate mutase-like	100
														Superfamily: Phosphoglycerate mutase-like	
														Family: Cofactor-dependent phosphoglycerate mutase	
													c1k6mA	**PDB header:**transferase, hydrolase	100
														Chain: A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2-	
														PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase	
													c4eo9A	**PDB header:**isomerase	100
														Chain: A: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	
														PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae	
													d1k6ma2	**Fold:** Phosphoglycerate mutase-like	100
														Superfamily: Phosphoglycerate mutase-like	
														Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain	
													c6yj6C	**PDB header:**transcription	100
														Chain: C: **PDB Molecule:**transcription factor tau 55 kda subunit	
														PDBTitle: structure of the tfiiic subcomplex taua	
													c2i1vB	**PDB header:**transferase, hydrolase	100
														Chain: B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	
														PDBTitle: crystal structure of pfkfb3 in complex with adp and fructose-2,6-2 bisphosphate	

AMC58019		MinD-like ATPase involved in chromosome partitioning or flagellar assembly [Cell cycle control]	CobQ/CobB/MinD/ParA nucleotide binding domain	Membrane 1.767 *	1hyqA	24,39	0,000027	RN08_1373	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2bekB	**PDB header:**chromosome segregation	100
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** B: **PDB Molecule:**segregation protein	
									1nth	A	Monomethylamine methyltransferase	0,00000007		**PDBTitle:** structure of the bacterial chromosome segregation protein soj	
									1l2q	A	monomethylamine methyltransferase	0,00000007			
									1hyq	A	CELL DIVISION INHIBITOR (MIND-1)	0,0000008			
									4v03	B	SITE-DETERMINING PROTEIN	0,000001	c4v02B	**PDB header:**cell cycle	100
									4v03	A	SITE-DETERMINING PROTEIN	0,000001		**Chain:** B: **PDB Molecule:**site-determining protein	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000009		**PDBTitle:** minc:mind cell division protein complex, aquifex aeolicus	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000009			
													d1g3qa	**Fold:** P-loop containing nucleoside triphosphate hydrolases	100
														Superfamily: P-loop containing nucleoside triphosphate hydrolases	
														Family: Nitrogenase iron protein-like	
													c3endA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**light-independent protochlorophyllide reductase	
														PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein	

													d1hyqa	**Fold:** P-loop containing nucleoside triphosphate hydrolases	100
														Superfamily: P-loop containing nucleoside triphosphate hydrolases	
														Family: Nitrogenase iron protein-like	
													c1hyqA	**PDB header:**cell cycle	100
														Chain: A: **PDB Molecule:**cell division inhibitor (mind-1)	
														PDBTitle: mind bacterial cell division regulator from a. fulgidus	
													c4pfsA	**PDB header:**ligase	100
														Chain: A: **PDB Molecule:**cobyrinic acid a,c-diamide synthase	
														PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis	
													c3kjgB	**PDB header:**hydrolase, metal binding protein	100
														Chain: B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase complex, accessory	
														PDBTitle: adp-bound state of cooc1	
													d1iona	**Fold:** P-loop containing nucleoside triphosphate hydrolases	100
														Superfamily: P-loop containing nucleoside triphosphate hydrolases	
														Family: Nitrogenase iron protein-like	
													c5j1jA	**PDB header:**transcription	100
														Chain: A: **PDB Molecule:**site-determining protein	
														PDBTitle: structure of flen-amppnp complex	
													c3vx3A	**PDB header:**adp binding protein	100
														Chain: A: **PDB Molecule:**atpase involved in chromosome partitioning, para/mind	
														PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb	

														from2 thermococcus kodakarensis kod1	
													c6g2gA	**PDB header:**cytosolic protein	100
														Chain: A: **PDB Molecule:**cytosolic fe-s cluster assembly factor cfd1	
														PDBTitle: fe-s assembly cfd1	
													d1cp2a	**Fold:** P-loop containing nucleoside triphosphate hydrolases	100
														Superfamily: P-loop containing nucleoside triphosphate hydrolases	
														Family: Nitrogenase iron protein-like	
													c3ez6B	**PDB header:**dna binding protein	100
														Chain: B: **PDB Molecule:**plasmid partition protein a	
														PDBTitle: structure of para-adp complex:tetragonal form	
													c4rz3B	**PDB header:**structural protein	100
														Chain: B: **PDB Molecule:**site-determining protein	
														PDBTitle: crystal structure of the mind-like atpase flhg	
AMC58037		No	Beta-fructofuranosidase, N-terminal domain	Membrane 3.702 *	1jb0L	17,5	1,7	No string found	No	No	No	No	c1ifpA	**PDB header:**virus	55,1
														Chain: A: **PDB Molecule:**major coat protein assembly	
														PDBTitle: inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly	
AMC58039		uncharacterized subfamily of vicinal oxygen chelate (VOC) family	Glyoxalase/Bleomycin resistance protein	Cytoplasmic 4.309 *	1f9zA	24,39	0,0000016	No String found	No	No	No	No	c6bu2A	**PDB header:**isomerase	99,7
														Chain: A: **PDB Molecule:**glyoxalase	

														PDBTitle: crystal structure of methylmalonyl-coa epimerase from mycobacterium2 tuberculosis	
AMC58062		Domain of unknown function (DUF1918)	Domain of unknown function (DUF1918)	Cytoplasmic 3.878 *	2a7yA	47,73	0,00000022	RN08_2547	No	No	No	No	c2a7yA	**PDB header:**structural genomics, unknown function	100
														Chain: A: **PDB Molecule:**hypothetical protein rv2302/mt2359	
														PDBTitle: solution structure of the conserved hypothetical protein rv2302 from2 the bacterium mycobacterium tuberculosis	
													d2a7ya1	**Fold:** SH3-like barrel	100
														Superfamily: Cell growth inhibitor/plasmid maintenance toxic component	
														Family: Rv2302-like	
AMC58066		Pimeloyl-ACP methyl ester carboxylesterase	Family of unknown function (DUF6143)	Cytoplasmic 3.068 *	2o2gA	56,86	0	RN08_0639	2o2g	A	Dienelactone hydrolase	0	c2o2gA	**PDB header:**hydrolase	100
									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**dienelactone hydrolase	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDBTitle:** crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution	
									6bo4	C	Transient receptor potential cation channel	0,000001			
									6bo4	B	Transient receptor potential cation channel	0,000001			
AMC58073		Poly-gamma-glutamate biosynthesis protein CapA/YwtB (capsule formation)	Bacterial capsule synthesis protein PGA_cap	Cytoplasmic 4.585 *	2z1aA	18,42	0,00036	No String found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	d2z06a1	**Fold:** Metallo-dependent phosphatases	100

									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Superfamily:** Metallo-dependent phosphatases	
														Family: TTHA0625-like	
													d1t71a	**Fold:** Metallo-dependent phosphatases	100
														Superfamily: Metallo-dependent phosphatases	
														Family: DR1281-like	
AMC58076		No	No	Extracellular 3.215 *	3e4oA	23,08	1,7	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	d2ersa1	**Fold:** Complement control module/SCR domain	20,4
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Superfamily:** Complement control module/SCR domain	
														Family: Complement control module/SCR domain	
AMC58079		No	No	Cytoplasmic 2.075 *	1qhhD	26,32	0,47	RN08_3526	No	No	No	No	d2ersa1	**Fold:** Complement control module/SCR domain	20,4
														Superfamily: Complement control module/SCR domain	
														Family: Complement control module/SCR domain	
AMC58097		No	UvrD-like helicase C-terminal domain	Extracellular 2.466 *	1qhhD	26,32	0,47	RN08_1055	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000002	c1qhhD	**PDB header:**hydrolase	99,4
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,0000002		**Chain:** D: **PDB Molecule:**protein (pcra (subunit))	
														PDB Title: structure of dna helicase with adpnp	
AMC58103		No	Peptidase propeptide and YPEB domain	Membrane 1.324 *	3emoC	23,53	2,3	No string found	2lra	A	POSSIBLE EXPORTED PROTEIN	0	c2kgyA	**PDB header:** immune system	100
									2kgy	A	POSSIBLE EXPORTED PROTEIN	0		**Chain:** A: **PDB Molecule:** possible exported protein	
									7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0		**PDB Title:** solution structure of rv0603 protein from mycobacterium tuberculosis2 h37rv	

									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0			
AMC58111		No	Antitoxin VbhA	Cytoplasmic 4.915 *	1vlbA	15.21	4,9	RN08_0418	1nth	A	Monomethylamine methyltransferase	0,000001	c6d0tA	**PDB header:**de novo protein	25,4
									1l2q	A	monomethylamine methyltransferase	0,000001		**Chain:** A: **PDB Molecule:**bb1	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002		**PDBTitle:** de novo design of a fluorescence-activating beta barrel - bb1	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			
AMC58114		SEC-C motif	Protein of unknown function (DUF3320)	Cytoplasmic 3.860 *	1lshA	12,09	0,57	No string found	No	No	No	No	d1ozbi	**Fold:** Sec-C motif	99,2
														Superfamily: Sec-C motif	
														Family: Sec-C motif	
AMC58115		No	Poliovirus 3A protein like	Extracellular 2.566 *	1rypD	15,05	1,7	No String Found	No	No	No	No	d1jvra	**Fold:** Retroviral matrix proteins	59,5
														Superfamily: Retroviral matrix proteins	
														Family: HTLV-II matrix protein	
AMC58135		Transcription regulator of the Arc/MetJ class	Bacterial antitoxin of type II TA system	Cytoplasmic 3.437 *	1q5vB	32	0,11	No string found	No	No	No	No	c6a7vU	**PDB header:**toxin/antitoxin	97,7
														Chain: U: **PDB Molecule:**antitoxin vapb11	
														PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex	
AMC58149		Predicted unusual protein kinase regulating ubiquinone biosynthesis, AarF/ABC1	ABC1 atypical kinase-like domain	Cytoplasmic 4.818 *	1cm8A	17,41	0,67	RN08_2316	5yk2	A	Probable conserved ATP-binding protein	0	c5yk2A	**PDB header:**transport protein	100

		/UbiB family													
									5yk1	A	Probable conserved ATP-binding protein	0		**Chain:** A: **PDB Molecule:**probable conserved atp-binding protein abc transporter	
									7cz2	A	ABC1 family protein	0		**PDBTitle:** the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis	
									7cyr	A	ABC1 family protein	0			
									5i35	A	Atypical kinase ADCK3, mitochondrial	0	c5yk2A	**PDB header:**transferase	100
									4ped	A	Chaperone activity of bc1 complex	0		**Chain:** A: **PDB Molecule:**chaperone activity of bc1 complex-like, mitochondrial	
														PDBTitle: mitochondrial adck3 employs an atypical protein kinase-like fold to2 enable coenzyme q biosynthes	
AMC58184		Helix-turn-helix domains	MarR family	Cytoplasmic 3.535 *	1ku9A	13,61	0,000091	NO STRING FOUND	4nb5	D	DNA binding protein	0	c4nb5D	**PDB header:**dna binding protein	100
									4nb5	C	DNA binding protein	0		**Chain:** D: **PDB Molecule:**dna binding protein	
									6bo4	C	Transient receptor potential cation channel	0,000004		**PDBTitle:** crystal structure of a transcriptional regulator	
									6bo4	B	Transient receptor potential cation channel	0,000004			
AMC58195		No	No	Extracellular 1.585 *	1vchD	13,43	8,5	No striing found	No	No	No	No	c6p4hE	**PDB header:**ribosome	16,2
														Chain: E: **PDB Molecule:**us3	
														PDBTitle: structure of a mammalian small ribosomal subunit in complex with the2 israeli acute paralysis virus ires (class 2)	

AMC58196		Uncharacterized protein	Uncharacterized protein conserved in bac	Cytoplasmic 3.235 *	1ewrB	12,14	0,72	No string founds	1nth	A	Monomethylamine methyltransferase	0,000001	c5dplB_	**PDB header:**transferase	73,9
									1l2q	A	monomethylamine methyltransferase	0,000001		**Chain:** B: **PDB Molecule:**protein lysine methyltransferase 2	
														PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy	
AMC58219		Sulfatase-modifying factor enzyme 1	Sulfatase-modifying factor enzyme 1	Extracellular 3.497 *	2q17E	42,57	0	RN08_0792	6muj	E	Formylglycine-generating enzyme	0	c2q17C	**PDB header:**unknown function	100
									6muj	D	Formylglycine-generating enzyme	0		**Chain:** C: **PDB Molecule:**formylglycine generating enzyme	
									2aii	X	Sulfatase modifying factor 1	0		**PDBTitle:** formylglycine generating enzyme from streptomyces coelicolor	
									1z70	X	C-alpha-formylglycine-generating enzyme 2	0			
									1y1j	X	C-alpha-formylglycine-generating enzyme 2	0			
									2hib	X	Sulfatase-modifying factor 1	0	c5nyyA_	**PDB header:**transferase	100
									2hi8	X	Sulfatase-modifying factor 1	0		**Chain:** A: **PDB Molecule:**non-specific serine/threonine protein kinase	
									7msy	A	CalU17	0		**PDBTitle:** formylglycine generating enzyme from t. curvata in complex with cd(ii)	
									7ml6	A	CalU17	0			
									6vqp	A	CalU17	0			
									4x8e	B	Sulfoxide synthase EgtB	0	c1y1fX_	**PDB header:**oxidoreductase	100
									4x8e	A	Sulfoxide synthase EgtB	0		**Chain:** X: **PDB Molecule:**c-alpha-formylglycine-generating enzyme	

									5hha	B	PvdO	0		**PDBTitle:** human formylglycine generating enzyme with cysteine sulfenic acid	
									5hha	A	PvdO	0			
									1nth	A	Monomethylamine methyltransferase	0,0000007			
									1l2q	A	monomethylamine methyltransferase	0,0000007	d1z70x1	**Fold:** C-type lectin-like	100
									6bo4	C	Transient receptor potential cation channel	0,000003		**Superfamily:** C-type lectin-like	
									6bo4	B	Transient receptor potential cation channel	0,000003		**Family:** Sulfatase-modifying factor-like	
									2y3c	A	TREPONEMA DENTICOLA VARIABLE PROTEIN 1	0,000006			
													c6vqpA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**calu17	
														PDBTitle: structure of calu17 from the calicheamicin biosynthesis pathway of2 micromonospora echinospora	
													d1y4ja1	**Fold:** C-type lectin-like	100
														Superfamily: C-type lectin-like	
														Family: Sulfatase-modifying factor-like	
													c4x8bA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**sulfoxide synthase egtb	
														PDBTitle: ergothioneine-biosynthetic sulfoxide synthase egtb, apo form	
													c5hhaB_	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**pvdo	

														PDBTitle: structure of pvdo from pseudomonas aeruginosa	
													c5aohA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**spore coat protein coth	
														PDBTitle: crystal structure of carf	
													c6qkjA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: egtb from chloracidobacterium thermophilum, a type ii sulfoxide2 synthase in complex with n,n,n-trimethyl-histidine	
													c5vf4A_	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: thermus aquaticus variable protein (taqvp) from diversity-generating2 retroelements (dgr)	
													c2y3cA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**treponema denticola variable protein 1	
														PDBTitle: treponema denticola variable protein 1	
													d1yu3a2	**Fold:** C-type lectin-like	100
														Superfamily: C-type lectin-like	
														Family: Mtd variable domain	
														PDB entry: PDBe RCSB PDB	
													d1yu0a2	**Fold:** C-type lectin-like	100
														Superfamily: C-type lectin-like	
														Family: Mtd variable domain	
													c2iouC	**PDB header:**viral protein/membrane protein	100

														Chain: C: **PDB Molecule:**major tropism determinant p1	
														PDBTitle: major tropism determinant p1 (mtd-p1) variant complexed with2 bordetella brochiseptica virulence factor pertactin extracellular3 domain (prn-e).	
AMC58233		O-Methyltransferase involved in polyketide biosynthesis	Leucine carboxyl methyltransferase	Extracellular 3.386 *	2uyoA	40,3	0	RN08_0167	6id6	A	Putative S-adenosyl-L-methionine-dependent methyltransferase	0	c6id6A	**PDB header:**transferase	100
									2ckd	B	PUTATIVE S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE	0		**Chain:** A: **PDB Molecule:**putative s-adenosyl-l-methionine-dependent	
									2ckd	A	PUTATIVE S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE	0		**PDBTitle:** crystal structure of rv0731c from mycobacterium tuberculosis at 1.632 angstroms.	
									6bo4	C	Transient receptor potential cation channel	0,000001			
									6bo4	B	Transient receptor potential cation channel	0,000001			
									1nth	A	Monomethylamine methyltransferase	0,000002	d2uyoa1	**Fold:** S-adenosyl-L-methionine-dependent methyltransferases	100
									1l2q	A	monomethylamine methyltransferase	0,000002		**Superfamily:** S-adenosyl-L-methionine-dependent methyltransferases	
														Family: ML2640-like	
													c3ieiD_	**PDB header:**transferase	100
														Chain: D: **PDB Molecule:**leucine carboxyl methyltransferase 1	
														PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine	
													c3mntA	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**leucine carboxyl methyltransferase 1	

														PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1	
													d1rjda	**Fold:** S-adenosyl-L-methionine-dependent methyltransferases	100
														Superfamily: S-adenosyl-L-methionine-dependent methyltransferases	
														Family: Leucine carboxy methyltransferase Ppm1	
AMC58246		TIGR03086 family protein	Mycothiol maleylpyruvate isomerase	Cytoplasmic 3.053 *	2nsfA	21,74	0,21	No string found	No	No	No	No	c2nsfA	**PDB header:**isomerase	100
														Chain: A: **PDB Molecule:**hypothetical protein cgl3021	
														PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase	
AMC58247		EspA/EspE family This family of proteins includes Mycobacterium tuberculosis EspA and EspE proteins	Domain of unknown function (DUF4226)	Extracellular 2.299 *	3caxA	11,84	8,3	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c4p40A	**PDB header:**transport protein	90,1
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**copn	
														PDBTitle: chlamydia pneumoniae copn	
AMC58248		No	No	Cytoplasmic 4.038 *	3c19A	18,71	2,3	No string found	No	No	No	No	c5jxfA	**PDB header:**hydrolase	84
														Chain: A: **PDB Molecule:**asp/glu-specific dipeptidyl-peptidase	
														PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp	
AMC58251		No	Nucleotidyltransferase of unknown functi	Cytoplasmic 4.124 *	1a04A	14,9	5,4	RN08_3582	No	No	No	No	c4e8iA	**PDB header:**transferase	86,1

														Chain: A: **PDB Molecule:**lincosamide resistance protein	
														PDBTitle: crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo	
AMC58255		No	No	Extracellular 2.973 *	1y0fB	33,99	0	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c1ygvA	**PDB header:**structural protein/contractile protein	99,8
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**collagen i alpha 1	
									7jjv	B	GrAFP antifreeze protein	0		**PDBTitle:** the structure of collagen type i. single type i collagen2 molecule: rigid refinment	
									7jjv	A	GrAFP antifreeze protein	0			
									3hr2	B	Collagen alpha-2(I) chain	0			
									3hqv	B	Collagen alpha-2(I) chain	0			
									3boi	B	6.5 kda glycine-rich antifreeze protection	0,000000001			
									3boi	A	6.5 kda glycine-rich antifreeze protection	0,000000001			
									5yvg	Y	RNA-binding protein FUS	0,000000005			
									5yvg	X	RNA-binding protein FUS	0,000000005			
									7mqa	SD	rRNA 2'-O-methyltransferase fibr...	0,00000001			
									7mqa	SC	rRNA 2'-O-methyltransferase fibr...	0,00000001			
									6nd4	D	Bud21	0,00000001			
									6nd4	c	Nop1.1	0,00000001			

									6lqv	3C	rRNA 2'-O-methyltransferase fibr...	0,00000001			
									6lqv	3B	rRNA 2'-O-methyltransferase fibr...	0,00000001			
AMC58256		No	No	Extracellular 2.817 *	1y0fB	43,59	0,032	No string found	No	No	No	No	c2klwA	**PDB header:**de novo protein	23,1
														Chain: A: **PDB Molecule:**(pkg)10	
														PDBTitle: solution structure of an abc collagen heterotrimer reveals a single-2 register helix stabilized by electrostatic interactions	
AMC58257		No	No	Extracellular 3.168 *	1y0fB	39,27	0	No string found	7jjv	B	GrAFP antifreeze protein	0	c1ygvA	**PDB header:**structural protein/contractile protein	99,3
									7jjv	A	GrAFP antifreeze protein	0		**Chain:** A: **PDB Molecule:**collagen i alpha 1	
									3hr2	C	Collagen alpha-1(I) chain	0		**PDBTitle:** the structure of collagen type i. single type i collagen2 molecule: rigid refinment	
									3hr2	A	Collagen alpha-1(I) chain	0			
									6wqk	E	MCherry fluorescent protein	0			
									6wqk	D	MCherry fluorescent protein	0			
									3bog	B	6.5 kda glycine-rich antifreeze protection	0			
									3bog	A	6.5 kda glycine-rich antifreeze protection	0			
									5yvg	Y	RNA-binding protein FUS	0			
									5yvg	X	RNA-binding protein FUS	0			
									3boi	B	6.5 kda glycine-rich antifreeze protection	0,0000000001			

									3boi	A	6.5 kda glycine-rich antifreeze protection	0,0000000001			
									7mqa	SD	rRNA 2'-O-methyltransferase fibr...	0,0000000002			
									7mqa	SC	rRNA 2'-O-methyltransferase fibr...	0,0000000002			
									6nd4	D	Bud21	0,0000000008			
									6nd4	c	Nop1.1	0,0000000008			
									7vop	e	Nucleoporin CAN	0,000000001			
									7vop	A	Nuclear pore complex protein Nup85	0,000000001			
									7bx7	F	Heterogeneous nuclear ribonucleoproteins (hnRNPs)	0,000000002			
									7bx7	E	Heterogeneous nuclear ribonucleoproteins (hnRNPs)	0,000000002			
									7nkx	Z	Transcription elongation factor	0,000000002			
									6f45	D	Receptor recognition protein	0,000000005			
									7nx1	A	Leukocyte tyrosine kinase receptor	0,00000008			
									3eiv	D	Single-stranded DNA-binding prote...	0,00000008			
									1nth	A	Monomethylamine methyltransferase	0,0000001			
AMC58260		No	No	Extracellular 3.020 *	2pneA	53,19	0,047	No string found	7jjv	B	GrAFP antifreeze protein	0,0000008	c1jrjA	**PDB header:**hormone/growth factor	40,5
									7jjv	A	GrAFP antifreeze protein	0,0000008		**Chain:** A: **PDB Molecule:**exendin-4	

									3boi	B	6.5 kda glycine-rich antifreeze protection	0,000005		**PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol	
									3boi	A	6.5 kda glycine-rich antifreeze protection	0,000005			
AMC58264		No	No	Extracellular 2.005 *	3e4vA	27,54	9	No string found	No	No	No	No	c4qysA	**PDB header:**lyase	39,3
														Chain: A: **PDB Molecule:**tryptophan synthase beta chain 2	
														PDBTitle: trpb2 enzymes	
AMC58272		3,4-dihydroxy-2-butanone 4-phosphate synthase	DASH complex subunit Dad2	Cytoplasmic 3.089 *	1knzB	20,79	5,7	No String Found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	no	No hits with confidence > 5%	
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0			
AMC58275		Diadenosine tetraphosphate (Ap4A) hydrolase or other HIT family hydrolase	HIT domain	Cytoplasmic 3.183 *	1y23B	28,99	0	RN08_0848	3p0t	B	Uncharacterized protein	0	c3p0tB	**PDB header:**unknown function	100
									3p0t	A	Uncharacterized protein	0		**Chain:** B: **PDB Molecule:**uncharacterized protein	
									7mqw	B	HIT family protein	0		**PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis	
									7mqw	A	HIT family protein	0			
									3lb5	D	Hit-like protein involved in cell-cycle regulation	0			
									3lb5	C	Hit-like protein involved in cell-cycle regulation	0	c3lb5B	**PDB header:**cell cycle	100
									2eo4	A	150aa long hypothetical histidine triad nucleotide-binding	0		**Chain:** B: **PDB Molecule:**hit-like protein involved in cell-cycle regulation	
									3l7x	A	Putative Hit-like protein involved in cell-cycle regulation	0,000000001		**PDBTitle:** crystal structure of hit-like protein involved in cell-cycle2	

														regulation from bartonella henselae with unknown ligand	
									3o0m	B	HIT family protein	0,000000002			
									3o0m	A	HIT family protein	0,000000002			
									1y23	E	Histidine triad protein	0,000000003	d1y23a	**Fold:** HIT-like	100
									1y23	D	Histidine triad protein	0,000000003		**Superfamily:** HIT-like	
									3oxk	A	Putative histidine triad family proteins	0,000000008		**Family:** HIT (HINT, histidine triad) family of protein kinase-interacting proteins	
									3omf	A	Putative histidine triad family proteins	0,000000008			
									3imi	D	HIT family protein	0,00000001			
									3imi	C	HIT family protein	0,00000001	c3o0mB	**PDB header:**hydrolase	100
									3o1z	A	Histidine triad nucleotide-binding (hHINT) proteins	0,00000001		**Chain:** B: **PDB Molecule:**hit family protein	
									6rhn	A	HISTIDINE TRIAD NUCLEOTIDE-BINDING (HHINT) PROTEINS	0,00000002		**PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis	
									5rhn	A	HISTIDINE TRIAD NUCLEOTIDE-BINDING (HHINT) PROTEINS	0,00000002			
									6yqm	BBB	Histidine triad nucleotide-binding (hHINT) proteins	0,0000002			
									6yqm	AAA	Histidine triad nucleotide-binding (hHINT) proteins	0,0000002	c2eo4A	**PDB header:**hydrolase	100
									1kpf	A	PROTEIN KINASE C INTERACTING PROTEIN	0,0000002		**Chain:** A: **PDB Molecule:**150aa long hypothetical histidine triad nucleotide-binding	

									1kpc	D	HUMAN PROTEIN KINASE C INTERACTIN...	0,0000002		**PDBTitle:** crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000007			
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000007			
													c3l7xA	**PDB header:**cell cycle	100
														Chain: A: **PDB Molecule:**putative hit-like protein involved in cell-cycle	
														PDBTitle: the crystal structure of smu.412c from streptococcus mutans ua159	
													c3imiB	**PDB header:**structural genomics, unknown function	100
														Chain: B: **PDB Molecule:**hit family protein	
														PDBTitle: 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'	
													c3ksvA	**PDB header:**unknown function	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: hypothetical protein from leishmania major	
													c3n1tE	**PDB header:**hydrolase	100
														Chain: E: **PDB Molecule:**hit-like protein hint	
														PDBTitle: crystal structure of the h101a mutant echint gmp complex	
													c6iq1A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**adenosine 5'-monophosphoramidase	
														PDBTitle: crystal structure of histidine triad nucleotide-binding protein from2 candida albicans	
													d1rzya	**Fold:** HIT-like	100

														Superfamily: HIT-like	
														Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins	
													d1kpfa	**Fold:** HIT-like	
														Superfamily: HIT-like	
														Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins	
													d1emsa1	**Fold:** HIT-like	100
														Superfamily: HIT-like	
														Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins	
													c3r6fA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**hit family protein	
														PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi	
AMC58278		SnoaL-like domain This family contains a large number of proteins that share the SnoaL fold.	SnoaL-like domain	Cytoplasmic 3.729 *	2q9uA	18,12	0,051	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c3i0yC	**PDB header:**isomerase	99
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** C: **PDB Molecule:**putative polyketide cyclase	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002		**PDBTitle:** crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002			
AMC58290		S-formylglutathione hydrolase FrmB [Defense mechanisms]	Putative esterase	Membrane 2.113 *	2uz0A	18,8	0,000000015	No string found	No	No	No	No	c4rgyA	**PDB header:**hydrolase	100

														Chain: A: **PDB Molecule:**esterase	
														PDBTitle: structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library	
													c3ls2D	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**s-formylglutathione hydrolase	
														PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125	
													c3azqA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**aminopeptidase	
														PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg	
													c3i6yA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**esterase apc40077	
														PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica	
AMC58291		DNA-binding transcriptional regulator YbjK [Transcription]	Bacterial regulatory proteins, tetR family	Cytoplasmic 2.148 *	2dg8B	22,03	0,0045	No string found	3iuv	A	uncharacterized TetR family protein	0,0000007	c3iuvA	**PDB header:**structural genomics, unknown function	99,7
									3htj	B	EbrA repressor	0,0000007		**Chain:** A: **PDB Molecule:**uncharacterized tetr family protein	
									3htj	A	EbrA repressor	0,0000007		**PDBTitle:** the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3	
									3kkd	C	transcriptional regulator	0,000003			
									3kkd	B	transcriptional regulator	0,000003			

									2dg8	D	putative tetR-family transcriptional regulatory gene	0,000003			
									2dg8	C	putative tetR-family transcriptional regulatory gene	0,000003			
									7aco	B	HTH-type transcriptional regulator	0,000006			
									7aco	A	HTH-type transcriptional regulator	0,000006			
AMC58305		L-ascorbate metabolism protein UlaG, beta-lactamase superfamily	Beta-lactamase superfamily domain	Cytoplasmic 4.386 *	1vjnA	15,09	0,0000007	No string found	6bo4	C	Transient receptor potential cation channel	0,000003	c4qn9A	**PDB header:**hydrolase	100
									6bo4	B	Transient receptor potential cation channel	0,000003		**Chain:** A: **PDB Molecule:**n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase	
									6bo4	D	Transient receptor potential cation channel	0,000003		**PDBTitle:** structure of human nape-pld	
									6bo4	A	Transient receptor potential cation channel	0,000003			
													c3x30A	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**upf0173 metal-dependent hydrolase tm_1162	
														PDBTitle: crystal structure of metallo-beta-lactamase from thermotoga maritima	
													c3bv6D	**PDB header:**hydrolase	100
														Chain: D: **PDB Molecule:**metal-dependent hydrolase	
														PDBTitle: crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold	
													c6hrgA	**PDB header:**hydrolase	100
														Chain: A: **PDB Molecule:**upf0173 metal-dependent hydrolase igni_1254	
														PDBTitle: structure of igni18, a novel metallo hydrolase from the2	

														hyperthermophilic archaeon ignicoccus hospitalis kin4/i	
													c6l7gB	**PDB header:**metal binding protein	100
														Chain: B: **PDB Molecule:**upf0173 metal-dependent hydrolase c7p97_11315	
														PDBTitle: metallo beta-lactamase fold protein (camp bound)	
													c2wylF_	**PDB header:**hydrolase	100
														Chain: F: **PDB Molecule:**l-ascorbate-6-phosphate lactonase ulag	
														PDBTitle: apo structure of a metallo-b-lactamase	
AMC58311		Flavin-utilizing monoxygenases	Family of unknown function (DUF6515)	Membrane 1.930 *	3c8nA	22,25	0	RN08_0458	3rao	B	Putative Luciferase-like monooxygenase	0	c6lr5B_	**PDB header:**oxidoreductase	100
									3rao	A	Putative Luciferase-like monooxygenase	0		**Chain:** B: **PDB Molecule:**hexachlorobenzene oxidative dehalogenase	
									5lxe	B	F420-dependent glucose-6-phosphate dehydrogenase (FGD1)	0		**PDBTitle:** hexachlorobenzene monooxygenase (hcba1) from nocardioides sp. strain2 pd653 complexed with fmn	
									5lxe	A	F420-dependent glucose-6-phosphate dehydrogenase (FGD1)	0			
									3c8n	D	Probable F420-dependent glucose-6-phosphate dehydrogenase (FGD1)	0			
									3c8n	C	Probable F420-dependent glucose-6-phosphate dehydrogenase (FGD1)	0	c3c8nB	**PDB header:**oxidoreductase	100
									3b4y	B	PROBABLE F420-DEPENDENT GLUCOSE-6-PHOSPHATE DEHYDROGENASE (FGD1)	0		**Chain:** B: **PDB Molecule:**probable f420-dependent glucose-6-phosphate dehydrogenase	
									3b4y	A	PROBABLE F420-DEPENDENT GLUCOSE-6-PHOSPHATE DEHYDROGENASE (FGD1)	0		**PDBTitle:** crystal structure of apo-fgd1 from mycobacterium tuberculosis	
									7bip	B	Luciferase-like monooxygenase	0			

									7bip	A	Luciferase-like monooxygenase	0			
									1nqk	A	Alkanesulfonate monooxygenase	0	c7bipB	**PDB header:**oxidoreductase	100
									1m41	B	FMNH2-dependent alkanesulfonate monooxygenase	0		**Chain:** B: **PDB Molecule:**luciferase-like monooxygenase	
									1m41	A	FMNH2-dependent alkanesulfonate monooxygenase	0		**PDBTitle:** crystal structure of monooxygenase rslo1 from streptomyces2 bottropensis	
									7k64	H	Alkanesulfonate monooxygenase	0,0000000001			
									7k64	G	Alkanesulfonate monooxygenase	0,0000000001			
									1ezw	A	COENZYME-F420-DEPENDENT N5,N10-METHYLENETETRAHYDROMETHANOPTERIN DEHYDROGENASE	0,0000000003	c3raoB	**PDB header:**structural genomics, unknown function	100
									1rhc	A	F420-dependent alcohol dehydrogenase	0,0000000005		**Chain:** B: **PDB Molecule:**putative luciferase-like monooxygenase	
									6teg	AAA	Pyrimidine monooxygenase RutA	0,000000003		**PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.	
									6tef	AAA	Pyrimidine monooxygenase RutA	0,000000003			
									1z69	D	Coenzyme-F420-dependent N(5),N(10)-methylenetetrahydromethanopterin dehydrogenase	0,00000007			
									1z69	C	Coenzyme-F420-dependent N(5),N(10)-methylenetetrahydromethanopterin dehydrogenase	0,00000007	d1ezwa	**Fold:** TIM beta/alpha-barrel	100
									7oh2	B	Alkanesulfonate monooxygenase	0,000001		**Superfamily:** Bacterial luciferase-like	
									7oh2	A	Alkanesulfonate monooxygenase	0,000001		**Family:** F420 dependent oxidoreductases	
									6ak1	B	Dimethyl-sulfide monooxygenase	0,000003			

									6ak1	A	Dimethyl-sulfide monooxygenase	0,000003			
									3sdo	B	Nitrilotriacetate monooxygenase	0,000009	c2b81D	**PDB header:**oxidoreductase	100
									3sdo	A	Nitrilotriacetate monooxygenase	0,000009		**Chain:** D: **PDB Molecule:**luciferase-like monooxygenase	
														PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus	
													c2i7gA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**monooxygenase	
														PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens	
													c7k14C	**PDB header:**flavoprotein, oxidoreductase	100
														Chain: C: **PDB Molecule:**alkanesulfonate monooxygenase	
														PDBTitle: ternary soak structure of alkanesulfonate monooxygenase msud from2 pseudomonas fluorescens with fmn and methanesulfonate	
													d1nqka	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Bacterial luciferase-like	
														Family: Ssud-like monoxygenases	
													c1z69D	**PDB header:**oxidoreductase	100
														Chain: D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)-	
														PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420	
													c5w4zA	**PDB header:**flavoprotein	100
														Chain: A: **PDB Molecule:**riboflavin lyase	

														PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin	
													c5wanA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**pyrimidine monooxygenase ruta	
														PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway	
													d1rhca	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Bacterial luciferase-like	
														Family: F420 dependent oxidoreductases	
													c7jv3D	**PDB header:**flavoprotein, oxidoreductase	100
														Chain: D: **PDB Molecule:**alkanesulfonate monooxygenase	
														PDBTitle: crystal structure of alkanesulfonate monooxygenase msud from2 pseudomonas fluorescens	
													c6ak1B	**PDB header:**oxidoreductase	100
														Chain: B: **PDB Molecule:**dimethyl-sulfide monooxygenase	
														PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans	
													c7oh2A	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**alkanesulfonate monooxygenase	
														PDBTitle: crystal structure of fmnh2-dependent monooxygenase for oxidative2 desulfurization of sulfoquinovose	
													c5tlcA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**dibenzothiophene desulfurization enzyme a	
														PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b	

													c3sdoB	**PDB header:**oxidoreductase	100
														Chain: B: **PDB Molecule:**nitrilotriacetate monooxygenase	
														PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei	
													c1tvlA	**PDB header:**oxidoreductase	100
														Chain: A: **PDB Molecule:**protein ytnj	
														PDBTitle: structure of ytnj from bacillus subtilis	
													d1tvla	**Fold:** TIM beta/alpha-barrel	100
														Superfamily: Bacterial luciferase-like	
														Family: Ssud-like monoxygenases	
AMC58316		Uncharacterized protein, linocin/CFP 29 family	Manganese-stabilising protein / photosys	Cytoplasmic 4.334 *	3dktA	34,72	0	No string found	7boj	A	29 kDa antigen Cfp29	e-125	c6i9gF_	**PDB header:**virus like particle	
									6i9g	O	Linocin-M18	e-122		**Chain:** F: **PDB Molecule:**linocin-m18	
									7oeu	E	Linocin_M18 bacteriocin protein	0		**PDBTitle:** crystal structure of encapsulin from mycolicibacterium hassiacum	
									7oeu	D	Linocin_M18 bacteriocin protein	0			
									7mu1	A	Maritimacin	0			
									7lik	A	Maritimacin	0	c7oeuE	**PDB header:**virus like particle	
									6wkv	X	Encapsulin	0		**Chain:** E: **PDB Molecule:**linocin_m18 bacteriocin protein	
									6wkv	W	Encapsulin	0		**PDBTitle:** model of open pentamer of the haliangium ochraceum encapsulin from2 symmetry expansion of icosahedral single particle reconstruction	

									1nth	A	Monomethylamine methyltransferase	0,00000005			
									1l2q	A	monomethylamine methyltransferase	0,00000005			
									6nj8	D	Encapsulating protein for a DyP-t	0,0000003	c3dktD	**PDB header:**structural protein/virus like particle	
									6nj8	C	Encapsulating protein for a DyP-t	0,0000003		**Chain:** D: **PDB Molecule:**maritimacin	
									7s4q	C	EncA	0,0000007		**PDBTitle:** crystal structure of thermotoga maritima encapsulin	
									7s4q	B	EncA	0,0000007			
									4pt2	B	Encapsulin protein	0,0000007			
									4pt2	A	Encapsulin protein	0,0000007	c4pt2B	**PDB header:**virus like particle	
														Chain: B: **PDB Molecule:**encapsulin protein	
														PDBTitle: myxococcus xanthus encapsulin protein (enca)	
													c6nj8D	**PDB header:**metal transport	
														Chain: D: **PDB Molecule:**encapsulating protein for a dyp-type peroxidase	
														PDBTitle: encapsulin iron storage compartment from quasibacillus thermotolerans	
													c2e0zA	**PDB header:**virus like particle	
														Chain: A: **PDB Molecule:**virus-like particle	
														PDBTitle: crystal structure of virus-like particle from pyrococcus2 furiosus	
AMC58319		Glyoxalase-like domain	No	Cytoplasmic 4.570 *	2rbbA	19,05	0,011	No string found	1nth	A	Monomethylamine methyltransferase	0,000002	c4lqbA	**PDB header:**unknown function	99,8

									1l2q	A	monomethylamine methyltransferase	0,000002		**Chain: A: PDB Molecule:**uncharacterized protein	
														PDBTitle: crystal structure of uncharacterized protein kfla3161	
AMC58326		DinB superfamily The DinB family are an uncharacterized family of potential enzymes	Bacterial SCP ortholog	Extracellular 1.767 *	2qztB	22,45	0,032	No string found	4zy7	B	Uncharacterized protein MSMEG_5817	0,0000000003	c4nssA	**PDB header:**unknown function	99,9
									4zy7	A	Uncharacterized protein MSMEG_5817	0,0000000003		**Chain: A: PDB Molecule:**mycobacterial protein	
									4nss	B	Mycobacterial protein	0,0000000003		**PDBTitle:** a structural and functional investigation of a novel protein from2 mycobacterium smegmatis implicated in mycobacterial macrophage3 survivability	
									4nss	A	Mycobacterial protein	0,0000000003			
AMC58330		Protein of unknown function (DUF3073)	Protein of unknown function (DUF3073)	Extracellular 2.401 *	2e5tA	34,48	7,2	No string found	No	No	No	No	c1trlB	**PDB header:**hydrolase (metalloprotease)	26,4
														Chain: B: PDB Molecule:thermolysin fragment 255 - 316	
														PDBTitle: nmr solution structure of the c-terminal fragment 255-316 of2 thermolysin: a dimer formed by subunits having the native structure	
AMC58335		heme-binding beta-barrel domain of human THAP4	THAP4-like, heme-binding beta-barrel dom	Cytoplasmic 3.452 *	2fwvA	95	0	RN08_0908	7bbm	A	UPF0678 fatty acid-binding protein	0,000000005	c2fwvA	**PDB header:**structural genomics, unknown function	100
									3emm	A	Uncharacterized protein At1g79260	0,000000008		**Chain: A: PDB Molecule:**hypothetical protein mtubf_01000852	
									2q4n	A	Uncharacterized protein At1g79260	0,000000008		**PDBTitle:** crystal structure of rv0813	
									2a13	A	At1g79260	0,000000008			

									4ymy	A	UPF0678 fatty acid-binding protein	0,00000002			
									3wje	B	UPF0678 fatty acid-binding protein	0,00000005	d2fr2a1	**Fold:** Lipocalins	100
									1nth	A	Monomethylamine methyltransferase	0,000002		**Superfamily:** Lipocalins	
									1l2q	A	monomethylamine methyltransferase	0,000002		**Family:** Rv2717c-like	
													d2a13a1	**Fold:** Lipocalins	100
														Superfamily: Lipocalins	
														Family: Rv2717c-like	
													c3ia8A	**PDB header:**metal binding protein	100
														Chain: A: **PDB Molecule:**thap domain-containing protein 4	
														PDBTitle: the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens	
AMC58348		DNA-binding transcriptional regulator, AcrR family	Glycosyl hydrolase catalytic core	Membrane 1.984 *	2of7A	18,95	0,0036	No string found	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002	c3e7qB	**PDB header:**transcription regulator	99,9
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000002		**Chain:** B: **PDB Molecule:**transcriptional regulator	
														PDBTitle: the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1	
AMC58353		TIGR04255 family protein	No	Cytoplasmic 2.848 *	1qnaB	10,33	1,8	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	d1f4nb	**Fold:** ROP-like	64,9
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Superfamily:** ROP protein	
														Family: ROP protein	

AMC58359		No	No	Membrane 2.784 *	3b9wA	22,77	4	No string foumd	No	No	No	No	c5gpdA	**PDB header:**dna binding protein	28,7
														Chain: A: **PDB Molecule:**sterol regulatory element-binding protein 1	
														PDBTitle: crystal structure of the binding domain of srebp from fission yeast	
AMC58360		Predicted nucleotidyltransferase	Nucleotidyl transferase AbiEii toxin, Ty	Extracellular 1.849 *	1a04A	15,1	4,5	RN08_3582	1nth	A	Monomethylamine methyltransferase	0,000004	c6j7nA	**PDB header:**toxin	98,3
									1l2q	A	monomethylamine methyltransferase	0,000004		**Chain:** A: **PDB Molecule:**guanylyltransferase-like toxin	
														PDBTitle: crystal structure of toxin tglt (unusual type guanylyltransferase-like2 toxin, rv1045) mutant d82a co-expressed with taka from mycobacterium3 tuberculosis	
AMC58361		Uncharacterized protein	Transcriptional regulator, AbiEi antitox	Cytoplasmic 3.414 *	2o3iA	14,65	5,5	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c2oqgA	**PDB header:**transcription	96,9
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,00000004		**PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,00000004			
									1nth	A	Monomethylamine methyltransferase	0,000007			
									1l2q	A	monomethylamine methyltransferase	0,000007			
AMC58363		Methyltransferase domain This family appears to have methyltransferase activity.	Methyltransferase domain	Cytoplasmic 4.069 *	3busA	26,51	0,000008	RN08_1569	3mgg	B	Methyltransferase	0	c6uvqA	**PDB header:**transferase	100

									3mgg	A	Methyltransferase	0		**Chain:** A: **PDB Molecule:**d-glucose o-methyltransferase	
									6uak	A	SAM dependent methyltransferase L	0,0000000006		**PDBTitle:** crystal structure of apo atmm	
									4pne	B	Methyltransferase-like protein	0,0000000007			
									4pne	A	Methyltransferase-like protein	0,0000000007			
									5f8f	C	Methyltransferase	0,0000003	c5wp5A	**PDB header:**transferase	100
									5f8f	B	Methyltransferase	0,0000003		**Chain:** A: **PDB Molecule:**phosphomethylethanolamine n-methyltransferase 2	
									5gm2	R	O-methylransferase	0,0000006		**PDBTitle:** arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah	
									5gm2	Q	O-methylransferase	0,0000006			
									2glu	B	ycgJ	0,000001			
									2glu	A	ycgJ	0,000001	c3mggB	**PDB header:**transferase	100
									1xxl	B	YcgJ protein	0,000001		**Chain:** B: **PDB Molecule:**methyltransferase	
									1xxl	A	YcgJ protein	0,000001		**PDBTitle:** crystal structure of methyl transferase from methanosarcina mazei	
									7qcc	A	Methyltransferase-like 27	0,000001			
									7qcb	A	Methyltransferase-like 27	0,000001			
									6uwd	A	D-glucose O-methyltransferase	0,000002	d2gh1a1	**Fold:** S-adenosyl-L-methionine-dependent methyltransferases	100
									6uvq	B	D-glucose O-methyltransferase	0,000006		**Superfamily:** S-adenosyl-L-methionine-dependent methyltransferases	

									3sm3	A	SAM-dependent methyltransferases	0,000000004		**Family:** BC2162-like	
									3d2l	D	SAM-dependent methyltransferase	0,000000004			
													c5w7kA_	**PDB header:**transferase	100
														Chain: A: **PDB Molecule:**oxag	
														PDBTitle: crystal structure of oxag	
AMC58375		No	No	Cytoplasmic 3.559 *	2i3eA	15,26	1,3	No string found	No	No	No	No	c3kngA	**PDB header:**oxidoreductase	70,3
														Chain: A: **PDB Molecule:**snoab	
														PDBTitle: crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution	
AMC58377		Ligand-binding SRPBCC domain of an uncharacterized subfamily of proteins	YetA-like protein	Cytoplasmic 3.808 *	2d4rA	17,01	0,000073	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c5z8oA	**PDB header:**unknown function	99,9
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**cyclase/dehydrase	
									5z8o	B	Cyclase/dehydrase	0		**PDBTitle:** structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis	
									5z8o	A	Cyclase/dehydrase	0			
AMC58379		Ligand-binding SRPBCC domain of an uncharacterized subfamily of proteins	Polyketide cyclase / dehydrase and lipid	Cytoplasmic 4.219 *	2d4rA	19,67	0,0044	No string found	No	No	No	No	c5z8oA_	**PDB header:**unknown function	99,9
														Chain: A: **PDB Molecule:**cyclase/dehydrase	
														PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis	

AMC58380		Ligand-binding SRPBCC domain of an uncharacterized subfamily of proteins	Polyketide cyclase / dehydrase and lipid	Cytoplasmic 3.547 *	2d4rA	20,55	0,0001	No string found	No	No	No	No	d2rera1	**Fold:** TBP-like	99,9
														Superfamily: Bet v1-like	
														Family: oligoketide cyclase/dehydrase-like	
AMC58385		Helicase conserved C-terminal domain	WYL domain	Membrane 2.841 *	2nvoA	11,89	1,4	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c6sj9A	**PDB header:**transcription	98,6
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain:** A: **PDB Molecule:**proteasome accessory factor b/c (pafbc)	
									1nth	A	Monomethylamine methyltransferase	0,000006		**PDBTitle:** proteasome accessory factor b/c (pafbc) of arthrobacter aurescens	
									1l2q	A	monomethylamine methyltransferase	0,000006			
AMC58386		No	No	Extracellular 2.479 *	2p3hA	22,22	0,42	No string found	7qho	X	Actinobacterial supercomplex, subu	0,0000006	c7q21V	**PDB header:**electron transport	100
									7qho	K	Actinobacterial supercomplex, subu	0,0000006		**Chain:** V: **PDB Molecule:**actinobacterial supercomplex, subunit c (ascc)	
														PDBTitle: iii2-iv2 respiratory supercomplex from corynebacterium glutamicum	
AMC58401		Protein of unknown function (DUF3027)	Protein of unknown function (DUF3027)	Extracellular 1.399 *	3citA	16,15	4,2	No string found	7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000005	c3d0fA	**PDB header:**transferase	57,6
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000005		**Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca	
														PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718	

AMC58402		Protein of unknown function (DUF3027)	Protein of unknown function (DUF3027)	Extracellular 3.183 *	1iugA	22,73	2,4	No string found	1nth	A	Monomethylamine methyltransferase	0,000001	d1js2a	**Fold:** HIPIP (high potential iron protein)	47,2
									1l2q	A	monomethylamine methyltransferase	0,000001		**Superfamily:** HIPIP (high potential iron protein)	
														Family: HIPIP (high potential iron protein)	
AMC58408		Protein of unknown function (DUF3027)	Protein of unknown function (DUF3071)	Cytoplasmic 3.936 *	1ixrB	20,86	1,4	RN08_2874	No	No	No	No	c3fmyA	**PDB header:**dna binding protein	89,9
														Chain: A: **PDB Molecule:**hth-type transcriptional regulator mqsa	
														PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)	
AMC58410		P-aminobenzoate N-oxygenase AurF	P-aminobenzoate N-oxygenase AurF	Cytoplasmic 3.997 *	3chtA	16,39	0,01	No string found	1nth	A	Monomethylamine methyltransferase	0,00000002	c3chtA	**PDB header:**oxidoreductase	100
									1l2q	A	monomethylamine methyltransferase	0,00000002		**Chain:** A: **PDB Molecule:**p-aminobenzoate n-oxygenase	
									7b1n	B	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000001		**PDBTitle:** crystal structure of di-iron aurf with partially bound ligand	
									7b1n	A	Cdp-diacylglycerol--serine o-phosphatidyltransferase	0,000001			
													c5hyhA	**PDB header:**metal binding protein	100
														Chain: A: **PDB Molecule:**uncharacterized protein	
														PDBTitle: cmli (chemically reduced state), arylamine oxygenase of2 chloramphenicol biosynthetic pathway	

AMC58414		Bacterial Ig domain This entry represents a wide variety of bacterial Ig domains.	Bacterial Ig domain	Extracellular 3.484 *	2ddrC	52,86	0,000012	No string found	7bzv	B	2-aminomuconic 6-semialdehyde dehydrogenase	0	c5uvgA	**PDB header:**hydrolase	100
									7bzv	A	2-aminomuconic 6-semialdehyde dehydrogenase	0		**Chain: A: PDB Molecule:**sphingomyelin phosphodiesterase 3,sphingomyelin	
									1nth	A	Monomethylamine methyltransferase	0,00000004		**PDBTitle:** crystal structure of the human neutral sphingomyelinase 2 (nsmase2)2 catalytic domain with insertion deleted and calcium bound	
									1l2q	A	monomethylamine methyltransferase	0,00000004			
AMC58418		Adenylate cyclase, class 3 [Signal transduction mechanisms]	Adenylate and Guanylate cyclase catalyti	Cytoplasmic 2.564 *	1fx4A	26,52	0	No string found	4wp3	F	Ma1120	0,0000000002	d1fx4a	**Fold:** Ferredoxin-like	100
									4wp3	E	Ma1120	0,0000000002		**Superfamily:** Nucleotide cyclase	
									1ybu	D	lipJ	0,00000002		**Family:** Adenylyl and guanylyl cyclase catalytic domain	
									1ybu	C	lipJ	0,00000002			
									1ybt	D	hydrolase, alpha/beta hydrolase fold	0,00000002			
									1ybt	C	hydrolase, alpha/beta hydrolase fold	0,00000002	d1fx2a	**Fold:** Ferredoxin-like	100
									5d15	B	Cyclase	0,00000003		**Superfamily:** Nucleotide cyclase	
									5d15	A	Cyclase	0,00000003		**Family:** Adenylyl and guanylyl cyclase catalytic domain	
									4wpa	B	Ma1120	0,00000003			
									4wpa	A	Ma1120	0,00000003			

									5d0h	B	Cyclase	0,0000003	c1ybuA	**PDB header:**hydrolase	100
									5d0h	A	Cyclase	0,0000003		**Chain:** A: **PDB Molecule:**lipj	
														PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.	
													c4wp3E	**PDB header:**lyase	100
														Chain: E: **PDB Molecule:**ma1120	
														PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type	
													c6fhtB	**PDB header:**lyase	100
														Chain: B: **PDB Molecule:**bacteriophytochrome,adenylate cyclase	
														PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form	
													c3mr7B	**PDB header:**hydrolase	100
														Chain: B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold	
														PDBTitle: crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi	
													c4yusA	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**family 3 adenylate cyclase	
														PDBTitle: crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form	
													c7r65C	**PDB header:**transferase	100
														Chain: C: **PDB Molecule:**adenylate/guanylate cyclase	

														PDBTitle: crystal structure of a bacterial cyclic ump synthase from burkholderia2 cepacia lk29	
													c2w01C	**PDB header:**lyase	100
														Chain: C: **PDB Molecule:**adenylate cyclase	
														PDBTitle: crystal structure of the guanylyl cyclase cya2	
													d1wc1a	**Fold:** Ferredoxin-like	100
														Superfamily: Nucleotide cyclase	
														Family: Adenylyl and guanylyl cyclase catalytic domain	
													c1wc6B	**PDB header:**lyase	100
														Chain: B: **PDB Molecule:**adenylate cyclase	
														PDBTitle: soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate	
													c5o5kC	**PDB header:**membrane protein	100
														Chain: C: **PDB Molecule:**adenylate cyclase	
														PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain	
													c6patB	**PDB header:**signaling protein	100
														Chain: B: **PDB Molecule:**soluble guanylyl cyclase beta-1 subunit	
														PDBTitle: active state of manduca sexta soluble guanylate cyclase	
													c3r5gB	**PDB header:**lyase	100
														Chain: B: **PDB Molecule:**cyab	
														PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa	
													c2wz1B	**PDB header:**lyase	100

														Chain: B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1	
														PDBTitle: structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.	
													c6jt1A	**PDB header:**signaling protein	100
														Chain: A: **PDB Molecule:**guanylate cyclase soluble subunit alpha-1	
														PDBTitle: structure of human soluble guanylate cyclase in the heme oxidised2 state	
													c5nbyA	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**beta subunit of photoactivated adenylyl cyclase	
														PDBTitle: structure of a bacterial light-regulated adenylyl cylcase	
													c4cllA_	**PDB header:**lyase	100
														Chain: A: **PDB Molecule:**adenylate cyclase type 10	
														PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate	
													c6jt1B	**PDB header:**signaling protein	100
														Chain: B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1	
														PDBTitle: structure of human soluble guanylate cyclase in the heme oxidised2 state	

SUUPPLEMENTARY TABLE 1

#node1	node2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
(3R)-hydroxyacyl-ACP dehydratase	RN08_0563	1806.RN08_0710	1806.RN08_0563	0	0	0.722	0.610	0	0	0	0.547	0.449
(3R)-hydroxyacyl-ACP dehydratase	RN08_0711	1806.RN08_0710	1806.RN08_0711	0.084	0	0.683	0	0.212	0.999	0	0.209	0.999
(3R)-hydroxyacyl-ACP dehydratase	RN08_0712	1806.RN08_0710	1806.RN08_0712	0.879	0	0.770	0.923	0.212	0	0	0.825	0.912

Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_0081	1806.RN08_0488	1806.RN08_0081	0.046	0	0	0	0.121	0	0.826	0	0.841
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_0489	1806.RN08_0488	1806.RN08_0489	0.957	0	0.685	0	0.480	0	0.993	0.986	0.999
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_1448	1806.RN08_0488	1806.RN08_1448	0.066	0	0.155	0	0.110	0	0.666	0	0.734
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_1748	1806.RN08_0488	1806.RN08_1748	0.067	0	0	0	0.277	0	0.993	0	0.995
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_1785	1806.RN08_0488	1806.RN08_1785	0.048	0	0	0	0.272	0	0.993	0	0.995
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_1786	1806.RN08_0488	1806.RN08_1786	0.048	0	0	0	0	0	0.993	0	0.993
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_2027	1806.RN08_0488	1806.RN08_2027	0.042	0	0.154	0.216	0	0	0.961	0.570	0.980
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_2590	1806.RN08_0488	1806.RN08_2590	0.067	0	0	0	0	0	0.993	0	0.993
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_2892	1806.RN08_0488	1806.RN08_2892	0.067	0	0	0	0.167	0	0	0.374	0.471
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_2893	1806.RN08_0488	1806.RN08_2893	0.042	0	0	0.114	0.306	0	0.993	0.729	0.998
Cdp-diacylglycerol--	RN08_3032	1806.RN08_0488	1806.RN08_3032	0.042	0	0	0.210	0	0	0.993	0.891	0.998

serine o-phosphatidyltransferase												
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_3175	1806.RN08_0488	1806.RN08_3175	0.378	0	0	0	0.381	0	0.993	0.082	0.997
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_3353	1806.RN08_0488	1806.RN08_3353	0	0	0.159	0	0.381	0	0.993	0	0.996
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_3690	1806.RN08_0488	1806.RN08_3690	0	0	0.181	0	0	0	0.961	0	0.967
Cdp-diacylglycerol--serine o-phosphatidyltransferase	RN08_4092	1806.RN08_0488	1806.RN08_4092	0.047	0	0.163	0	0	0	0	0.351	0.437
Cyclase	RN08_2590	1806.RN08_2701	1806.RN08_2590	0.043	0	0	0	0	0	0.465	0	0.466
DNA binding protein	RN08_0067	1806.RN08_0063	1806.RN08_0067	0.275	0	0.223	0	0.212	0.999	0	0.153	0.999
DNA binding protein	RN08_2598	1806.RN08_0063	1806.RN08_2598	0.049	0	0.347	0	0	0.258	0	0.153	0.557
DNA binding protein	RN08_2746	1806.RN08_0063	1806.RN08_2746	0	0	0.317	0.391	0	0	0.993	0.799	0.997
DNA binding protein	RN08_3175	1806.RN08_0063	1806.RN08_3175	0.049	0	0.164	0	0	0	0.479	0	0.550
Glucosyl-3-phosphoglycerate phosphatase	RN08_1272	1806.RN08_2682	1806.RN08_1272	0.078	0	0	0	0.381	0	0	0	0.405
Glucosyl-3-phosphoglycerate phosphatase	RN08_1604	1806.RN08_2682	1806.RN08_1604	0.079	0	0.164	0	0	0	0.977	0.202	0.984
Glucosyl-3-phosphoglycerate phosphatase	RN08_1748	1806.RN08_2682	1806.RN08_1748	0	0	0	0	0.381	0	0.258	0	0.521
Glucosyl-3-phosphoglycerate phosphatase	RN08_2680	1806.RN08_2682	1806.RN08_2680	0.957	0	0	0	0.381	0	0	0.807	0.994
Glucosyl-3-phosphoglycerate phosphatase	RN08_2681	1806.RN08_2682	1806.RN08_2681	0.943	0	0	0	0.212	0	0	0.825	0.991
HIT family protein	RN08_2894	1806.RN08_1411	1806.RN08_2894	0	0	0.241	0.325	0	0	0.791	0	0.820

HIT family protein	RN08_4092	1806.RN08_1411	1806.RN08_4092	0.413	0	0.154	0	0	0	0	0	0.482
RN08_0001	RN08_0067	1806.RN08_0001	1806.RN08_0067	0.079	0	0.237	0	0.266	0.766	0	0.982	0.997
RN08_0001	RN08_2598	1806.RN08_0001	1806.RN08_2598	0.067	0	0.253	0	0.267	0	0	0.551	0.740
RN08_0001	RN08_2892	1806.RN08_0001	1806.RN08_2892	0.047	0	0	0	0.529	0	0	0	0.532
RN08_0067	RN08_0001	1806.RN08_0067	1806.RN08_0001	0.079	0	0.237	0	0.266	0.766	0	0.982	0.997
RN08_0067	DNA binding protein	1806.RN08_0067	1806.RN08_0063	0.275	0	0.223	0	0.212	0.999	0	0.153	0.999
RN08_0067	RN08_2598	1806.RN08_0067	1806.RN08_2598	0.092	0	0.452	0	0.466	0.745	0.956	0.311	0.997
RN08_0067	RN08_3314	1806.RN08_0067	1806.RN08_3314	0.042	0	0	0	0	0	0.412	0.094	0.445
RN08_0081	RN08_0438	1806.RN08_0081	1806.RN08_0438	0.078	0	0	0	0	0	0.637	0.104	0.674
RN08_0081	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_0081	1806.RN08_0488	0.046	0	0	0	0.121	0	0.826	0	0.841
RN08_0081	RN08_0949	1806.RN08_0081	1806.RN08_0949	0	0	0	0	0	0	0.626	0	0.626
RN08_0081	RN08_1210	1806.RN08_0081	1806.RN08_1210	0.078	0	0	0	0	0	0.637	0.104	0.674
RN08_0081	RN08_1448	1806.RN08_0081	1806.RN08_1448	0.044	0	0	0	0	0	0.961	0.160	0.966
RN08_0081	RN08_1449	1806.RN08_0081	1806.RN08_1449	0.066	0	0	0	0	0	0.977	0.401	0.986
RN08_0081	RN08_1748	1806.RN08_0081	1806.RN08_1748	0.069	0	0.151	0	0.272	0.199	0.993	0.789	0.999
RN08_0081	RN08_1784	1806.RN08_0081	1806.RN08_1784	0	0	0	0	0	0	0	0.608	0.608
RN08_0081	RN08_1785	1806.RN08_0081	1806.RN08_1785	0	0	0	0	0.112	0	0.826	0.208	0.867
RN08_0081	RN08_1786	1806.RN08_0081	1806.RN08_1786	0	0	0	0	0	0	0.826	0.156	0.847
RN08_0081	RN08_2027	1806.RN08_0081	1806.RN08_2027	0	0	0	0	0	0	0.422	0.055	0.430
RN08_0081	RN08_2431	1806.RN08_0081	1806.RN08_2431	0.047	0	0	0	0	0	0	0.422	0.426
RN08_0081	RN08_2590	1806.RN08_0081	1806.RN08_2590	0	0	0	0	0	0	0.977	0.613	0.991
RN08_0081	RN08_2893	1806.RN08_0081	1806.RN08_2893	0.121	0	0	0	0	0	0.422	0.055	0.478
RN08_0081	RN08_3032	1806.RN08_0081	1806.RN08_3032	0	0	0	0	0	0	0.422	0.055	0.430
RN08_0081	RN08_3313	1806.RN08_0081	1806.RN08_3313	0.047	0	0	0	0	0	0.791	0.098	0.805

RN08_0081	RN08_3314	1806.RN08_0081	1806.RN08_3314	0	0	0	0	0.212	0	0.952	0.424	0.976
RN08_0081	RN08_3353	1806.RN08_0081	1806.RN08_3353	0	0	0	0	0.271	0	0.993	0.862	0.999
RN08_0081	RN08_3690	1806.RN08_0081	1806.RN08_3690	0	0	0	0	0	0	0.993	0	0.993
RN08_0081	RN08_3872	1806.RN08_0081	1806.RN08_3872	0	0	0	0	0	0	0.961	0.046	0.961
RN08_0438	RN08_0081	1806.RN08_0438	1806.RN08_0081	0.078	0	0	0	0	0	0.637	0.104	0.674
RN08_0438	RN08_1210	1806.RN08_0438	1806.RN08_1210	0	0	0.768	0.513	0.212	0	0.961	0.521	0.985
RN08_0438	RN08_1272	1806.RN08_0438	1806.RN08_1272	0.085	0	0.163	0	0.268	0	0.986	0.308	0.994
RN08_0438	RN08_1448	1806.RN08_0438	1806.RN08_1448	0.066	0	0.155	0	0.212	0	0.961	0.181	0.977
RN08_0438	RN08_1449	1806.RN08_0438	1806.RN08_1449	0.049	0	0	0	0.080	0	0.266	0.261	0.462
RN08_0438	RN08_1748	1806.RN08_0438	1806.RN08_1748	0.118	0	0	0	0.298	0	0.986	0.263	0.993
RN08_0438	RN08_2453	1806.RN08_0438	1806.RN08_2453	0.077	0	0	0	0	0.114	0.651	0.068	0.698
RN08_0438	RN08_2590	1806.RN08_0438	1806.RN08_2590	0.066	0	0.213	0	0.212	0	0.607	0.388	0.835
RN08_0438	RN08_2724	1806.RN08_0438	1806.RN08_2724	0.083	0	0	0	0.110	0	0.961	0.105	0.968
RN08_0438	RN08_3314	1806.RN08_0438	1806.RN08_3314	0	0	0	0	0.072	0.114	0.445	0.203	0.588
RN08_0438	RN08_3353	1806.RN08_0438	1806.RN08_3353	0	0	0.161	0	0	0	0.484	0.054	0.555
RN08_0438	RN08_3689	1806.RN08_0438	1806.RN08_3689	0.084	0	0.773	0.492	0.110	0	0.986	0.647	0.995
RN08_0438	RN08_3690	1806.RN08_0438	1806.RN08_3690	0.081	0	0.359	0	0.239	0	0.986	0.234	0.994
RN08_0489	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_0489	1806.RN08_0488	0.957	0	0.685	0	0.480	0	0.993	0.986	0.999
RN08_0489	RN08_1604	1806.RN08_0489	1806.RN08_1604	0	0	0	0	0.161	0	0	0.326	0.410
RN08_0489	RN08_2027	1806.RN08_0489	1806.RN08_2027	0.042	0	0	0	0.074	0.154	0.422	0.261	0.621
RN08_0489	RN08_2453	1806.RN08_0489	1806.RN08_2453	0	0	0.198	0	0	0	0.770	0.054	0.810
RN08_0489	RN08_2893	1806.RN08_0489	1806.RN08_2893	0.042	0	0	0	0.074	0.154	0.422	0.519	0.753
RN08_0489	RN08_3032	1806.RN08_0489	1806.RN08_3032	0.042	0	0	0	0.074	0.154	0.422	0.374	0.679
RN08_0489	RN08_3175	1806.RN08_0489	1806.RN08_3175	0.378	0	0	0	0.246	0	0	0.418	0.703

RN08_0489	RN08_3314	1806.RN08_0489	1806.RN08_3314	0.378	0	0.151	0	0	0	0	0	0.449
RN08_0489	RN08_3872	1806.RN08_0489	1806.RN08_3872	0	0	0.155	0	0.381	0	0	0	0.455
RN08_0563	(3R)-hydroxyacyl-ACP dehydratase	1806.RN08_0563	1806.RN08_0710	0	0	0.722	0.610	0	0	0	0.547	0.449
RN08_0563	RN08_0711	1806.RN08_0563	1806.RN08_0711	0.084	0	0.732	0	0.212	0.915	0	0.852	0.997
RN08_0563	RN08_0712	1806.RN08_0563	1806.RN08_0712	0	0	0.782	0.569	0	0	0	0.676	0.543
RN08_0711	RN08_0563	1806.RN08_0711	1806.RN08_0563	0.084	0	0.732	0	0.212	0.915	0	0.852	0.997
RN08_0711	(3R)-hydroxyacyl-ACP dehydratase	1806.RN08_0711	1806.RN08_0710	0.084	0	0.683	0	0.212	0.999	0	0.209	0.999
RN08_0711	RN08_0712	1806.RN08_0711	1806.RN08_0712	0.887	0	0.727	0	0.212	0.999	0	0.999	0.999
RN08_0711	RN08_3872	1806.RN08_0711	1806.RN08_3872	0	0	0.166	0	0.272	0	0	0.183	0.461
RN08_0712	RN08_0563	1806.RN08_0712	1806.RN08_0563	0	0	0.782	0.569	0	0	0	0.676	0.543
RN08_0712	(3R)-hydroxyacyl-ACP dehydratase	1806.RN08_0712	1806.RN08_0710	0.879	0	0.770	0.923	0.212	0	0	0.825	0.912
RN08_0712	RN08_0711	1806.RN08_0712	1806.RN08_0711	0.887	0	0.727	0	0.212	0.999	0	0.999	0.999
RN08_0949	RN08_0081	1806.RN08_0949	1806.RN08_0081	0	0	0	0	0	0	0.626	0	0.626
RN08_0949	RN08_1449	1806.RN08_0949	1806.RN08_1449	0	0	0	0	0	0	0	0.410	0.410
RN08_0949	RN08_1748	1806.RN08_0949	1806.RN08_1748	0.066	0	0	0	0	0.114	0.946	0.854	0.993
RN08_0949	RN08_2453	1806.RN08_0949	1806.RN08_2453	0	0	0	0	0	0.119	0.991	0.425	0.995
RN08_0949	RN08_3313	1806.RN08_0949	1806.RN08_3313	0	0	0.155	0	0.074	0	0.927	0.657	0.978
RN08_0949	RN08_3314	1806.RN08_0949	1806.RN08_3314	0	0	0.177	0	0.052	0	0.400	0.536	0.754
RN08_0949	RN08_4092	1806.RN08_0949	1806.RN08_4092	0	0	0.143	0	0	0	0.223	0.633	0.734
RN08_1210	RN08_0081	1806.RN08_1210	1806.RN08_0081	0.078	0	0	0	0	0	0.637	0.104	0.674
RN08_1210	RN08_0438	1806.RN08_1210	1806.RN08_0438	0	0	0.768	0.513	0.212	0	0.961	0.521	0.985
RN08_1210	RN08_1272	1806.RN08_1210	1806.RN08_1272	0.085	0	0	0	0.268	0	0.986	0.772	0.998
RN08_1210	RN08_1448	1806.RN08_1210	1806.RN08_1448	0.066	0	0	0	0.212	0	0.961	0.345	0.979
RN08_1210	RN08_1449	1806.RN08_1210	1806.RN08_1449	0.049	0	0	0	0.080	0	0.266	0.414	0.573

RN08_1210	RN08_1748	1806.RN08_1210	1806.RN08_1748	0.118	0	0	0	0.298	0	0.986	0.263	0.993
RN08_1210	RN08_1784	1806.RN08_1210	1806.RN08_1784	0	0	0	0	0.144	0	0	0.376	0.443
RN08_1210	RN08_2431	1806.RN08_1210	1806.RN08_2431	0	0	0.160	0	0	0	0	0.758	0.788
RN08_1210	RN08_2453	1806.RN08_1210	1806.RN08_2453	0.077	0	0	0	0.212	0.114	0.986	0.068	0.990
RN08_1210	RN08_2590	1806.RN08_1210	1806.RN08_2590	0.066	0	0	0	0	0	0.607	0.575	0.830
RN08_1210	RN08_2724	1806.RN08_1210	1806.RN08_2724	0.083	0	0	0	0.110	0	0.961	0.650	0.987
RN08_1210	RN08_3314	1806.RN08_1210	1806.RN08_3314	0	0	0	0	0.072	0.114	0.445	0.584	0.785
RN08_1210	RN08_3353	1806.RN08_1210	1806.RN08_3353	0	0	0	0	0	0	0.484	0.054	0.491
RN08_1210	RN08_3689	1806.RN08_1210	1806.RN08_3689	0.084	0	0.774	0.500	0.110	0	0.986	0.820	0.995
RN08_1210	RN08_3690	1806.RN08_1210	1806.RN08_3690	0.081	0	0.276	0	0.073	0	0.986	0.347	0.993
RN08_1210	RN08_3872	1806.RN08_1210	1806.RN08_3872	0	0	0	0	0	0	0	0.469	0.469
RN08_1272	RN08_0438	1806.RN08_1272	1806.RN08_0438	0.085	0	0.163	0	0.268	0	0.986	0.308	0.994
RN08_1272	RN08_1210	1806.RN08_1272	1806.RN08_1210	0.085	0	0	0	0.268	0	0.986	0.772	0.998
RN08_1272	RN08_1448	1806.RN08_1272	1806.RN08_1448	0.047	0	0	0	0.212	0	0.961	0.299	0.977
RN08_1272	RN08_1449	1806.RN08_1272	1806.RN08_1449	0	0	0	0	0.381	0	0	0.388	0.605
RN08_1272	RN08_1748	1806.RN08_1272	1806.RN08_1748	0	0	0.168	0	0.381	0	0.993	0.233	0.997
RN08_1272	RN08_1785	1806.RN08_1272	1806.RN08_1785	0.048	0	0.173	0	0	0	0	0.346	0.440
RN08_1272	RN08_2590	1806.RN08_1272	1806.RN08_2590	0.080	0	0	0	0	0	0	0.569	0.587
RN08_1272	Glucosyl-3-phosphoglycerate phosphatase	1806.RN08_1272	1806.RN08_2682	0.078	0	0	0	0.381	0	0	0	0.405
RN08_1272	RN08_2724	1806.RN08_1272	1806.RN08_2724	0.044	0	0	0	0	0	0.952	0.548	0.977
RN08_1272	RN08_3313	1806.RN08_1272	1806.RN08_3313	0	0	0	0	0.145	0	0	0.722	0.752
RN08_1272	RN08_3314	1806.RN08_1272	1806.RN08_3314	0.047	0	0	0	0	0	0.439	0.668	0.807
RN08_1272	RN08_3353	1806.RN08_1272	1806.RN08_3353	0	0	0	0	0	0	0.248	0.413	0.540
RN08_1272	RN08_3689	1806.RN08_1272	1806.RN08_3689	0.282	0	0	0	0.323	0	0.993	0.854	0.999
RN08_1272	RN08_3690	1806.RN08_1272	1806.RN08_3690	0.254	0	0	0	0	0	0.308	0.375	0.649

RN08_1448	RN08_0081	1806.RN08_1448	1806.RN08_0081	0.044	0	0	0	0	0	0.961	0.160	0.966
RN08_1448	RN08_0438	1806.RN08_1448	1806.RN08_0438	0.066	0	0.155	0	0.212	0	0.961	0.181	0.977
RN08_1448	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_1448	1806.RN08_0488	0.066	0	0.155	0	0.110	0	0.666	0	0.734
RN08_1448	RN08_1210	1806.RN08_1448	1806.RN08_1210	0.066	0	0	0	0.212	0	0.961	0.345	0.979
RN08_1448	RN08_1272	1806.RN08_1448	1806.RN08_1272	0.047	0	0	0	0.212	0	0.961	0.299	0.977
RN08_1448	RN08_1449	1806.RN08_1448	1806.RN08_1449	0.577	0	0.168	0	0.990	0	0.669	0.903	0.999
RN08_1448	RN08_1748	1806.RN08_1448	1806.RN08_1748	0.069	0	0.234	0	0.244	0.185	0.669	0.914	0.985
RN08_1448	RN08_1782	1806.RN08_1448	1806.RN08_1782	0	0	0.155	0	0.381	0	0	0	0.455
RN08_1448	RN08_1785	1806.RN08_1448	1806.RN08_1785	0.068	0	0.185	0	0	0	0.666	0.080	0.735
RN08_1448	RN08_1786	1806.RN08_1448	1806.RN08_1786	0	0	0.214	0	0	0.144	0.666	0.274	0.815
RN08_1448	RN08_2453	1806.RN08_1448	1806.RN08_2453	0.047	0	0.163	0	0.114	0	0.826	0.353	0.906
RN08_1448	RN08_2590	1806.RN08_1448	1806.RN08_2590	0.066	0	0.185	0	0	0	0.826	0.096	0.864
RN08_1448	RN08_2724	1806.RN08_1448	1806.RN08_2724	0.066	0	0	0	0.111	0	0.991	0.160	0.993
RN08_1448	RN08_3313	1806.RN08_1448	1806.RN08_3313	0.081	0	0.546	0	0.121	0	0	0.199	0.667
RN08_1448	RN08_3314	1806.RN08_1448	1806.RN08_3314	0.378	0	0.364	0.235	0.116	0	0	0.336	0.675
RN08_1448	RN08_3353	1806.RN08_1448	1806.RN08_3353	0.066	0	0	0	0	0	0.647	0.066	0.665
RN08_1448	RN08_3689	1806.RN08_1448	1806.RN08_3689	0.185	0	0	0	0.176	0	0.826	0.438	0.926
RN08_1448	RN08_3690	1806.RN08_1448	1806.RN08_3690	0.132	0	0	0	0.181	0	0.826	0.491	0.929
RN08_1448	RN08_4092	1806.RN08_1448	1806.RN08_4092	0.047	0	0.177	0	0	0	0	0.327	0.426
RN08_1449	RN08_0081	1806.RN08_1449	1806.RN08_0081	0.066	0	0	0	0	0	0.977	0.401	0.986
RN08_1449	RN08_0438	1806.RN08_1449	1806.RN08_0438	0.049	0	0	0	0.080	0	0.266	0.261	0.462
RN08_1449	RN08_0949	1806.RN08_1449	1806.RN08_0949	0	0	0	0	0	0	0	0.410	0.410
RN08_1449	RN08_1210	1806.RN08_1449	1806.RN08_1210	0.049	0	0	0	0.080	0	0.266	0.414	0.573
RN08_1449	RN08_1272	1806.RN08_1449	1806.RN08_1272	0	0	0	0	0.381	0	0	0.388	0.605

RN08_1449	RN08_1448	1806.RN08_1449	1806.RN08_1448	0.577	0	0.168	0	0.990	0	0.669	0.903	0.999
RN08_1449	RN08_1604	1806.RN08_1449	1806.RN08_1604	0.067	0	0.153	0	0.381	0	0	0.161	0.535
RN08_1449	RN08_1748	1806.RN08_1449	1806.RN08_1748	0.069	0	0.151	0.297	0.512	0.106	0.993	0.836	0.999
RN08_1449	RN08_1784	1806.RN08_1449	1806.RN08_1784	0	0	0	0	0.109	0	0	0.689	0.711
RN08_1449	RN08_1785	1806.RN08_1449	1806.RN08_1785	0	0	0	0.141	0.570	0	0	0.209	0.635
RN08_1449	RN08_1786	1806.RN08_1449	1806.RN08_1786	0	0	0	0	0.570	0	0	0.179	0.632
RN08_1449	RN08_2453	1806.RN08_1449	1806.RN08_2453	0.047	0	0	0	0	0.127	0	0.688	0.718
RN08_1449	RN08_2590	1806.RN08_1449	1806.RN08_2590	0.066	0	0.179	0	0	0	0.642	0.395	0.812
RN08_1449	RN08_3313	1806.RN08_1449	1806.RN08_3313	0.091	0	0.192	0	0.290	0	0	0.421	0.658
RN08_1449	RN08_3314	1806.RN08_1449	1806.RN08_3314	0.081	0	0.153	0	0.522	0	0.669	0.322	0.901
RN08_1449	RN08_3689	1806.RN08_1449	1806.RN08_3689	0.068	0	0	0	0	0	0	0.411	0.428
RN08_1449	RN08_3690	1806.RN08_1449	1806.RN08_3690	0	0	0	0	0.110	0	0	0.701	0.723
RN08_1449	RN08_3872	1806.RN08_1449	1806.RN08_3872	0	0	0	0	0	0	0.336	0.462	0.627
RN08_1604	RN08_0489	1806.RN08_1604	1806.RN08_0489	0	0	0	0	0.161	0	0	0.326	0.410
RN08_1604	RN08_1449	1806.RN08_1604	1806.RN08_1449	0.067	0	0.153	0	0.381	0	0	0.161	0.535
RN08_1604	RN08_1748	1806.RN08_1604	1806.RN08_1748	0.076	0	0	0	0.381	0	0	0.121	0.453
RN08_1604	RN08_2598	1806.RN08_1604	1806.RN08_2598	0.105	0	0	0	0.246	0	0	0.651	0.744
RN08_1604	RN08_2680	1806.RN08_1604	1806.RN08_2680	0.067	0	0	0	0	0	0.642	0	0.652
RN08_1604	Glucosyl-3-phosphoglycerate phosphatase	1806.RN08_1604	1806.RN08_2682	0.079	0	0.164	0	0	0	0.977	0.202	0.984
RN08_1604	RN08_3313	1806.RN08_1604	1806.RN08_3313	0.049	0	0	0	0.367	0	0	0.192	0.471
RN08_1748	RN08_0081	1806.RN08_1748	1806.RN08_0081	0.069	0	0.151	0	0.272	0.199	0.993	0.789	0.999
RN08_1748	RN08_0438	1806.RN08_1748	1806.RN08_0438	0.118	0	0	0	0.298	0	0.986	0.263	0.993
RN08_1748	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_1748	1806.RN08_0488	0.067	0	0	0	0.277	0	0.993	0	0.995

RN08_1748	RN08_0949	1806.RN08_1748	1806.RN08_0949	0.066	0	0	0	0	0.114	0.946	0.854	0.993
RN08_1748	RN08_1210	1806.RN08_1748	1806.RN08_1210	0.118	0	0	0	0.298	0	0.986	0.263	0.993
RN08_1748	RN08_1272	1806.RN08_1748	1806.RN08_1272	0	0	0.168	0	0.381	0	0.993	0.233	0.997
RN08_1748	RN08_1448	1806.RN08_1748	1806.RN08_1448	0.069	0	0.234	0	0.244	0.185	0.669	0.914	0.985
RN08_1748	RN08_1449	1806.RN08_1748	1806.RN08_1449	0.069	0	0.151	0.297	0.512	0.106	0.993	0.836	0.999
RN08_1748	RN08_1604	1806.RN08_1748	1806.RN08_1604	0.076	0	0	0	0.381	0	0	0.121	0.453
RN08_1748	RN08_1784	1806.RN08_1748	1806.RN08_1784	0.042	0	0	0	0.457	0.246	0	0.677	0.856
RN08_1748	RN08_1785	1806.RN08_1748	1806.RN08_1785	0.066	0	0	0.118	0.114	0	0.826	0.207	0.867
RN08_1748	RN08_1786	1806.RN08_1748	1806.RN08_1786	0.049	0	0	0	0.118	0	0.826	0.274	0.880
RN08_1748	RN08_2027	1806.RN08_1748	1806.RN08_2027	0	0	0	0	0	0	0.422	0.069	0.439
RN08_1748	RN08_2431	1806.RN08_1748	1806.RN08_2431	0.139	0	0	0	0.073	0.110	0	0.356	0.481
RN08_1748	RN08_2453	1806.RN08_1748	1806.RN08_2453	0.047	0	0	0	0.275	0	0.993	0.981	0.999
RN08_1748	RN08_2590	1806.RN08_1748	1806.RN08_2590	0.048	0	0	0	0.111	0	0.993	0.103	0.994
RN08_1748	Glucosyl-3-phosphoglycerate phosphatase	1806.RN08_1748	1806.RN08_2682	0	0	0	0	0.381	0	0.258	0	0.521
RN08_1748	RN08_2724	1806.RN08_1748	1806.RN08_2724	0.044	0	0	0	0	0	0.991	0.055	0.991
RN08_1748	RN08_2893	1806.RN08_1748	1806.RN08_2893	0	0	0	0	0	0	0.422	0.069	0.439
RN08_1748	RN08_3032	1806.RN08_1748	1806.RN08_3032	0	0	0	0	0	0	0.422	0.069	0.439
RN08_1748	RN08_3313	1806.RN08_1748	1806.RN08_3313	0.118	0	0.493	0	0.246	0.182	0.791	0.857	0.990
RN08_1748	RN08_3314	1806.RN08_1748	1806.RN08_3314	0.118	0	0.255	0	0.277	0	0.993	0.625	0.999
RN08_1748	RN08_3353	1806.RN08_1748	1806.RN08_3353	0.069	0	0	0	0.324	0	0.993	0.156	0.996
RN08_1748	RN08_3689	1806.RN08_1748	1806.RN08_3689	0	0	0	0	0.248	0	0.993	0	0.995
RN08_1748	RN08_3690	1806.RN08_1748	1806.RN08_3690	0.047	0	0	0	0.296	0	0.993	0.075	0.995
RN08_1748	RN08_3872	1806.RN08_1748	1806.RN08_3872	0	0	0.154	0	0.275	0.085	0.993	0.320	0.997
RN08_1748	RN08_4092	1806.RN08_1748	1806.RN08_4092	0.089	0	0	0	0	0	0.389	0.985	0.991
RN08_1782	RN08_1448	1806.RN08_1782	1806.RN08_1448	0	0	0.155	0	0.381	0	0	0	0.455

RN08_1782	RN08_1784	1806.RN08_1782	1806.RN08_1784	0.445	0	0.711	0	0.298	0	0.954	0.857	0.999
RN08_1782	RN08_1785	1806.RN08_1782	1806.RN08_1785	0.453	0	0.726	0	0.274	0	0	0.854	0.982
RN08_1782	RN08_1786	1806.RN08_1782	1806.RN08_1786	0.470	0	0.745	0	0.274	0	0	0.863	0.985
RN08_1782	RN08_2431	1806.RN08_1782	1806.RN08_2431	0.042	0	0.722	0	0.277	0	0.963	0.863	0.999
RN08_1784	RN08_0081	1806.RN08_1784	1806.RN08_0081	0	0	0	0	0	0	0	0.608	0.608
RN08_1784	RN08_1210	1806.RN08_1784	1806.RN08_1210	0	0	0	0	0.144	0	0	0.376	0.443
RN08_1784	RN08_1449	1806.RN08_1784	1806.RN08_1449	0	0	0	0	0.109	0	0	0.689	0.711
RN08_1784	RN08_1748	1806.RN08_1784	1806.RN08_1748	0.042	0	0	0	0.457	0.246	0	0.677	0.856
RN08_1784	RN08_1782	1806.RN08_1784	1806.RN08_1782	0.445	0	0.711	0	0.298	0	0.954	0.857	0.999
RN08_1784	RN08_1785	1806.RN08_1784	1806.RN08_1785	0.577	0	0.781	0	0.145	0	0.826	0.858	0.998
RN08_1784	RN08_1786	1806.RN08_1784	1806.RN08_1786	0.577	0	0.778	0	0.888	0	0.826	0.917	0.999
RN08_1784	RN08_2431	1806.RN08_1784	1806.RN08_2431	0.577	0	0.773	0	0.720	0	0.963	0.978	0.999
RN08_1784	RN08_2598	1806.RN08_1784	1806.RN08_2598	0	0	0	0	0	0.433	0	0	0.433
RN08_1784	RN08_3175	1806.RN08_1784	1806.RN08_3175	0	0	0	0	0.381	0	0	0.093	0.415
RN08_1784	RN08_3313	1806.RN08_1784	1806.RN08_3313	0	0	0.228	0	0.075	0	0	0.647	0.726
RN08_1784	RN08_3314	1806.RN08_1784	1806.RN08_3314	0.081	0	0.299	0	0.146	0	0	0.226	0.517
RN08_1785	RN08_0081	1806.RN08_1785	1806.RN08_0081	0	0	0	0	0.112	0	0.826	0.208	0.867
RN08_1785	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_1785	1806.RN08_0488	0.048	0	0	0	0.272	0	0.993	0	0.995
RN08_1785	RN08_1272	1806.RN08_1785	1806.RN08_1272	0.048	0	0.173	0	0	0	0	0.346	0.440
RN08_1785	RN08_1448	1806.RN08_1785	1806.RN08_1448	0.068	0	0.185	0	0	0	0.666	0.080	0.735
RN08_1785	RN08_1449	1806.RN08_1785	1806.RN08_1449	0	0	0	0.141	0.570	0	0	0.209	0.635
RN08_1785	RN08_1748	1806.RN08_1785	1806.RN08_1748	0.066	0	0	0.118	0.114	0	0.826	0.207	0.867
RN08_1785	RN08_1782	1806.RN08_1785	1806.RN08_1782	0.453	0	0.726	0	0.274	0	0	0.854	0.982
RN08_1785	RN08_1784	1806.RN08_1785	1806.RN08_1784	0.577	0	0.781	0	0.145	0	0.826	0.858	0.998

RN08_1785	RN08_1786	1806.RN08_1785	1806.RN08_1786	0.577	0	0.782	0	0.878	0.999	0.826	0.978	0.999
RN08_1785	RN08_2027	1806.RN08_1785	1806.RN08_2027	0.131	0	0	0	0	0	0.423	0	0.477
RN08_1785	RN08_2431	1806.RN08_1785	1806.RN08_2431	0.577	0	0.776	0	0.571	0	0.826	0.732	0.998
RN08_1785	RN08_2590	1806.RN08_1785	1806.RN08_2590	0	0	0	0	0.274	0	0.993	0.152	0.995
RN08_1785	RN08_2893	1806.RN08_1785	1806.RN08_2893	0.130	0	0	0	0	0	0.423	0	0.477
RN08_1785	RN08_3032	1806.RN08_1785	1806.RN08_3032	0	0	0	0	0	0	0.423	0	0.423
RN08_1785	RN08_3313	1806.RN08_1785	1806.RN08_3313	0.066	0	0.266	0	0.075	0	0	0.261	0.469
RN08_1785	RN08_3314	1806.RN08_1785	1806.RN08_3314	0.044	0	0.399	0	0.249	0	0	0.200	0.609
RN08_1785	RN08_3353	1806.RN08_1785	1806.RN08_3353	0	0	0	0	0.212	0	0.961	0.290	0.976
RN08_1785	RN08_3690	1806.RN08_1785	1806.RN08_3690	0.077	0	0	0	0.072	0	0.961	0.063	0.965
RN08_1786	RN08_0081	1806.RN08_1786	1806.RN08_0081	0	0	0	0	0	0	0.826	0.156	0.847
RN08_1786	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_1786	1806.RN08_0488	0.048	0	0	0	0	0	0.993	0	0.993
RN08_1786	RN08_1448	1806.RN08_1786	1806.RN08_1448	0	0	0.214	0	0	0.144	0.666	0.274	0.815
RN08_1786	RN08_1449	1806.RN08_1786	1806.RN08_1449	0	0	0	0	0.570	0	0	0.179	0.632
RN08_1786	RN08_1748	1806.RN08_1786	1806.RN08_1748	0.049	0	0	0	0.118	0	0.826	0.274	0.880
RN08_1786	RN08_1782	1806.RN08_1786	1806.RN08_1782	0.470	0	0.745	0	0.274	0	0	0.863	0.985
RN08_1786	RN08_1784	1806.RN08_1786	1806.RN08_1784	0.577	0	0.778	0	0.888	0	0.826	0.917	0.999
RN08_1786	RN08_1785	1806.RN08_1786	1806.RN08_1785	0.577	0	0.782	0	0.878	0.999	0.826	0.978	0.999
RN08_1786	RN08_2027	1806.RN08_1786	1806.RN08_2027	0.133	0	0	0	0	0	0.423	0	0.478
RN08_1786	RN08_2431	1806.RN08_1786	1806.RN08_2431	0.577	0	0.779	0	0.675	0	0.669	0.862	0.998
RN08_1786	RN08_2590	1806.RN08_1786	1806.RN08_2590	0	0	0	0	0.277	0	0.993	0.162	0.995
RN08_1786	RN08_2893	1806.RN08_1786	1806.RN08_2893	0.121	0	0	0	0	0	0.423	0	0.471
RN08_1786	RN08_3032	1806.RN08_1786	1806.RN08_3032	0	0	0	0	0	0	0.423	0	0.423
RN08_1786	RN08_3313	1806.RN08_1786	1806.RN08_3313	0	0	0.294	0	0.212	0	0	0.179	0.503

RN08_1786	RN08_3314	1806.RN08_1786	1806.RN08_3314	0.043	0	0.476	0	0.332	0	0	0.205	0.698
RN08_1786	RN08_3353	1806.RN08_1786	1806.RN08_3353	0	0	0	0	0	0	0.961	0.393	0.975
RN08_1786	RN08_3690	1806.RN08_1786	1806.RN08_3690	0.077	0	0	0	0.072	0	0.961	0.063	0.965
RN08_1786	RN08_4092	1806.RN08_1786	1806.RN08_4092	0	0	0.178	0	0	0	0	0.407	0.492
RN08_2027	RN08_0081	1806.RN08_2027	1806.RN08_0081	0	0	0	0	0	0	0.422	0.055	0.430
RN08_2027	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_2027	1806.RN08_0488	0.042	0	0.154	0.216	0	0	0.961	0.570	0.980
RN08_2027	RN08_0489	1806.RN08_2027	1806.RN08_0489	0.042	0	0	0	0.074	0.154	0.422	0.261	0.621
RN08_2027	RN08_1748	1806.RN08_2027	1806.RN08_1748	0	0	0	0	0	0	0.422	0.069	0.439
RN08_2027	RN08_1785	1806.RN08_2027	1806.RN08_1785	0.131	0	0	0	0	0	0.423	0	0.477
RN08_2027	RN08_1786	1806.RN08_2027	1806.RN08_1786	0.133	0	0	0	0	0	0.423	0	0.478
RN08_2027	RN08_2590	1806.RN08_2027	1806.RN08_2590	0.046	0	0	0	0	0	0.423	0	0.426
RN08_2027	RN08_2892	1806.RN08_2027	1806.RN08_2892	0.577	0	0	0	0	0	0	0.440	0.753
RN08_2027	RN08_2893	1806.RN08_2027	1806.RN08_2893	0.577	0	0	0.141	0	0	0.826	0.520	0.956
RN08_2027	RN08_2894	1806.RN08_2027	1806.RN08_2894	0.577	0	0.170	0	0	0	0	0	0.634
RN08_2027	RN08_3032	1806.RN08_2027	1806.RN08_3032	0	0	0.599	0.320	0	0	0.993	0.761	0.998
RN08_2027	RN08_3175	1806.RN08_2027	1806.RN08_3175	0.042	0	0	0	0.114	0	0.826	0.769	0.961
RN08_2027	RN08_3353	1806.RN08_2027	1806.RN08_3353	0	0	0.164	0	0.272	0	0.183	0	0.459
RN08_2431	RN08_0081	1806.RN08_2431	1806.RN08_0081	0.047	0	0	0	0	0	0	0.422	0.426
RN08_2431	RN08_1210	1806.RN08_2431	1806.RN08_1210	0	0	0.160	0	0	0	0	0.758	0.788
RN08_2431	RN08_1748	1806.RN08_2431	1806.RN08_1748	0.139	0	0	0	0.073	0.110	0	0.356	0.481
RN08_2431	RN08_1782	1806.RN08_2431	1806.RN08_1782	0.042	0	0.722	0	0.277	0	0.963	0.863	0.999
RN08_2431	RN08_1784	1806.RN08_2431	1806.RN08_1784	0.577	0	0.773	0	0.720	0	0.963	0.978	0.999
RN08_2431	RN08_1785	1806.RN08_2431	1806.RN08_1785	0.577	0	0.776	0	0.571	0	0.826	0.732	0.998
RN08_2431	RN08_1786	1806.RN08_2431	1806.RN08_1786	0.577	0	0.779	0	0.675	0	0.669	0.862	0.998

RN08_2431	RN08_2453	1806.RN08_2431	1806.RN08_2453	0.043	0	0	0	0	0	0.418	0.096	0.453
RN08_2431	RN08_3313	1806.RN08_2431	1806.RN08_3313	0	0	0.245	0	0.069	0	0	0.660	0.740
RN08_2431	RN08_3314	1806.RN08_2431	1806.RN08_3314	0	0	0.388	0	0.212	0	0	0.302	0.634
RN08_2431	RN08_4092	1806.RN08_2431	1806.RN08_4092	0.044	0	0	0	0	0	0	0.431	0.433
RN08_2453	RN08_0438	1806.RN08_2453	1806.RN08_0438	0.077	0	0	0	0	0.114	0.651	0.068	0.698
RN08_2453	RN08_0489	1806.RN08_2453	1806.RN08_0489	0	0	0.198	0	0	0	0.770	0.054	0.810
RN08_2453	RN08_0949	1806.RN08_2453	1806.RN08_0949	0	0	0	0	0	0.119	0.991	0.425	0.995
RN08_2453	RN08_1210	1806.RN08_2453	1806.RN08_1210	0.077	0	0	0	0.212	0.114	0.986	0.068	0.990
RN08_2453	RN08_1448	1806.RN08_2453	1806.RN08_1448	0.047	0	0.163	0	0.114	0	0.826	0.353	0.906
RN08_2453	RN08_1449	1806.RN08_2453	1806.RN08_1449	0.047	0	0	0	0	0.127	0	0.688	0.718
RN08_2453	RN08_1748	1806.RN08_2453	1806.RN08_1748	0.047	0	0	0	0.275	0	0.993	0.981	0.999
RN08_2453	RN08_2431	1806.RN08_2453	1806.RN08_2431	0.043	0	0	0	0	0	0.418	0.096	0.453
RN08_2453	RN08_3313	1806.RN08_2453	1806.RN08_3313	0.577	0	0.175	0	0.119	0.166	0.414	0.912	0.984
RN08_2453	RN08_3314	1806.RN08_2453	1806.RN08_3314	0.331	0	0.152	0	0.237	0.123	0.403	0.266	0.795
RN08_2453	RN08_3353	1806.RN08_2453	1806.RN08_3353	0	0	0	0	0.212	0	0.407	0.305	0.647
RN08_2453	RN08_4092	1806.RN08_2453	1806.RN08_4092	0.145	0	0.160	0	0.274	0	0.993	0.062	0.996
RN08_2590	hydrolase	1806.RN08_2590	1806.RN08_0054	0.047	0	0	0	0	0	0.423	0	0.427
RN08_2590	RN08_0081	1806.RN08_2590	1806.RN08_0081	0	0	0	0	0	0	0.977	0.613	0.991
RN08_2590	RN08_0438	1806.RN08_2590	1806.RN08_0438	0.066	0	0.213	0	0.212	0	0.607	0.388	0.835
RN08_2590	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_2590	1806.RN08_0488	0.067	0	0	0	0	0	0.993	0	0.993
RN08_2590	RN08_1210	1806.RN08_2590	1806.RN08_1210	0.066	0	0	0	0	0	0.607	0.575	0.830
RN08_2590	RN08_1272	1806.RN08_2590	1806.RN08_1272	0.080	0	0	0	0	0	0	0.569	0.587
RN08_2590	RN08_1448	1806.RN08_2590	1806.RN08_1448	0.066	0	0.185	0	0	0	0.826	0.096	0.864
RN08_2590	RN08_1449	1806.RN08_2590	1806.RN08_1449	0.066	0	0.179	0	0	0	0.642	0.395	0.812

RN08_2590	RN08_1748	1806.RN08_2590	1806.RN08_1748	0.048	0	0	0	0.111	0	0.993	0.103	0.994
RN08_2590	RN08_1785	1806.RN08_2590	1806.RN08_1785	0	0	0	0	0.274	0	0.993	0.152	0.995
RN08_2590	RN08_1786	1806.RN08_2590	1806.RN08_1786	0	0	0	0	0.277	0	0.993	0.162	0.995
RN08_2590	RN08_2027	1806.RN08_2590	1806.RN08_2027	0.046	0	0	0	0	0	0.423	0	0.426
RN08_2590	Cyclase	1806.RN08_2590	1806.RN08_2701	0.043	0	0	0	0	0	0.465	0	0.466
RN08_2590	RN08_2893	1806.RN08_2590	1806.RN08_2893	0.046	0	0	0	0	0	0.423	0	0.426
RN08_2590	RN08_3032	1806.RN08_2590	1806.RN08_3032	0.046	0	0	0	0	0	0.423	0	0.426
RN08_2590	RN08_3314	1806.RN08_2590	1806.RN08_3314	0	0	0.165	0	0	0	0.659	0.162	0.741
RN08_2590	RN08_3353	1806.RN08_2590	1806.RN08_3353	0	0	0	0	0.110	0	0.993	0.156	0.994
RN08_2590	RN08_3689	1806.RN08_2590	1806.RN08_3689	0.081	0	0.169	0	0	0	0.993	0.227	0.995
RN08_2590	RN08_3690	1806.RN08_2590	1806.RN08_3690	0.047	0	0	0	0	0	0.423	0.339	0.605
RN08_2598	RN08_0001	1806.RN08_2598	1806.RN08_0001	0.067	0	0.253	0	0.267	0	0	0.551	0.740
RN08_2598	DNA binding protein	1806.RN08_2598	1806.RN08_0063	0.049	0	0.347	0	0	0.258	0	0.153	0.557
RN08_2598	RN08_0067	1806.RN08_2598	1806.RN08_0067	0.092	0	0.452	0	0.466	0.745	0.956	0.311	0.997
RN08_2598	RN08_1604	1806.RN08_2598	1806.RN08_1604	0.105	0	0	0	0.246	0	0	0.651	0.744
RN08_2598	RN08_1784	1806.RN08_2598	1806.RN08_1784	0	0	0	0	0	0.433	0	0	0.433
RN08_2598	RN08_2746	1806.RN08_2598	1806.RN08_2746	0.049	0	0.321	0	0	0.258	0	0.153	0.540
RN08_2598	RN08_3032	1806.RN08_2598	1806.RN08_3032	0.046	0	0	0	0	0	0	0.577	0.579
RN08_2598	RN08_3175	1806.RN08_2598	1806.RN08_3175	0.084	0	0.319	0	0.114	0	0	0.064	0.413
RN08_2680	RN08_1604	1806.RN08_2680	1806.RN08_1604	0.067	0	0	0	0	0	0.642	0	0.652
RN08_2680	RN08_2681	1806.RN08_2680	1806.RN08_2681	0.957	0	0	0	0.278	0	0	0.886	0.996
RN08_2680	Glucosyl-3-phosphoglycerate phosphatase	1806.RN08_2680	1806.RN08_2682	0.957	0	0	0	0.381	0	0	0.807	0.994
RN08_2681	RN08_2680	1806.RN08_2681	1806.RN08_2680	0.957	0	0	0	0.278	0	0	0.886	0.996
RN08_2681	Glucosyl-3-phosphoglycerate phosphatase	1806.RN08_2681	1806.RN08_2682	0.943	0	0	0	0.212	0	0	0.825	0.991

RN08_2681	RN08_2892	1806.RN08_2681	1806.RN08_2892	0	0	0.201	0	0.381	0	0	0	0.484
RN08_2724	RN08_0438	1806.RN08_2724	1806.RN08_0438	0.083	0	0	0	0.110	0	0.961	0.105	0.968
RN08_2724	RN08_1210	1806.RN08_2724	1806.RN08_1210	0.083	0	0	0	0.110	0	0.961	0.650	0.987
RN08_2724	RN08_1272	1806.RN08_2724	1806.RN08_1272	0.044	0	0	0	0	0	0.952	0.548	0.977
RN08_2724	RN08_1448	1806.RN08_2724	1806.RN08_1448	0.066	0	0	0	0.111	0	0.991	0.160	0.993
RN08_2724	RN08_1748	1806.RN08_2724	1806.RN08_1748	0.044	0	0	0	0	0	0.991	0.055	0.991
RN08_2724	RN08_3689	1806.RN08_2724	1806.RN08_3689	0.069	0	0	0	0	0	0.993	0.305	0.995
RN08_2746	DNA binding protein	1806.RN08_2746	1806.RN08_0063	0	0	0.317	0.391	0	0	0.993	0.799	0.997
RN08_2746	RN08_2598	1806.RN08_2746	1806.RN08_2598	0.049	0	0.321	0	0	0.258	0	0.153	0.540
RN08_2746	RN08_3175	1806.RN08_2746	1806.RN08_3175	0.049	0	0	0	0	0	0.479	0	0.483
RN08_2892	RN08_0001	1806.RN08_2892	1806.RN08_0001	0.047	0	0	0	0.529	0	0	0	0.532
RN08_2892	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_2892	1806.RN08_0488	0.067	0	0	0	0.167	0	0	0.374	0.471
RN08_2892	RN08_2027	1806.RN08_2892	1806.RN08_2027	0.577	0	0	0	0	0	0	0.440	0.753
RN08_2892	RN08_2681	1806.RN08_2892	1806.RN08_2681	0	0	0.201	0	0.381	0	0	0	0.484
RN08_2892	RN08_2893	1806.RN08_2892	1806.RN08_2893	0.975	0	0.279	0	0.381	0	0	0.904	0.999
RN08_2892	RN08_2894	1806.RN08_2892	1806.RN08_2894	0.948	0	0.161	0	0.381	0	0	0.604	0.988
RN08_2892	RN08_3175	1806.RN08_2892	1806.RN08_3175	0.068	0	0.191	0	0	0	0.791	0.384	0.890
RN08_2893	RN08_0081	1806.RN08_2893	1806.RN08_0081	0.121	0	0	0	0	0	0.422	0.055	0.478
RN08_2893	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_2893	1806.RN08_0488	0.042	0	0	0.114	0.306	0	0.993	0.729	0.998
RN08_2893	RN08_0489	1806.RN08_2893	1806.RN08_0489	0.042	0	0	0	0.074	0.154	0.422	0.519	0.753
RN08_2893	RN08_1748	1806.RN08_2893	1806.RN08_1748	0	0	0	0	0	0	0.422	0.069	0.439
RN08_2893	RN08_1785	1806.RN08_2893	1806.RN08_1785	0.130	0	0	0	0	0	0.423	0	0.477

RN08_2893	RN08_1786	1806.RN08_2893	1806.RN08_1786	0.121	0	0	0	0	0	0.423	0	0.471
RN08_2893	RN08_2027	1806.RN08_2893	1806.RN08_2027	0.577	0	0	0.141	0	0	0.826	0.520	0.956
RN08_2893	RN08_2590	1806.RN08_2893	1806.RN08_2590	0.046	0	0	0	0	0	0.423	0	0.426
RN08_2893	RN08_2892	1806.RN08_2893	1806.RN08_2892	0.975	0	0.279	0	0.381	0	0	0.904	0.999
RN08_2893	RN08_2894	1806.RN08_2893	1806.RN08_2894	0.948	0	0.278	0	0.381	0	0	0.613	0.990
RN08_2893	RN08_3032	1806.RN08_2893	1806.RN08_3032	0	0	0	0.254	0	0	0.993	0.863	0.997
RN08_2893	RN08_3175	1806.RN08_2893	1806.RN08_3175	0.042	0	0	0	0.381	0	0.993	0.095	0.996
RN08_2894	HIT family protein	1806.RN08_2894	1806.RN08_1411	0	0	0.241	0.325	0	0	0.791	0	0.820
RN08_2894	RN08_2027	1806.RN08_2894	1806.RN08_2027	0.577	0	0.170	0	0	0	0	0	0.634
RN08_2894	RN08_2892	1806.RN08_2894	1806.RN08_2892	0.948	0	0.161	0	0.381	0	0	0.604	0.988
RN08_2894	RN08_2893	1806.RN08_2894	1806.RN08_2893	0.948	0	0.278	0	0.381	0	0	0.613	0.990
RN08_3032	RN08_0081	1806.RN08_3032	1806.RN08_0081	0	0	0	0	0	0	0.422	0.055	0.430
RN08_3032	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_3032	1806.RN08_0488	0.042	0	0	0.210	0	0	0.993	0.891	0.998
RN08_3032	RN08_0489	1806.RN08_3032	1806.RN08_0489	0.042	0	0	0	0.074	0.154	0.422	0.374	0.679
RN08_3032	RN08_1748	1806.RN08_3032	1806.RN08_1748	0	0	0	0	0	0	0.422	0.069	0.439
RN08_3032	RN08_1785	1806.RN08_3032	1806.RN08_1785	0	0	0	0	0	0	0.423	0	0.423
RN08_3032	RN08_1786	1806.RN08_3032	1806.RN08_1786	0	0	0	0	0	0	0.423	0	0.423
RN08_3032	RN08_2027	1806.RN08_3032	1806.RN08_2027	0	0	0.599	0.320	0	0	0.993	0.761	0.998
RN08_3032	RN08_2590	1806.RN08_3032	1806.RN08_2590	0.046	0	0	0	0	0	0.423	0	0.426
RN08_3032	RN08_2598	1806.RN08_3032	1806.RN08_2598	0.046	0	0	0	0	0	0	0.577	0.579
RN08_3032	RN08_2893	1806.RN08_3032	1806.RN08_2893	0	0	0	0.254	0	0	0.993	0.863	0.997
RN08_3032	RN08_3175	1806.RN08_3032	1806.RN08_3175	0.042	0	0	0	0	0	0.826	0.586	0.925
RN08_3175	DNA binding protein	1806.RN08_3175	1806.RN08_0063	0.049	0	0.164	0	0	0	0.479	0	0.550
RN08_3175	Cdp-diacylglycerol--	1806.RN08_3175	1806.RN08_0488	0.378	0	0	0	0.381	0	0.993	0.082	0.997

	serine o-phosphatidyltransferase											
RN08_3175	RN08_0489	1806.RN08_3175	1806.RN08_0489	0.378	0	0	0	0.246	0	0	0.418	0.703
RN08_3175	RN08_1784	1806.RN08_3175	1806.RN08_1784	0	0	0	0	0.381	0	0	0.093	0.415
RN08_3175	RN08_2027	1806.RN08_3175	1806.RN08_2027	0.042	0	0	0	0.114	0	0.826	0.769	0.961
RN08_3175	RN08_2598	1806.RN08_3175	1806.RN08_2598	0.084	0	0.319	0	0.114	0	0	0.064	0.413
RN08_3175	RN08_2746	1806.RN08_3175	1806.RN08_2746	0.049	0	0	0	0	0	0.479	0	0.483
RN08_3175	RN08_2892	1806.RN08_3175	1806.RN08_2892	0.068	0	0.191	0	0	0	0.791	0.384	0.890
RN08_3175	RN08_2893	1806.RN08_3175	1806.RN08_2893	0.042	0	0	0	0.381	0	0.993	0.095	0.996
RN08_3175	RN08_3032	1806.RN08_3175	1806.RN08_3032	0.042	0	0	0	0	0	0.826	0.586	0.925
RN08_3313	RN08_0081	1806.RN08_3313	1806.RN08_0081	0.047	0	0	0	0	0	0.791	0.098	0.805
RN08_3313	RN08_0949	1806.RN08_3313	1806.RN08_0949	0	0	0.155	0	0.074	0	0.927	0.657	0.978
RN08_3313	RN08_1272	1806.RN08_3313	1806.RN08_1272	0	0	0	0	0.145	0	0	0.722	0.752
RN08_3313	RN08_1448	1806.RN08_3313	1806.RN08_1448	0.081	0	0.546	0	0.121	0	0	0.199	0.667
RN08_3313	RN08_1449	1806.RN08_3313	1806.RN08_1449	0.091	0	0.192	0	0.290	0	0	0.421	0.658
RN08_3313	RN08_1604	1806.RN08_3313	1806.RN08_1604	0.049	0	0	0	0.367	0	0	0.192	0.471
RN08_3313	RN08_1748	1806.RN08_3313	1806.RN08_1748	0.118	0	0.493	0	0.246	0.182	0.791	0.857	0.990
RN08_3313	RN08_1784	1806.RN08_3313	1806.RN08_1784	0	0	0.228	0	0.075	0	0	0.647	0.726
RN08_3313	RN08_1785	1806.RN08_3313	1806.RN08_1785	0.066	0	0.266	0	0.075	0	0	0.261	0.469
RN08_3313	RN08_1786	1806.RN08_3313	1806.RN08_1786	0	0	0.294	0	0.212	0	0	0.179	0.503
RN08_3313	RN08_2431	1806.RN08_3313	1806.RN08_2431	0	0	0.245	0	0.069	0	0	0.660	0.740
RN08_3313	RN08_2453	1806.RN08_3313	1806.RN08_2453	0.577	0	0.175	0	0.119	0.166	0.414	0.912	0.984
RN08_3313	RN08_3314	1806.RN08_3313	1806.RN08_3314	0.716	0	0.620	0	0.550	0.207	0.961	0.785	0.999
RN08_3313	RN08_3872	1806.RN08_3313	1806.RN08_3872	0	0	0.197	0	0.081	0	0.993	0.289	0.996
RN08_3313	RN08_4092	1806.RN08_3313	1806.RN08_4092	0.260	0	0.222	0	0.110	0	0.389	0.094	0.665
RN08_3314	hydrolase	1806.RN08_3314	1806.RN08_0054	0	0	0	0	0	0	0.371	0.090	0.403

RN08_3314	RN08_0067	1806.RN08_3314	1806.RN08_0067	0.042	0	0	0	0	0	0.412	0.094	0.445
RN08_3314	RN08_0081	1806.RN08_3314	1806.RN08_0081	0	0	0	0	0.212	0	0.952	0.424	0.976
RN08_3314	RN08_0438	1806.RN08_3314	1806.RN08_0438	0	0	0	0	0.072	0.114	0.445	0.203	0.588
RN08_3314	RN08_0489	1806.RN08_3314	1806.RN08_0489	0.378	0	0.151	0	0	0	0	0	0.449
RN08_3314	RN08_0949	1806.RN08_3314	1806.RN08_0949	0	0	0.177	0	0.052	0	0.400	0.536	0.754
RN08_3314	RN08_1210	1806.RN08_3314	1806.RN08_1210	0	0	0	0	0.072	0.114	0.445	0.584	0.785
RN08_3314	RN08_1272	1806.RN08_3314	1806.RN08_1272	0.047	0	0	0	0	0	0.439	0.668	0.807
RN08_3314	RN08_1448	1806.RN08_3314	1806.RN08_1448	0.378	0	0.364	0.235	0.116	0	0	0.336	0.675
RN08_3314	RN08_1449	1806.RN08_3314	1806.RN08_1449	0.081	0	0.153	0	0.522	0	0.669	0.322	0.901
RN08_3314	RN08_1748	1806.RN08_3314	1806.RN08_1748	0.118	0	0.255	0	0.277	0	0.993	0.625	0.999
RN08_3314	RN08_1784	1806.RN08_3314	1806.RN08_1784	0.081	0	0.299	0	0.146	0	0	0.226	0.517
RN08_3314	RN08_1785	1806.RN08_3314	1806.RN08_1785	0.044	0	0.399	0	0.249	0	0	0.200	0.609
RN08_3314	RN08_1786	1806.RN08_3314	1806.RN08_1786	0.043	0	0.476	0	0.332	0	0	0.205	0.698
RN08_3314	RN08_2431	1806.RN08_3314	1806.RN08_2431	0	0	0.388	0	0.212	0	0	0.302	0.634
RN08_3314	RN08_2453	1806.RN08_3314	1806.RN08_2453	0.331	0	0.152	0	0.237	0.123	0.403	0.266	0.795
RN08_3314	RN08_2590	1806.RN08_3314	1806.RN08_2590	0	0	0.165	0	0	0	0.659	0.162	0.741
RN08_3314	RN08_3313	1806.RN08_3314	1806.RN08_3313	0.716	0	0.620	0	0.550	0.207	0.961	0.785	0.999
RN08_3314	RN08_3353	1806.RN08_3314	1806.RN08_3353	0	0	0.163	0	0	0	0.333	0.206	0.518
RN08_3314	RN08_3689	1806.RN08_3314	1806.RN08_3689	0.104	0	0	0	0	0	0.430	0	0.467
RN08_3314	RN08_3690	1806.RN08_3314	1806.RN08_3690	0	0	0	0	0	0	0.371	0.090	0.403
RN08_3314	RN08_3872	1806.RN08_3314	1806.RN08_3872	0	0	0.164	0	0.110	0.263	0.987	0.988	0.999
RN08_3314	RN08_4092	1806.RN08_3314	1806.RN08_4092	0.219	0	0.212	0	0	0	0.993	0.756	0.999
RN08_3353	RN08_0081	1806.RN08_3353	1806.RN08_0081	0	0	0	0	0.271	0	0.993	0.862	0.999
RN08_3353	RN08_0438	1806.RN08_3353	1806.RN08_0438	0	0	0.161	0	0	0	0.484	0.054	0.555
RN08_3353	Cdp-diacylglycerol--serine o-	1806.RN08_3353	1806.RN08_0488	0	0	0.159	0	0.381	0	0.993	0	0.996

	phosphatidyltransferase											
RN08_3353	RN08_1210	1806.RN08_3353	1806.RN08_1210	0	0	0	0	0	0	0.484	0.054	0.491
RN08_3353	RN08_1272	1806.RN08_3353	1806.RN08_1272	0	0	0	0	0	0	0.248	0.413	0.540
RN08_3353	RN08_1448	1806.RN08_3353	1806.RN08_1448	0.066	0	0	0	0	0	0.647	0.066	0.665
RN08_3353	RN08_1748	1806.RN08_3353	1806.RN08_1748	0.069	0	0	0	0.324	0	0.993	0.156	0.996
RN08_3353	RN08_1785	1806.RN08_3353	1806.RN08_1785	0	0	0	0	0.212	0	0.961	0.290	0.976
RN08_3353	RN08_1786	1806.RN08_3353	1806.RN08_1786	0	0	0	0	0	0	0.961	0.393	0.975
RN08_3353	RN08_2027	1806.RN08_3353	1806.RN08_2027	0	0	0.164	0	0.272	0	0.183	0	0.459
RN08_3353	RN08_2453	1806.RN08_3353	1806.RN08_2453	0	0	0	0	0.212	0	0.407	0.305	0.647
RN08_3353	RN08_2590	1806.RN08_3353	1806.RN08_2590	0	0	0	0	0.110	0	0.993	0.156	0.994
RN08_3353	RN08_3314	1806.RN08_3353	1806.RN08_3314	0	0	0.163	0	0	0	0.333	0.206	0.518
RN08_3353	RN08_3689	1806.RN08_3353	1806.RN08_3689	0	0	0.172	0	0	0	0.600	0	0.655
RN08_3353	RN08_3690	1806.RN08_3353	1806.RN08_3690	0	0	0.152	0	0	0	0.993	0	0.994
RN08_3689	RN08_0438	1806.RN08_3689	1806.RN08_0438	0.084	0	0.773	0.492	0.110	0	0.986	0.647	0.995
RN08_3689	RN08_1210	1806.RN08_3689	1806.RN08_1210	0.084	0	0.774	0.500	0.110	0	0.986	0.820	0.995
RN08_3689	RN08_1272	1806.RN08_3689	1806.RN08_1272	0.282	0	0	0	0.323	0	0.993	0.854	0.999
RN08_3689	RN08_1448	1806.RN08_3689	1806.RN08_1448	0.185	0	0	0	0.176	0	0.826	0.438	0.926
RN08_3689	RN08_1449	1806.RN08_3689	1806.RN08_1449	0.068	0	0	0	0	0	0	0.411	0.428
RN08_3689	RN08_1748	1806.RN08_3689	1806.RN08_1748	0	0	0	0	0.248	0	0.993	0	0.995
RN08_3689	RN08_2590	1806.RN08_3689	1806.RN08_2590	0.081	0	0.169	0	0	0	0.993	0.227	0.995
RN08_3689	RN08_2724	1806.RN08_3689	1806.RN08_2724	0.069	0	0	0	0	0	0.993	0.305	0.995
RN08_3689	RN08_3314	1806.RN08_3689	1806.RN08_3314	0.104	0	0	0	0	0	0.430	0	0.467
RN08_3689	RN08_3353	1806.RN08_3689	1806.RN08_3353	0	0	0.172	0	0	0	0.600	0	0.655
RN08_3689	RN08_3690	1806.RN08_3689	1806.RN08_3690	0.947	0	0.539	0	0.381	0	0.993	0.558	0.999
RN08_3690	RN08_0081	1806.RN08_3690	1806.RN08_0081	0	0	0	0	0	0	0.993	0	0.993

RN08_3690	RN08_0438	1806.RN08_3690	1806.RN08_0438	0.081	0	0.359	0	0.239	0	0.986	0.234	0.994
RN08_3690	Cdp-diacylglycerol--serine o-phosphatidyltransferase	1806.RN08_3690	1806.RN08_0488	0	0	0.181	0	0	0	0.961	0	0.967
RN08_3690	RN08_1210	1806.RN08_3690	1806.RN08_1210	0.081	0	0.276	0	0.073	0	0.986	0.347	0.993
RN08_3690	RN08_1272	1806.RN08_3690	1806.RN08_1272	0.254	0	0	0	0	0	0.308	0.375	0.649
RN08_3690	RN08_1448	1806.RN08_3690	1806.RN08_1448	0.132	0	0	0	0.181	0	0.826	0.491	0.929
RN08_3690	RN08_1449	1806.RN08_3690	1806.RN08_1449	0	0	0	0	0.110	0	0	0.701	0.723
RN08_3690	RN08_1748	1806.RN08_3690	1806.RN08_1748	0.047	0	0	0	0.296	0	0.993	0.075	0.995
RN08_3690	RN08_1785	1806.RN08_3690	1806.RN08_1785	0.077	0	0	0	0.072	0	0.961	0.063	0.965
RN08_3690	RN08_1786	1806.RN08_3690	1806.RN08_1786	0.077	0	0	0	0.072	0	0.961	0.063	0.965
RN08_3690	RN08_2590	1806.RN08_3690	1806.RN08_2590	0.047	0	0	0	0	0	0.423	0.339	0.605
RN08_3690	RN08_3314	1806.RN08_3690	1806.RN08_3314	0	0	0	0	0	0	0.371	0.090	0.403
RN08_3690	RN08_3353	1806.RN08_3690	1806.RN08_3353	0	0	0.152	0	0	0	0.993	0	0.994
RN08_3690	RN08_3689	1806.RN08_3690	1806.RN08_3689	0.947	0	0.539	0	0.381	0	0.993	0.558	0.999
RN08_3872	RN08_0081	1806.RN08_3872	1806.RN08_0081	0	0	0	0	0	0	0.961	0.046	0.961
RN08_3872	RN08_0489	1806.RN08_3872	1806.RN08_0489	0	0	0.155	0	0.381	0	0	0	0.455
RN08_3872	RN08_0711	1806.RN08_3872	1806.RN08_0711	0	0	0.166	0	0.272	0	0	0.183	0.461
RN08_3872	RN08_1210	1806.RN08_3872	1806.RN08_1210	0	0	0	0	0	0	0	0.469	0.469
RN08_3872	RN08_1449	1806.RN08_3872	1806.RN08_1449	0	0	0	0	0	0	0.336	0.462	0.627
RN08_3872	RN08_1748	1806.RN08_3872	1806.RN08_1748	0	0	0.154	0	0.275	0.085	0.993	0.320	0.997
RN08_3872	RN08_3313	1806.RN08_3872	1806.RN08_3313	0	0	0.197	0	0.081	0	0.993	0.289	0.996
RN08_3872	RN08_3314	1806.RN08_3872	1806.RN08_3314	0	0	0.164	0	0.110	0.263	0.987	0.988	0.999
RN08_3872	RN08_4092	1806.RN08_3872	1806.RN08_4092	0	0	0	0	0	0	0.993	0.182	0.994
RN08_4092	Cdp-diacylglycerol--serine o-	1806.RN08_4092	1806.RN08_0488	0.047	0	0.163	0	0	0	0	0.351	0.437

	phosphatidyltransferase											
RN08_4092	RN08_0949	1806.RN08_4092	1806.RN08_0949	0	0	0.143	0	0	0	0.223	0.633	0.734
RN08_4092	HIT family protein	1806.RN08_4092	1806.RN08_1411	0.413	0	0.154	0	0	0	0	0	0.482
RN08_4092	RN08_1448	1806.RN08_4092	1806.RN08_1448	0.047	0	0.177	0	0	0	0	0.327	0.426
RN08_4092	RN08_1748	1806.RN08_4092	1806.RN08_1748	0.089	0	0	0	0	0	0.389	0.985	0.991
RN08_4092	RN08_1786	1806.RN08_4092	1806.RN08_1786	0	0	0.178	0	0	0	0	0.407	0.492
RN08_4092	RN08_2431	1806.RN08_4092	1806.RN08_2431	0.044	0	0	0	0	0	0	0.431	0.433
RN08_4092	RN08_2453	1806.RN08_4092	1806.RN08_2453	0.145	0	0.160	0	0.274	0	0.993	0.062	0.996
RN08_4092	RN08_3313	1806.RN08_4092	1806.RN08_3313	0.260	0	0.222	0	0.110	0	0.389	0.094	0.665
RN08_4092	RN08_3314	1806.RN08_4092	1806.RN08_3314	0.219	0	0.212	0	0	0	0.993	0.756	0.999
RN08_4092	RN08_3872	1806.RN08_4092	1806.RN08_3872	0	0	0	0	0	0	0.993	0.182	0.994
hydrolase	RN08_2590	1806.RN08_0054	1806.RN08_2590	0.047	0	0	0	0	0	0.423	0	0.427
hydrolase	RN08_3314	1806.RN08_0054	1806.RN08_3314	0	0	0	0	0	0	0.371	0.090	0.403

SUPPLEMENTARY TABLE 2

RN08_0067	1806.RN08_0067	GO Component	GO:1990077	Primosome complex
RN08_0067	1806.RN08_0067	STRING clusters	CL:1718	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	STRING clusters	CL:1719	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	STRING clusters	CL:1720	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	STRING clusters	CL:1721	DNA repair, and DNA replication
RN08_0067	1806.RN08_0067	STRING clusters	CL:1723	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	STRING clusters	CL:1724	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	STRING clusters	CL:1726	DNA repair, and Mismatch repair
RN08_0067	1806.RN08_0067	KEGG	mmic03030	DNA replication
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0067	ATP-binding
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0235	DNA replication
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0238	DNA-binding

RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0347	Helicase
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0378	Hydrolase
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0547	Nucleotide-binding
RN08_0067	1806.RN08_0067	UniProt Keywords	KW-0639	Primosome
RN08_0081	1806.RN08_0081	GO Process	GO:0005975	Carbohydrate metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0005996	Monosaccharide metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0006006	Glucose metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0006094	Gluconeogenesis
RN08_0081	1806.RN08_0081	GO Process	GO:0008152	Metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0009058	Biosynthetic process
RN08_0081	1806.RN08_0081	GO Process	GO:0016051	Carbohydrate biosynthetic process
RN08_0081	1806.RN08_0081	GO Process	GO:0019318	Hexose metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0019319	Hexose biosynthetic process
RN08_0081	1806.RN08_0081	GO Process	GO:0044238	Primary metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0044281	Small molecule metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_0081	1806.RN08_0081	GO Process	GO:0046364	Monosaccharide biosynthetic process
RN08_0081	1806.RN08_0081	GO Process	GO:0071704	Organic substance metabolic process
RN08_0081	1806.RN08_0081	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_0081	1806.RN08_0081	GO Function	GO:0003824	Catalytic activity
RN08_0081	1806.RN08_0081	GO Function	GO:0003941	L-serine ammonia-lyase activity
RN08_0081	1806.RN08_0081	GO Function	GO:0005488	Binding
RN08_0081	1806.RN08_0081	GO Function	GO:0016829	Lyase activity
RN08_0081	1806.RN08_0081	GO Function	GO:0016840	Carbon-nitrogen lyase activity
RN08_0081	1806.RN08_0081	GO Function	GO:0016841	Ammonia-lyase activity
RN08_0081	1806.RN08_0081	GO Function	GO:0043167	Ion binding
RN08_0081	1806.RN08_0081	GO Function	GO:0043169	Cation binding
RN08_0081	1806.RN08_0081	GO Function	GO:0046872	Metal ion binding
RN08_0081	1806.RN08_0081	GO Function	GO:0051536	Iron-sulfur cluster binding
RN08_0081	1806.RN08_0081	GO Function	GO:0051539	4 iron, 4 sulfur cluster binding
RN08_0081	1806.RN08_0081	GO Function	GO:0051540	Metal cluster binding
RN08_0081	1806.RN08_0081	GO Component	GO:0005886	Plasma membrane
RN08_0081	1806.RN08_0081	GO Component	GO:0016020	Membrane
RN08_0081	1806.RN08_0081	GO Component	GO:0071944	Cell periphery
RN08_0081	1806.RN08_0081	GO Component	GO:0110165	Cellular anatomical entity
RN08_0081	1806.RN08_0081	STRING clusters	CL:154	Serine biosynthesis, and L-serine ammonia-lyase activity
RN08_0081	1806.RN08_0081	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_0081	1806.RN08_0081	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_0081	1806.RN08_0081	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_0081	1806.RN08_0081	STRING clusters	CL:87	Mixed, incl. lysine biosynthesis, and arginine biosynthetic process
RN08_0081	1806.RN08_0081	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_0081	1806.RN08_0081	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_0081	1806.RN08_0081	KEGG	mmic01100	Metabolic pathways
RN08_0081	1806.RN08_0081	KEGG	mmic01110	Biosynthesis of secondary metabolites

RN08_0081	1806.RN08_0081	KEGG	mmic01200	Carbon metabolism
RN08_0081	1806.RN08_0081	KEGG	mmic01230	Biosynthesis of amino acids
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0004	4Fe-4S
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0312	Gluconeogenesis
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0408	Iron
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0411	Iron-sulfur
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0456	Lyase
RN08_0081	1806.RN08_0081	UniProt Keywords	KW-0479	Metal-binding
RN08_0438	1806.RN08_0438	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006082	Organic acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006534	Cysteine metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006555	Methionine metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0008152	Metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009058	Biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009069	Serine family amino acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009086	Methionine biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009092	Homoserine metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0009987	Cellular process
RN08_0438	1806.RN08_0438	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0019346	Transsulfuration
RN08_0438	1806.RN08_0438	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0043436	Oxoacid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044237	Cellular metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044238	Primary metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044249	Cellular biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044281	Small molecule metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0050667	Homocysteine metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:0071265	L-methionine biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0071266	De novo l-methionine biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0071268	Homocysteine biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:0071704	Organic substance metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:1901564	Organonitrogen compound metabolic process

RN08_0438	1806.RN08_0438	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_0438	1806.RN08_0438	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_0438	1806.RN08_0438	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_0438	1806.RN08_0438	GO Function	GO:0003824	Catalytic activity
RN08_0438	1806.RN08_0438	GO Function	GO:0005488	Binding
RN08_0438	1806.RN08_0438	GO Function	GO:0016740	Transferase activity
RN08_0438	1806.RN08_0438	GO Function	GO:0016765	Transferase activity, transferring alkyl or aryl (other than methyl) groups
RN08_0438	1806.RN08_0438	GO Function	GO:0016829	Lyase activity
RN08_0438	1806.RN08_0438	GO Function	GO:0016846	Carbon-sulfur lyase activity
RN08_0438	1806.RN08_0438	GO Function	GO:0019842	Vitamin binding
RN08_0438	1806.RN08_0438	GO Function	GO:0030170	Pyridoxal phosphate binding
RN08_0438	1806.RN08_0438	GO Function	GO:0036094	Small molecule binding
RN08_0438	1806.RN08_0438	GO Function	GO:0043167	Ion binding
RN08_0438	1806.RN08_0438	GO Function	GO:0043168	Anion binding
RN08_0438	1806.RN08_0438	GO Function	GO:0070279	Vitamin b6 binding
RN08_0438	1806.RN08_0438	GO Function	GO:0097159	Organic cyclic compound binding
RN08_0438	1806.RN08_0438	GO Function	GO:1901363	Heterocyclic compound binding
RN08_0438	1806.RN08_0438	GO Component	GO:0005622	Intracellular
RN08_0438	1806.RN08_0438	GO Component	GO:0005737	Cytoplasm
RN08_0438	1806.RN08_0438	GO Component	GO:0110165	Cellular anatomical entity
RN08_0438	1806.RN08_0438	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_0438	1806.RN08_0438	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_0438	1806.RN08_0438	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_0438	1806.RN08_0438	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_0438	1806.RN08_0438	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_0438	1806.RN08_0438	STRING clusters	CL:529	Cysteine biosynthetic process from serine, and de novo l-methionine biosynthetic process
RN08_0438	1806.RN08_0438	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_0438	1806.RN08_0438	KEGG	mmic00920	Sulfur metabolism
RN08_0438	1806.RN08_0438	KEGG	mmic01100	Metabolic pathways
RN08_0438	1806.RN08_0438	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_0438	1806.RN08_0438	UniProt Keywords	KW-0486	Methionine biosynthesis
RN08_0438	1806.RN08_0438	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_0438	1806.RN08_0438	UniProt Keywords	KW-0808	Transferase
RN08_0489	1806.RN08_0489	GO Process	GO:0006629	Lipid metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0006644	Phospholipid metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0006646	Phosphatidylethanolamine biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0006650	Glycerophospholipid metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0006793	Phosphorus metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0008152	Metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0008610	Lipid biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0008654	Phospholipid biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0009058	Biosynthetic process

RN08_0489	1806.RN08_0489	GO Process	GO:0009987	Cellular process
RN08_0489	1806.RN08_0489	GO Process	GO:0019637	Organophosphate metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0044237	Cellular metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0044238	Primary metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0044249	Cellular biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0045017	Glycerolipid biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0046337	Phosphatidylethanolamine metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0046474	Glycerophospholipid biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:0046486	Glycerolipid metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0071704	Organic substance metabolic process
RN08_0489	1806.RN08_0489	GO Process	GO:0090407	Organophosphate biosynthetic process
RN08_0489	1806.RN08_0489	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_0489	1806.RN08_0489	GO Function	GO:0003824	Catalytic activity
RN08_0489	1806.RN08_0489	GO Function	GO:0004609	Phosphatidylserine decarboxylase activity
RN08_0489	1806.RN08_0489	GO Function	GO:0016829	Lyase activity
RN08_0489	1806.RN08_0489	GO Function	GO:0016830	Carbon-carbon lyase activity
RN08_0489	1806.RN08_0489	GO Function	GO:0016831	Carboxy-lyase activity
RN08_0489	1806.RN08_0489	GO Component	GO:0005886	Plasma membrane
RN08_0489	1806.RN08_0489	GO Component	GO:0016020	Membrane
RN08_0489	1806.RN08_0489	GO Component	GO:0071944	Cell periphery
RN08_0489	1806.RN08_0489	GO Component	GO:0110165	Cellular anatomical entity
RN08_0489	1806.RN08_0489	STRING clusters	CL:2743	Glycerophospholipid metabolism, and acylglycerol O-acyltransferase activity
RN08_0489	1806.RN08_0489	STRING clusters	CL:2744	Glycerophospholipid metabolism, and polyol catabolic process
RN08_0489	1806.RN08_0489	STRING clusters	CL:2745	Glycerophospholipid metabolism
RN08_0489	1806.RN08_0489	STRING clusters	CL:2787	Inositol phosphate metabolism, and CDP-alcohol phosphatidyltransferase activity
RN08_0489	1806.RN08_0489	KEGG	mmic00564	Glycerophospholipid metabolism
RN08_0489	1806.RN08_0489	KEGG	mmic01100	Metabolic pathways
RN08_0489	1806.RN08_0489	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0210	Decarboxylase
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0443	Lipid metabolism
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0444	Lipid biosynthesis
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0456	Lyase
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0472	Membrane
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0594	Phospholipid biosynthesis
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0670	Pyruvate
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-0865	Zymogen
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-1003	Cell membrane
RN08_0489	1806.RN08_0489	UniProt Keywords	KW-1208	Phospholipid metabolism

RN08_0563	1806.RN08_0563	GO Process	GO:0001676	Long-chain fatty acid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0006082	Organic acid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0006629	Lipid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0006631	Fatty acid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0006633	Fatty acid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0008152	Metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0008610	Lipid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0009058	Biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0009987	Cellular process
RN08_0563	1806.RN08_0563	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0030497	Fatty acid elongation
RN08_0563	1806.RN08_0563	GO Process	GO:0032787	Monocarboxylic acid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0042759	Long-chain fatty acid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0043436	Oxoacid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044237	Cellular metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044238	Primary metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044249	Cellular biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044281	Small molecule metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:0071704	Organic substance metabolic process
RN08_0563	1806.RN08_0563	GO Process	GO:0072330	Monocarboxylic acid biosynthetic process
RN08_0563	1806.RN08_0563	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_0563	1806.RN08_0563	GO Function	GO:0003824	Catalytic activity
RN08_0563	1806.RN08_0563	GO Function	GO:0016829	Lyase activity
RN08_0563	1806.RN08_0563	GO Function	GO:0016835	Carbon-oxygen lyase activity
RN08_0563	1806.RN08_0563	GO Function	GO:0016836	Hydro-lyase activity
RN08_0563	1806.RN08_0563	GO Function	GO:0019171	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
RN08_0563	1806.RN08_0563	GO Component	GO:0005618	Cell wall
RN08_0563	1806.RN08_0563	GO Component	GO:0005886	Plasma membrane
RN08_0563	1806.RN08_0563	GO Component	GO:0016020	Membrane
RN08_0563	1806.RN08_0563	GO Component	GO:0030312	External encapsulating structure
RN08_0563	1806.RN08_0563	GO Component	GO:0071944	Cell periphery
RN08_0563	1806.RN08_0563	GO Component	GO:0110165	Cellular anatomical entity
RN08_0563	1806.RN08_0563	STRING clusters	CL:2219	Mostly uncharacterized, incl. protein catabolic process, and mycothiol metabolic process
RN08_0563	1806.RN08_0563	STRING clusters	CL:2220	Mostly uncharacterized, incl. protein catabolic process, and mycothiol metabolic process
RN08_0563	1806.RN08_0563	STRING clusters	CL:2221	Mostly uncharacterized, incl. protein catabolic process, and mycothiol metabolic process
RN08_0563	1806.RN08_0563	STRING clusters	CL:2319	Mixed, incl. proteasomal protein catabolic process, and mycothiol metabolic process
RN08_0563	1806.RN08_0563	STRING clusters	CL:2379	Mixed, incl. cyclopropane-fatty-acyl-phospholipid synthase activity, and biosynthesis of type ii polyketide backbone
RN08_0563	1806.RN08_0563	STRING clusters	CL:2380	Mixed, incl. cyclopropane-fatty-acyl-phospholipid synthase activity, and 3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
RN08_0563	1806.RN08_0563	KEGG	mmic01100	Metabolic pathways
RN08_0563	1806.RN08_0563	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_0711	1806.RN08_0711	GO Process	GO:0006082	Organic acid metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0008152	Metabolic process

RN08_0711	1806.RN08_0711	GO Process	GO:0009987	Cellular process
RN08_0711	1806.RN08_0711	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0032787	Monocarboxylic acid metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0043436	Oxoacid metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0044237	Cellular metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0044281	Small molecule metabolic process
RN08_0711	1806.RN08_0711	GO Process	GO:0071704	Organic substance metabolic process
RN08_0711	1806.RN08_0711	GO Function	GO:0003824	Catalytic activity
RN08_0711	1806.RN08_0711	GO Function	GO:0016829	Lyase activity
RN08_0711	1806.RN08_0711	GO Component	GO:0005886	Plasma membrane
RN08_0711	1806.RN08_0711	GO Component	GO:0016020	Membrane
RN08_0711	1806.RN08_0711	GO Component	GO:0071944	Cell periphery
RN08_0711	1806.RN08_0711	GO Component	GO:0110165	Cellular anatomical entity
RN08_0711	1806.RN08_0711	STRING clusters	CL:6263	Mixed, incl. fatty acid metabolism, and oxidoreductase activity, acting on the ch-ch group of donors
RN08_0711	1806.RN08_0711	STRING clusters	CL:6264	Mixed, incl. fatty acid metabolism, and oxidoreductase activity, acting on the ch-ch group of donors
RN08_0711	1806.RN08_0711	STRING clusters	CL:6568	Mixed, incl. coa carboxylase activity, and fatty acid synthase activity
RN08_0711	1806.RN08_0711	STRING clusters	CL:6570	Mixed, incl. coa carboxylase activity, and fatty acid synthase activity
RN08_0711	1806.RN08_0711	STRING clusters	CL:6602	Fatty acid synthase activity, and 3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
RN08_0711	1806.RN08_0711	KEGG	mmic01100	Metabolic pathways
RN08_0711	1806.RN08_0711	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_0712	1806.RN08_0712	GO Process	GO:0001676	Long-chain fatty acid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0006082	Organic acid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0006629	Lipid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0006631	Fatty acid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0006633	Fatty acid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0008152	Metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0008610	Lipid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0009058	Biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0009987	Cellular process
RN08_0712	1806.RN08_0712	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0030497	Fatty acid elongation
RN08_0712	1806.RN08_0712	GO Process	GO:0032787	Monocarboxylic acid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0042759	Long-chain fatty acid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0043436	Oxoacid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044237	Cellular metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044238	Primary metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044249	Cellular biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044281	Small molecule metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:0071704	Organic substance metabolic process
RN08_0712	1806.RN08_0712	GO Process	GO:0072330	Monocarboxylic acid biosynthetic process
RN08_0712	1806.RN08_0712	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_0712	1806.RN08_0712	GO Function	GO:0003824	Catalytic activity
RN08_0712	1806.RN08_0712	GO Function	GO:0016829	Lyase activity

RN08_0712	1806.RN08_0712	GO Function	GO:0016835	Carbon-oxygen lyase activity
RN08_0712	1806.RN08_0712	GO Function	GO:0016836	Hydro-lyase activity
RN08_0712	1806.RN08_0712	GO Function	GO:0019171	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
RN08_0712	1806.RN08_0712	GO Component	GO:0005886	Plasma membrane
RN08_0712	1806.RN08_0712	GO Component	GO:0016020	Membrane
RN08_0712	1806.RN08_0712	GO Component	GO:0071944	Cell periphery
RN08_0712	1806.RN08_0712	GO Component	GO:0110165	Cellular anatomical entity
RN08_0712	1806.RN08_0712	STRING clusters	CL:6263	Mixed, incl. fatty acid metabolism, and oxidoreductase activity, acting on the ch-ch group of donors
RN08_0712	1806.RN08_0712	STRING clusters	CL:6264	Mixed, incl. fatty acid metabolism, and oxidoreductase activity, acting on the ch-ch group of donors
RN08_0712	1806.RN08_0712	STRING clusters	CL:6568	Mixed, incl. coa carboxylase activity, and fatty acid synthase activity
RN08_0712	1806.RN08_0712	STRING clusters	CL:6570	Mixed, incl. coa carboxylase activity, and fatty acid synthase activity
RN08_0712	1806.RN08_0712	STRING clusters	CL:6602	Fatty acid synthase activity, and 3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity
RN08_0712	1806.RN08_0712	KEGG	mmic01100	Metabolic pathways
RN08_0712	1806.RN08_0712	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_0949	1806.RN08_0949	GO Process	GO:0008152	Metabolic process
RN08_0949	1806.RN08_0949	GO Function	GO:0000287	Magnesium ion binding
RN08_0949	1806.RN08_0949	GO Function	GO:0003824	Catalytic activity
RN08_0949	1806.RN08_0949	GO Function	GO:0005488	Binding
RN08_0949	1806.RN08_0949	GO Function	GO:0016829	Lyase activity
RN08_0949	1806.RN08_0949	GO Function	GO:0016830	Carbon-carbon lyase activity
RN08_0949	1806.RN08_0949	GO Function	GO:0016831	Carboxy-lyase activity
RN08_0949	1806.RN08_0949	GO Function	GO:0019842	Vitamin binding
RN08_0949	1806.RN08_0949	GO Function	GO:0030976	Thiamine pyrophosphate binding
RN08_0949	1806.RN08_0949	GO Function	GO:0036094	Small molecule binding
RN08_0949	1806.RN08_0949	GO Function	GO:0043167	Ion binding
RN08_0949	1806.RN08_0949	GO Function	GO:0043168	Anion binding
RN08_0949	1806.RN08_0949	GO Function	GO:0043169	Cation binding
RN08_0949	1806.RN08_0949	GO Function	GO:0046872	Metal ion binding
RN08_0949	1806.RN08_0949	GO Function	GO:0097159	Organic cyclic compound binding
RN08_0949	1806.RN08_0949	GO Function	GO:1901363	Heterocyclic compound binding
RN08_0949	1806.RN08_0949	GO Function	GO:1901681	Sulfur compound binding
RN08_0949	1806.RN08_0949	GO Component	GO:0005622	Intracellular
RN08_0949	1806.RN08_0949	GO Component	GO:0005737	Cytoplasm
RN08_0949	1806.RN08_0949	GO Component	GO:0005829	Cytosol
RN08_0949	1806.RN08_0949	GO Component	GO:0005886	Plasma membrane
RN08_0949	1806.RN08_0949	GO Component	GO:0016020	Membrane
RN08_0949	1806.RN08_0949	GO Component	GO:0071944	Cell periphery
RN08_0949	1806.RN08_0949	GO Component	GO:0110165	Cellular anatomical entity
RN08_0949	1806.RN08_0949	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_0949	1806.RN08_0949	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_0949	1806.RN08_0949	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_0949	1806.RN08_0949	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_0949	1806.RN08_0949	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_0949	1806.RN08_0949	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_0949	1806.RN08_0949	KEGG	mmic00380	Tryptophan metabolism
RN08_0949	1806.RN08_0949	KEGG	mmic01100	Metabolic pathways

RN08_0949	1806.RN08_0949	UniProt Keywords	KW-0460	Magnesium
RN08_0949	1806.RN08_0949	UniProt Keywords	KW-0479	Metal-binding
RN08_0949	1806.RN08_0949	UniProt Keywords	KW-0786	Thiamine pyrophosphate
RN08_1210	1806.RN08_1210	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006082	Organic acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006534	Cysteine metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006555	Methionine metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0008152	Metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009058	Biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009069	Serine family amino acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009086	Methionine biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009092	Homoserine metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0009987	Cellular process
RN08_1210	1806.RN08_1210	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0019346	Transsulfuration
RN08_1210	1806.RN08_1210	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044237	Cellular metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044238	Primary metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044281	Small molecule metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:0050667	Homocysteine metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:0071704	Organic substance metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1210	1806.RN08_1210	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1210	1806.RN08_1210	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1210	1806.RN08_1210	GO Function	GO:0003824	Catalytic activity
RN08_1210	1806.RN08_1210	GO Function	GO:0003962	Cystathionine gamma-synthase activity
RN08_1210	1806.RN08_1210	GO Function	GO:0005488	Binding
RN08_1210	1806.RN08_1210	GO Function	GO:0016740	Transferase activity
RN08_1210	1806.RN08_1210	GO Function	GO:0016765	Transferase activity, transferring alkyl or aryl (other than methyl) groups
RN08_1210	1806.RN08_1210	GO Function	GO:0019842	Vitamin binding

RN08_1210	1806.RN08_1210	GO Function	GO:0030170	Pyridoxal phosphate binding
RN08_1210	1806.RN08_1210	GO Function	GO:0036094	Small molecule binding
RN08_1210	1806.RN08_1210	GO Function	GO:0043167	Ion binding
RN08_1210	1806.RN08_1210	GO Function	GO:0043168	Anion binding
RN08_1210	1806.RN08_1210	GO Function	GO:0070279	Vitamin b6 binding
RN08_1210	1806.RN08_1210	GO Function	GO:0097159	Organic cyclic compound binding
RN08_1210	1806.RN08_1210	GO Function	GO:1901363	Heterocyclic compound binding
RN08_1210	1806.RN08_1210	GO Component	GO:0005622	Intracellular
RN08_1210	1806.RN08_1210	GO Component	GO:0005737	Cytoplasm
RN08_1210	1806.RN08_1210	GO Component	GO:0110165	Cellular anatomical entity
RN08_1210	1806.RN08_1210	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_1210	1806.RN08_1210	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_1210	1806.RN08_1210	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_1210	1806.RN08_1210	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_1210	1806.RN08_1210	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_1210	1806.RN08_1210	STRING clusters	CL:517	S-methyltransferase activity, and adenosylhomocysteinase activity
RN08_1210	1806.RN08_1210	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_1210	1806.RN08_1210	KEGG	mmic00450	Selenocompound metabolism
RN08_1210	1806.RN08_1210	KEGG	mmic00920	Sulfur metabolism
RN08_1210	1806.RN08_1210	KEGG	mmic01100	Metabolic pathways
RN08_1210	1806.RN08_1210	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1210	1806.RN08_1210	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1210	1806.RN08_1210	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_1272	1806.RN08_1272	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0006082	Organic acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0006555	Methionine metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0008152	Metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0009058	Biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0009086	Methionine biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0009987	Cellular process
RN08_1272	1806.RN08_1272	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0032259	Methylation
RN08_1272	1806.RN08_1272	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0044237	Cellular metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0044238	Primary metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0044281	Small molecule metabolic process

RN08_1272	1806.RN08_1272	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:0071704	Organic substance metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1272	1806.RN08_1272	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1272	1806.RN08_1272	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1272	1806.RN08_1272	GO Function	GO:0003824	Catalytic activity
RN08_1272	1806.RN08_1272	GO Function	GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity
RN08_1272	1806.RN08_1272	GO Function	GO:0005488	Binding
RN08_1272	1806.RN08_1272	GO Function	GO:0008168	Methyltransferase activity
RN08_1272	1806.RN08_1272	GO Function	GO:0008172	S-methyltransferase activity
RN08_1272	1806.RN08_1272	GO Function	GO:0008270	Zinc ion binding
RN08_1272	1806.RN08_1272	GO Function	GO:0016740	Transferase activity
RN08_1272	1806.RN08_1272	GO Function	GO:0016741	Transferase activity, transferring one-carbon groups
RN08_1272	1806.RN08_1272	GO Function	GO:0042085	5-methyltetrahydropteroyltri-L-glutamate-dependent methyltransferase activity
RN08_1272	1806.RN08_1272	GO Function	GO:0043167	Ion binding
RN08_1272	1806.RN08_1272	GO Function	GO:0043169	Cation binding
RN08_1272	1806.RN08_1272	GO Function	GO:0046872	Metal ion binding
RN08_1272	1806.RN08_1272	GO Function	GO:0046914	Transition metal ion binding
RN08_1272	1806.RN08_1272	GO Component	GO:0005618	Cell wall
RN08_1272	1806.RN08_1272	GO Component	GO:0005622	Intracellular
RN08_1272	1806.RN08_1272	GO Component	GO:0005737	Cytoplasm
RN08_1272	1806.RN08_1272	GO Component	GO:0005829	Cytosol
RN08_1272	1806.RN08_1272	GO Component	GO:0005886	Plasma membrane
RN08_1272	1806.RN08_1272	GO Component	GO:0016020	Membrane
RN08_1272	1806.RN08_1272	GO Component	GO:0030312	External encapsulating structure
RN08_1272	1806.RN08_1272	GO Component	GO:0071944	Cell periphery
RN08_1272	1806.RN08_1272	GO Component	GO:0110165	Cellular anatomical entity
RN08_1272	1806.RN08_1272	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_1272	1806.RN08_1272	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_1272	1806.RN08_1272	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_1272	1806.RN08_1272	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_1272	1806.RN08_1272	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_1272	1806.RN08_1272	STRING clusters	CL:517	S-methyltransferase activity, and adenosylhomocysteinase activity
RN08_1272	1806.RN08_1272	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_1272	1806.RN08_1272	KEGG	mmic00450	Selenocompound metabolism
RN08_1272	1806.RN08_1272	KEGG	mmic01100	Metabolic pathways
RN08_1272	1806.RN08_1272	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1272	1806.RN08_1272	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0479	Metal-binding
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0486	Methionine biosynthesis

RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0489	Methyltransferase
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0677	Repeat
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0808	Transferase
RN08_1272	1806.RN08_1272	UniProt Keywords	KW-0862	Zinc
RN08_1448	1806.RN08_1448	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006082	Organic acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006549	Isoleucine metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006555	Methionine metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006566	Threonine metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0008152	Metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009058	Biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009086	Methionine biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009088	Threonine biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0009987	Cellular process
RN08_1448	1806.RN08_1448	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044237	Cellular metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044238	Primary metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044281	Small molecule metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:0055114	Oxidation-reduction process
RN08_1448	1806.RN08_1448	GO Process	GO:0071704	Organic substance metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1448	1806.RN08_1448	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1448	1806.RN08_1448	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1448	1806.RN08_1448	GO Function	GO:0000166	Nucleotide binding
RN08_1448	1806.RN08_1448	GO Function	GO:0003824	Catalytic activity
RN08_1448	1806.RN08_1448	GO Function	GO:0004412	Homoserine dehydrogenase activity

RN08_1448	1806.RN08_1448	GO Function	GO:0005488	Binding
RN08_1448	1806.RN08_1448	GO Function	GO:0016491	Oxidoreductase activity
RN08_1448	1806.RN08_1448	GO Function	GO:0016614	Oxidoreductase activity, acting on ch-oh group of donors
RN08_1448	1806.RN08_1448	GO Function	GO:0016616	Oxidoreductase activity, acting on the ch-oh group of donors, nad or nadp as acceptor
RN08_1448	1806.RN08_1448	GO Function	GO:0036094	Small molecule binding
RN08_1448	1806.RN08_1448	GO Function	GO:0050661	NADP binding
RN08_1448	1806.RN08_1448	GO Function	GO:0097159	Organic cyclic compound binding
RN08_1448	1806.RN08_1448	GO Function	GO:1901265	Nucleoside phosphate binding
RN08_1448	1806.RN08_1448	GO Function	GO:1901363	Heterocyclic compound binding
RN08_1448	1806.RN08_1448	GO Component	GO:0005618	Cell wall
RN08_1448	1806.RN08_1448	GO Component	GO:0005886	Plasma membrane
RN08_1448	1806.RN08_1448	GO Component	GO:0016020	Membrane
RN08_1448	1806.RN08_1448	GO Component	GO:0030312	External encapsulating structure
RN08_1448	1806.RN08_1448	GO Component	GO:0071944	Cell periphery
RN08_1448	1806.RN08_1448	GO Component	GO:0110165	Cellular anatomical entity
RN08_1448	1806.RN08_1448	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1448	1806.RN08_1448	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1448	1806.RN08_1448	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1448	1806.RN08_1448	STRING clusters	CL:87	Mixed, incl. lysine biosynthesis, and arginine biosynthetic process
RN08_1448	1806.RN08_1448	STRING clusters	CL:89	Lysine biosynthesis, and arginine biosynthetic process
RN08_1448	1806.RN08_1448	STRING clusters	CL:90	Lysine biosynthetic process, and threonine biosynthesis
RN08_1448	1806.RN08_1448	STRING clusters	CL:91	Lysine biosynthetic process, and threonine biosynthesis
RN08_1448	1806.RN08_1448	STRING clusters	CL:93	Threonine biosynthesis, and aspartate kinase activity
RN08_1448	1806.RN08_1448	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_1448	1806.RN08_1448	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_1448	1806.RN08_1448	KEGG	mmic00300	Lysine biosynthesis
RN08_1448	1806.RN08_1448	KEGG	mmic01100	Metabolic pathways
RN08_1448	1806.RN08_1448	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1448	1806.RN08_1448	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_1448	1806.RN08_1448	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0100	Branched-chain amino acid biosynthesis
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0412	Isoleucine biosynthesis
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0486	Methionine biosynthesis
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0521	NADP
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0560	Oxidoreductase
RN08_1448	1806.RN08_1448	UniProt Keywords	KW-0791	Threonine biosynthesis
RN08_1449	1806.RN08_1449	GO Process	GO:0006082	Organic acid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0006566	Threonine metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0006807	Nitrogen compound metabolic process

RN08_1449	1806.RN08_1449	GO Process	GO:0008152	Metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0009058	Biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0009088	Threonine biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0009987	Cellular process
RN08_1449	1806.RN08_1449	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0044237	Cellular metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0044238	Primary metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0044281	Small molecule metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:0071704	Organic substance metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1449	1806.RN08_1449	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1449	1806.RN08_1449	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1449	1806.RN08_1449	GO Function	GO:0003824	Catalytic activity
RN08_1449	1806.RN08_1449	GO Function	GO:0004795	Threonine synthase activity
RN08_1449	1806.RN08_1449	GO Function	GO:0005488	Binding
RN08_1449	1806.RN08_1449	GO Function	GO:0016829	Lyase activity
RN08_1449	1806.RN08_1449	GO Function	GO:0016835	Carbon-oxygen lyase activity
RN08_1449	1806.RN08_1449	GO Function	GO:0016838	Carbon-oxygen lyase activity, acting on phosphates
RN08_1449	1806.RN08_1449	GO Function	GO:0019842	Vitamin binding
RN08_1449	1806.RN08_1449	GO Function	GO:0030170	Pyridoxal phosphate binding
RN08_1449	1806.RN08_1449	GO Function	GO:0036094	Small molecule binding
RN08_1449	1806.RN08_1449	GO Function	GO:0043167	Ion binding
RN08_1449	1806.RN08_1449	GO Function	GO:0043168	Anion binding
RN08_1449	1806.RN08_1449	GO Function	GO:0070279	Vitamin b6 binding
RN08_1449	1806.RN08_1449	GO Function	GO:0097159	Organic cyclic compound binding
RN08_1449	1806.RN08_1449	GO Function	GO:1901363	Heterocyclic compound binding
RN08_1449	1806.RN08_1449	GO Component	GO:0005622	Intracellular
RN08_1449	1806.RN08_1449	GO Component	GO:0005737	Cytoplasm
RN08_1449	1806.RN08_1449	GO Component	GO:0005829	Cytosol
RN08_1449	1806.RN08_1449	GO Component	GO:0005886	Plasma membrane
RN08_1449	1806.RN08_1449	GO Component	GO:0016020	Membrane
RN08_1449	1806.RN08_1449	GO Component	GO:0071944	Cell periphery
RN08_1449	1806.RN08_1449	GO Component	GO:0110165	Cellular anatomical entity
RN08_1449	1806.RN08_1449	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1449	1806.RN08_1449	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1449	1806.RN08_1449	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1449	1806.RN08_1449	STRING clusters	CL:87	Mixed, incl. lysine biosynthesis, and arginine biosynthetic process

RN08_1449	1806.RN08_1449	STRING clusters	CL:89	Lysine biosynthesis, and arginine biosynthetic process
RN08_1449	1806.RN08_1449	STRING clusters	CL:90	Lysine biosynthetic process, and threonine biosynthesis
RN08_1449	1806.RN08_1449	STRING clusters	CL:91	Lysine biosynthetic process, and threonine biosynthesis
RN08_1449	1806.RN08_1449	STRING clusters	CL:93	Threonine biosynthesis, and aspartate kinase activity
RN08_1449	1806.RN08_1449	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_1449	1806.RN08_1449	KEGG	mmic00750	Vitamin B6 metabolism
RN08_1449	1806.RN08_1449	KEGG	mmic01100	Metabolic pathways
RN08_1449	1806.RN08_1449	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1449	1806.RN08_1449	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_1449	1806.RN08_1449	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1449	1806.RN08_1449	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1449	1806.RN08_1449	UniProt Keywords	KW-0456	Lyase
RN08_1449	1806.RN08_1449	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_1449	1806.RN08_1449	UniProt Keywords	KW-0791	Threonine biosynthesis
RN08_1604	1806.RN08_1604	GO Process	GO:0005975	Carbohydrate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006082	Organic acid metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006090	Pyruvate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006091	Generation of precursor metabolites and energy
RN08_1604	1806.RN08_1604	GO Process	GO:0006096	Glycolytic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006139	Nucleobase-containing compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006163	Purine nucleotide metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006165	Nucleoside diphosphate phosphorylation
RN08_1604	1806.RN08_1604	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006753	Nucleoside phosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006757	ATP generation from ADP
RN08_1604	1806.RN08_1604	GO Process	GO:0006793	Phosphorus metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0008152	Metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009056	Catabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009117	Nucleotide metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009132	Nucleoside diphosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009135	Purine nucleoside diphosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009150	Purine ribonucleotide metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009179	Purine ribonucleoside diphosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009185	Ribonucleoside diphosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009259	Ribonucleotide metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0009987	Cellular process
RN08_1604	1806.RN08_1604	GO Process	GO:0016052	Carbohydrate catabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0016310	Phosphorylation
RN08_1604	1806.RN08_1604	GO Process	GO:0019637	Organophosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0019693	Ribose phosphate metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0032787	Monocarboxylic acid metabolic process

RN08_1604	1806.RN08_1604	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0044237	Cellular metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0044238	Primary metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0044281	Small molecule metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0046031	ADP metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0046034	ATP metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0046483	Heterocycle metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0046939	Nucleotide phosphorylation
RN08_1604	1806.RN08_1604	GO Process	GO:0055086	Nucleobase-containing small molecule metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0071704	Organic substance metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:0072521	Purine-containing compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:1901135	Carbohydrate derivative metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1604	1806.RN08_1604	GO Process	GO:1901575	Organic substance catabolic process
RN08_1604	1806.RN08_1604	GO Function	GO:0000166	Nucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0003824	Catalytic activity
RN08_1604	1806.RN08_1604	GO Function	GO:0004618	Phosphoglycerate kinase activity
RN08_1604	1806.RN08_1604	GO Function	GO:0005488	Binding
RN08_1604	1806.RN08_1604	GO Function	GO:0005524	ATP binding
RN08_1604	1806.RN08_1604	GO Function	GO:0016301	Kinase activity
RN08_1604	1806.RN08_1604	GO Function	GO:0016740	Transferase activity
RN08_1604	1806.RN08_1604	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_1604	1806.RN08_1604	GO Function	GO:0016774	Phosphotransferase activity, carboxyl group as acceptor
RN08_1604	1806.RN08_1604	GO Function	GO:0017076	Purine nucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0030554	Adenyl nucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0032553	Ribonucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0032555	Purine ribonucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0032559	Adenyl ribonucleotide binding
RN08_1604	1806.RN08_1604	GO Function	GO:0035639	Purine ribonucleoside triphosphate binding
RN08_1604	1806.RN08_1604	GO Function	GO:0036094	Small molecule binding
RN08_1604	1806.RN08_1604	GO Function	GO:0043167	Ion binding
RN08_1604	1806.RN08_1604	GO Function	GO:0043168	Anion binding
RN08_1604	1806.RN08_1604	GO Function	GO:0097159	Organic cyclic compound binding
RN08_1604	1806.RN08_1604	GO Function	GO:0097367	Carbohydrate derivative binding
RN08_1604	1806.RN08_1604	GO Function	GO:1901265	Nucleoside phosphate binding
RN08_1604	1806.RN08_1604	GO Function	GO:1901363	Heterocyclic compound binding
RN08_1604	1806.RN08_1604	GO Component	GO:0005622	Intracellular
RN08_1604	1806.RN08_1604	GO Component	GO:0005737	Cytoplasm
RN08_1604	1806.RN08_1604	GO Component	GO:0110165	Cellular anatomical entity
RN08_1604	1806.RN08_1604	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_1604	1806.RN08_1604	STRING clusters	CL:837	Carbohydrate metabolic process, and vitamin b6 metabolic process
RN08_1604	1806.RN08_1604	STRING clusters	CL:838	Mixed, incl. pentose phosphate pathway, and glycolytic process
RN08_1604	1806.RN08_1604	STRING clusters	CL:839	Mixed, incl. pentose phosphate pathway, and glycolytic process
RN08_1604	1806.RN08_1604	STRING clusters	CL:840	Mixed, incl. glycolytic process, and pentose phosphate pathway
RN08_1604	1806.RN08_1604	STRING clusters	CL:841	Mixed, incl. pentose phosphate pathway, and intramolecular transferase activity, phosphotransferases

RN08_1604	1806.RN08_1604	STRING clusters	CL:843	Pentose phosphate pathway, and Glycolysis
RN08_1604	1806.RN08_1604	STRING clusters	CL:845	Glycolysis, and Pentose phosphate pathway
RN08_1604	1806.RN08_1604	STRING clusters	CL:847	Mixed, incl. transketolase activity, and phosphoglycerate kinase activity
RN08_1604	1806.RN08_1604	KEGG	mmic00010	Glycolysis / Gluconeogenesis
RN08_1604	1806.RN08_1604	KEGG	mmic01100	Metabolic pathways
RN08_1604	1806.RN08_1604	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1604	1806.RN08_1604	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_1604	1806.RN08_1604	KEGG	mmic01200	Carbon metabolism
RN08_1604	1806.RN08_1604	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0067	ATP-binding
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0324	Glycolysis
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0418	Kinase
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0547	Nucleotide-binding
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0808	Transferase
RN08_1604	1806.RN08_1604	UniProt Keywords	KW-0963	Cytoplasm
RN08_1748	1806.RN08_1748	GO Process	GO:0006082	Organic acid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0006549	Isoleucine metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0006566	Threonine metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0008152	Metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009058	Biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0009987	Cellular process
RN08_1748	1806.RN08_1748	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0044237	Cellular metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0044238	Primary metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0044281	Small molecule metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:0071704	Organic substance metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1748	1806.RN08_1748	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1748	1806.RN08_1748	GO Process	GO:1901605	Alpha-amino acid metabolic process

RN08_1748	1806.RN08_1748	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1748	1806.RN08_1748	GO Function	GO:0003824	Catalytic activity
RN08_1748	1806.RN08_1748	GO Function	GO:0004794	L-threonine ammonia-lyase activity
RN08_1748	1806.RN08_1748	GO Function	GO:0005488	Binding
RN08_1748	1806.RN08_1748	GO Function	GO:0016829	Lyase activity
RN08_1748	1806.RN08_1748	GO Function	GO:0016840	Carbon-nitrogen lyase activity
RN08_1748	1806.RN08_1748	GO Function	GO:0016841	Ammonia-lyase activity
RN08_1748	1806.RN08_1748	GO Function	GO:0019842	Vitamin binding
RN08_1748	1806.RN08_1748	GO Function	GO:0030170	Pyridoxal phosphate binding
RN08_1748	1806.RN08_1748	GO Function	GO:0036094	Small molecule binding
RN08_1748	1806.RN08_1748	GO Function	GO:0043167	Ion binding
RN08_1748	1806.RN08_1748	GO Function	GO:0043168	Anion binding
RN08_1748	1806.RN08_1748	GO Function	GO:0070279	Vitamin b6 binding
RN08_1748	1806.RN08_1748	GO Function	GO:0097159	Organic cyclic compound binding
RN08_1748	1806.RN08_1748	GO Function	GO:1901363	Heterocyclic compound binding
RN08_1748	1806.RN08_1748	GO Component	GO:0005886	Plasma membrane
RN08_1748	1806.RN08_1748	GO Component	GO:0016020	Membrane
RN08_1748	1806.RN08_1748	GO Component	GO:0071944	Cell periphery
RN08_1748	1806.RN08_1748	GO Component	GO:0110165	Cellular anatomical entity
RN08_1748	1806.RN08_1748	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_1748	1806.RN08_1748	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_1748	1806.RN08_1748	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_1748	1806.RN08_1748	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_1748	1806.RN08_1748	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_1748	1806.RN08_1748	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_1748	1806.RN08_1748	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_1748	1806.RN08_1748	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_1748	1806.RN08_1748	KEGG	mmic01100	Metabolic pathways
RN08_1748	1806.RN08_1748	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1748	1806.RN08_1748	KEGG	mmic01200	Carbon metabolism
RN08_1748	1806.RN08_1748	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1748	1806.RN08_1748	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1748	1806.RN08_1748	UniProt Keywords	KW-0100	Branched-chain amino acid biosynthesis
RN08_1748	1806.RN08_1748	UniProt Keywords	KW-0412	Isoleucine biosynthesis
RN08_1748	1806.RN08_1748	UniProt Keywords	KW-0456	Lyase
RN08_1748	1806.RN08_1748	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_1782	1806.RN08_1782	GO Process	GO:0000162	Tryptophan biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006082	Organic acid metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006568	Tryptophan metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006576	Cellular biogenic amine metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006586	Indolalkylamine metabolic process

RN08_1782	1806.RN08_1782	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0008152	Metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009058	Biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009072	Aromatic amino acid family metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009073	Aromatic amino acid family biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009308	Amine metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009309	Amine biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0009987	Cellular process
RN08_1782	1806.RN08_1782	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0042401	Cellular biogenic amine biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0042430	Indole-containing compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0042435	Indole-containing compound biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044106	Cellular amine metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044237	Cellular metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044238	Primary metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044281	Small molecule metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0046219	Indolalkylamine biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:0046483	Heterocycle metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:0071704	Organic substance metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1782	1806.RN08_1782	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1782	1806.RN08_1782	GO Function	GO:0000287	Magnesium ion binding
RN08_1782	1806.RN08_1782	GO Function	GO:0003824	Catalytic activity
RN08_1782	1806.RN08_1782	GO Function	GO:0004049	Anthranilate synthase activity
RN08_1782	1806.RN08_1782	GO Function	GO:0005488	Binding
RN08_1782	1806.RN08_1782	GO Function	GO:0016829	Lyase activity
RN08_1782	1806.RN08_1782	GO Function	GO:0016830	Carbon-carbon lyase activity
RN08_1782	1806.RN08_1782	GO Function	GO:0016833	Oxo-acid-lyase activity
RN08_1782	1806.RN08_1782	GO Function	GO:0043167	Ion binding
RN08_1782	1806.RN08_1782	GO Function	GO:0043169	Cation binding
RN08_1782	1806.RN08_1782	GO Function	GO:0046872	Metal ion binding

RN08_1782	1806.RN08_1782	GO Component	GO:0005886	Plasma membrane
RN08_1782	1806.RN08_1782	GO Component	GO:0016020	Membrane
RN08_1782	1806.RN08_1782	GO Component	GO:0071944	Cell periphery
RN08_1782	1806.RN08_1782	GO Component	GO:0110165	Cellular anatomical entity
RN08_1782	1806.RN08_1782	STRING clusters	CL:166	Aromatic amino acid family biosynthetic process, and isochorismate synthase activity
RN08_1782	1806.RN08_1782	STRING clusters	CL:167	Aromatic amino acid family biosynthetic process
RN08_1782	1806.RN08_1782	STRING clusters	CL:168	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1782	1806.RN08_1782	STRING clusters	CL:195	Tryptophan biosynthetic process
RN08_1782	1806.RN08_1782	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1782	1806.RN08_1782	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1782	1806.RN08_1782	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1782	1806.RN08_1782	KEGG	mmic00400	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1782	1806.RN08_1782	KEGG	mmic01100	Metabolic pathways
RN08_1782	1806.RN08_1782	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1782	1806.RN08_1782	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1782	1806.RN08_1782	KEGG	mmic02024	Quorum sensing
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0057	Aromatic amino acid biosynthesis
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0175	Coiled coil
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0456	Lyase
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0460	Magnesium
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0479	Metal-binding
RN08_1782	1806.RN08_1782	UniProt Keywords	KW-0822	Tryptophan biosynthesis
RN08_1784	1806.RN08_1784	GO Process	GO:0000162	Tryptophan biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006082	Organic acid metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006568	Tryptophan metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006576	Cellular biogenic amine metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006586	Indolalkylamine metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0008152	Metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009058	Biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009072	Aromatic amino acid family metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009073	Aromatic amino acid family biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009308	Amine metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009309	Amine biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0009987	Cellular process
RN08_1784	1806.RN08_1784	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0018130	Heterocycle biosynthetic process

RN08_1784	1806.RN08_1784	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0042401	Cellular biogenic amine biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0042430	Indole-containing compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0042435	Indole-containing compound biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044106	Cellular amine metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044237	Cellular metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044238	Primary metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044281	Small molecule metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0046219	Indolalkylamine biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:0046483	Heterocycle metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:0071704	Organic substance metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1784	1806.RN08_1784	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1784	1806.RN08_1784	GO Function	GO:0003824	Catalytic activity
RN08_1784	1806.RN08_1784	GO Function	GO:0004425	indole-3-glycerol-phosphate synthase activity
RN08_1784	1806.RN08_1784	GO Function	GO:0016829	Lyase activity
RN08_1784	1806.RN08_1784	GO Function	GO:0016830	Carbon-carbon lyase activity
RN08_1784	1806.RN08_1784	GO Function	GO:0016831	Carboxy-lyase activity
RN08_1784	1806.RN08_1784	GO Component	GO:0005618	Cell wall
RN08_1784	1806.RN08_1784	GO Component	GO:0005886	Plasma membrane
RN08_1784	1806.RN08_1784	GO Component	GO:0016020	Membrane
RN08_1784	1806.RN08_1784	GO Component	GO:0030312	External encapsulating structure
RN08_1784	1806.RN08_1784	GO Component	GO:0071944	Cell periphery
RN08_1784	1806.RN08_1784	GO Component	GO:0110165	Cellular anatomical entity
RN08_1784	1806.RN08_1784	STRING clusters	CL:166	Aromatic amino acid family biosynthetic process, and isochorismate synthase activity
RN08_1784	1806.RN08_1784	STRING clusters	CL:167	Aromatic amino acid family biosynthetic process
RN08_1784	1806.RN08_1784	STRING clusters	CL:168	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1784	1806.RN08_1784	STRING clusters	CL:195	Tryptophan biosynthetic process
RN08_1784	1806.RN08_1784	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1784	1806.RN08_1784	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1784	1806.RN08_1784	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1784	1806.RN08_1784	KEGG	mmic00400	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1784	1806.RN08_1784	KEGG	mmic01100	Metabolic pathways
RN08_1784	1806.RN08_1784	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1784	1806.RN08_1784	KEGG	mmic01230	Biosynthesis of amino acids

RN08_1784	1806.RN08_1784	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1784	1806.RN08_1784	UniProt Keywords	KW-0057	Aromatic amino acid biosynthesis
RN08_1784	1806.RN08_1784	UniProt Keywords	KW-0210	Decarboxylase
RN08_1784	1806.RN08_1784	UniProt Keywords	KW-0456	Lyase
RN08_1784	1806.RN08_1784	UniProt Keywords	KW-0822	Tryptophan biosynthesis
RN08_1785	1806.RN08_1785	GO Process	GO:0000162	Tryptophan biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006082	Organic acid metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006568	Tryptophan metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006576	Cellular biogenic amine metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006586	Indolalkylamine metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0008152	Metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009058	Biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009072	Aromatic amino acid family metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009073	Aromatic amino acid family biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009308	Amine metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009309	Amine biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0009987	Cellular process
RN08_1785	1806.RN08_1785	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0042401	Cellular biogenic amine biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0042430	Indole-containing compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0042435	Indole-containing compound biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044106	Cellular amine metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044237	Cellular metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044238	Primary metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044281	Small molecule metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0046219	Indolalkylamine biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:0046483	Heterocycle metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:0071704	Organic substance metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901362	Organic cyclic compound biosynthetic process

RN08_1785	1806.RN08_1785	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1785	1806.RN08_1785	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1785	1806.RN08_1785	GO Function	GO:0003824	Catalytic activity
RN08_1785	1806.RN08_1785	GO Function	GO:0004834	Tryptophan synthase activity
RN08_1785	1806.RN08_1785	GO Function	GO:0016829	Lyase activity
RN08_1785	1806.RN08_1785	GO Function	GO:0016835	Carbon-oxygen lyase activity
RN08_1785	1806.RN08_1785	GO Function	GO:0016836	Hydro-lyase activity
RN08_1785	1806.RN08_1785	GO Component	GO:0005622	Intracellular
RN08_1785	1806.RN08_1785	GO Component	GO:0005737	Cytoplasm
RN08_1785	1806.RN08_1785	GO Component	GO:0110165	Cellular anatomical entity
RN08_1785	1806.RN08_1785	STRING clusters	CL:166	Aromatic amino acid family biosynthetic process, and isochorismate synthase activity
RN08_1785	1806.RN08_1785	STRING clusters	CL:167	Aromatic amino acid family biosynthetic process
RN08_1785	1806.RN08_1785	STRING clusters	CL:168	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1785	1806.RN08_1785	STRING clusters	CL:195	Tryptophan biosynthetic process
RN08_1785	1806.RN08_1785	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1785	1806.RN08_1785	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1785	1806.RN08_1785	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1785	1806.RN08_1785	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_1785	1806.RN08_1785	KEGG	mmic00400	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1785	1806.RN08_1785	KEGG	mmic01100	Metabolic pathways
RN08_1785	1806.RN08_1785	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1785	1806.RN08_1785	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1785	1806.RN08_1785	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1785	1806.RN08_1785	UniProt Keywords	KW-0057	Aromatic amino acid biosynthesis
RN08_1785	1806.RN08_1785	UniProt Keywords	KW-0456	Lyase
RN08_1785	1806.RN08_1785	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_1785	1806.RN08_1785	UniProt Keywords	KW-0822	Tryptophan biosynthesis
RN08_1786	1806.RN08_1786	GO Process	GO:0000162	Tryptophan biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006082	Organic acid metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006568	Tryptophan metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006576	Cellular biogenic amine metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006586	Indolalkylamine metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0008152	Metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0009058	Biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0009072	Aromatic amino acid family metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0009073	Aromatic amino acid family biosynthetic process

RN08_1786	1806.RN08_1786	GO Process	GO:0009308	Amine metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0009309	Amine biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0009987	Cellular process
RN08_1786	1806.RN08_1786	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0042401	Cellular biogenic amine biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0042430	Indole-containing compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0042435	Indole-containing compound biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0043436	Oxoacid metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044106	Cellular amine metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044237	Cellular metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044238	Primary metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044249	Cellular biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044281	Small molecule metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0046219	Indolalkylamine biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:0046483	Heterocycle metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:0071704	Organic substance metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_1786	1806.RN08_1786	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_1786	1806.RN08_1786	GO Function	GO:0003824	Catalytic activity
RN08_1786	1806.RN08_1786	GO Function	GO:0004834	Tryptophan synthase activity
RN08_1786	1806.RN08_1786	GO Function	GO:0016829	Lyase activity
RN08_1786	1806.RN08_1786	GO Function	GO:0016835	Carbon-oxygen lyase activity
RN08_1786	1806.RN08_1786	GO Function	GO:0016836	Hydro-lyase activity
RN08_1786	1806.RN08_1786	GO Component	GO:0005622	Intracellular
RN08_1786	1806.RN08_1786	GO Component	GO:0005737	Cytoplasm
RN08_1786	1806.RN08_1786	GO Component	GO:0005829	Cytosol
RN08_1786	1806.RN08_1786	GO Component	GO:0005886	Plasma membrane
RN08_1786	1806.RN08_1786	GO Component	GO:0016020	Membrane
RN08_1786	1806.RN08_1786	GO Component	GO:0071944	Cell periphery
RN08_1786	1806.RN08_1786	GO Component	GO:0110165	Cellular anatomical entity
RN08_1786	1806.RN08_1786	STRING clusters	CL:166	Aromatic amino acid family biosynthetic process, and isochorismate synthase activity
RN08_1786	1806.RN08_1786	STRING clusters	CL:167	Aromatic amino acid family biosynthetic process
RN08_1786	1806.RN08_1786	STRING clusters	CL:168	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1786	1806.RN08_1786	STRING clusters	CL:195	Tryptophan biosynthetic process
RN08_1786	1806.RN08_1786	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process

RN08_1786	1806.RN08_1786	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_1786	1806.RN08_1786	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_1786	1806.RN08_1786	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_1786	1806.RN08_1786	KEGG	mmic00400	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_1786	1806.RN08_1786	KEGG	mmic01100	Metabolic pathways
RN08_1786	1806.RN08_1786	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_1786	1806.RN08_1786	KEGG	mmic01230	Biosynthesis of amino acids
RN08_1786	1806.RN08_1786	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_1786	1806.RN08_1786	UniProt Keywords	KW-0057	Aromatic amino acid biosynthesis
RN08_1786	1806.RN08_1786	UniProt Keywords	KW-0456	Lyase
RN08_1786	1806.RN08_1786	UniProt Keywords	KW-0822	Tryptophan biosynthesis
RN08_2027	1806.RN08_2027	GO Process	GO:0006629	Lipid metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0006644	Phospholipid metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0006650	Glycerophospholipid metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0006793	Phosphorus metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0008152	Metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0008610	Lipid biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0008654	Phospholipid biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0009058	Biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0009987	Cellular process
RN08_2027	1806.RN08_2027	GO Process	GO:0019637	Organophosphate metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0044237	Cellular metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0044238	Primary metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0045017	Glycerolipid biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0046474	Glycerophospholipid biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:0046486	Glycerolipid metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0071704	Organic substance metabolic process
RN08_2027	1806.RN08_2027	GO Process	GO:0090407	Organophosphate biosynthetic process
RN08_2027	1806.RN08_2027	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2027	1806.RN08_2027	GO Function	GO:0003824	Catalytic activity
RN08_2027	1806.RN08_2027	GO Function	GO:0008444	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
RN08_2027	1806.RN08_2027	GO Function	GO:0016740	Transferase activity
RN08_2027	1806.RN08_2027	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_2027	1806.RN08_2027	GO Function	GO:0016780	Phosphotransferase activity, for other substituted phosphate groups
RN08_2027	1806.RN08_2027	GO Function	GO:0017169	CDP-alcohol phosphatidyltransferase activity
RN08_2027	1806.RN08_2027	GO Component	GO:0005886	Plasma membrane
RN08_2027	1806.RN08_2027	GO Component	GO:0016020	Membrane
RN08_2027	1806.RN08_2027	GO Component	GO:0016021	Integral component of membrane
RN08_2027	1806.RN08_2027	GO Component	GO:0031224	Intrinsic component of membrane
RN08_2027	1806.RN08_2027	GO Component	GO:0071944	Cell periphery
RN08_2027	1806.RN08_2027	GO Component	GO:0110165	Cellular anatomical entity

RN08_2027	1806.RN08_2027	STRING clusters	CL:2743	Glycerophospholipid metabolism, and acylglycerol O-acyltransferase activity
RN08_2027	1806.RN08_2027	STRING clusters	CL:2744	Glycerophospholipid metabolism, and polyol catabolic process
RN08_2027	1806.RN08_2027	STRING clusters	CL:2745	Glycerophospholipid metabolism
RN08_2027	1806.RN08_2027	STRING clusters	CL:2787	Inositol phosphate metabolism, and CDP-alcohol phosphatidyltransferase activity
RN08_2027	1806.RN08_2027	KEGG	mmic00564	Glycerophospholipid metabolism
RN08_2027	1806.RN08_2027	KEGG	mmic01100	Metabolic pathways
RN08_2027	1806.RN08_2027	UniProt Keywords	KW-0472	Membrane
RN08_2027	1806.RN08_2027	UniProt Keywords	KW-0808	Transferase
RN08_2027	1806.RN08_2027	UniProt Keywords	KW-0812	Transmembrane
RN08_2027	1806.RN08_2027	UniProt Keywords	KW-1133	Transmembrane helix
RN08_2431	1806.RN08_2431	GO Process	GO:0000162	Tryptophan biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006082	Organic acid metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006568	Tryptophan metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006576	Cellular biogenic amine metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006586	Indolalkylamine metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0008152	Metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009058	Biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009072	Aromatic amino acid family metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009073	Aromatic amino acid family biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009308	Amine metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009309	Amine biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0009987	Cellular process
RN08_2431	1806.RN08_2431	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0042401	Cellular biogenic amine biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0042430	Indole-containing compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0042435	Indole-containing compound biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0043436	Oxoacid metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044106	Cellular amine metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044237	Cellular metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044238	Primary metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044281	Small molecule metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0046219	Indolalkylamine biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:0046394	Carboxylic acid biosynthetic process

RN08_2431	1806.RN08_2431	GO Process	GO:0046483	Heterocycle metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:0071704	Organic substance metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_2431	1806.RN08_2431	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_2431	1806.RN08_2431	GO Function	GO:0000287	Magnesium ion binding
RN08_2431	1806.RN08_2431	GO Function	GO:0003824	Catalytic activity
RN08_2431	1806.RN08_2431	GO Function	GO:0004048	Anthranilate phosphoribosyltransferase activity
RN08_2431	1806.RN08_2431	GO Function	GO:0005488	Binding
RN08_2431	1806.RN08_2431	GO Function	GO:0016740	Transferase activity
RN08_2431	1806.RN08_2431	GO Function	GO:0016757	Transferase activity, transferring glycosyl groups
RN08_2431	1806.RN08_2431	GO Function	GO:0016763	Transferase activity, transferring pentosyl groups
RN08_2431	1806.RN08_2431	GO Function	GO:0043167	Ion binding
RN08_2431	1806.RN08_2431	GO Function	GO:0043169	Cation binding
RN08_2431	1806.RN08_2431	GO Function	GO:0046872	Metal ion binding
RN08_2431	1806.RN08_2431	GO Component	GO:0005576	Extracellular region
RN08_2431	1806.RN08_2431	GO Component	GO:0005622	Intracellular
RN08_2431	1806.RN08_2431	GO Component	GO:0005737	Cytoplasm
RN08_2431	1806.RN08_2431	GO Component	GO:0005829	Cytosol
RN08_2431	1806.RN08_2431	GO Component	GO:0005886	Plasma membrane
RN08_2431	1806.RN08_2431	GO Component	GO:0016020	Membrane
RN08_2431	1806.RN08_2431	GO Component	GO:0071944	Cell periphery
RN08_2431	1806.RN08_2431	GO Component	GO:0110165	Cellular anatomical entity
RN08_2431	1806.RN08_2431	STRING clusters	CL:166	Aromatic amino acid family biosynthetic process, and isochorismate synthase activity
RN08_2431	1806.RN08_2431	STRING clusters	CL:167	Aromatic amino acid family biosynthetic process
RN08_2431	1806.RN08_2431	STRING clusters	CL:168	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_2431	1806.RN08_2431	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_2431	1806.RN08_2431	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_2431	1806.RN08_2431	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_2431	1806.RN08_2431	KEGG	mmic00400	Phenylalanine, tyrosine and tryptophan biosynthesis
RN08_2431	1806.RN08_2431	KEGG	mmic01100	Metabolic pathways
RN08_2431	1806.RN08_2431	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_2431	1806.RN08_2431	KEGG	mmic01230	Biosynthesis of amino acids
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0057	Aromatic amino acid biosynthesis
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0328	Glycosyltransferase
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0460	Magnesium
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0479	Metal-binding

RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0808	Transferase
RN08_2431	1806.RN08_2431	UniProt Keywords	KW-0822	Tryptophan biosynthesis
RN08_2453	1806.RN08_2453	GO Process	GO:0006082	Organic acid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0006549	Isoleucine metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0006551	Leucine metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0006573	Valine metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0008152	Metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009058	Biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009098	Leucine biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009099	Valine biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0009987	Cellular process
RN08_2453	1806.RN08_2453	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0043436	Oxoacid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0044237	Cellular metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0044238	Primary metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0044281	Small molecule metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:0071704	Organic substance metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2453	1806.RN08_2453	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_2453	1806.RN08_2453	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_2453	1806.RN08_2453	GO Function	GO:0003824	Catalytic activity
RN08_2453	1806.RN08_2453	GO Function	GO:0004084	Branched-chain-amino-acid transaminase activity
RN08_2453	1806.RN08_2453	GO Function	GO:0008483	Transaminase activity
RN08_2453	1806.RN08_2453	GO Function	GO:0016740	Transferase activity
RN08_2453	1806.RN08_2453	GO Function	GO:0016769	Transferase activity, transferring nitrogenous groups
RN08_2453	1806.RN08_2453	GO Function	GO:0052654	L-leucine transaminase activity
RN08_2453	1806.RN08_2453	GO Function	GO:0052655	L-valine transaminase activity
RN08_2453	1806.RN08_2453	GO Function	GO:0052656	L-isoleucine transaminase activity
RN08_2453	1806.RN08_2453	GO Component	GO:0005622	Intracellular
RN08_2453	1806.RN08_2453	GO Component	GO:0005737	Cytoplasm
RN08_2453	1806.RN08_2453	GO Component	GO:0005829	Cytosol
RN08_2453	1806.RN08_2453	GO Component	GO:0110165	Cellular anatomical entity
RN08_2453	1806.RN08_2453	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process

RN08_2453	1806.RN08_2453	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_2453	1806.RN08_2453	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_2453	1806.RN08_2453	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_2453	1806.RN08_2453	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_2453	1806.RN08_2453	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disu
RN08_2453	1806.RN08_2453	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_2453	1806.RN08_2453	KEGG	mmic00280	Valine, leucine and isoleucine degradation
RN08_2453	1806.RN08_2453	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_2453	1806.RN08_2453	KEGG	mmic00770	Pantothenate and CoA biosynthesis
RN08_2453	1806.RN08_2453	KEGG	mmic01100	Metabolic pathways
RN08_2453	1806.RN08_2453	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_2453	1806.RN08_2453	KEGG	mmic01210	2-Oxocarboxylic acid metabolism
RN08_2453	1806.RN08_2453	KEGG	mmic01230	Biosynthesis of amino acids
RN08_2453	1806.RN08_2453	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_2453	1806.RN08_2453	UniProt Keywords	KW-0032	Aminotransferase
RN08_2453	1806.RN08_2453	UniProt Keywords	KW-0100	Branched-chain amino acid biosynthesis
RN08_2453	1806.RN08_2453	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_2453	1806.RN08_2453	UniProt Keywords	KW-0808	Transferase
RN08_2590	1806.RN08_2590	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006082	Organic acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006534	Cysteine metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006535	Cysteine biosynthetic process from serine
RN08_2590	1806.RN08_2590	GO Process	GO:0006563	L-serine metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0008152	Metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0009058	Biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0009069	Serine family amino acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0009070	Serine family amino acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0009987	Cellular process
RN08_2590	1806.RN08_2590	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0019344	Cysteine biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0043436	Oxoacid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044237	Cellular metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044238	Primary metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044281	Small molecule metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:0044283	Small molecule biosynthetic process

RN08_2590	1806.RN08_2590	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:0071704	Organic substance metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2590	1806.RN08_2590	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_2590	1806.RN08_2590	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_2590	1806.RN08_2590	GO Function	GO:0003824	Catalytic activity
RN08_2590	1806.RN08_2590	GO Function	GO:0008374	O-acyltransferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0009001	Serine o-acetyltransferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0016407	Acetyltransferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0016412	Serine o-acyltransferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0016413	O-acetyltransferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0016740	Transferase activity
RN08_2590	1806.RN08_2590	GO Function	GO:0016746	Transferase activity, transferring acyl groups
RN08_2590	1806.RN08_2590	GO Function	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
RN08_2590	1806.RN08_2590	GO Component	GO:0005622	Intracellular
RN08_2590	1806.RN08_2590	GO Component	GO:0005737	Cytoplasm
RN08_2590	1806.RN08_2590	GO Component	GO:0005829	Cytosol
RN08_2590	1806.RN08_2590	GO Component	GO:0110165	Cellular anatomical entity
RN08_2590	1806.RN08_2590	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_2590	1806.RN08_2590	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_2590	1806.RN08_2590	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_2590	1806.RN08_2590	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_2590	1806.RN08_2590	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_2590	1806.RN08_2590	STRING clusters	CL:529	Cysteine biosynthetic process from serine, and de novo l-methionine biosynthetic process
RN08_2590	1806.RN08_2590	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_2590	1806.RN08_2590	KEGG	mmic00920	Sulfur metabolism
RN08_2590	1806.RN08_2590	KEGG	mmic01100	Metabolic pathways
RN08_2590	1806.RN08_2590	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_2590	1806.RN08_2590	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_2590	1806.RN08_2590	KEGG	mmic01200	Carbon metabolism
RN08_2590	1806.RN08_2590	KEGG	mmic01230	Biosynthesis of amino acids
RN08_2590	1806.RN08_2590	UniProt Keywords	KW-0808	Transferase
RN08_2598	1806.RN08_2598	GO Process	GO:0006139	Nucleobase-containing compound metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0006259	DNA metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0006260	DNA replication
RN08_2598	1806.RN08_2598	GO Process	GO:0006261	DNA-dependent DNA replication
RN08_2598	1806.RN08_2598	GO Process	GO:0006269	DNA replication, synthesis of RNA primer
RN08_2598	1806.RN08_2598	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0008152	Metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0009058	Biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0009059	Macromolecule biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0009987	Cellular process
RN08_2598	1806.RN08_2598	GO Process	GO:0016070	RNA metabolic process

RN08_2598	1806.RN08_2598	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0032774	RNA biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0034645	Cellular macromolecule biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0034654	Nucleobase-containing compound biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0043170	Macromolecule metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0044237	Cellular metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0044238	Primary metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0044260	Cellular macromolecule metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:0046483	Heterocycle metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0071704	Organic substance metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:0090304	Nucleic acid metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_2598	1806.RN08_2598	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_2598	1806.RN08_2598	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2598	1806.RN08_2598	GO Function	GO:0003676	Nucleic acid binding
RN08_2598	1806.RN08_2598	GO Function	GO:0003677	DNA binding
RN08_2598	1806.RN08_2598	GO Function	GO:0003824	Catalytic activity
RN08_2598	1806.RN08_2598	GO Function	GO:0003896	DNA primase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0003899	DNA-directed 5-3 RNA polymerase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0005488	Binding
RN08_2598	1806.RN08_2598	GO Function	GO:0008270	Zinc ion binding
RN08_2598	1806.RN08_2598	GO Function	GO:0016740	Transferase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_2598	1806.RN08_2598	GO Function	GO:0016779	Nucleotidyltransferase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0034062	5-3 RNA polymerase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0043167	Ion binding
RN08_2598	1806.RN08_2598	GO Function	GO:0043169	Cation binding
RN08_2598	1806.RN08_2598	GO Function	GO:0046872	Metal ion binding
RN08_2598	1806.RN08_2598	GO Function	GO:0046914	Transition metal ion binding
RN08_2598	1806.RN08_2598	GO Function	GO:0097159	Organic cyclic compound binding
RN08_2598	1806.RN08_2598	GO Function	GO:0097747	RNA polymerase activity
RN08_2598	1806.RN08_2598	GO Function	GO:0140098	Catalytic activity, acting on rna
RN08_2598	1806.RN08_2598	GO Function	GO:1901363	Heterocyclic compound binding
RN08_2598	1806.RN08_2598	GO Component	GO:0005622	Intracellular
RN08_2598	1806.RN08_2598	GO Component	GO:0005657	Replication fork
RN08_2598	1806.RN08_2598	GO Component	GO:0005694	Chromosome
RN08_2598	1806.RN08_2598	GO Component	GO:0030894	Replisome
RN08_2598	1806.RN08_2598	GO Component	GO:0032991	Protein-containing complex
RN08_2598	1806.RN08_2598	GO Component	GO:0032993	protein-DNA complex
RN08_2598	1806.RN08_2598	GO Component	GO:0043226	Organelle
RN08_2598	1806.RN08_2598	GO Component	GO:0043228	Non-membrane-bounded organelle
RN08_2598	1806.RN08_2598	GO Component	GO:0043229	Intracellular organelle
RN08_2598	1806.RN08_2598	GO Component	GO:0043232	Intracellular non-membrane-bounded organelle

RN08_2598	1806.RN08_2598	GO Component	GO:0110165	Cellular anatomical entity
RN08_2598	1806.RN08_2598	GO Component	GO:1990077	Primosome complex
RN08_2598	1806.RN08_2598	STRING clusters	CL:1688	Mixed, incl. trna threonylcarbamoyladenosine modification, and dna primase activity
RN08_2598	1806.RN08_2598	KEGG	mmic03030	DNA replication
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0235	DNA replication
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0238	DNA-binding
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0240	DNA-directed RNA polymerase
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0460	Magnesium
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0479	Metal-binding
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0548	Nucleotidyltransferase
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0639	Primosome
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0804	Transcription
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0808	Transferase
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0862	Zinc
RN08_2598	1806.RN08_2598	UniProt Keywords	KW-0863	Zinc-finger
RN08_2680	1806.RN08_2680	GO Function	GO:0005488	Binding
RN08_2680	1806.RN08_2680	GO Function	GO:0008289	Lipid binding
RN08_2680	1806.RN08_2680	GO Component	GO:0005886	Plasma membrane
RN08_2680	1806.RN08_2680	GO Component	GO:0016020	Membrane
RN08_2680	1806.RN08_2680	GO Component	GO:0071944	Cell periphery
RN08_2680	1806.RN08_2680	GO Component	GO:0110165	Cellular anatomical entity
RN08_2680	1806.RN08_2680	STRING clusters	CL:4150	Mixed, incl. establishment of competence for transformation, and positive regulation of carbohydrate metabolic process
RN08_2680	1806.RN08_2680	STRING clusters	CL:4171	Establishment of competence for transformation, and o-octanoyltransferase activity
RN08_2680	1806.RN08_2680	KEGG	mmic00230	Purine metabolism
RN08_2680	1806.RN08_2680	KEGG	mmic01100	Metabolic pathways
RN08_2680	1806.RN08_2680	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_2680	1806.RN08_2680	UniProt Keywords	KW-0446	Lipid-binding
RN08_2681	1806.RN08_2681	GO Process	GO:0009987	Cellular process
RN08_2681	1806.RN08_2681	GO Process	GO:0016043	Cellular component organization
RN08_2681	1806.RN08_2681	GO Process	GO:0022607	Cellular component assembly
RN08_2681	1806.RN08_2681	GO Process	GO:0043933	Protein-containing complex subunit organization
RN08_2681	1806.RN08_2681	GO Process	GO:0044085	Cellular component biogenesis
RN08_2681	1806.RN08_2681	GO Process	GO:0051259	Protein complex oligomerization
RN08_2681	1806.RN08_2681	GO Process	GO:0051262	Protein tetramerization
RN08_2681	1806.RN08_2681	GO Process	GO:0065003	Protein-containing complex assembly
RN08_2681	1806.RN08_2681	GO Process	GO:0071840	Cellular component organization or biogenesis
RN08_2681	1806.RN08_2681	GO Function	GO:0003824	Catalytic activity

RN08_2681	1806.RN08_2681	GO Function	GO:0008374	O-acyltransferase activity
RN08_2681	1806.RN08_2681	GO Function	GO:0016414	O-octanoyltransferase activity
RN08_2681	1806.RN08_2681	GO Function	GO:0016415	Octanoyltransferase activity
RN08_2681	1806.RN08_2681	GO Function	GO:0016740	Transferase activity
RN08_2681	1806.RN08_2681	GO Function	GO:0016746	Transferase activity, transferring acyl groups
RN08_2681	1806.RN08_2681	GO Function	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
RN08_2681	1806.RN08_2681	GO Component	GO:0005886	Plasma membrane
RN08_2681	1806.RN08_2681	GO Component	GO:0016020	Membrane
RN08_2681	1806.RN08_2681	GO Component	GO:0071944	Cell periphery
RN08_2681	1806.RN08_2681	GO Component	GO:0110165	Cellular anatomical entity
RN08_2681	1806.RN08_2681	STRING clusters	CL:4150	Mixed, incl. establishment of competence for transformation, and positive regulation of carbohydrate metabolic process
RN08_2681	1806.RN08_2681	STRING clusters	CL:4171	Establishment of competence for transformation, and o-octanoyltransferase activity
RN08_2681	1806.RN08_2681	KEGG	mmic01040	Biosynthesis of unsaturated fatty acids
RN08_2724	1806.RN08_2724	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006082	Organic acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006555	Methionine metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006575	Cellular modified amino acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0008152	Metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0009058	Biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0009086	Methionine biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0009987	Cellular process
RN08_2724	1806.RN08_2724	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0032259	Methylation
RN08_2724	1806.RN08_2724	GO Process	GO:0033477	S-methylmethionine metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0033528	S-methylmethionine cycle
RN08_2724	1806.RN08_2724	GO Process	GO:0043436	Oxoacid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044237	Cellular metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044238	Primary metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044281	Small molecule metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:0071704	Organic substance metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2724	1806.RN08_2724	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_2724	1806.RN08_2724	GO Process	GO:1901607	Alpha-amino acid biosynthetic process

RN08_2724	1806.RN08_2724	GO Function	GO:0003824	Catalytic activity
RN08_2724	1806.RN08_2724	GO Function	GO:0005488	Binding
RN08_2724	1806.RN08_2724	GO Function	GO:0008168	Methyltransferase activity
RN08_2724	1806.RN08_2724	GO Function	GO:0008172	S-methyltransferase activity
RN08_2724	1806.RN08_2724	GO Function	GO:0008270	Zinc ion binding
RN08_2724	1806.RN08_2724	GO Function	GO:0008757	S-adenosylmethionine-dependent methyltransferase activity
RN08_2724	1806.RN08_2724	GO Function	GO:0008898	S-adenosylmethionine-homocysteine S-methyltransferase activity
RN08_2724	1806.RN08_2724	GO Function	GO:0016740	Transferase activity
RN08_2724	1806.RN08_2724	GO Function	GO:0016741	Transferase activity, transferring one-carbon groups
RN08_2724	1806.RN08_2724	GO Function	GO:0043167	Ion binding
RN08_2724	1806.RN08_2724	GO Function	GO:0043169	Cation binding
RN08_2724	1806.RN08_2724	GO Function	GO:0046872	Metal ion binding
RN08_2724	1806.RN08_2724	GO Function	GO:0046914	Transition metal ion binding
RN08_2724	1806.RN08_2724	GO Function	GO:0047150	Betaine-homocysteine s-methyltransferase activity
RN08_2724	1806.RN08_2724	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_2724	1806.RN08_2724	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_2724	1806.RN08_2724	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_2724	1806.RN08_2724	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_2724	1806.RN08_2724	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_2724	1806.RN08_2724	STRING clusters	CL:517	S-methyltransferase activity, and adenosylhomocysteinase activity
RN08_2724	1806.RN08_2724	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_2724	1806.RN08_2724	KEGG	mmic01100	Metabolic pathways
RN08_2724	1806.RN08_2724	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_2724	1806.RN08_2724	UniProt Keywords	KW-0479	Metal-binding
RN08_2724	1806.RN08_2724	UniProt Keywords	KW-0489	Methyltransferase
RN08_2724	1806.RN08_2724	UniProt Keywords	KW-0808	Transferase
RN08_2724	1806.RN08_2724	UniProt Keywords	KW-0862	Zinc
RN08_2746	1806.RN08_2746	GO Process	GO:0006260	DNA replication
RN08_2746	1806.RN08_2746	GO Process	GO:0008152	Metabolic process
RN08_2746	1806.RN08_2746	GO Process	GO:0009058	Biosynthetic process
RN08_2746	1806.RN08_2746	GO Process	GO:0009059	Macromolecule biosynthetic process
RN08_2746	1806.RN08_2746	GO Process	GO:0009987	Cellular process
RN08_2746	1806.RN08_2746	GO Process	GO:0034645	Cellular macromolecule biosynthetic process
RN08_2746	1806.RN08_2746	GO Process	GO:0043170	Macromolecule metabolic process
RN08_2746	1806.RN08_2746	GO Process	GO:0044237	Cellular metabolic process
RN08_2746	1806.RN08_2746	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2746	1806.RN08_2746	GO Process	GO:0044260	Cellular macromolecule metabolic process
RN08_2746	1806.RN08_2746	GO Process	GO:0071704	Organic substance metabolic process
RN08_2746	1806.RN08_2746	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2746	1806.RN08_2746	GO Function	GO:0003676	Nucleic acid binding
RN08_2746	1806.RN08_2746	GO Function	GO:0003677	DNA binding
RN08_2746	1806.RN08_2746	GO Function	GO:0003697	Single-stranded dna binding
RN08_2746	1806.RN08_2746	GO Function	GO:0005488	Binding
RN08_2746	1806.RN08_2746	GO Function	GO:0097159	Organic cyclic compound binding

RN08_2746	1806.RN08_2746	GO Function	GO:1901363	Heterocyclic compound binding
RN08_2746	1806.RN08_2746	GO Component	GO:0009295	Nucleoid
RN08_2746	1806.RN08_2746	GO Component	GO:0110165	Cellular anatomical entity
RN08_2746	1806.RN08_2746	STRING clusters	CL:1718	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	STRING clusters	CL:1719	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	STRING clusters	CL:1720	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	STRING clusters	CL:1721	DNA repair, and DNA replication
RN08_2746	1806.RN08_2746	STRING clusters	CL:1723	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	STRING clusters	CL:1724	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	STRING clusters	CL:1726	DNA repair, and Mismatch repair
RN08_2746	1806.RN08_2746	KEGG	mmic03030	DNA replication
RN08_2746	1806.RN08_2746	KEGG	mmic03430	Mismatch repair
RN08_2746	1806.RN08_2746	KEGG	mmic03440	Homologous recombination
RN08_2746	1806.RN08_2746	UniProt Keywords	KW-0238	DNA-binding
RN08_2892	1806.RN08_2892	GO Process	GO:0006629	Lipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006643	Membrane lipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006644	Phospholipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006650	Glycerophospholipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006664	Glycolipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006793	Phosphorus metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0008152	Metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0008610	Lipid biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:0009058	Biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:0009247	Glycolipid biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:0009987	Cellular process
RN08_2892	1806.RN08_2892	GO Process	GO:0019637	Organophosphate metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0044237	Cellular metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0044238	Primary metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0046467	Membrane lipid biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:0046486	Glycerolipid metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0046488	Phosphatidylinositol metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:0071704	Organic substance metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:1901135	Carbohydrate derivative metabolic process
RN08_2892	1806.RN08_2892	GO Process	GO:1901137	Carbohydrate derivative biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2892	1806.RN08_2892	GO Process	GO:1903509	Liposaccharide metabolic process
RN08_2892	1806.RN08_2892	GO Function	GO:0003824	Catalytic activity
RN08_2892	1806.RN08_2892	GO Function	GO:0016740	Transferase activity
RN08_2892	1806.RN08_2892	GO Function	GO:0016746	Transferase activity, transferring acyl groups
RN08_2892	1806.RN08_2892	GO Component	GO:0005886	Plasma membrane
RN08_2892	1806.RN08_2892	GO Component	GO:0016020	Membrane
RN08_2892	1806.RN08_2892	GO Component	GO:0016021	Integral component of membrane
RN08_2892	1806.RN08_2892	GO Component	GO:0031224	Intrinsic component of membrane

RN08_2892	1806.RN08_2892	GO Component	GO:0071944	Cell periphery
RN08_2892	1806.RN08_2892	GO Component	GO:0110165	Cellular anatomical entity
RN08_2892	1806.RN08_2892	STRING clusters	CL:3771	Mixed, incl. external encapsulating structure organization, and transmembrane helix
RN08_2892	1806.RN08_2892	STRING clusters	CL:3773	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2892	1806.RN08_2892	STRING clusters	CL:3775	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2892	1806.RN08_2892	STRING clusters	CL:3776	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2892	1806.RN08_2892	STRING clusters	CL:4022	Mixed, incl. mannosylation, and lipoarabinomannan (lam) biosynthesis
RN08_2892	1806.RN08_2892	STRING clusters	CL:4024	Mixed, incl. threonyl-trna aminoacylation, and atp adenylyltransferase activity
RN08_2892	1806.RN08_2892	KEGG	mmic01100	Metabolic pathways
RN08_2892	1806.RN08_2892	UniProt Keywords	KW-0012	Acyltransferase
RN08_2892	1806.RN08_2892	UniProt Keywords	KW-0808	Transferase
RN08_2893	1806.RN08_2893	GO Process	GO:0006629	Lipid metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0006644	Phospholipid metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0006793	Phosphorus metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0008152	Metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0008610	Lipid biosynthetic process
RN08_2893	1806.RN08_2893	GO Process	GO:0008654	Phospholipid biosynthetic process
RN08_2893	1806.RN08_2893	GO Process	GO:0009058	Biosynthetic process
RN08_2893	1806.RN08_2893	GO Process	GO:0009987	Cellular process
RN08_2893	1806.RN08_2893	GO Process	GO:0019637	Organophosphate metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0044237	Cellular metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0044238	Primary metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2893	1806.RN08_2893	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0071704	Organic substance metabolic process
RN08_2893	1806.RN08_2893	GO Process	GO:0090407	Organophosphate biosynthetic process
RN08_2893	1806.RN08_2893	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2893	1806.RN08_2893	GO Function	GO:0003824	Catalytic activity
RN08_2893	1806.RN08_2893	GO Function	GO:0005488	Binding
RN08_2893	1806.RN08_2893	GO Function	GO:0016740	Transferase activity
RN08_2893	1806.RN08_2893	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_2893	1806.RN08_2893	GO Function	GO:0016780	Phosphotransferase activity, for other substituted phosphate groups
RN08_2893	1806.RN08_2893	GO Function	GO:0043167	Ion binding
RN08_2893	1806.RN08_2893	GO Function	GO:0043169	Cation binding
RN08_2893	1806.RN08_2893	GO Function	GO:0046872	Metal ion binding
RN08_2893	1806.RN08_2893	GO Component	GO:0005886	Plasma membrane
RN08_2893	1806.RN08_2893	GO Component	GO:0016020	Membrane
RN08_2893	1806.RN08_2893	GO Component	GO:0016021	Integral component of membrane
RN08_2893	1806.RN08_2893	GO Component	GO:0031224	Intrinsic component of membrane
RN08_2893	1806.RN08_2893	GO Component	GO:0071944	Cell periphery
RN08_2893	1806.RN08_2893	GO Component	GO:0110165	Cellular anatomical entity
RN08_2893	1806.RN08_2893	STRING clusters	CL:3771	Mixed, incl. external encapsulating structure organization, and transmembrane helix
RN08_2893	1806.RN08_2893	STRING clusters	CL:3773	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2893	1806.RN08_2893	STRING clusters	CL:3775	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups

RN08_2893	1806.RN08_2893	STRING clusters	CL:3776	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2893	1806.RN08_2893	STRING clusters	CL:4022	Mixed, incl. mannosylation, and lipoarabinomannan (lam) biosynthesis
RN08_2893	1806.RN08_2893	STRING clusters	CL:4024	Mixed, incl. threonyl-trna aminoacylation, and atp adenylyltransferase activity
RN08_2893	1806.RN08_2893	KEGG	mmic00564	Glycerophospholipid metabolism
RN08_2893	1806.RN08_2893	KEGG	mmic01100	Metabolic pathways
RN08_2893	1806.RN08_2893	UniProt Keywords	KW-0472	Membrane
RN08_2893	1806.RN08_2893	UniProt Keywords	KW-0808	Transferase
RN08_2893	1806.RN08_2893	UniProt Keywords	KW-0812	Transmembrane
RN08_2893	1806.RN08_2893	UniProt Keywords	KW-1133	Transmembrane helix
RN08_2894	1806.RN08_2894	GO Process	GO:0006139	Nucleobase-containing compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0006725	Cellular aromatic compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0006753	Nucleoside phosphate metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0006793	Phosphorus metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0008152	Metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0009056	Catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0009058	Biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0009117	Nucleotide metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0009166	Nucleotide catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0009987	Cellular process
RN08_2894	1806.RN08_2894	GO Process	GO:0015959	Diadenosine polyphosphate metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0015961	Diadenosine polyphosphate catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0015965	Diadenosine tetraphosphate metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0015967	Diadenosine tetraphosphate catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0018130	Heterocycle biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0019438	Aromatic compound biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0019439	Aromatic compound catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0019637	Organophosphate metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0034404	Nucleobase-containing small molecule biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0034641	Cellular nitrogen compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0034654	Nucleobase-containing compound biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0034655	Nucleobase-containing compound catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044237	Cellular metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044238	Primary metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044248	Cellular catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044249	Cellular biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044270	Cellular nitrogen compound catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044271	Cellular nitrogen compound biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044281	Small molecule metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:0046434	Organophosphate catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0046483	Heterocycle metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0046700	Heterocycle catabolic process

RN08_2894	1806.RN08_2894	GO Process	GO:0055086	Nucleobase-containing small molecule metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:0071704	Organic substance metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901292	Nucleoside phosphate catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901360	Organic cyclic compound metabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901361	Organic cyclic compound catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901362	Organic cyclic compound biosynthetic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901575	Organic substance catabolic process
RN08_2894	1806.RN08_2894	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_2894	1806.RN08_2894	GO Function	GO:0000166	Nucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0003824	Catalytic activity
RN08_2894	1806.RN08_2894	GO Function	GO:0003877	ATP adenylyltransferase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0004551	Nucleotide diphosphatase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0005488	Binding
RN08_2894	1806.RN08_2894	GO Function	GO:0005524	ATP binding
RN08_2894	1806.RN08_2894	GO Function	GO:0008796	bis(5-nucleosyl)-tetraphosphatase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0016462	Pyrophosphatase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0016740	Transferase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_2894	1806.RN08_2894	GO Function	GO:0016779	Nucleotidyltransferase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0016787	Hydrolase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0016817	Hydrolase activity, acting on acid anhydrides
RN08_2894	1806.RN08_2894	GO Function	GO:0016818	Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
RN08_2894	1806.RN08_2894	GO Function	GO:0017076	Purine nucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0030554	Adenyl nucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0032553	Ribonucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0032555	Purine ribonucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0032559	Adenyl ribonucleotide binding
RN08_2894	1806.RN08_2894	GO Function	GO:0035639	Purine ribonucleoside triphosphate binding
RN08_2894	1806.RN08_2894	GO Function	GO:0036094	Small molecule binding
RN08_2894	1806.RN08_2894	GO Function	GO:0043167	Ion binding
RN08_2894	1806.RN08_2894	GO Function	GO:0043168	Anion binding
RN08_2894	1806.RN08_2894	GO Function	GO:0070566	Adenylyltransferase activity
RN08_2894	1806.RN08_2894	GO Function	GO:0097159	Organic cyclic compound binding
RN08_2894	1806.RN08_2894	GO Function	GO:0097367	Carbohydrate derivative binding
RN08_2894	1806.RN08_2894	GO Function	GO:1901265	Nucleoside phosphate binding
RN08_2894	1806.RN08_2894	GO Function	GO:1901363	Heterocyclic compound binding
RN08_2894	1806.RN08_2894	GO Component	GO:0005886	Plasma membrane
RN08_2894	1806.RN08_2894	GO Component	GO:0016020	Membrane
RN08_2894	1806.RN08_2894	GO Component	GO:0071944	Cell periphery
RN08_2894	1806.RN08_2894	GO Component	GO:0110165	Cellular anatomical entity
RN08_2894	1806.RN08_2894	STRING clusters	CL:3771	Mixed, incl. external encapsulating structure organization, and transmembrane helix
RN08_2894	1806.RN08_2894	STRING clusters	CL:3773	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2894	1806.RN08_2894	STRING clusters	CL:3775	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2894	1806.RN08_2894	STRING clusters	CL:3776	Mixed, incl. external encapsulating structure organization, and transferase activity, transferring hexosyl groups
RN08_2894	1806.RN08_2894	STRING clusters	CL:4022	Mixed, incl. mannosylation, and lipoarabinomannan (lam) biosynthesis
RN08_2894	1806.RN08_2894	STRING clusters	CL:4024	Mixed, incl. threonyl-trna aminoacylation, and atp adenylyltransferase activity
RN08_2894	1806.RN08_2894	KEGG	mmic00230	Purine metabolism

RN08_2894	1806.RN08_2894	KEGG	mmic01100	Metabolic pathways
RN08_3032	1806.RN08_3032	GO Process	GO:0006629	Lipid metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0006644	Phospholipid metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0006650	Glycerophospholipid metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0006793	Phosphorus metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0008152	Metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0008610	Lipid biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0008654	Phospholipid biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0009058	Biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0009987	Cellular process
RN08_3032	1806.RN08_3032	GO Process	GO:0019637	Organophosphate metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0044237	Cellular metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0044238	Primary metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0045017	Glycerolipid biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0046474	Glycerophospholipid biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:0046486	Glycerolipid metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0071704	Organic substance metabolic process
RN08_3032	1806.RN08_3032	GO Process	GO:0090407	Organophosphate biosynthetic process
RN08_3032	1806.RN08_3032	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3032	1806.RN08_3032	GO Function	GO:0003824	Catalytic activity
RN08_3032	1806.RN08_3032	GO Function	GO:0008444	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
RN08_3032	1806.RN08_3032	GO Function	GO:0016740	Transferase activity
RN08_3032	1806.RN08_3032	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_3032	1806.RN08_3032	GO Function	GO:0016780	Phosphotransferase activity, for other substituted phosphate groups
RN08_3032	1806.RN08_3032	GO Function	GO:0017169	CDP-alcohol phosphatidyltransferase activity
RN08_3032	1806.RN08_3032	GO Component	GO:0005618	Cell wall
RN08_3032	1806.RN08_3032	GO Component	GO:0005886	Plasma membrane
RN08_3032	1806.RN08_3032	GO Component	GO:0016020	Membrane
RN08_3032	1806.RN08_3032	GO Component	GO:0016021	Integral component of membrane
RN08_3032	1806.RN08_3032	GO Component	GO:0030312	External encapsulating structure
RN08_3032	1806.RN08_3032	GO Component	GO:0031224	Intrinsic component of membrane
RN08_3032	1806.RN08_3032	GO Component	GO:0071944	Cell periphery
RN08_3032	1806.RN08_3032	GO Component	GO:0110165	Cellular anatomical entity
RN08_3032	1806.RN08_3032	STRING clusters	CL:2743	Glycerophospholipid metabolism, and acylglycerol O-acyltransferase activity
RN08_3032	1806.RN08_3032	STRING clusters	CL:2744	Glycerophospholipid metabolism, and polyol catabolic process
RN08_3032	1806.RN08_3032	STRING clusters	CL:2745	Glycerophospholipid metabolism
RN08_3032	1806.RN08_3032	STRING clusters	CL:2787	Inositol phosphate metabolism, and CDP-alcohol phosphatidyltransferase activity
RN08_3032	1806.RN08_3032	KEGG	mmic00564	Glycerophospholipid metabolism
RN08_3032	1806.RN08_3032	KEGG	mmic01100	Metabolic pathways
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0443	Lipid metabolism
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0444	Lipid biosynthesis

RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0472	Membrane
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0594	Phospholipid biosynthesis
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0808	Transferase
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-0812	Transmembrane
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-1133	Transmembrane helix
RN08_3032	1806.RN08_3032	UniProt Keywords	KW-1208	Phospholipid metabolism
RN08_3175	1806.RN08_3175	GO Process	GO:0006629	Lipid metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0006644	Phospholipid metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0006650	Glycerophospholipid metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0006793	Phosphorus metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0008152	Metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0008610	Lipid biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0008654	Phospholipid biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0009058	Biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0009987	Cellular process
RN08_3175	1806.RN08_3175	GO Process	GO:0016024	CDP-diacylglycerol biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0019637	Organophosphate metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0044237	Cellular metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0044238	Primary metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0044255	Cellular lipid metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0045017	Glycerolipid biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0046341	CDP-diacylglycerol metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0046474	Glycerophospholipid biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:0046486	Glycerolipid metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0071704	Organic substance metabolic process
RN08_3175	1806.RN08_3175	GO Process	GO:0090407	Organophosphate biosynthetic process
RN08_3175	1806.RN08_3175	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3175	1806.RN08_3175	GO Function	GO:0003824	Catalytic activity
RN08_3175	1806.RN08_3175	GO Function	GO:0004605	Phosphatidate cytidylyltransferase activity
RN08_3175	1806.RN08_3175	GO Function	GO:0016740	Transferase activity
RN08_3175	1806.RN08_3175	GO Function	GO:0016772	Transferase activity, transferring phosphorus-containing groups
RN08_3175	1806.RN08_3175	GO Function	GO:0016779	Nucleotidyltransferase activity
RN08_3175	1806.RN08_3175	GO Function	GO:0070567	Cytidylyltransferase activity
RN08_3175	1806.RN08_3175	GO Component	GO:0005618	Cell wall
RN08_3175	1806.RN08_3175	GO Component	GO:0005886	Plasma membrane
RN08_3175	1806.RN08_3175	GO Component	GO:0016020	Membrane
RN08_3175	1806.RN08_3175	GO Component	GO:0016021	Integral component of membrane
RN08_3175	1806.RN08_3175	GO Component	GO:0030312	External encapsulating structure
RN08_3175	1806.RN08_3175	GO Component	GO:0031224	Intrinsic component of membrane
RN08_3175	1806.RN08_3175	GO Component	GO:0071944	Cell periphery

RN08_3175	1806.RN08_3175	GO Component	GO:0110165	Cellular anatomical entity
RN08_3175	1806.RN08_3175	STRING clusters	CL:2743	Glycerophospholipid metabolism, and acylglycerol O-acyltransferase activity
RN08_3175	1806.RN08_3175	STRING clusters	CL:2744	Glycerophospholipid metabolism, and polyol catabolic process
RN08_3175	1806.RN08_3175	STRING clusters	CL:2745	Glycerophospholipid metabolism
RN08_3175	1806.RN08_3175	STRING clusters	CL:2787	Inositol phosphate metabolism, and CDP-alcohol phosphatidyltransferase activity
RN08_3175	1806.RN08_3175	KEGG	mmic00564	Glycerophospholipid metabolism
RN08_3175	1806.RN08_3175	KEGG	mmic01100	Metabolic pathways
RN08_3175	1806.RN08_3175	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3175	1806.RN08_3175	UniProt Keywords	KW-0472	Membrane
RN08_3175	1806.RN08_3175	UniProt Keywords	KW-0548	Nucleotidyltransferase
RN08_3175	1806.RN08_3175	UniProt Keywords	KW-0808	Transferase
RN08_3175	1806.RN08_3175	UniProt Keywords	KW-0812	Transmembrane
RN08_3175	1806.RN08_3175	UniProt Keywords	KW-1133	Transmembrane helix
RN08_3313	1806.RN08_3313	GO Process	GO:0006082	Organic acid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0006549	Isoleucine metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0006573	Valine metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0008152	Metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009058	Biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009099	Valine biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0009987	Cellular process
RN08_3313	1806.RN08_3313	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0044237	Cellular metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0044238	Primary metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0044281	Small molecule metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:0055114	Oxidation-reduction process
RN08_3313	1806.RN08_3313	GO Process	GO:0071704	Organic substance metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3313	1806.RN08_3313	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3313	1806.RN08_3313	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3313	1806.RN08_3313	GO Function	GO:0000166	Nucleotide binding

RN08_3313	1806.RN08_3313	GO Function	GO:0000287	Magnesium ion binding
RN08_3313	1806.RN08_3313	GO Function	GO:0003824	Catalytic activity
RN08_3313	1806.RN08_3313	GO Function	GO:0004455	Ketol-acid reductoisomerase activity
RN08_3313	1806.RN08_3313	GO Function	GO:0005488	Binding
RN08_3313	1806.RN08_3313	GO Function	GO:0016491	Oxidoreductase activity
RN08_3313	1806.RN08_3313	GO Function	GO:0016614	Oxidoreductase activity, acting on ch-oh group of donors
RN08_3313	1806.RN08_3313	GO Function	GO:0016616	Oxidoreductase activity, acting on the ch-oh group of donors, nad or nadp as acceptor
RN08_3313	1806.RN08_3313	GO Function	GO:0036094	Small molecule binding
RN08_3313	1806.RN08_3313	GO Function	GO:0043167	Ion binding
RN08_3313	1806.RN08_3313	GO Function	GO:0043169	Cation binding
RN08_3313	1806.RN08_3313	GO Function	GO:0046872	Metal ion binding
RN08_3313	1806.RN08_3313	GO Function	GO:0050661	NADP binding
RN08_3313	1806.RN08_3313	GO Function	GO:0097159	Organic cyclic compound binding
RN08_3313	1806.RN08_3313	GO Function	GO:1901265	Nucleoside phosphate binding
RN08_3313	1806.RN08_3313	GO Function	GO:1901363	Heterocyclic compound binding
RN08_3313	1806.RN08_3313	GO Component	GO:0005622	Intracellular
RN08_3313	1806.RN08_3313	GO Component	GO:0005737	Cytoplasm
RN08_3313	1806.RN08_3313	GO Component	GO:0005829	Cytosol
RN08_3313	1806.RN08_3313	GO Component	GO:0005886	Plasma membrane
RN08_3313	1806.RN08_3313	GO Component	GO:0016020	Membrane
RN08_3313	1806.RN08_3313	GO Component	GO:0071944	Cell periphery
RN08_3313	1806.RN08_3313	GO Component	GO:0110165	Cellular anatomical entity
RN08_3313	1806.RN08_3313	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_3313	1806.RN08_3313	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3313	1806.RN08_3313	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3313	1806.RN08_3313	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_3313	1806.RN08_3313	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_3313	1806.RN08_3313	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_3313	1806.RN08_3313	STRING clusters	CL:666	Valine, leucine and isoleucine biosynthesis
RN08_3313	1806.RN08_3313	STRING clusters	CL:668	Acetolactate synthase activity
RN08_3313	1806.RN08_3313	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_3313	1806.RN08_3313	KEGG	mmic00770	Pantothenate and CoA biosynthesis
RN08_3313	1806.RN08_3313	KEGG	mmic01100	Metabolic pathways
RN08_3313	1806.RN08_3313	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3313	1806.RN08_3313	KEGG	mmic01210	2-Oxocarboxylic acid metabolism
RN08_3313	1806.RN08_3313	KEGG	mmic01230	Biosynthesis of amino acids
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0100	Branched-chain amino acid biosynthesis
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0413	Isomerase
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0460	Magnesium
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0479	Metal-binding

RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0521	NADP
RN08_3313	1806.RN08_3313	UniProt Keywords	KW-0560	Oxidoreductase
RN08_3314	1806.RN08_3314	GO Process	GO:0006082	Organic acid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0006549	Isoleucine metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0006573	Valine metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0008152	Metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009058	Biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009099	Valine biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0009987	Cellular process
RN08_3314	1806.RN08_3314	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0044237	Cellular metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0044238	Primary metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0044281	Small molecule metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:0050790	Regulation of catalytic activity
RN08_3314	1806.RN08_3314	GO Process	GO:0065007	Biological regulation
RN08_3314	1806.RN08_3314	GO Process	GO:0065009	Regulation of molecular function
RN08_3314	1806.RN08_3314	GO Process	GO:0071704	Organic substance metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3314	1806.RN08_3314	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3314	1806.RN08_3314	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3314	1806.RN08_3314	GO Function	GO:0003824	Catalytic activity
RN08_3314	1806.RN08_3314	GO Function	GO:0003984	Acetolactate synthase activity
RN08_3314	1806.RN08_3314	GO Function	GO:0016740	Transferase activity
RN08_3314	1806.RN08_3314	GO Function	GO:0016744	Transferase activity, transferring aldehyde or ketonic groups
RN08_3314	1806.RN08_3314	GO Function	GO:0030234	Enzyme regulator activity
RN08_3314	1806.RN08_3314	GO Function	GO:0098772	Molecular function regulator
RN08_3314	1806.RN08_3314	GO Function	GO:1990610	Acetolactate synthase regulator activity
RN08_3314	1806.RN08_3314	GO Component	GO:0005618	Cell wall
RN08_3314	1806.RN08_3314	GO Component	GO:0005622	Intracellular
RN08_3314	1806.RN08_3314	GO Component	GO:0005737	Cytoplasm
RN08_3314	1806.RN08_3314	GO Component	GO:0005829	Cytosol
RN08_3314	1806.RN08_3314	GO Component	GO:0005886	Plasma membrane

RN08_3314	1806.RN08_3314	GO Component	GO:0005948	Acetolactate synthase complex
RN08_3314	1806.RN08_3314	GO Component	GO:0016020	Membrane
RN08_3314	1806.RN08_3314	GO Component	GO:0030312	External encapsulating structure
RN08_3314	1806.RN08_3314	GO Component	GO:0032991	Protein-containing complex
RN08_3314	1806.RN08_3314	GO Component	GO:0071944	Cell periphery
RN08_3314	1806.RN08_3314	GO Component	GO:0110165	Cellular anatomical entity
RN08_3314	1806.RN08_3314	GO Component	GO:1902494	Catalytic complex
RN08_3314	1806.RN08_3314	GO Component	GO:1990234	Transferase complex
RN08_3314	1806.RN08_3314	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_3314	1806.RN08_3314	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3314	1806.RN08_3314	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3314	1806.RN08_3314	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_3314	1806.RN08_3314	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_3314	1806.RN08_3314	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_3314	1806.RN08_3314	STRING clusters	CL:666	Valine, leucine and isoleucine biosynthesis
RN08_3314	1806.RN08_3314	STRING clusters	CL:668	Acetolactate synthase activity
RN08_3314	1806.RN08_3314	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_3314	1806.RN08_3314	KEGG	mmic00650	Butanoate metabolism
RN08_3314	1806.RN08_3314	KEGG	mmic00660	C5-Branched dibasic acid metabolism
RN08_3314	1806.RN08_3314	KEGG	mmic00770	Pantothenate and CoA biosynthesis
RN08_3314	1806.RN08_3314	KEGG	mmic01100	Metabolic pathways
RN08_3314	1806.RN08_3314	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3314	1806.RN08_3314	KEGG	mmic01210	2-Oxocarboxylic acid metabolism
RN08_3314	1806.RN08_3314	KEGG	mmic01230	Biosynthesis of amino acids
RN08_3314	1806.RN08_3314	UniProt Keywords	KW-0175	Coiled coil
RN08_3353	1806.RN08_3353	GO Process	GO:0006082	Organic acid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006464	Cellular protein modification process
RN08_3353	1806.RN08_3353	GO Process	GO:0006470	Protein dephosphorylation
RN08_3353	1806.RN08_3353	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006563	L-serine metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006564	L-serine biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006793	Phosphorus metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006796	Phosphate-containing compound metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0008152	Metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0009058	Biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0009069	Serine family amino acid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0009070	Serine family amino acid biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0009987	Cellular process
RN08_3353	1806.RN08_3353	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0016311	Dephosphorylation
RN08_3353	1806.RN08_3353	GO Process	GO:0019538	Protein metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0036211	Protein modification process

RN08_3353	1806.RN08_3353	GO Process	GO:0043170	Macromolecule metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0043412	Macromolecule modification
RN08_3353	1806.RN08_3353	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044237	Cellular metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044238	Primary metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044260	Cellular macromolecule metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044267	Cellular protein metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044281	Small molecule metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:0071704	Organic substance metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3353	1806.RN08_3353	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3353	1806.RN08_3353	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3353	1806.RN08_3353	GO Function	GO:0000287	Magnesium ion binding
RN08_3353	1806.RN08_3353	GO Function	GO:0003824	Catalytic activity
RN08_3353	1806.RN08_3353	GO Function	GO:0004647	Phosphoserine phosphatase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0004721	Phosphoprotein phosphatase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0004722	Protein serine/threonine phosphatase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0005488	Binding
RN08_3353	1806.RN08_3353	GO Function	GO:0016597	Amino acid binding
RN08_3353	1806.RN08_3353	GO Function	GO:0016787	Hydrolase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0016788	Hydrolase activity, acting on ester bonds
RN08_3353	1806.RN08_3353	GO Function	GO:0016791	Phosphatase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0031406	Carboxylic acid binding
RN08_3353	1806.RN08_3353	GO Function	GO:0036094	Small molecule binding
RN08_3353	1806.RN08_3353	GO Function	GO:0042578	Phosphoric ester hydrolase activity
RN08_3353	1806.RN08_3353	GO Function	GO:0043167	Ion binding
RN08_3353	1806.RN08_3353	GO Function	GO:0043168	Anion binding
RN08_3353	1806.RN08_3353	GO Function	GO:0043169	Cation binding
RN08_3353	1806.RN08_3353	GO Function	GO:0043177	Organic acid binding
RN08_3353	1806.RN08_3353	GO Function	GO:0046872	Metal ion binding
RN08_3353	1806.RN08_3353	GO Function	GO:0140096	Catalytic activity, acting on a protein
RN08_3353	1806.RN08_3353	GO Component	GO:0005576	Extracellular region
RN08_3353	1806.RN08_3353	GO Component	GO:0005622	Intracellular
RN08_3353	1806.RN08_3353	GO Component	GO:0005737	Cytoplasm
RN08_3353	1806.RN08_3353	GO Component	GO:0018995	Host cellular component
RN08_3353	1806.RN08_3353	GO Component	GO:0030430	Host cell cytoplasm
RN08_3353	1806.RN08_3353	GO Component	GO:0033643	Host cell part
RN08_3353	1806.RN08_3353	GO Component	GO:0033646	Host intracellular part
RN08_3353	1806.RN08_3353	GO Component	GO:0033655	Host cell cytoplasm part
RN08_3353	1806.RN08_3353	GO Component	GO:0043656	Host intracellular region
RN08_3353	1806.RN08_3353	GO Component	GO:0043657	Host cell
RN08_3353	1806.RN08_3353	GO Component	GO:0044164	Host cell cytosol

RN08_3353	1806.RN08_3353	GO Component	GO:0110165	Cellular anatomical entity
RN08_3353	1806.RN08_3353	STRING clusters	CL:154	Serine biosynthesis, and L-serine ammonia-lyase activity
RN08_3353	1806.RN08_3353	STRING clusters	CL:84	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_3353	1806.RN08_3353	STRING clusters	CL:85	Cellular amino acid biosynthetic process, and nucleoside monophosphate biosynthetic process
RN08_3353	1806.RN08_3353	STRING clusters	CL:86	Amino-acid biosynthesis, and transaminase activity
RN08_3353	1806.RN08_3353	STRING clusters	CL:87	Mixed, incl. lysine biosynthesis, and arginine biosynthetic process
RN08_3353	1806.RN08_3353	KEGG	mmic00260	Glycine, serine and threonine metabolism
RN08_3353	1806.RN08_3353	KEGG	mmic00680	Methane metabolism
RN08_3353	1806.RN08_3353	KEGG	mmic01100	Metabolic pathways
RN08_3353	1806.RN08_3353	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3353	1806.RN08_3353	KEGG	mmic01120	Microbial metabolism in diverse environments
RN08_3353	1806.RN08_3353	KEGG	mmic01200	Carbon metabolism
RN08_3353	1806.RN08_3353	KEGG	mmic01230	Biosynthesis of amino acids
RN08_3689	1806.RN08_3689	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006082	Organic acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006534	Cysteine metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006555	Methionine metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0008152	Metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009058	Biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009069	Serine family amino acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009086	Methionine biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009092	Homoserine metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0009987	Cellular process
RN08_3689	1806.RN08_3689	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0019346	Transsulfuration
RN08_3689	1806.RN08_3689	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044237	Cellular metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044238	Primary metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044281	Small molecule metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0050667	Homocysteine metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:0071265	L-methionine biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0071266	De novo l-methionine biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:0071704	Organic substance metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:1901566	Organonitrogen compound biosynthetic process

RN08_3689	1806.RN08_3689	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3689	1806.RN08_3689	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3689	1806.RN08_3689	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3689	1806.RN08_3689	GO Function	GO:0003824	Catalytic activity
RN08_3689	1806.RN08_3689	GO Function	GO:0003961	O-acetylhomoserine aminocarboxypropyltransferase activity
RN08_3689	1806.RN08_3689	GO Function	GO:0005488	Binding
RN08_3689	1806.RN08_3689	GO Function	GO:0016740	Transferase activity
RN08_3689	1806.RN08_3689	GO Function	GO:0016765	Transferase activity, transferring alkyl or aryl (other than methyl) groups
RN08_3689	1806.RN08_3689	GO Function	GO:0019842	Vitamin binding
RN08_3689	1806.RN08_3689	GO Function	GO:0030170	Pyridoxal phosphate binding
RN08_3689	1806.RN08_3689	GO Function	GO:0036094	Small molecule binding
RN08_3689	1806.RN08_3689	GO Function	GO:0043167	Ion binding
RN08_3689	1806.RN08_3689	GO Function	GO:0043168	Anion binding
RN08_3689	1806.RN08_3689	GO Function	GO:0070279	Vitamin b6 binding
RN08_3689	1806.RN08_3689	GO Function	GO:0097159	Organic cyclic compound binding
RN08_3689	1806.RN08_3689	GO Function	GO:1901363	Heterocyclic compound binding
RN08_3689	1806.RN08_3689	GO Component	GO:0005622	Intracellular
RN08_3689	1806.RN08_3689	GO Component	GO:0005634	Nucleus
RN08_3689	1806.RN08_3689	GO Component	GO:0005737	Cytoplasm
RN08_3689	1806.RN08_3689	GO Component	GO:0005829	Cytosol
RN08_3689	1806.RN08_3689	GO Component	GO:0043226	Organelle
RN08_3689	1806.RN08_3689	GO Component	GO:0043227	Membrane-bounded organelle
RN08_3689	1806.RN08_3689	GO Component	GO:0043229	Intracellular organelle
RN08_3689	1806.RN08_3689	GO Component	GO:0043231	Intracellular membrane-bounded organelle
RN08_3689	1806.RN08_3689	GO Component	GO:0110165	Cellular anatomical entity
RN08_3689	1806.RN08_3689	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_3689	1806.RN08_3689	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_3689	1806.RN08_3689	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_3689	1806.RN08_3689	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_3689	1806.RN08_3689	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_3689	1806.RN08_3689	STRING clusters	CL:529	Cysteine biosynthetic process from serine, and de novo l-methionine biosynthetic process
RN08_3689	1806.RN08_3689	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_3689	1806.RN08_3689	KEGG	mmic01100	Metabolic pathways
RN08_3689	1806.RN08_3689	UniProt Keywords	KW-0663	Pyridoxal phosphate
RN08_3690	1806.RN08_3690	GO Process	GO:0000096	Sulfur amino acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0006082	Organic acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0006555	Methionine metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0006790	Sulfur compound metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0008152	Metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0009058	Biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0009066	Aspartate family amino acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process

RN08_3690	1806.RN08_3690	GO Process	GO:0009086	Methionine biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0009987	Cellular process
RN08_3690	1806.RN08_3690	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044237	Cellular metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044238	Primary metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044272	Sulfur compound biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044281	Small molecule metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:0071704	Organic substance metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3690	1806.RN08_3690	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3690	1806.RN08_3690	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3690	1806.RN08_3690	GO Function	GO:0003824	Catalytic activity
RN08_3690	1806.RN08_3690	GO Function	GO:0004414	Homoserine o-acetyltransferase activity
RN08_3690	1806.RN08_3690	GO Function	GO:0008374	O-acyltransferase activity
RN08_3690	1806.RN08_3690	GO Function	GO:0016407	Acetyltransferase activity
RN08_3690	1806.RN08_3690	GO Function	GO:0016413	O-acetyltransferase activity
RN08_3690	1806.RN08_3690	GO Function	GO:0016740	Transferase activity
RN08_3690	1806.RN08_3690	GO Function	GO:0016746	Transferase activity, transferring acyl groups
RN08_3690	1806.RN08_3690	GO Function	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
RN08_3690	1806.RN08_3690	GO Component	GO:0005622	Intracellular
RN08_3690	1806.RN08_3690	GO Component	GO:0005737	Cytoplasm
RN08_3690	1806.RN08_3690	GO Component	GO:0110165	Cellular anatomical entity
RN08_3690	1806.RN08_3690	STRING clusters	CL:510	Mixed, incl. sulfur amino acid metabolic process, and sulfur metabolism
RN08_3690	1806.RN08_3690	STRING clusters	CL:511	Mixed, incl. sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_3690	1806.RN08_3690	STRING clusters	CL:512	Sulfur amino acid metabolic process, and atpase-coupled sulfate transmembrane transporter activity
RN08_3690	1806.RN08_3690	STRING clusters	CL:513	Methionine biosynthetic process, and cysteine biosynthetic process from serine
RN08_3690	1806.RN08_3690	STRING clusters	CL:515	Sulfur amino acid biosynthetic process
RN08_3690	1806.RN08_3690	STRING clusters	CL:529	Cysteine biosynthetic process from serine, and de novo l-methionine biosynthetic process
RN08_3690	1806.RN08_3690	KEGG	mmic00270	Cysteine and methionine metabolism
RN08_3690	1806.RN08_3690	KEGG	mmic00920	Sulfur metabolism
RN08_3690	1806.RN08_3690	KEGG	mmic01100	Metabolic pathways
RN08_3690	1806.RN08_3690	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3690	1806.RN08_3690	KEGG	mmic01230	Biosynthesis of amino acids
RN08_3690	1806.RN08_3690	UniProt Keywords	KW-0012	Acyltransferase
RN08_3690	1806.RN08_3690	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_3690	1806.RN08_3690	UniProt Keywords	KW-0486	Methionine biosynthesis
RN08_3690	1806.RN08_3690	UniProt Keywords	KW-0808	Transferase

RN08_3690	1806.RN08_3690	UniProt Keywords	KW-0963	Cytoplasm
RN08_3872	1806.RN08_3872	GO Process	GO:0006082	Organic acid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0006549	Isoleucine metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0006573	Valine metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0008152	Metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009058	Biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009097	Isoleucine biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009099	Valine biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0009987	Cellular process
RN08_3872	1806.RN08_3872	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0043436	Oxoacid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0044237	Cellular metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0044238	Primary metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0044249	Cellular biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0044281	Small molecule metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:0071704	Organic substance metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:1901564	Organonitrogen compound metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_3872	1806.RN08_3872	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_3872	1806.RN08_3872	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_3872	1806.RN08_3872	GO Function	GO:0000166	Nucleotide binding
RN08_3872	1806.RN08_3872	GO Function	GO:0003824	Catalytic activity
RN08_3872	1806.RN08_3872	GO Function	GO:0003984	Acetolactate synthase activity
RN08_3872	1806.RN08_3872	GO Function	GO:0005488	Binding
RN08_3872	1806.RN08_3872	GO Function	GO:0016740	Transferase activity
RN08_3872	1806.RN08_3872	GO Function	GO:0016744	Transferase activity, transferring aldehyde or ketonic groups
RN08_3872	1806.RN08_3872	GO Function	GO:0019842	Vitamin binding
RN08_3872	1806.RN08_3872	GO Function	GO:0030976	Thiamine pyrophosphate binding
RN08_3872	1806.RN08_3872	GO Function	GO:0036094	Small molecule binding
RN08_3872	1806.RN08_3872	GO Function	GO:0043167	Ion binding
RN08_3872	1806.RN08_3872	GO Function	GO:0043168	Anion binding
RN08_3872	1806.RN08_3872	GO Function	GO:0043169	Cation binding
RN08_3872	1806.RN08_3872	GO Function	GO:0046872	Metal ion binding
RN08_3872	1806.RN08_3872	GO Function	GO:0050660	Flavin adenine dinucleotide binding
RN08_3872	1806.RN08_3872	GO Function	GO:0097159	Organic cyclic compound binding
RN08_3872	1806.RN08_3872	GO Function	GO:1901265	Nucleoside phosphate binding
RN08_3872	1806.RN08_3872	GO Function	GO:1901363	Heterocyclic compound binding

RN08_3872	1806.RN08_3872	GO Function	GO:1901681	Sulfur compound binding
RN08_3872	1806.RN08_3872	GO Component	GO:0005576	Extracellular region
RN08_3872	1806.RN08_3872	GO Component	GO:0005618	Cell wall
RN08_3872	1806.RN08_3872	GO Component	GO:0005886	Plasma membrane
RN08_3872	1806.RN08_3872	GO Component	GO:0016020	Membrane
RN08_3872	1806.RN08_3872	GO Component	GO:0030312	External encapsulating structure
RN08_3872	1806.RN08_3872	GO Component	GO:0071944	Cell periphery
RN08_3872	1806.RN08_3872	GO Component	GO:0110165	Cellular anatomical entity
RN08_3872	1806.RN08_3872	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_3872	1806.RN08_3872	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3872	1806.RN08_3872	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_3872	1806.RN08_3872	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_3872	1806.RN08_3872	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_3872	1806.RN08_3872	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_3872	1806.RN08_3872	STRING clusters	CL:666	Valine, leucine and isoleucine biosynthesis
RN08_3872	1806.RN08_3872	STRING clusters	CL:668	Acetolactate synthase activity
RN08_3872	1806.RN08_3872	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_3872	1806.RN08_3872	KEGG	mmic00650	Butanoate metabolism
RN08_3872	1806.RN08_3872	KEGG	mmic00660	C5-Branched dibasic acid metabolism
RN08_3872	1806.RN08_3872	KEGG	mmic00770	Pantothenate and CoA biosynthesis
RN08_3872	1806.RN08_3872	KEGG	mmic01100	Metabolic pathways
RN08_3872	1806.RN08_3872	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_3872	1806.RN08_3872	KEGG	mmic01210	2-Oxocarboxylic acid metabolism
RN08_3872	1806.RN08_3872	KEGG	mmic01230	Biosynthesis of amino acids
RN08_4092	1806.RN08_4092	GO Process	GO:0006082	Organic acid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0006520	Cellular amino acid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0006551	Leucine metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0006807	Nitrogen compound metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0008152	Metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0008652	Cellular amino acid biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0009058	Biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0009081	Branched-chain amino acid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0009082	Branched-chain amino acid biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0009098	Leucine biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0009987	Cellular process
RN08_4092	1806.RN08_4092	GO Process	GO:0016053	Organic acid biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0019752	Carboxylic acid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0043436	Oxoacid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0044237	Cellular metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0044238	Primary metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0044249	Cellular biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0044281	Small molecule metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:0044283	Small molecule biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0046394	Carboxylic acid biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:0071704	Organic substance metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:1901564	Organonitrogen compound metabolic process

RN08_4092	1806.RN08_4092	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:1901576	Organic substance biosynthetic process
RN08_4092	1806.RN08_4092	GO Process	GO:1901605	Alpha-amino acid metabolic process
RN08_4092	1806.RN08_4092	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
RN08_4092	1806.RN08_4092	GO Function	GO:0003824	Catalytic activity
RN08_4092	1806.RN08_4092	GO Function	GO:0003852	2-isopropylmalate synthase activity
RN08_4092	1806.RN08_4092	GO Function	GO:0016740	Transferase activity
RN08_4092	1806.RN08_4092	GO Function	GO:0016746	Transferase activity, transferring acyl groups
RN08_4092	1806.RN08_4092	GO Function	GO:0046912	Transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer
RN08_4092	1806.RN08_4092	GO Component	GO:0005576	Extracellular region
RN08_4092	1806.RN08_4092	GO Component	GO:0005886	Plasma membrane
RN08_4092	1806.RN08_4092	GO Component	GO:0016020	Membrane
RN08_4092	1806.RN08_4092	GO Component	GO:0071944	Cell periphery
RN08_4092	1806.RN08_4092	GO Component	GO:0110165	Cellular anatomical entity
RN08_4092	1806.RN08_4092	STRING clusters	CL:623	Mixed, incl. carbohydrate metabolic process, and branched-chain amino acid metabolic process
RN08_4092	1806.RN08_4092	STRING clusters	CL:624	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_4092	1806.RN08_4092	STRING clusters	CL:625	Mixed, incl. pyruvate metabolism, and 2-oxocarboxylic acid metabolism
RN08_4092	1806.RN08_4092	STRING clusters	CL:626	Citrate cycle (TCA cycle), and branched-chain amino acid biosynthetic process
RN08_4092	1806.RN08_4092	STRING clusters	CL:627	Citrate cycle (TCA cycle), and Valine, leucine and isoleucine biosynthesis
RN08_4092	1806.RN08_4092	STRING clusters	CL:629	Valine, leucine and isoleucine biosynthesis, and oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
RN08_4092	1806.RN08_4092	STRING clusters	CL:631	Mixed, incl. oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, and isocitrate dehydrogenase activity
RN08_4092	1806.RN08_4092	STRING clusters	CL:632	Mixed, incl. oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, and malic enzyme activity
RN08_4092	1806.RN08_4092	STRING clusters	CL:645	Mixed, incl. malic enzyme activity, and 2-isopropylmalate synthase activity
RN08_4092	1806.RN08_4092	KEGG	mmic00290	Valine, leucine and isoleucine biosynthesis
RN08_4092	1806.RN08_4092	KEGG	mmic00620	Pyruvate metabolism
RN08_4092	1806.RN08_4092	KEGG	mmic01100	Metabolic pathways
RN08_4092	1806.RN08_4092	KEGG	mmic01110	Biosynthesis of secondary metabolites
RN08_4092	1806.RN08_4092	KEGG	mmic01210	2-Oxocarboxylic acid metabolism
RN08_4092	1806.RN08_4092	KEGG	mmic01230	Biosynthesis of amino acids
RN08_4092	1806.RN08_4092	UniProt Keywords	KW-0028	Amino-acid biosynthesis
RN08_4092	1806.RN08_4092	UniProt Keywords	KW-0100	Branched-chain amino acid biosynthesis
RN08_4092	1806.RN08_4092	UniProt Keywords	KW-0432	Leucine biosynthesis
RN08_4092	1806.RN08_4092	UniProt Keywords	KW-0808	Transferase
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Process	GO:0008152	Metabolic process
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Process	GO:0032259	Methylation
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Function	GO:0003824	Catalytic activity
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Function	GO:0008168	Methyltransferase activity
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Function	GO:0016740	Transferase activity
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Function	GO:0016741	Transferase activity, transferring one-carbon groups
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Component	GO:0005886	Plasma membrane
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Component	GO:0016020	Membrane

S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Component	GO:0071944	Cell periphery
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	GO Component	GO:0110165	Cellular anatomical entity
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	STRING clusters	CL:5251	Mixed, incl. s-adenosyl-l-methionine, and lipoarabinomannan (lam) biosynthesis
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	STRING clusters	CL:5329	S-adenosyl-L-methionine, and response to salicylic acid
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	KEGG	mmic01110	Biosynthesis of secondary metabolites
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	UniProt Keywords	KW-0489	Methyltransferase
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	UniProt Keywords	KW-0808	Transferase
S-adenosyl-L-methionine-dependent methyltransferase	1806.RN08_2098	UniProt Keywords	KW-0949	S-adenosyl-L-methionine
hydrolase	1806.RN08_0054	GO Process	GO:0000096	Sulfur amino acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0000097	Sulfur amino acid biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0006082	Organic acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0006520	Cellular amino acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0006555	Methionine metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0006790	Sulfur compound metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0006807	Nitrogen compound metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0008152	Metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0008652	Cellular amino acid biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0009058	Biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0009066	Aspartate family amino acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0009067	Aspartate family amino acid biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0009086	Methionine biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0009987	Cellular process
hydrolase	1806.RN08_0054	GO Process	GO:0016053	Organic acid biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0019752	Carboxylic acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0043436	Oxoacid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0044237	Cellular metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0044238	Primary metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0044249	Cellular biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0044272	Sulfur compound biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0044281	Small molecule metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:0044283	Small molecule biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0046394	Carboxylic acid biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:0071704	Organic substance metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:1901564	Organonitrogen compound metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:1901566	Organonitrogen compound biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:1901576	Organic substance biosynthetic process
hydrolase	1806.RN08_0054	GO Process	GO:1901605	Alpha-amino acid metabolic process
hydrolase	1806.RN08_0054	GO Process	GO:1901607	Alpha-amino acid biosynthetic process
hydrolase	1806.RN08_0054	GO Function	GO:0003824	Catalytic activity
hydrolase	1806.RN08_0054	GO Function	GO:0008374	O-acyltransferase activity
hydrolase	1806.RN08_0054	GO Function	GO:0016740	Transferase activity
hydrolase	1806.RN08_0054	GO Function	GO:0016746	Transferase activity, transferring acyl groups
hydrolase	1806.RN08_0054	GO Function	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
hydrolase	1806.RN08_0054	GO Component	GO:0005622	Intracellular

hydrolase	1806.RN08_0054	GO Component	GO:0005737	Cytoplasm
hydrolase	1806.RN08_0054	GO Component	GO:0110165	Cellular anatomical entity
hydrolase	1806.RN08_0054	STRING clusters	CL:6910	Mixed, incl. triglyceride lipase activity, and n,n-dimethylaniline monooxygenase activity
hydrolase	1806.RN08_0054	STRING clusters	CL:6911	Mixed, incl. triglyceride lipase activity, and short-chain carboxylesterase activity
hydrolase	1806.RN08_0054	STRING clusters	CL:6913	Mixed, incl. short-chain carboxylesterase activity, and triglyceride lipase activity
hydrolase	1806.RN08_0054	STRING clusters	CL:6916	Short-chain carboxylesterase activity, and triglyceride lipase activity
hydrolase	1806.RN08_0054	KEGG	mmic00270	Cysteine and methionine metabolism
hydrolase	1806.RN08_0054	KEGG	mmic00920	Sulfur metabolism
hydrolase	1806.RN08_0054	KEGG	mmic01100	Metabolic pathways
hydrolase	1806.RN08_0054	KEGG	mmic01110	Biosynthesis of secondary metabolites
hydrolase	1806.RN08_0054	KEGG	mmic01230	Biosynthesis of amino acids
hydrolase	1806.RN08_0054	UniProt Keywords	KW-0378	Hydrolase