

**Supplementary Table S3. Classification of acetylated proteins according to their biological process, molecular function and cellular localization.**

Biological Process			
Protein_ID	Description	GO_ID	GO_Term
gij148660799	ribose-phosphate pyrophosphokinase	GO:0071840	cellular component organization or biogenesis
gij148661845	antigen Hsp20	GO:0071840	cellular component organization or biogenesis
gij148662038	glutamine synthetase	GO:0071840	cellular component organization or biogenesis
gij148663281	molecular chaperone GroEL	GO:0071840	cellular component organization or biogenesis
gij148663282	co-chaperonin GroES	GO:0071840	cellular component organization or biogenesis
gij148663668	polyketide synthase	GO:0071840	cellular component organization or biogenesis
gij148661961	hypothetical protein	GO:0071840	cellular component organization or biogenesis
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0071840	cellular component organization or biogenesis
gij148661325	acyl-CoA synthetase	GO:0071840	cellular component organization or biogenesis
gij148662787	acyl-CoA synthetase	GO:0071840	cellular component organization or biogenesis
gij148663669	long-chain-fatty-acid--CoA ligase	GO:0071840	cellular component organization or biogenesis
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0071840	cellular component organization or biogenesis
gij148660416	methoxy mycolic acid synthase 4	GO:0071840	cellular component organization or biogenesis
gij148661276	3-oxoacyl-ACP reductase	GO:0071840	cellular component organization or biogenesis
gij148662726	ribosome recycling factor	GO:0071840	cellular component organization or biogenesis
gij148660129	fructose-bisphosphate aldolase	GO:0071840	cellular component organization or biogenesis
gij148663111	S-adenosyl-L-homocysteine hydrolase	GO:0071840	cellular component organization or biogenesis
gij148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0071840	cellular component organization or biogenesis
gij148661325	acyl-CoA synthetase	GO:0002376	immune system process
gij148662787	acyl-CoA synthetase	GO:0002376	immune system process
gij148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0008152	metabolic process
gij148662852	ketol-acid reductoisomerase	GO:0008152	metabolic process
gij148661183	S-adenosylmethionine synthetase	GO:0008152	metabolic process
gij148663111	S-adenosyl-L-homocysteine hydrolase	GO:0008152	metabolic process
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0008152	metabolic process
gij148659975	phosphoenolpyruvate carboxykinase	GO:0008152	metabolic process
gij148660799	ribose-phosphate pyrophosphokinase	GO:0008152	metabolic process
gij148661955	hypothetical protein	GO:0008152	metabolic process
gij148660947	pterin-4-alpha-carbinolamine dehydratase	GO:0008152	metabolic process
gij148662028	glycine cleavage system aminomethyltransferase T	GO:0008152	metabolic process
gij148662987	two component transcriptional regulatory protein DevR	GO:0008152	metabolic process
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0008152	metabolic process
gij148659912	short-chain type dehydrogenase/reductase	GO:0008152	metabolic process
gij148659921	NAD(P) transhydrogenase subunit beta	GO:0008152	metabolic process
gij148659995	acyl-CoA dehydrogenase	GO:0008152	metabolic process
gij148660007	3-ketoacyl-ACP reductase	GO:0008152	metabolic process
gij148660009	acyl-CoA dehydrogenase	GO:0008152	metabolic process
gij148660036	acyl-CoA dehydrogenase	GO:0008152	metabolic process
gij148660104	iron-sulfur-binding reductase	GO:0008152	metabolic process
gij148660172	f420-dependent glucose-6-phosphate dehydrogenase Fgd1	GO:0008152	metabolic process
gij148660204	short chain dehydrogenase	GO:0008152	metabolic process
gij148660228	dihydroipoamide dehydrogenase	GO:0008152	metabolic process
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0008152	metabolic process
gij148660460	elongation factor Tu	GO:0008152	metabolic process
gij148660529	MmsA	GO:0008152	metabolic process
gij148660593	thiosulfate sulfurtransferase CysA2	GO:0008152	metabolic process
gij148660602	fatty acid desaturase	GO:0008152	metabolic process
gij148660637	fatty oxidation complex subunit alpha	GO:0008152	metabolic process
gij148661113	thioredoxin-related protein	GO:0008152	metabolic process
gij148661276	3-oxoacyl-ACP reductase	GO:0008152	metabolic process
gij148661329	hypothetical protein	GO:0008152	metabolic process
gij148661530	hypothetical protein	GO:0008152	metabolic process
gij148661816	20-beta-hydroxysteroid dehydrogenase FabG3	GO:0008152	metabolic process
gij148662062	pyruvate dehydrogenase subunit E1	GO:0008152	metabolic process
gij148662102	dehydrogenase	GO:0008152	metabolic process
gij148662311	NAD-dependent glutamate dehydrogenase Gdh	GO:0008152	metabolic process
gij148662940	zinc-type alcohol dehydrogenase AdhD	GO:0008152	metabolic process
gij148662971	thiosulfate sulfurtransferase CysA3	GO:0008152	metabolic process
gij148662995	acyl-CoA dehydrogenase	GO:0008152	metabolic process
gij148663007	NADH dehydrogenase subunit H	GO:0008152	metabolic process
gij148663086	short chain dehydrogenase	GO:0008152	metabolic process
gij148663137	acyl-CoA dehydrogenase	GO:0008152	metabolic process
gij148663251	hypothetical protein	GO:0008152	metabolic process
gij148659759	DNA polymerase III subunit beta	GO:0008152	metabolic process
gij148660118	molecular chaperone DnaJ	GO:0008152	metabolic process
gij148663281	molecular chaperone GroEL	GO:0008152	metabolic process
gij148662038	glutamine synthetase	GO:0008152	metabolic process
gij148662065	acyl carrier protein	GO:0008152	metabolic process
gij148661422	lipid-transfer protein	GO:0008152	metabolic process
gij148662003	long-chain-fatty-acid--CoA ligase	GO:0008152	metabolic process
gij148662787	acyl-CoA synthetase	GO:0008152	metabolic process
gij148663669	long-chain-fatty-acid--CoA ligase	GO:0008152	metabolic process
gij148661317	acyl-CoA synthetase	GO:0008152	metabolic process
gij148661325	acyl-CoA synthetase	GO:0008152	metabolic process
gij148661643	malate synthase G	GO:0008152	metabolic process
gij148663668	polyketide synthase	GO:0008152	metabolic process
gij148660459	elongation factor G	GO:0008152	metabolic process
gij148660331	polyprenyl-diphosphate synthase GrcC1	GO:0008152	metabolic process
gij148660416	methoxy mycolic acid synthase 4	GO:0008152	metabolic process
gij148660879	serine hydroxymethyltransferase	GO:0008152	metabolic process
gij148661633	hypothetical protein	GO:0008152	metabolic process
gij148660661	phosphoserine aminotransferase	GO:0008152	metabolic process
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0008152	metabolic process
gij148661496	CTP synthetase	GO:0008152	metabolic process
gij148663456	hypothetical protein	GO:0008152	metabolic process
gij148661961	hypothetical protein	GO:0008152	metabolic process
gij148659826	isocitrate dehydrogenase (NADP) Icd2	GO:0008152	metabolic process
gij148660013	succinate dehydrogenase flavoprotein subunit	GO:0008152	metabolic process
gij148660233	isocitrate lyase Icl	GO:0008152	metabolic process
gij148660667	citrate synthase 2	GO:0008152	metabolic process
gij148660674	type II citrate synthase	GO:0008152	metabolic process
gij148660730	succinyl-CoA synthetase subunit beta	GO:0008152	metabolic process
gij148660731	succinyl-CoA synthetase subunit alpha	GO:0008152	metabolic process

gij148660884	fumarate hydratase	GO:0008152	metabolic process
gij148661027	malate dehydrogenase	GO:0008152	metabolic process
gij148661035	alpha-ketoglutarate decarboxylase	GO:0008152	metabolic process
gij148661529	succinic semialdehyde dehydrogenase	GO:0008152	metabolic process
gij148662032	dihydrolipoamide acetyltransferase	GO:0008152	metabolic process
gij148660908	6-phosphogluconate dehydrogenase	GO:0008152	metabolic process
gij148661240	transaldolase	GO:0008152	metabolic process
gij148660129	fructose-bisphosphate aldolase	GO:0008152	metabolic process
gij148660256	phosphoglyceromutase	GO:0008152	metabolic process
gij148663444	cysteinyl-tRNA synthetase	GO:0008152	metabolic process
gij148661454	argininosuccinate synthase	GO:0008152	metabolic process
gij148660116	molecular chaperone DnaK	GO:0008152	metabolic process
gij148661845	antigen Hsp20	GO:0008152	metabolic process
gij148661281	hypothetical protein	GO:0008152	metabolic process
gij148661956	hypothetical protein	GO:0008152	metabolic process
gij148662295	ATP-dependent Clp protease proteolytic subunit	GO:0008152	metabolic process
gij148663282	co-chaperonin GroES	GO:0008152	metabolic process
gij148663076	isochorismate synthase EntC	GO:0008152	metabolic process
gij148663491	inorganic pyrophosphatase	GO:0008152	metabolic process
gij148660035	acyl-CoA synthetase	GO:0008152	metabolic process
gij148660320	acyl-CoA synthetase	GO:0008152	metabolic process
gij148660636	acetyl-CoA acetyltransferase	GO:0008152	metabolic process
gij148661112	acetyl-CoA acetyltransferase	GO:0008152	metabolic process
gij148661268	aconitate hydratase	GO:0008152	metabolic process
gij148661733	fatty-acid-CoA ligase	GO:0008152	metabolic process
gij148663419	acetyl-CoA acetyltransferase	GO:0008152	metabolic process
gij148663642	enoyl-CoA hydratase	GO:0008152	metabolic process
gij148662625	polynucleotide phosphorylase	GO:0008152	metabolic process
gij148662842	glutamyl-tRNA synthetase	GO:0008152	metabolic process
gij148661080	arginyl-tRNA synthetase	GO:0008152	metabolic process
gij148660203	molybdopterin biosynthesis protein MoeA2	GO:0008152	metabolic process
gij148662726	ribosome recycling factor	GO:0008152	metabolic process
gij148662733	elongation factor Ts	GO:0008152	metabolic process
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0008152	metabolic process
gij148660426	50S ribosomal protein L7/L12	GO:0008152	metabolic process
gij148660458	30S ribosomal protein S7	GO:0008152	metabolic process
gij148660475	30S ribosomal protein S10	GO:0008152	metabolic process
gij148661425	30S ribosomal protein S1	GO:0008152	metabolic process
gij148662734	30S ribosomal protein S2	GO:0008152	metabolic process
gij148662753	30S ribosomal protein S16	GO:0008152	metabolic process
gij148662825	50S ribosomal protein L28	GO:0008152	metabolic process
gij148663323	30S ribosomal protein S4	GO:0008152	metabolic process
gij148662881	electron transfer flavoprotein subunit beta	GO:0008152	metabolic process
gij148662446	pyridoxal biosynthesis lyase PdxS	GO:0008152	metabolic process
gij148660205	molecular chaperone GroEL	GO:0008152	metabolic process
gij148661094	ATP synthase F0F1 subunit B	GO:0008152	metabolic process
gij148661096	ATP synthase F0F1 subunit alpha	GO:0008152	metabolic process
gij148661098	ATP synthase F0F1 subunit beta	GO:0008152	metabolic process
gij148662385	hypothetical protein	GO:0008152	metabolic process
gij148663717	hypothetical protein	GO:0008152	metabolic process
gij148662080	transcriptional regulatory protein	GO:0008152	metabolic process
gij148660441	DNA-directed RNA polymerase subunit beta	GO:0008152	metabolic process
gij148660442	DNA-directed RNA polymerase subunit beta'	GO:0008152	metabolic process
gij148663322	DNA-directed RNA polymerase subunit alpha	GO:0008152	metabolic process
gij148662987	two component transcriptional regulatory protein DevR	GO:0023052	signaling
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0023052	signaling
gij148662987	two component transcriptional regulatory protein DevR	GO:0065007	biological regulation
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0065007	biological regulation
gij148662385	hypothetical protein	GO:0065007	biological regulation
gij148661845	antigen Hsp20	GO:0065007	biological regulation
gij148661961	hypothetical protein	GO:0065007	biological regulation
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0065007	biological regulation
gij148660228	dihydrolipoamide dehydrogenase	GO:0065007	biological regulation
gij148661113	thioredoxin-related protein	GO:0065007	biological regulation
gij148662032	dihydrolipoamide acetyltransferase	GO:0065007	biological regulation
gij148661633	hypothetical protein	GO:0065007	biological regulation
gij148661325	acyl-CoA synthetase	GO:0065007	biological regulation
gij148662787	acyl-CoA synthetase	GO:0065007	biological regulation
gij148660118	molecular chaperone DnaJ	GO:0065007	biological regulation
gij148661816	20-beta-hydroxysteroid dehydrogenase FabG3	GO:0065007	biological regulation
gij148663717	hypothetical protein	GO:0065007	biological regulation
gij148663282	co-chaperonin GroES	GO:0065007	biological regulation
gij148662987	two component transcriptional regulatory protein DevR	GO:0050896	response to stimulus
gij148660233	isocitrate lyase Icl	GO:0050896	response to stimulus
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0050896	response to stimulus
gij148663281	molecular chaperone GroEL	GO:0050896	response to stimulus
gij148660205	molecular chaperone GroEL	GO:0050896	response to stimulus
gij148660460	elongation factor Tu	GO:0050896	response to stimulus
gij148660116	molecular chaperone DnaK	GO:0050896	response to stimulus
gij148660118	molecular chaperone DnaJ	GO:0050896	response to stimulus
gij148661845	antigen Hsp20	GO:0050896	response to stimulus
gij148661810	hypothetical protein	GO:0050896	response to stimulus
gij148659975	phosphoenolpyruvate carboxykinase	GO:0050896	response to stimulus
gij148660009	acyl-CoA dehydrogenase	GO:0050896	response to stimulus
gij148660602	fatty acid desaturase	GO:0050896	response to stimulus
gij148661112	acetyl-CoA acetyltransferase	GO:0050896	response to stimulus
gij148663419	acetyl-CoA acetyltransferase	GO:0050896	response to stimulus
gij148663717	hypothetical protein	GO:0050896	response to stimulus
gij148661325	acyl-CoA synthetase	GO:0050896	response to stimulus
gij148662787	acyl-CoA synthetase	GO:0050896	response to stimulus
gij148662080	transcriptional regulatory protein	GO:0050896	response to stimulus
gij148661431	hypothetical protein	GO:0050896	response to stimulus
gij148661268	aconitate hydratase	GO:0050896	response to stimulus
gij148663086	short chain dehydrogenase	GO:0050896	response to stimulus
gij148662038	glutamine synthetase	GO:0050896	response to stimulus
gij148660007	3-ketoacyl-ACP reductase	GO:0050896	response to stimulus
gij148660441	DNA-directed RNA polymerase subunit beta	GO:0050896	response to stimulus
gij148663282	co-chaperonin GroES	GO:0050896	response to stimulus

gij148662940	zinc-type alcohol dehydrogenase AdhD	GO:0050896	response to stimulus
gij148660879	serine hydroxymethyltransferase	GO:0050896	response to stimulus
gij148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0009987	cellular process
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0009987	cellular process
gij148662852	ketol-acid reductoisomerase	GO:0009987	cellular process
gij148661183	S-adenosylmethionine synthetase	GO:0009987	cellular process
gij148663111	S-adenosyl-L-homocysteine hydrolase	GO:0009987	cellular process
gij148661096	ATP synthase FOF1 subunit alpha	GO:0009987	cellular process
gij148661098	ATP synthase FOF1 subunit beta	GO:0009987	cellular process
gij148659975	phosphoenolpyruvate carboxykinase	GO:0009987	cellular process
gij148660799	ribose-phosphate pyrophosphokinase	GO:0009987	cellular process
gij148661955	hypothetical protein	GO:0009987	cellular process
gij148660947	pterin-4-alpha-carbinolamine dehydratase	GO:0009987	cellular process
gij148662028	glycine cleavage system aminomethyltransferase T	GO:0009987	cellular process
gij148662987	two component transcriptional regulatory protein DevR	GO:0009987	cellular process
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0009987	cellular process
gij148659759	DNA polymerase III subunit beta	GO:0009987	cellular process
gij148660118	molecular chaperone DnaJ	GO:0009987	cellular process
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0009987	cellular process
gij148661961	hypothetical protein	GO:0009987	cellular process
gij148663281	molecular chaperone GroEL	GO:0009987	cellular process
gij148660228	dihydrolipoamide dehydrogenase	GO:0009987	cellular process
gij148661113	thioredoxin-related protein	GO:0009987	cellular process
gij148662032	dihydrolipoamide acetyltransferase	GO:0009987	cellular process
gij148662065	acyl carrier protein	GO:0009987	cellular process
gij148660602	fatty acid desaturase	GO:0009987	cellular process
gij148661422	lipid-transfer protein	GO:0009987	cellular process
gij148662003	long-chain-fatty-acid--CoA ligase	GO:0009987	cellular process
gij148662787	acyl-CoA synthetase	GO:0009987	cellular process
gij148663251	hypothetical protein	GO:0009987	cellular process
gij148663669	long-chain-fatty-acid--CoA ligase	GO:0009987	cellular process
gij148660637	fatty oxidation complex subunit alpha	GO:0009987	cellular process
gij148661317	acyl-CoA synthetase	GO:0009987	cellular process
gij148661325	acyl-CoA synthetase	GO:0009987	cellular process
gij148661643	malate synthase G	GO:0009987	cellular process
gij148663668	polyketide synthase	GO:0009987	cellular process
gij148660459	elongation factor G	GO:0009987	cellular process
gij148660460	elongation factor Tu	GO:0009987	cellular process
gij148660331	polyprenyl-diphosphate synthase GrcC1	GO:0009987	cellular process
gij148660007	3-ketoacyl-ACP reductase	GO:0009987	cellular process
gij148661276	3-oxoacyl-ACP reductase	GO:0009987	cellular process
gij148661810	hypothetical protein	GO:0009987	cellular process
gij148661845	antigen Hsp20	GO:0009987	cellular process
gij148661633	hypothetical protein	GO:0009987	cellular process
gij148660661	phosphoserine aminotransferase	GO:0009987	cellular process
gij148660233	isocitrate lyase Icl	GO:0009987	cellular process
gij148662080	transcriptional regulatory protein	GO:0009987	cellular process
gij148660116	molecular chaperone DnaK	GO:0009987	cellular process
gij148662038	glutamine synthetase	GO:0009987	cellular process
gij148661496	CTP synthetase	GO:0009987	cellular process
gij148663456	hypothetical protein	GO:0009987	cellular process
gij148659826	isocitrate dehydrogenase (NADP) Icd2	GO:0009987	cellular process
gij148660013	succinate dehydrogenase flavoprotein subunit	GO:0009987	cellular process
gij148660667	citrate synthase 2	GO:0009987	cellular process
gij148660674	type II citrate synthase	GO:0009987	cellular process
gij148660730	succinyl-CoA synthetase subunit beta	GO:0009987	cellular process
gij148660731	succinyl-CoA synthetase subunit alpha	GO:0009987	cellular process
gij148660884	fumarate hydratase	GO:0009987	cellular process
gij148661027	malate dehydrogenase	GO:0009987	cellular process
gij148661035	alpha-ketoglutarate decarboxylase	GO:0009987	cellular process
gij148661529	succinic semialdehyde dehydrogenase	GO:0009987	cellular process
gij148660908	6-phosphogluconate dehydrogenase	GO:0009987	cellular process
gij148661240	transaldolase	GO:0009987	cellular process
gij148660129	fructose-bisphosphate aldolase	GO:0009987	cellular process
gij148660256	phosphoglyceromutase	GO:0009987	cellular process
gij148662062	pyruvate dehydrogenase subunit E1	GO:0009987	cellular process
gij148663444	cysteinyl-tRNA synthetase	GO:0009987	cellular process
gij148661454	argininosuccinate synthase	GO:0009987	cellular process
gij148660879	serine hydroxymethyltransferase	GO:0009987	cellular process
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0009987	cellular process
gij148660416	methoxy mycolic acid synthase 4	GO:0009987	cellular process
gij148663282	co-chaperonin GroES	GO:0009987	cellular process
gij148661816	20-beta-hydroxysteroid dehydrogenase FabG3	GO:0009987	cellular process
gij148663076	isochorismate synthase EntC	GO:0009987	cellular process
gij148663491	inorganic pyrophosphatase	GO:0009987	cellular process
gij148662625	polynucleotide phosphorylase	GO:0009987	cellular process
gij148662842	glutamyl-tRNA synthetase	GO:0009987	cellular process
gij148661080	arginyl-tRNA synthetase	GO:0009987	cellular process
gij148663717	hypothetical protein	GO:0009987	cellular process
gij148660203	molybdopterin biosynthesis protein MoeA2	GO:0009987	cellular process
gij148662726	ribosome recycling factor	GO:0009987	cellular process
gij148662733	elongation factor Ts	GO:0009987	cellular process
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0009987	cellular process
gij148660426	50S ribosomal protein L7/L12	GO:0009987	cellular process
gij148660458	30S ribosomal protein S7	GO:0009987	cellular process
gij148660475	30S ribosomal protein S10	GO:0009987	cellular process
gij148661425	30S ribosomal protein S1	GO:0009987	cellular process
gij148662734	30S ribosomal protein S2	GO:0009987	cellular process
gij148662753	30S ribosomal protein S16	GO:0009987	cellular process
gij148662825	50S ribosomal protein L28	GO:0009987	cellular process
gij148663323	30S ribosomal protein S4	GO:0009987	cellular process
gij148662881	electron transfer flavoprotein subunit beta	GO:0009987	cellular process
gij148662446	pyridoxal biosynthesis lyase PdxS	GO:0009987	cellular process
gij148660205	molecular chaperone GroEL	GO:0009987	cellular process
gij148661094	ATP synthase FOF1 subunit B	GO:0009987	cellular process
gij148662385	hypothetical protein	GO:0009987	cellular process
gij148660441	DNA-directed RNA polymerase subunit beta	GO:0009987	cellular process
gij148660442	DNA-directed RNA polymerase subunit beta'	GO:0009987	cellular process

gij148663322	DNA-directed RNA polymerase subunit alpha	GO:0009987	cellular process
gij148660205	molecular chaperone GroEL	GO:0022610	biological adhesion
gij148661845	antigen Hsp20	GO:0040007	growth
gij148661325	acyl-CoA synthetase	GO:0040007	growth
gij148662787	acyl-CoA synthetase	GO:0040007	growth
gij148662940	zinc-type alcohol dehydrogenase AdhD	GO:0040007	growth
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0040007	growth
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0040007	growth
gij148662385	hypothetical protein	GO:0040007	growth
gij148660104	iron-sulfur-binding reductase	GO:0040007	growth
gij148660116	molecular chaperone DnaK	GO:0040007	growth
gij148660118	molecular chaperone DnaJ	GO:0040007	growth
gij148660205	molecular chaperone GroEL	GO:0040007	growth
gij148660228	dihydrolipoamide dehydrogenase	GO:0040007	growth
gij148660331	polyprenyl-diphosphate synthase GrcC1	GO:0040007	growth
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0040007	growth
gij148660426	50S ribosomal protein L7/L12	GO:0040007	growth
gij148660441	DNA-directed RNA polymerase subunit beta	GO:0040007	growth
gij148660442	DNA-directed RNA polymerase subunit beta'	GO:0040007	growth
gij148660458	30S ribosomal protein S7	GO:0040007	growth
gij148660459	elongation factor G	GO:0040007	growth
gij148660460	elongation factor Tu	GO:0040007	growth
gij148660475	30S ribosomal protein S10	GO:0040007	growth
gij148660602	fatty acid desaturase	GO:0040007	growth
gij148660661	phosphoserine aminotransferase	GO:0040007	growth
gij148660730	succinyl-CoA synthetase subunit beta	GO:0040007	growth
gij148660731	succinyl-CoA synthetase subunit alpha	GO:0040007	growth
gij148660799	ribose-phosphate pyrophosphokinase	GO:0040007	growth
gij148660884	fumarate hydratase	GO:0040007	growth
gij148660908	6-phosphogluconate dehydrogenase	GO:0040007	growth
gij148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0040007	growth
gij148661035	alpha-ketoglutarate decarboxylase	GO:0040007	growth
gij148661080	arginyl-tRNA synthetase	GO:0040007	growth
gij148661094	ATP synthase F0F1 subunit B	GO:0040007	growth
gij148661096	ATP synthase F0F1 subunit alpha	GO:0040007	growth
gij148661098	ATP synthase F0F1 subunit beta	GO:0040007	growth
gij148661183	S-adenosylmethionine synthetase	GO:0040007	growth
gij148661240	transaldolase	GO:0040007	growth
gij148661268	aconitate hydratase	GO:0040007	growth
gij148661273	hypothetical protein	GO:0040007	growth
gij148661425	30S ribosomal protein S1	GO:0040007	growth
gij148661454	argininosuccinate synthase	GO:0040007	growth
gij148661496	CTP synthetase	GO:0040007	growth
gij148661961	hypothetical protein	GO:0040007	growth
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0040007	growth
gij148662028	glycine cleavage system aminomethyltransferase T	GO:0040007	growth
gij148662032	dihydrolipoamide acetyltransferase	GO:0040007	growth
gij148662038	glutamine synthetase	GO:0040007	growth
gij148662065	acyl carrier protein	GO:0040007	growth
gij148662295	ATP-dependent Clp protease proteolytic subunit	GO:0040007	growth
gij148662446	pyridoxal biosynthesis lyase PdxS	GO:0040007	growth
gij148662726	ribosome recycling factor	GO:0040007	growth
gij148662733	elongation factor Ts	GO:0040007	growth
gij148662734	30S ribosomal protein S2	GO:0040007	growth
gij148662842	glutamyl-tRNA synthetase	GO:0040007	growth
gij148662852	ketol-acid reductoisomerase	GO:0040007	growth
gij148662881	electron transfer flavoprotein subunit beta	GO:0040007	growth
gij148662995	acyl-CoA dehydrogenase	GO:0040007	growth
gij148663111	S-adenosyl-L-homocysteine hydrolase	GO:0040007	growth
gij148663281	molecular chaperone GroEL	GO:0040007	growth
gij148663282	co-chaperonin GroES	GO:0040007	growth
gij148663322	DNA-directed RNA polymerase subunit alpha	GO:0040007	growth
gij148663323	30S ribosomal protein S4	GO:0040007	growth
gij148663444	cysteinyl-tRNA synthetase	GO:0040007	growth
gij148663668	polyketide synthase	GO:0040007	growth
gij148663669	long-chain-fatty-acid--CoA ligase	GO:0040007	growth
gij148661096	ATP synthase F0F1 subunit alpha	GO:0051179	localization
gij148661098	ATP synthase F0F1 subunit beta	GO:0051179	localization
gij148663732	hypothetical protein	GO:0051179	localization
gij148663717	hypothetical protein	GO:0051179	localization
gij148661094	ATP synthase F0F1 subunit B	GO:0051179	localization
gij148661961	hypothetical protein	GO:0032502	developmental process
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0032502	developmental process
gij148662987	two component transcriptional regulatory protein DevR	GO:0032502	developmental process
gij148661845	antigen Hsp20	GO:0051704	multi-organism process
gij148661325	acyl-CoA synthetase	GO:0051704	multi-organism process
gij148662787	acyl-CoA synthetase	GO:0051704	multi-organism process
gij148662940	zinc-type alcohol dehydrogenase AdhD	GO:0051704	multi-organism process
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0051704	multi-organism process
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0051704	multi-organism process
gij148660205	molecular chaperone GroEL	GO:0051704	multi-organism process
gij148660233	isocitrate lyase Icl	GO:0051704	multi-organism process
gij148662032	dihydrolipoamide acetyltransferase	GO:0051704	multi-organism process
gij148662038	glutamine synthetase	GO:0051704	multi-organism process
gij148662987	two component transcriptional regulatory protein DevR	GO:0051704	multi-organism process
gij148663717	hypothetical protein	GO:0051704	multi-organism process
gij148659975	phosphoenolpyruvate carboxykinase	GO:0051704	multi-organism process
gij148660009	acyl-CoA dehydrogenase	GO:0051704	multi-organism process
gij148660602	fatty acid desaturase	GO:0051704	multi-organism process
gij148661112	acetyl-CoA acetyltransferase	GO:0051704	multi-organism process
gij148663419	acetyl-CoA acetyltransferase	GO:0051704	multi-organism process
gij148660879	serine hydroxymethyltransferase	GO:0051704	multi-organism process
<b>Molecular Function</b>			
<b>Protein_ID</b>	<b>Description</b>	<b>GO_ID</b>	<b>GO_Term</b>
gij148660228	dihydrolipoamide dehydrogenase	GO:0016209	antioxidant activity
gij148661530	hypothetical protein	GO:0016209	antioxidant activity
gij148662032	dihydrolipoamide acetyltransferase	GO:0016209	antioxidant activity
gij148660172	f420-dependent glucose-6-phosphate dehydrogenase FgdI	GO:0003824	catalytic activity



gii148660908	6-phosphogluconate dehydrogenase	GO:0003824	catalytic activity
gii148660104	iron-sulfur-binding reductase	GO:0003824	catalytic activity
gii148659975	phosphoenolpyruvate carboxykinase	GO:0003824	catalytic activity
gii148660441	DNA-directed RNA polymerase subunit beta	GO:0003824	catalytic activity
gii148660442	DNA-directed RNA polymerase subunit beta'	GO:0003824	catalytic activity
gii148663322	DNA-directed RNA polymerase subunit alpha	GO:0003824	catalytic activity
gii148660593	thiosulfate sulfurtransferase CysA2	GO:0003824	catalytic activity
gii148662971	thiosulfate sulfurtransferase CysA3	GO:0003824	catalytic activity
gii148661329	hypothetical protein	GO:0003824	catalytic activity
gii148660459	elongation factor G	GO:0003824	catalytic activity
gii148660460	elongation factor Tu	GO:0003824	catalytic activity
gii148659759	DNA polymerase III subunit beta	GO:0003824	catalytic activity
gii148660799	ribose-phosphate pyrophosphokinase	GO:0003824	catalytic activity
gii148661955	hypothetical protein	GO:0003824	catalytic activity
gii148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0003824	catalytic activity
gii148661496	CTP synthetase	GO:0003824	catalytic activity
gii148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0003824	catalytic activity
gii148661096	ATP synthase FOF1 subunit alpha	GO:0003824	catalytic activity
gii148661098	ATP synthase FOF1 subunit beta	GO:0003824	catalytic activity
gii148660228	dihydrolipoamide dehydrogenase	GO:0003824	catalytic activity
gii148660731	succinyl-CoA synthetase subunit alpha	GO:0003824	catalytic activity
gii148660416	methoxy mycolic acid synthase 4	GO:0003824	catalytic activity
gii148662032	dihydrolipoamide acetyltransferase	GO:0003824	catalytic activity
gii148659912	short-chain type dehydrogenase/reductase	GO:0003824	catalytic activity
gii148660637	fatty oxidation complex subunit alpha	GO:0003824	catalytic activity
gii148663456	hypothetical protein	GO:0003824	catalytic activity
gii148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0003824	catalytic activity
gii148662102	dehydrogenase	GO:0003824	catalytic activity
gii148660529	MmsA	GO:0003824	catalytic activity
gii148663007	NADH dehydrogenase subunit H	GO:0003824	catalytic activity
gii148660256	phosphoglyceromutase	GO:0003824	catalytic activity
gii148660320	acyl-CoA synthetase	GO:0003824	catalytic activity
gii148659921	NAD(P) transhydrogenase subunit beta	GO:0003824	catalytic activity
gii148662995	acyl-CoA dehydrogenase	GO:0003824	catalytic activity
gii148663137	acyl-CoA dehydrogenase	GO:0003824	catalytic activity
gii148661268	aconitate hydratase	GO:0003824	catalytic activity
gii148661183	S-adenosylmethionine synthetase	GO:0003824	catalytic activity
gii148661643	malate synthase G	GO:0003824	catalytic activity
gii148660667	citrate synthase 2	GO:0003824	catalytic activity
gii148660674	type II citrate synthase	GO:0003824	catalytic activity
gii148661733	fatty-acid--CoA ligase	GO:0003824	catalytic activity
gii148662003	long-chain-fatty-acid--CoA ligase	GO:0003824	catalytic activity
gii148662787	acyl-CoA synthetase	GO:0003824	catalytic activity
gii148661529	succinic semialdehyde dehydrogenase	GO:0003824	catalytic activity
gii148663444	cysteinyI-tRNA synthetase	GO:0003824	catalytic activity
gii148662852	ketol-acid reductoisomerase	GO:0003824	catalytic activity
gii148660233	isocitrate lyase Icl	GO:0003824	catalytic activity
gii148659826	isocitrate dehydrogenase (NADP) Icd2	GO:0003824	catalytic activity
gii148661035	alpha-ketoglutarate decarboxylase	GO:0003824	catalytic activity
gii148661454	argininosuccinate synthase	GO:0003824	catalytic activity
gii148662625	polynucleotide phosphorylase	GO:0003824	catalytic activity
gii148662028	glycine cleavage system aminomethyltransferase T	GO:0003824	catalytic activity
gii148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0003824	catalytic activity
gii148660204	short chain dehydrogenase	GO:0003824	catalytic activity
gii148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0003824	catalytic activity
gii148661530	hypothetical protein	GO:0003824	catalytic activity
gii148663086	short chain dehydrogenase	GO:0003824	catalytic activity
gii148663251	hypothetical protein	GO:0003824	catalytic activity
gii148662940	zinc-type alcohol dehydrogenase AdhD	GO:0003824	catalytic activity
gii148663491	inorganic pyrophosphatase	GO:0003824	catalytic activity
gii148660967	hypothetical protein	GO:0003824	catalytic activity
gii148661027	malate dehydrogenase	GO:0003824	catalytic activity
gii148662842	glutamyl-tRNA synthetase	GO:0003824	catalytic activity
gii148661080	arginyl-tRNA synthetase	GO:0003824	catalytic activity
gii148660035	acyl-CoA synthetase	GO:0003824	catalytic activity
gii148661317	acyl-CoA synthetase	GO:0003824	catalytic activity
gii148661325	acyl-CoA synthetase	GO:0003824	catalytic activity
gii148663669	long-chain-fatty-acid--CoA ligase	GO:0003824	catalytic activity
gii148660730	succinyl-CoA synthetase subunit beta	GO:0003824	catalytic activity
gii148663111	S-adenosyl-L-homocysteine hydrolase	GO:0003824	catalytic activity
gii148660879	serine hydroxymethyltransferase	GO:0003824	catalytic activity
gii148661113	thioredoxin-related protein	GO:0003824	catalytic activity
gii148661240	transaldolase	GO:0003824	catalytic activity
gii148661956	hypothetical protein	GO:0003824	catalytic activity
gii148661281	hypothetical protein	GO:0003824	catalytic activity
gii148663642	enoyl-CoA hydratase	GO:0003824	catalytic activity
gii148662038	glutamine synthetase	GO:0003824	catalytic activity
gii148661816	20-beta-hydroxysteroid dehydrogenase FabG3	GO:0003824	catalytic activity
gii148662311	NAD-dependent glutamate dehydrogenase Gdh	GO:0003824	catalytic activity
gii148662446	pyridoxal biosynthesis lyase PdxS	GO:0003824	catalytic activity
gii148660013	succinate dehydrogenase flavoprotein subunit	GO:0003824	catalytic activity
gii148662080	transcriptional regulatory protein	GO:0003824	catalytic activity
gii148662062	pyruvate dehydrogenase subunit E1	GO:0003824	catalytic activity
gii148662825	50S ribosomal protein L28	GO:0003824	catalytic activity
gii148660884	fumarate hydratase	GO:0003824	catalytic activity
gii148660129	fructose-bisphosphate aldolase	GO:0003824	catalytic activity
gii148660602	fatty acid desaturase	GO:0003824	catalytic activity
gii148663668	polyketide synthase	GO:0003824	catalytic activity
gii148660116	molecular chaperone DnaK	GO:0003824	catalytic activity
gii148661094	ATP synthase FOF1 subunit B	GO:0003824	catalytic activity
gii148660007	3-ketoacyl-ACP reductase	GO:0003824	catalytic activity
gii148661276	3-oxoacyl-ACP reductase	GO:0003824	catalytic activity
gii148659995	acyl-CoA dehydrogenase	GO:0003824	catalytic activity
gii148660009	acyl-CoA dehydrogenase	GO:0003824	catalytic activity
gii148660036	acyl-CoA dehydrogenase	GO:0003824	catalytic activity
gii148661422	lipid-transfer protein	GO:0003824	catalytic activity
gii148660636	acetyl-CoA acetyltransferase	GO:0003824	catalytic activity
gii148661112	acetyl-CoA acetyltransferase	GO:0003824	catalytic activity

gij148663419	acetyl-CoA acetyltransferase	GO:0003824	catalytic activity
gij148662295	ATP-dependent Clp protease proteolytic subunit	GO:0003824	catalytic activity
gij148660947	pterin-4-alpha-carbinolamine dehydratase	GO:0003824	catalytic activity
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0003824	catalytic activity
gij148660661	phosphoserine aminotransferase	GO:0003824	catalytic activity
gij148660203	molybdopterin biosynthesis protein MoeA2	GO:0003824	catalytic activity
gij148660331	polyprenyl-diphosphate synthase GrcC1	GO:0003824	catalytic activity
gij148663076	isochorismate synthase EntC	GO:0003824	catalytic activity
gij148662987	two component transcriptional regulatory protein DevR	GO:0060089	molecular transducer activity
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0060089	molecular transducer activity
gij148661096	ATP synthase F0F1 subunit alpha	GO:0005215	transporter activity
gij148661098	ATP synthase F0F1 subunit beta	GO:0005215	transporter activity
gij148661094	ATP synthase F0F1 subunit B	GO:0005215	transporter activity
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0005215	transporter activity
gij148660426	50S ribosomal protein L7/L12	GO:0005198	structural molecule activity
gij148660458	30S ribosomal protein S7	GO:0005198	structural molecule activity
gij148660475	30S ribosomal protein S10	GO:0005198	structural molecule activity
gij148661425	30S ribosomal protein S1	GO:0005198	structural molecule activity
gij148662734	30S ribosomal protein S2	GO:0005198	structural molecule activity
gij148662753	30S ribosomal protein S16	GO:0005198	structural molecule activity
gij148662825	50S ribosomal protein L28	GO:0005198	structural molecule activity
gij148663323	30S ribosomal protein S4	GO:0005198	structural molecule activity
gij148662987	two component transcriptional regulatory protein DevR	GO:0001071	nucleic acid binding transcription factor activity
gij148660593	thiosulfate sulfurtransferase CysA2	GO:0009055	electron carrier activity
gij148661035	alpha-ketoglutarate decarboxylase	GO:0009055	electron carrier activity
gij148661113	thioredoxin-related protein	GO:0009055	electron carrier activity
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0009055	electron carrier activity
gij148662881	electron transfer flavoprotein subunit beta	GO:0009055	electron carrier activity
gij148662971	thiosulfate sulfurtransferase CysA3	GO:0009055	electron carrier activity
gij148663322	DNA-directed RNA polymerase subunit alpha	GO:0005488	binding
gij148659826	isocitrate dehydrogenase (NADP) Icd2	GO:0005488	binding
gij148660730	succinyl-CoA synthetase subunit beta	GO:0005488	binding
gij148660799	ribose-phosphate pyrophosphokinase	GO:0005488	binding
gij148660988	tetrahydrodipicolinate N-succinyltransferase	GO:0005488	binding
gij148661035	alpha-ketoglutarate decarboxylase	GO:0005488	binding
gij148661183	S-adenosylmethionine synthetase	GO:0005488	binding
gij148661643	malate synthase G	GO:0005488	binding
gij148662038	glutamine synthetase	GO:0005488	binding
gij148662062	pyruvate dehydrogenase subunit E1	GO:0005488	binding
gij148663491	inorganic pyrophosphatase	GO:0005488	binding
gij148660458	30S ribosomal protein S7	GO:0005488	binding
gij148663323	30S ribosomal protein S4	GO:0005488	binding
gij148660661	phosphoserine aminotransferase	GO:0005488	binding
gij148660879	serine hydroxymethyltransferase	GO:0005488	binding
gij148660602	fatty acid desaturase	GO:0005488	binding
gij148660203	molybdopterin biosynthesis protein MoeA2	GO:0005488	binding
gij148662013	ubiquinol-cytochrome C reductase QcrB	GO:0005488	binding
gij148663282	co-chaperonin GroES	GO:0005488	binding
gij148659975	phosphoenolpyruvate carboxykinase	GO:0005488	binding
gij148663668	polyketide synthase	GO:0005488	binding
gij148661268	aconitate hydratase	GO:0005488	binding
gij148660104	iron-sulfur-binding reductase	GO:0005488	binding
gij148660459	elongation factor G	GO:0005488	binding
gij148660460	elongation factor Tu	GO:0005488	binding
gij148660116	molecular chaperone DnaK	GO:0005488	binding
gij148660118	molecular chaperone DnaJ	GO:0005488	binding
gij148660205	molecular chaperone GroEL	GO:0005488	binding
gij148660731	succinyl-CoA synthetase subunit alpha	GO:0005488	binding
gij148660967	hypothetical protein	GO:0005488	binding
gij148661080	arginyl-tRNA synthetase	GO:0005488	binding
gij148661096	ATP synthase F0F1 subunit alpha	GO:0005488	binding
gij148661098	ATP synthase F0F1 subunit beta	GO:0005488	binding
gij148661454	argininosuccinate synthase	GO:0005488	binding
gij148661496	CTP synthetase	GO:0005488	binding
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	GO:0005488	binding
gij148662003	long-chain-fatty-acid--CoA ligase	GO:0005488	binding
gij148662295	ATP-dependent Clp protease proteolytic subunit	GO:0005488	binding
gij148662787	acyl-CoA synthetase	GO:0005488	binding
gij148662842	glutamyl-tRNA synthetase	GO:0005488	binding
gij148663281	molecular chaperone GroEL	GO:0005488	binding
gij148663444	cysteinyl-tRNA synthetase	GO:0005488	binding
gij148663669	long-chain-fatty-acid--CoA ligase	GO:0005488	binding
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	GO:0005488	binding
gij148660416	methoxy mycolic acid synthase 4	GO:0005488	binding
gij148660475	30S ribosomal protein S10	GO:0005488	binding
gij148661633	hypothetical protein	GO:0005488	binding
gij148661961	hypothetical protein	GO:0005488	binding
gij148662032	dihydrolipoamide acetyltransferase	GO:0005488	binding
gij148662065	acyl carrier protein	GO:0005488	binding
gij148662311	NAD-dependent glutamate dehydrogenase Gdh	GO:0005488	binding
gij148660129	fructose-bisphosphate aldolase	GO:0005488	binding
gij148662940	zinc-type alcohol dehydrogenase AdhD	GO:0005488	binding
gij148659912	short-chain type dehydrogenase/reductase	GO:0005488	binding
gij148660204	short chain dehydrogenase	GO:0005488	binding
gij148660637	fatty oxidation complex subunit alpha	GO:0005488	binding
gij148661027	malate dehydrogenase	GO:0005488	binding
gij148661317	acyl-CoA synthetase	GO:0005488	binding
gij148661325	acyl-CoA synthetase	GO:0005488	binding
gij148661816	20-beta-hydroxysteroid dehydrogenase FabG3	GO:0005488	binding
gij148663086	short chain dehydrogenase	GO:0005488	binding
gij148660228	dihydrolipoamide dehydrogenase	GO:0005488	binding
gij148663111	S-adenosyl-L-homocysteine hydrolase	GO:0005488	binding
gij148661276	3-oxoacyl-ACP reductase	GO:0005488	binding
gij148662733	elongation factor Ts	GO:0005488	binding
gij148661425	30S ribosomal protein S1	GO:0005488	binding
gij148662625	polynucleotide phosphorylase	GO:0005488	binding
gij148659759	DNA polymerase III subunit beta	GO:0005488	binding
gij148660441	DNA-directed RNA polymerase subunit beta	GO:0005488	binding

gij148660442	DNA-directed RNA polymerase subunit beta'	GO:0005488	binding
gij148662385	hypothetical protein	GO:0005488	binding
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	GO:0005488	binding
gij148662987	two component transcriptional regulatory protein DevR	GO:0005488	binding
gij148663717	hypothetical protein	GO:0005488	binding
gij148660593	thiosulfate sulfurtransferase CysA2	GO:0005488	binding
gij148662971	thiosulfate sulfurtransferase CysA3	GO:0005488	binding
gij148663456	hypothetical protein	GO:0005488	binding
gij148661845	antigen Hsp20	GO:0005488	binding
gij148663007	NADH dehydrogenase subunit H	GO:0005488	binding
gij148662852	ketol-acid reductoisomerase	GO:0005488	binding
gij148659921	NAD(P) transhydrogenase subunit beta	GO:0005488	binding
gij148660007	3-ketoacyl-ACP reductase	GO:0005488	binding
gij148660908	6-phosphogluconate dehydrogenase	GO:0005488	binding
gij148660009	acyl-CoA dehydrogenase	GO:0005488	binding
gij148660013	succinate dehydrogenase flavoprotein subunit	GO:0005488	binding
gij148660036	acyl-CoA dehydrogenase	GO:0005488	binding
gij148662102	dehydrogenase	GO:0005488	binding
gij148662995	acyl-CoA dehydrogenase	GO:0005488	binding
gij148663137	acyl-CoA dehydrogenase	GO:0005488	binding
gij148662726	ribosome recycling factor	GO:0005488	binding
gij148660172	f420-dependent glucose-6-phosphate dehydrogenase Fgd1	GO:0005488	binding
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	GO:0005488	binding
<b>Cellular localization</b>			
<b>Protein_ID</b>	<b>Discription</b>	<b>Location</b>	
gij148661845	antigen Hsp20	Cellwall	
gij148659759	DNA polymerase III subunit beta	Cytoplasmic	
gij148659826	isocitrate dehydrogenase (NADP) Icd2	Cytoplasmic	
gij148659912	short-chain type dehydrogenase/reductase	Cytoplasmic	
gij148659975	phosphoenolpyruvate carboxykinase	Cytoplasmic	
gij148659995	acyl-CoA dehydrogenase	Cytoplasmic	
gij148660007	3-ketoacyl-ACP reductase	Cytoplasmic	
gij148660009	acyl-CoA dehydrogenase	Cytoplasmic	
gij148660035	acyl-CoA synthetase	Cytoplasmic	
gij148660036	acyl-CoA dehydrogenase	Cytoplasmic	
gij148660116	molecular chaperone DnaK	Cytoplasmic	
gij148660118	molecular chaperone DnaJ	Cytoplasmic	
gij148660129	fructose-bisphosphate aldolase	Cytoplasmic	
gij148660172	f420-dependent glucose-6-phosphate dehydrogenase Fgd1	Cytoplasmic	
gij148660203	molybdopterin biosynthesis protein MoeA2	Cytoplasmic	
gij148660205	molecular chaperone GroEL	Cytoplasmic	
gij148660228	dihydrolipoamide dehydrogenase	Cytoplasmic	
gij148660233	isocitrate lyase Icl	Cytoplasmic	
gij148660320	acyl-CoA synthetase	Cytoplasmic	
gij148660331	polyprenyl-diphosphate synthase GrcC1	Cytoplasmic	
gij148660416	methoxy mycolic acid synthase 4	Cytoplasmic	
gij148660426	50S ribosomal protein L7/L12	Cytoplasmic	
gij148660441	DNA-directed RNA polymerase subunit beta	Cytoplasmic	
gij148660442	DNA-directed RNA polymerase subunit beta'	Cytoplasmic	
gij148660458	30S ribosomal protein S7	Cytoplasmic	
gij148660459	elongation factor G	Cytoplasmic	
gij148660460	elongation factor Tu	Cytoplasmic	
gij148660475	30S ribosomal protein S10	Cytoplasmic	
gij148660529	MmsA	Cytoplasmic	
gij148660593	thiosulfate sulfurtransferase CysA2	Cytoplasmic	
gij148660602	fatty acid desaturase	Cytoplasmic	
gij148660636	acetyl-CoA acetyltransferase	Cytoplasmic	
gij148660637	fatty oxidation complex subunit alpha	Cytoplasmic	
gij148660667	citrate synthase 2	Cytoplasmic	
gij148660674	type II citrate synthase	Cytoplasmic	
gij148660730	succinyl-CoA synthetase subunit beta	Cytoplasmic	
gij148660799	ribose-phosphate pyrophosphokinase	Cytoplasmic	
gij148660879	serine hydroxymethyltransferase	Cytoplasmic	
gij148660884	fumarate hydratase	Cytoplasmic	
gij148660908	6-phosphogluconate dehydrogenase	Cytoplasmic	
gij148660947	pterin-4-alpha-carbinolamine dehydratase	Cytoplasmic	
gij148661035	alpha-ketoglutarate decarboxylase	Cytoplasmic	
gij148661080	arginyl-tRNA synthetase	Cytoplasmic	
gij148661096	ATP synthase FOF1 subunit alpha	Cytoplasmic	
gij148661112	acetyl-CoA acetyltransferase	Cytoplasmic	
gij148661113	thioredoxin-related protein	Cytoplasmic	
gij148661183	S-adenosylmethionine synthetase	Cytoplasmic	
gij148661240	transaldolase	Cytoplasmic	
gij148661268	aconitate hydratase	Cytoplasmic	
gij148661273	hypothetical protein	Cytoplasmic	
gij148661276	3-oxoacyl-ACP reductase	Cytoplasmic	
gij148661317	acyl-CoA synthetase	Cytoplasmic	
gij148661325	acyl-CoA synthetase	Cytoplasmic	
gij148661329	hypothetical protein	Cytoplasmic	
gij148661422	lipid-transfer protein	Cytoplasmic	
gij148661425	30S ribosomal protein S1	Cytoplasmic	
gij148661454	argininosuccinate synthase	Cytoplasmic	
gij148661496	CTP synthetase	Cytoplasmic	
gij148661529	succinic semialdehyde dehydrogenase	Cytoplasmic	
gij148661633	hypothetical protein	Cytoplasmic	
gij148661643	malate synthase G	Cytoplasmic	
gij148661733	fatty-acid--CoA ligase	Cytoplasmic	
gij148661816	20-beta-hydroxysteroid dehydrogenase FabG3	Cytoplasmic	
gij148661955	hypothetical protein	Cytoplasmic	
gij148661961	hypothetical protein	Cytoplasmic	
gij148661974	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	Cytoplasmic	
gij148661988	hypothetical protein	Cytoplasmic	
gij148662003	long-chain-fatty-acid--CoA ligase	Cytoplasmic	
gij148662028	glycine cleavage system aminomethyltransferase T	Cytoplasmic	
gij148662032	dihydrolipoamide acetyltransferase	Cytoplasmic	
gij148662038	glutamine synthetase	Cytoplasmic	
gij148662062	pyruvate dehydrogenase subunit E1	Cytoplasmic	
gij148662065	acyl carrier protein	Cytoplasmic	

gij148662080	transcriptional regulatory protein	Cytoplasmic	
gij148662295	ATP-dependent Clp protease proteolytic subunit	Cytoplasmic	
gij148662446	pyridoxal biosynthesis lyase PdxS	Cytoplasmic	
gij148662586	hypothetical protein	Cytoplasmic	
gij148662625	polynucleotide phosphorylase	Cytoplasmic	
gij148662726	ribosome recycling factor	Cytoplasmic	
gij148662733	elongation factor Ts	Cytoplasmic	
gij148662734	30S ribosomal protein S2	Cytoplasmic	
gij148662753	30S ribosomal protein S16	Cytoplasmic	
gij148662787	acyl-CoA synthetase	Cytoplasmic	
gij148662842	glutamyl-tRNA synthetase	Cytoplasmic	
gij148662852	ketol-acid reductoisomerase	Cytoplasmic	
gij148662881	electron transfer flavoprotein subunit beta	Cytoplasmic	
gij148662940	zinc-type alcohol dehydrogenase AdhD	Cytoplasmic	
gij148662971	thiosulfate sulfurtransferase CysA3	Cytoplasmic	
gij148662987	two component transcriptional regulatory protein DevR	Cytoplasmic	
gij148662995	acyl-CoA dehydrogenase	Cytoplasmic	
gij148663076	isochorismate synthase EntC	Cytoplasmic	
gij148663086	short chain dehydrogenase	Cytoplasmic	
gij148663109	two component sensory transduction transcriptional regulatory protein MtrA	Cytoplasmic	
gij148663111	S-adenosyl-L-homocysteine hydrolase	Cytoplasmic	
gij148663137	acyl-CoA dehydrogenase	Cytoplasmic	
gij148663251	hypothetical protein	Cytoplasmic	
gij148663281	molecular chaperone GroEL	Cytoplasmic	
gij148663282	co-chaperonin GroES	Cytoplasmic	
gij148663322	DNA-directed RNA polymerase subunit alpha	Cytoplasmic	
gij148663323	30S ribosomal protein S4	Cytoplasmic	
gij148663419	acetyl-CoA acetyltransferase	Cytoplasmic	
gij148663433	2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase	Cytoplasmic	
gij148663444	cysteinyl-tRNA synthetase	Cytoplasmic	
gij148663456	hypothetical protein	Cytoplasmic	
gij148663491	inorganic pyrophosphatase	Cytoplasmic	
gij148663669	long-chain-fatty-acid-CoA ligase	Cytoplasmic	
gij148663717	hypothetical protein	Cytoplasmic	
gij148659921	NAD(P) transhydrogenase subunit beta	Cytoplasmic Membrane	
gij148660013	succinate dehydrogenase flavoprotein subunit	Cytoplasmic Membrane	
gij148660104	iron-sulfur-binding reductase	Cytoplasmic Membrane	
gij148660733	transmembrane protein	Cytoplasmic Membrane	
gij148660967	hypothetical protein	Cytoplasmic Membrane	
gij148661098	ATP synthase F0F1 subunit beta	Cytoplasmic Membrane	
gij148661281	hypothetical protein	Cytoplasmic Membrane	
gij148661810	hypothetical protein	Cytoplasmic Membrane	
gij148662013	ubiquinol-cytochrome C reductase QcrB	Cytoplasmic Membrane	
gij148662311	NAD-dependent glutamate dehydrogenase Gdh	Cytoplasmic Membrane	
gij148663007	NADH dehydrogenase subunit H	Cytoplasmic Membrane	
gij148663558	hypothetical protein	Cytoplasmic Membrane	
gij148663668	polyketide synthase	Cytoplasmic Membrane	
gij148660204	short chain dehydrogenase	Unknown	
gij148660256	phosphoglyceromutase	Unknown	
gij148660410	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	Unknown	
gij148660608	hypothetical protein	Unknown	
gij148660661	phosphoserine aminotransferase	Unknown	
gij148660731	succinyl-CoA synthetase subunit alpha	Unknown	
gij148660988	tetrahydrodipicolinate N-succinyltransferase	Unknown	
gij148661027	malate dehydrogenase	Unknown	
gij148661094	ATP synthase F0F1 subunit B	Unknown	
gij148661431	hypothetical protein	Unknown	
gij148661530	hypothetical protein	Unknown	
gij148661956	hypothetical protein	Unknown	
gij148662102	dehydrogenase	Unknown	
gij148662385	hypothetical protein	Unknown	
gij148662825	50S ribosomal protein L28	Unknown	
gij148663642	enoyl-CoA hydratase	Unknown	
gij148663732	hypothetical protein	Unknown	