

Electronic Supplementary Information (ESI)

Multi-omics based characterization of antibiotic response in clinical isogenic isolates of methicillin-susceptible/-resistant *Staphylococcus aureus*

Sung-Hyun Jo^a, Won-Suk Song^b, Han-Gyu Park^a, Jae-Seung Lee^a, Hyo-Jin Jeon^a, Yeon-Hee Lee^c, Wooseong Kim^d, Hwang-Soo Joo^c, Yung-Hun Yang^e, Jae-Seok Kim^f, and Yun-Gon Kim^{a,*}

^a*Department of Chemical Engineering, College of Engineering, Soongsil University, Seoul 06978, Republic of Korea*

^b*School of Chemical and Biological Engineering, Seoul National University, Seoul 08826, Republic of Korea*

^c*Department of Biotechnology, Duksung Women's University, Seoul 01369, Republic of Korea*

^d*College of Pharmacy, Graduate School of Pharmaceutical Sciences, Ewha Womans University, Seoul 03760, Republic of Korea*

^e*Department of Microbial Engineering, College of Engineering, Konkuk University, Seoul 05029, Republic of Korea*

^f*Department of Laboratory Medicine, Kangdong Sacred Heart Hospital, Hallym University College of Medicine, Seoul 05355, Republic of Korea*

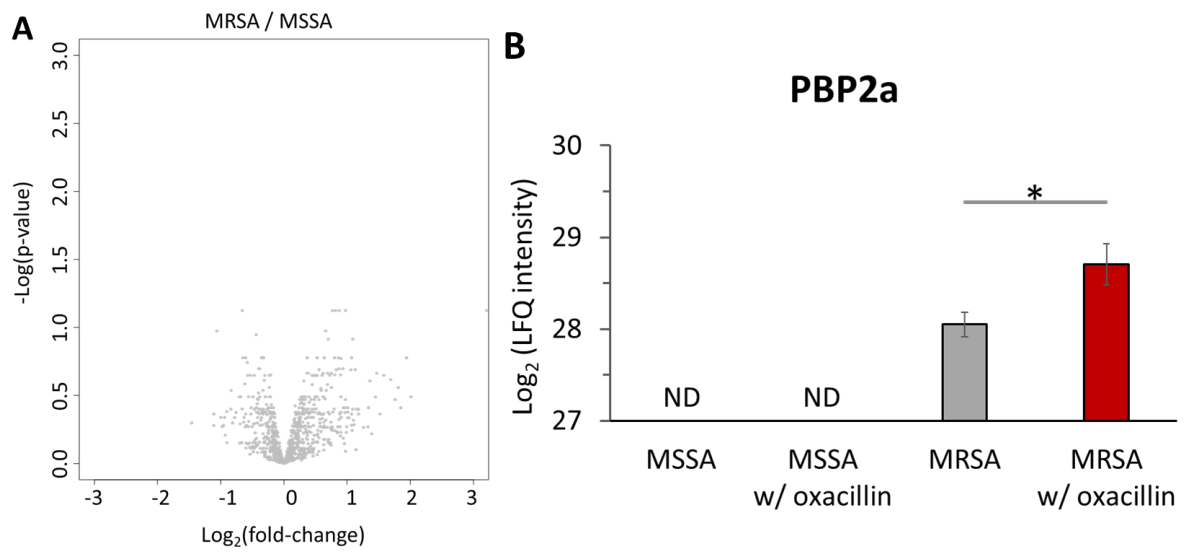


Fig S1. Volcano plot of proteomic analysis for MSSA and MRSA without oxacillin. There are no statistically significant proteins. (B) Penicillin-binding protein 2a (PBP2a) encoded by the *mecA* gene was up-regulated in oxacillin treated MRSA than MRSA without oxacillin. PBP2a was not detected in MSSA. The symbol (*) indicates a statistically significant difference (n = 4, p < 0.05). Error bars indicate standard deviation.

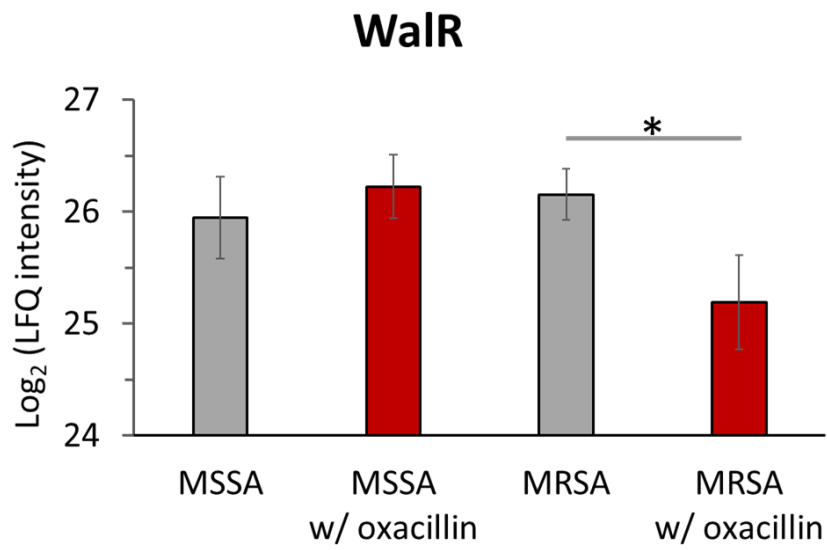


Fig S2. Bar graph of LFQ intensity level of WalK. The symbol (*) indicates a statistically significant difference ($n = 4$, $p < 0.05$). Error bars indicate standard deviation.

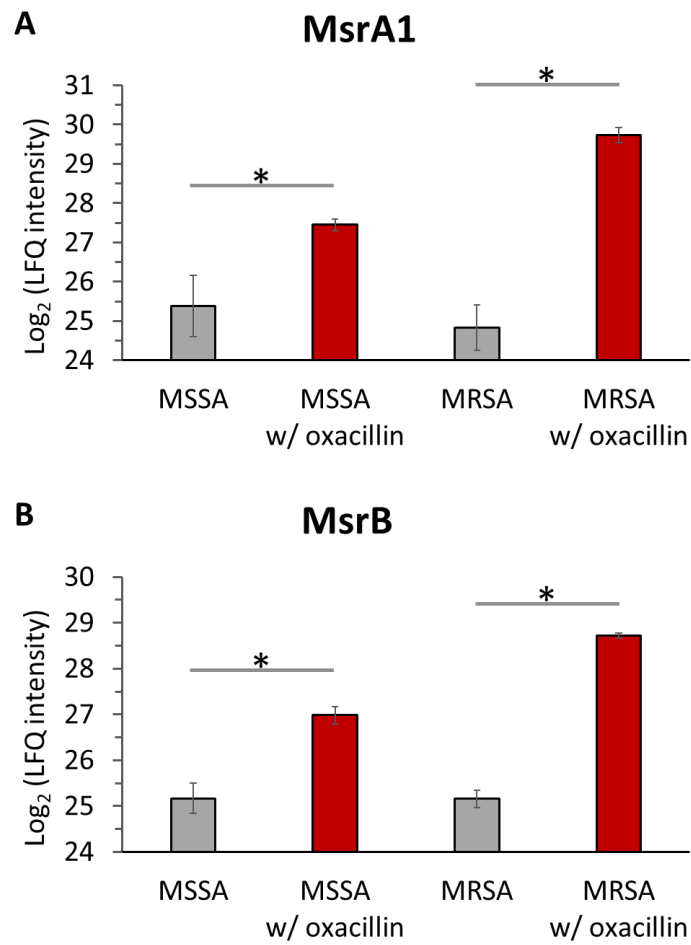


Fig S3. Bar graph of LFQ intensity levels of (A) MsrA1 and (B) MsrB (Methionine sulfoxide reductases). The symbol (*) indicates a statistically significant difference (n = 4, p < 0.05). Error bars indicate standard deviation.

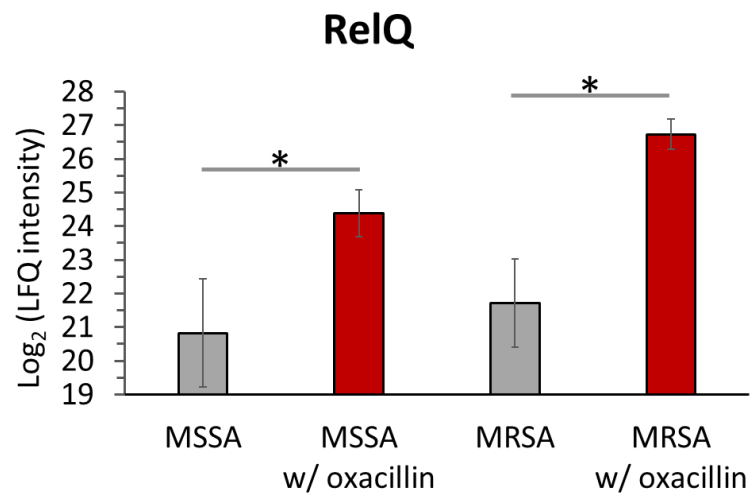


Fig S4. Bar graph of LFQ intensity level of RelQ. The symbol (*) indicates a statistically significant difference (n = 4, p < 0.05). Error bars indicate standard deviation.

Table S1. List of identified proteins in the intracellular proteome analysis.

RAST IDs	Protein function (the seed)	Gene name	log2 fold change (MRSA with oxacillin / MSSA with oxacillin)	log2 fold change (MRSA/ MSSA)	log2 fold change (MRSA with oxacillin/ MRSA)	log2 fold change (MSSA with oxacillin/ MSSA)	adjusted p-value (MRSA with oxacillin/ MSSA with oxacillin)	adjusted p-value (MRSA/ MSSA)	adjusted p-value (MRSA with oxacillin/ MRSA)	adjusted p-value (MSSA with oxacillin/ MSSA)
fig 6666666.474.865.peg.1111	Penicillin-binding protein PBP2a, methicillin resistance determinant MecA, transpeptidase	mecA	Not detectable in MSSA							
fig 6666666.474.865.peg.1125	ORFID:MW0043		1.73	3.21	-0.887	0.592	0.118	0.0751	0.32	0.519
fig 6666666.474.865.peg.191	3'->5' exoribonuclease Bsu YhaM		-0.468	2.01	-0.0654	2.42	0.734	0.323	0.959	0.027
fig 6666666.474.865.peg.1105	FIG01108167: hypothetical protein		0.123	1.94	-1.3	0.516	0.911	0.167	0.0737	0.486
fig 6666666.474.865.peg.1408	Potassium efflux system KefA protein / Small-conductance mechanosensitive channel		1.84	1.85	1.81	1.82	0.168	0.389	0.0975	0.0975
fig 6666666.474.865.peg.2370	SOS-response repressor and protease LexA (EC 3.4.21.88)		-0.464	1.81	-0.924	1.35	0.694	0.276	0.296	0.126
fig 6666666.474.865.peg.1855	Cell division inhibitor Slr1223 (YfcH in EC), contains epimerase/dehydratase and DUF1731 domains		-0.941	1.76	-0.0355	2.66	0.456	0.339	0.976	0.012
fig 6666666.474.865.peg.887	LPXTG specific sortase A		0.236	1.69	0.205	1.66	0.832	0.242	0.827	0.0396
fig 6666666.474.865.peg.2386	Sodium:alanine symporter family protein		-0.535	1.58	-0.0506	2.07	0.561	0.225	0.955	0.00752
fig 6666666.474.865.peg.1571	Membrane-associated protein containing RNA-binding TRAM domain and ribonuclease PIN-domain, YacL B.subtilis ortholog		-0.303	1.52	-0.286	1.53	0.84	0.432	0.823	0.147
fig 6666666.474.865.peg.2635	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)		-0.0844	1.47	-0.0628	1.49	0.931	0.217	0.932	0.0219
fig 6666666.474.865.peg.714	Multidrug resistance protein [function not yet clear]		-0.623	1.45	-0.516	1.55	0.541	0.324	0.532	0.0504
fig 6666666.474.865.peg.2490	MazG nucleotide pyrophosphohydrolase		-3.13	1.39	-3.77	0.745	0.0806	0.605	0.0137	0.62
fig 6666666.474.865.peg.710	FIG01107838: hypothetical protein		0.00595	1.36	0.314	1.67	0.992	0.247	0.659	0.0149
fig 6666666.474.865.peg.1418	Phage protein		-1.39	1.34	-1.06	1.66	0.159	0.389	0.188	0.0444
fig 6666666.474.865.peg.193	DNA repair exonuclease family protein YhaO		-1.03	1.33	-1.44	0.919	0.502	0.537	0.224	0.443
fig 6666666.474.865.peg.1607	Adhesin of unknown specificity SdrE, similar to bone sialoprotein-binding protein Bbp		-1.17	1.26	-2.25	0.168	0.435	0.543	0.0542	0.891
fig 6666666.474.865.peg.1499	Esterase/lipase family protein		0.179	1.18	1.66	2.67	0.868	0.399	0.0285	0.00219

fig/6666666.474 865.peg.1004	Phage infection protein		-0.811	1.18	-1.4	0.587	0.454	0.433	0.0957	0.495
fig/6666666.474 865.peg.52	tRNA S(4)U 4-thiouridine synthase (former ThiI)		-0.0852	1.15	0.257	1.5	0.945	0.399	0.764	0.0442
fig/6666666.474 865.peg.59	Phosphoserine aminotransferase, putative (EC 2.6.1.52)		0.535	1.14	-0.643	-0.034	0.845	0.791	0.779	0.988
fig/6666666.474 865.peg.2123	COG1399 protein in cluster with ribosomal protein L32p, Firmicutes subfamily		-0.522	1.13	0.567	2.22	0.367	0.204	0.218	0.000282
fig/6666666.474 865.peg.2282	FIG002344: Hydrolase (HAD superfamily)		0.491	1.11	0.315	0.933	0.694	0.519	0.774	0.319
fig/6666666.474 865.peg.2348	FIG01107992: hypothetical protein		-0.985	1.1	-2	0.0912	0.358	0.48	0.0245	0.92
fig/6666666.474 865.peg.1104	LSU m3Psi1915 methyltransferase RlmH		0.602	1.09	0.0258	0.513	0.162	0.122	0.955	0.146
fig/6666666.474 865.peg.999	immunodominant antigen B		-0.0779	1.09	-0.769	0.399	0.946	0.399	0.256	0.57
fig/6666666.474 865.peg.1573	Serine acetyltransferase (EC 2.3.1.30)		-0.93	1.08	-1.19	0.815	0.483	0.571	0.248	0.436
fig/6666666.474 865.peg.2442	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)		-0.934	1.07	-1.58	0.426	0.0619	0.167	0.000971	0.286
fig/6666666.474 865.peg.2139	DNA polymerase X family		-0.419	1.07	-0.209	1.28	0.726	0.522	0.846	0.154
fig/6666666.474 865.peg.2469	Probable 5'-3' exonuclease Bsu YpcP		0.134	1.07	0.182	1.12	0.908	0.433	0.843	0.14
fig/6666666.474 865.peg.2196	Aspartate carbamoyltransferase (EC 2.1.3.2)		0.0868	1.06	-0.599	0.376	0.897	0.205	0.17	0.397
fig/6666666.474 865.peg.2720	CsdL (EC-YgdL) protein of the HesA/MoeB/ThiF family, part of the CsdA-E-L sulfur transfer pathway		-0.071	1.03	0.127	1.23	0.962	0.461	0.892	0.113
fig/6666666.474 865.peg.2616	Alkaline shock protein		-0.879	1.01	-0.156	1.73	0.238	0.389	0.831	0.00929
fig/6666666.474 865.peg.55	Free methionine-(R)-sulfoxide reductase, contains GAF domain		0.383	1.01	0.928	1.56	0.711	0.461	0.223	0.0459
fig/6666666.474 865.peg.12	GTP-binding protein EngB		0.303	1.01	-0.619	0.0859	0.734	0.419	0.364	0.907
fig/6666666.474 865.peg.668	Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily F2 (as in PMID19099556)	msrR	1.62	0.993	2.48	1.85	0.131	0.536	0.00868	0.0385
fig/6666666.474 865.peg.81	FIG002434: Uncharacterized protein YtpQ		-1.12	0.988	-1.16	0.943	0.368	0.59	0.239	0.344
fig/6666666.474 865.peg.476	Hypothetical protein ywlG		0.124	0.976	-1.04	-0.193	0.966	0.813	0.59	0.92
fig/6666666.474 865.peg.1657	Predicted hydrolase		0.0202	0.974	0.62	1.57	0.963	0.0751	0.0199	4.09E-05
fig/6666666.474 865.peg.2741	FIG01108101: hypothetical protein		1.75	0.973	4.12	3.34	0.016	0.339	4.18E-06	4.27E-05
fig/6666666.474 865.peg.2439	FIG01108295: hypothetical protein		0.755	0.965	-0.619	-0.41	0.351	0.422	0.341	0.543

fig/6666666.474 865.peg.2705	peptidase, U32 family small subunit [C1]		0.0121	0.958	-0.216	0.73	0.984	0.389	0.749	0.206
fig/6666666.474 865.peg.361	Leukocidin LukS-PV		-1.58	0.955	-2.57	-0.04	0.331	0.714	0.0523	0.978
fig/6666666.474 865.peg.2120	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)		-0.295	0.94	0.471	1.71	0.694	0.389	0.409	0.00633
fig/6666666.474 865.peg.2258	Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage		0.962	0.939	1.75	1.73	0.475	0.652	0.0949	0.0985
fig/6666666.474 865.peg.2039	Menaquinone-specific isochorismate synthase (EC 5.4.4.2)		-0.352	0.934	-0.302	0.984	0.461	0.201	0.428	0.014
fig/6666666.474 865.peg.1683	N-acetylmannosaminyltransferase (EC 2.4.1.187)		-0.568	0.906	0.185	1.66	0.513	0.458	0.817	0.019
fig/6666666.474 865.peg.2649	UPF0135 protein Bsu YqfO @ Bsu YqfO NIF3/CutA domain		-0.57	0.904	0.119	1.59	0.645	0.59	0.919	0.0775
fig/6666666.474 865.peg.1329	ESAT-6/Esx family secreted protein EsxA/Yuke		0.298	0.902	-3.57	-2.97	0.658	0.323	5.16E-06	4.23E-05
fig/6666666.474 865.peg.1803	Lipoteichoic acid synthase LtaS Type Ib		-0.106	0.902	-0.0971	0.91	0.83	0.169	0.815	0.014
fig/6666666.474 865.peg.875	Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11)		-0.962	0.901	-0.138	1.73	0.19	0.419	0.849	0.009
fig/6666666.474 865.peg.1464	FIG01108224: hypothetical protein		-0.1	0.898	-0.612	0.386	0.914	0.422	0.31	0.539
fig/6666666.474 865.peg.2391	Peptide methionine sulfoxide reductase regulator MsrR		0.351	0.897	1.5	2.04	0.481	0.223	0.0012	0.000146
fig/6666666.474 865.peg.865	GTP pyrophosphokinase (EC 2.7.6.5)	relQ	1.12	0.895	5.01	4.78	0.351	0.626	9.88E-05	0.000225
fig/6666666.474 865.peg.852	DNA/RNA helicase of DEAD/DEAH box family		-0.0119	0.889	-1.37	-0.469	0.989	0.537	0.0832	0.567
fig/6666666.474 865.peg.493	Pantothenate kinase type II, eukaryotic (EC 2.7.1.33)		-0.117	0.885	-0.0129	0.99	0.903	0.433	0.988	0.119
fig/6666666.474 865.peg.1703	Acetyltransferase GNAT family		0.321	0.877	0.97	1.53	0.282	0.0751	0.000938	3.53E-05
fig/6666666.474 865.peg.2025	FIG01108367: hypothetical protein		0.105	0.874	-1.74	-0.971	0.832	0.201	0.000152	0.011
fig/6666666.474 865.peg.2174	Cell division protein MraZ	mraZ	1.07	0.872	3	2.79	0.19	0.475	0.000362	0.000843
fig/6666666.474 865.peg.600	SSU ribosomal protein S17p (S11e)		0.289	0.86	-0.627	-0.0555	0.461	0.167	0.0439	0.872
fig/6666666.474 865.peg.226	Hypothetical protein FIG009695		-0.212	0.854	-3.12	-2.05	0.845	0.537	0.000766	0.0127
fig/6666666.474 865.peg.1843	Excinuclease ABC subunit B		0.0962	0.849	-0.38	0.372	0.948	0.595	0.697	0.684
fig/6666666.474 865.peg.1854	NAD-dependent malic enzyme (EC 1.1.1.38)		-0.528	0.847	-1.66	-0.283	0.646	0.586	0.0503	0.756
fig/6666666.474 865.peg.703	ABC-type transport system, ATPase component		0.234	0.827	-2.26	-1.67	0.615	0.205	1.30E-05	0.000247

fig 6666666.474 865.peg.1503	Cystathionine gamma-lyase (EC 4.4.1.1)		1.1	0.819	0.705	0.429	0.00175	0.0751	0.00649	0.0695
fig 6666666.474 865.peg.1086	NAD(P)HX dehydratase		-0.478	0.808	-1.98	-0.699	0.658	0.574	0.016	0.378
fig 6666666.474 865.peg.2084	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)		0.574	0.805	2.77	3	0.178	0.223	2.45E-06	2.20E-06
fig 6666666.474 865.peg.2000	GTP pyrophosphokinase (EC 2.7.6.5)	relP	-0.28	0.801	-0.35	0.731	0.475	0.167	0.248	0.0219
fig 6666666.474 865.peg.2117	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)		0.249	0.793	1.73	2.27	0.704	0.397	0.00227	0.000363
fig 6666666.474 865.peg.2708	Putative Holliday junction resolvase YqgF		0.124	0.774	0.0746	0.724	0.868	0.419	0.908	0.154
fig 6666666.474 865.peg.1546	Peptidyl-tRNA hydrolase (EC 3.1.1.29)		-0.538	0.772	0.00955	1.32	0.581	0.57	0.994	0.0726
fig 6666666.474 865.peg.2618	Biotin carboxyl carrier protein of acetyl-CoA carboxylase		0.236	0.771	-0.107	0.428	0.394	0.0751	0.66	0.0531
fig 6666666.474 865.peg.969	Choline dehydrogenase (EC 1.1.99.1)		-0.0407	0.765	-6.66	-5.85	0.967	0.542	5.21E-07	2.92E-06
fig 6666666.474 865.peg.1783	Transcriptional repressor of the fructose operon, DeoR family		0.849	0.761	-0.285	-0.374	0.35	0.57	0.734	0.622
fig 6666666.474 865.peg.2614	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)		-1.36	0.753	-0.257	1.86	0.109	0.538	0.745	0.0117
fig 6666666.474 865.peg.2592	Ribonuclease Z (EC 3.1.26.11)		-0.102	0.752	-0.847	0.00727	0.843	0.276	0.0254	0.987
fig 6666666.474 865.peg.25	NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)		-0.404	0.751	-0.699	0.456	0.311	0.217	0.0325	0.154
fig 6666666.474 865.peg.1872	Clumping factor ClfA, fibrinogen-binding protein	clfA	0.39	0.746	-1.38	-1.02	0.789	0.733	0.196	0.343
fig 6666666.474 865.peg.2302	Aluminum resistance protein		-0.991	0.746	-1.05	0.689	0.243	0.554	0.13	0.326
fig 6666666.474 865.peg.1719	FIG01107967: hypothetical protein		0.563	0.743	1.17	1.35	0.461	0.497	0.0518	0.0298
fig 6666666.474 865.peg.1649	hypothetical fig 282458.1.peg.581 homolog		-0.162	0.737	-0.342	0.557	0.911	0.703	0.762	0.571
fig 6666666.474 865.peg.2491	probable metal-dependent peptidase		0.767	0.725	2.04	1.99	0.0556	0.225	1.80E-05	3.53E-05
fig 6666666.474 865.peg.1495	Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 homolog		0.109	0.721	-0.321	0.291	0.893	0.433	0.566	0.586
fig 6666666.474 865.peg.2180	Cell division protein FtsQ		0.15	0.71	-1.54	-0.981	0.915	0.708	0.0962	0.292
fig 6666666.474 865.peg.1327	FIG01108182: hypothetical protein		-0.198	0.709	-3.03	-2.12	0.868	0.664	0.0016	0.0154
fig 6666666.474 865.peg.2441	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)		-0.131	0.702	-1.07	-0.241	0.678	0.122	0.000253	0.296
fig 6666666.474 865.peg.1606	Adhesin of unknown specificity SdrD		0.833	0.7	0.196	0.0634	0.445	0.691	0.846	0.941

fig/6666666.474 865.peg.767	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)		-0.168	0.699	-1.46	-0.589	0.79	0.419	0.00473	0.2
fig/6666666.474 865.peg.111	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)		-0.406	0.691	-0.455	0.642	0.252	0.217	0.116	0.0338
fig/6666666.474 865.peg.2177	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)	pbpA	0.229	0.688	0.868	1.33	0.609	0.263	0.0135	0.00105
fig/6666666.474 865.peg.489	Hypothetical protein MW2050		-0.619	0.688	0.0899	1.4	0.446	0.542	0.911	0.0332
fig/6666666.474 865.peg.33	Citrate synthase (si) (EC 2.3.3.1)		0.34	0.671	0.324	0.656	0.429	0.29	0.331	0.0529
fig/6666666.474 865.peg.2054	FmtA protein involved in methicillin resistance	fmtA	0.635	0.663	1.98	2.01	0.321	0.479	0.00119	0.00127
fig/6666666.474 865.peg.2709	FIG01055109: hypothetical protein		0.016	0.66	-0.481	0.163	0.963	0.106	0.0236	0.432
fig/6666666.474 865.peg.1315	Ribokinase (EC 2.7.1.15)		0.0869	0.654	0.033	0.6	0.926	0.543	0.962	0.324
fig/6666666.474 865.peg.2273	Transcriptional regulator in cluster with Zn-dependent hydrolase		0.378	0.652	-0.222	0.0518	0.711	0.664	0.803	0.946
fig/6666666.474 865.peg.2495	5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)		-0.471	0.651	0.113	1.24	0.281	0.335	0.787	0.00282
fig/6666666.474 865.peg.2610	DNA repair protein RecN		-0.224	0.637	0.47	1.33	0.764	0.529	0.396	0.0209
fig/6666666.474 865.peg.2198	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)		0.156	0.636	-0.574	-0.0936	0.64	0.167	0.0214	0.718
fig/6666666.474 865.peg.2625	Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2)		0.0131	0.636	-0.767	-0.144	0.967	0.167	0.00409	0.562
fig/6666666.474 865.peg.2423	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)		-0.466	0.634	-1.54	-0.441	0.475	0.497	0.00592	0.392
fig/6666666.474 865.peg.612	Hypoxanthine/guanine permease PbuG		1.11	0.633	1.92	1.45	0.118	0.539	0.00332	0.0174
fig/6666666.474 865.peg.60	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)		-0.911	0.632	1.38	2.92	0.517	0.796	0.202	0.0123
fig/6666666.474 865.peg.1528	Signal peptidase-like protein		-0.117	0.632	-0.459	0.29	0.933	0.727	0.636	0.764
fig/6666666.474 865.peg.715	TetR family regulatory protein of MDR cluster		-0.525	0.629	-0.231	0.923	0.591	0.665	0.787	0.203
fig/6666666.474 865.peg.2621	FIG01108536: hypothetical protein		0.609	0.628	0.0455	0.0651	0.251	0.432	0.931	0.89
fig/6666666.474 865.peg.2683	Hydrolase (HAD superfamily), YqeK		-0.849	0.627	-0.741	0.735	0.0456	0.323	0.0304	0.034
fig/6666666.474 865.peg.669	Histidinol-phosphatase [alternative form] (EC 3.1.3.15)		0.105	0.626	0.166	0.687	0.868	0.432	0.742	0.113
fig/6666666.474 865.peg.101	Predicted cell-wall-anchored protein SasC (LPXTG motif)		-0.617	0.622	-1.1	0.143	0.254	0.433	0.0182	0.767
fig/6666666.474 865.peg.1021	FIG01108094: hypothetical protein		-0.567	0.622	-1.21	-0.0216	0.437	0.542	0.0364	0.973

fig 6666666.474 865.peg.2172	Uncharacterized N-acetyltransferase BT9727_3663 (EC 2.3.1.-)		0.616	0.622	0.225	0.231	0.0619	0.217	0.396	0.388
fig 6666666.474 865.peg.1082	FIG002958: hypothetical protein		0.132	0.619	-0.389	0.0985	0.773	0.323	0.237	0.784
fig 6666666.474 865.peg.752	Transcriptional regulator SarZ (Staphylococcal accessory regulator Z)	sarZ	-1.01	0.608	0.18	1.8	0.0658	0.437	0.723	0.000943
fig 6666666.474 865.peg.1613	Glucosamine-6-phosphate deaminase (EC 3.5.99.6)		-0.75	0.605	0.596	1.95	0.183	0.467	0.195	0.000712
fig 6666666.474 865.peg.270	Nicotinamidase (EC 3.5.1.19)		-0.311	0.604	0.656	1.57	0.354	0.225	0.0198	6.13E-05
fig 6666666.474 865.peg.929	Immunodominant staphylococcal antigen A precursor		0.178	0.59	-0.408	0.00331	0.658	0.29	0.162	0.991
fig 6666666.474 865.peg.1102	Virulence-associated cell-wall-anchored protein SasH (LPXTG motif); 5'-nucleotidase (EC 3.1.3.5)	sasH	-1.86	0.588	-4.11	-1.66	0.016	0.581	6.66E-06	0.0086
fig 6666666.474 865.peg.1635	Phosphomevalonate kinase (EC 2.7.4.2)		0.184	0.583	0.859	1.26	0.643	0.281	0.00649	0.000562
fig 6666666.474 865.peg.280	FIG01107873: hypothetical protein		0.392	0.581	-0.172	0.0167	0.562	0.537	0.777	0.977
fig 6666666.474 865.peg.2086	Trk system potassium uptake protein TrkA		-2.05	0.576	-0.2	2.42	0.00389	0.533	0.73	0.000263
fig 6666666.474 865.peg.2295	Glycerol kinase (EC 2.7.1.30)		-0.189	0.574	0.894	1.66	0.73	0.433	0.0332	0.00105
fig 6666666.474 865.peg.800	FIG01107902: hypothetical protein		1.45	0.572	3.79	2.91	0.0173	0.503	1.88E-06	3.53E-05
fig 6666666.474 865.peg.1028	Biofilm operon icaABCD HTH-type negative transcriptional regulator IcaR		-0.239	0.568	-0.617	0.19	0.722	0.536	0.213	0.721
fig 6666666.474 865.peg.678	phosphoglycolate phosphatase		-0.699	0.568	-0.386	0.881	0.189	0.473	0.38	0.048
fig 6666666.474 865.peg.2218	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)		0.31	0.557	0.434	0.68	0.529	0.422	0.251	0.0732
fig 6666666.474 865.peg.1449	Nitroreductase family protein		0.323	0.556	0.307	0.54	0.243	0.204	0.175	0.0232
fig 6666666.474 865.peg.2707	FIG01108372: hypothetical protein		0.189	0.556	0.176	0.543	0.658	0.339	0.601	0.0813
fig 6666666.474 865.peg.398	Response regulator of the competence regulon ComE	agrA	-1.29	0.556	-0.872	0.979	0.093	0.647	0.156	0.112
fig 6666666.474 865.peg.1353	Acid phosphatase (EC 3.1.3.2)		0.256	0.554	-3.47	-3.17	0.866	0.814	0.0031	0.0057
fig 6666666.474 865.peg.224	Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.-)	sgtB	0.708	0.535	5.7	5.53	0.257	0.57	9.16E-08	2.50E-07
fig 6666666.474 865.peg.1612	FIG011895: hypothetical protein		-0.011	0.535	0.578	1.12	0.988	0.699	0.391	0.0908
fig 6666666.474 865.peg.2725	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I	relA	-0.0229	0.535	-0.0118	0.547	0.967	0.43	0.979	0.138
fig 6666666.474 865.peg.2260	DNA polymerase III alpha subunit (EC 2.7.7.7)		0.87	0.533	-0.109	-0.446	0.199	0.608	0.869	0.426

fig/6666666.474 865.peg.2293	Glycerol uptake operon antiterminator regulatory protein		-0.996	0.529	-0.977	0.548	0.202	0.691	0.124	0.397
fig/6666666.474 865.peg.233	Ribonuclease BN (EC 3.1.-.-)		-0.231	0.528	-0.819	-0.0599	0.453	0.225	0.00285	0.826
fig/6666666.474 865.peg.1615	6-phospho-3-hexuloisomerase		-0.784	0.527	-0.254	1.06	0.251	0.621	0.689	0.0612
fig/6666666.474 865.peg.2464	Putative Staphylococcal surface anchored protein		-0.775	0.527	-0.511	0.791	0.658	0.861	0.73	0.552
fig/6666666.474 865.peg.2201	Orotate phosphoribosyltransferase (EC 2.4.2.10)		0.129	0.526	-0.667	-0.27	0.64	0.167	0.00336	0.174
fig/6666666.474 865.peg.1595	chaperone protein HchA		-0.485	0.525	-1.74	-0.727	0.154	0.323	2.37E-05	0.0153
fig/6666666.474 865.peg.2097	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)		0.179	0.52	-0.056	0.285	0.842	0.694	0.945	0.676
fig/6666666.474 865.peg.2144	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)		-0.441	0.51	-0.44	0.512	0.25	0.397	0.161	0.102
fig/6666666.474 865.peg.480	Peptide chain release factor 1		0.136	0.506	-0.383	-0.013	0.667	0.225	0.0949	0.957
fig/6666666.474 865.peg.1844	Excinuclease ABC subunit A		-0.529	0.498	-0.98	0.0463	0.0607	0.225	0.000428	0.859
fig/6666666.474 865.peg.2667	tRNA-t(6)A37 methyltransferase		0.0114	0.492	0.0437	0.524	0.974	0.323	0.891	0.0506
fig/6666666.474 865.peg.1707	Bacitracin export ATP-binding protein BceA		-0.53	0.49	-0.673	0.347	0.15	0.397	0.0292	0.244
fig/6666666.474 865.peg.2062	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)		-0.131	0.485	-0.16	0.455	0.667	0.226	0.485	0.0445
fig/6666666.474 865.peg.2228	acyl carrier protein ACP		-0.515	0.485	-1.41	-0.41	0.125	0.339	9.99E-05	0.131
fig/6666666.474 865.peg.1878	Cold shock protein CspC		0.493	0.484	-0.917	-0.926	0.211	0.419	0.00877	0.00883
fig/6666666.474 865.peg.37	Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)		0.284	0.481	0.34	0.537	0.285	0.225	0.115	0.019
fig/6666666.474 865.peg.2704	peptidase, U32 family large subunit [C1]		-0.293	0.48	0.161	0.934	0.677	0.621	0.789	0.0695
fig/6666666.474 865.peg.2079	LSU m5C1962 methyltransferase Rlml		0.0503	0.477	0.618	1.04	0.906	0.369	0.0297	0.00165
fig/6666666.474 865.peg.1767	Undecaprenyl-diphosphatase (EC 3.6.1.27)		0.867	0.475	3.25	2.86	0.238	0.699	7.82E-05	0.000305
fig/6666666.474 865.peg.1149	tRNA dihydrouridine synthase B (EC 1.-.-.-)		-0.552	0.475	-0.982	0.0453	0.594	0.774	0.202	0.955
fig/6666666.474 865.peg.1857	Central glycolytic genes regulator		0.0302	0.466	-0.555	-0.119	0.963	0.525	0.161	0.783
fig/6666666.474 865.peg.2134	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)		-0.163	0.465	-0.781	-0.153	0.726	0.458	0.0282	0.677
fig/6666666.474 865.peg.1920	Glyoxylate reductase (EC 1.1.1.79) / Glyoxylate reductase (EC 1.1.1.26) / Hydroxypyruvate reductase (EC 1.1.1.81)		0.0374	0.462	1.25	1.67	0.981	0.879	0.301	0.164

fig/6666666.474 865.peg.1195	Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)		-0.511	0.461	-0.858	0.114	0.691	0.831	0.375	0.913
fig/6666666.474 865.peg.1680	Manganese ABC transporter, ATP-binding protein SitB		-1.1	0.459	-2.29	-0.729	0.0967	0.664	0.000482	0.167
fig/6666666.474 865.peg.970	Betaine aldehyde dehydrogenase (EC 1.2.1.8)		-3.29	0.459	-10.7	-6.95	0.0346	0.882	1.16E-06	7.30E-05
fig/6666666.474 865.peg.1050	FIG01108092: hypothetical protein		-0.481	0.458	-2.71	-1.77	0.658	0.799	0.00285	0.0319
fig/6666666.474 865.peg.1998	Adenylate cyclase		-0.14	0.449	1.54	2.13	0.871	0.708	0.0148	0.00233
fig/6666666.474 865.peg.69	Formate--tetrahydrofolate ligase (EC 6.3.4.3)		-0.264	0.448	-0.737	-0.0253	0.322	0.263	0.00277	0.914
fig/6666666.474 865.peg.1690	Lipid A export ATP-binding/permease protein MsbA	abcA	-0.494	0.444	0.903	1.84	0.15	0.399	0.00409	2.67E-05
fig/6666666.474 865.peg.2424	4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)		1.3	0.444	0.0632	-0.791	0.15	0.781	0.947	0.286
fig/6666666.474 865.peg.2682	Ribosomal silencing factor RsfA (former Iojap)		0.255	0.444	0.0452	0.234	0.303	0.225	0.849	0.235
fig/6666666.474 865.peg.2185	FIG001960: FtsZ-interacting protein related to cell division		0.845	0.438	0.455	0.0485	0.0244	0.419	0.115	0.884
fig/6666666.474 865.peg.2349	Cardiolipin synthetase (EC 2.7.8.-)		0.254	0.432	0.451	0.63	0.489	0.419	0.113	0.0338
fig/6666666.474 865.peg.1604	Predicted flavoprotein		-0.291	0.431	0.0156	0.737	0.324	0.338	0.957	0.00551
fig/6666666.474 865.peg.108	Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23); putative		-0.48	0.429	0.952	1.86	0.221	0.458	0.00671	6.13E-05
fig/6666666.474 865.peg.507	oxidoreductase ylbE		-0.527	0.429	-0.706	0.25	0.324	0.592	0.1	0.572
fig/6666666.474 865.peg.695	Formiminoglutamase (EC 3.5.3.8)		0.317	0.422	-0.643	-0.537	0.703	0.744	0.298	0.391
fig/6666666.474 865.peg.2203	FIG01107914: hypothetical protein		0.33	0.419	0.396	0.486	0.777	0.827	0.676	0.579
fig/6666666.474 865.peg.822	M42 glutamyl aminopeptidase, cellulase		-0.0086	0.419	0.0709	0.498	0.984	0.538	0.874	0.184
fig/6666666.474 865.peg.452	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)		-0.386	0.413	0.0695	0.868	0.251	0.419	0.832	0.00502
fig/6666666.474 865.peg.2040	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase (EC 2.2.1.9)		-2.39	0.408	-1.93	0.871	0.016	0.811	0.015	0.239
fig/6666666.474 865.peg.2612	(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)		0.123	0.401	-0.302	-0.0251	0.691	0.355	0.183	0.918
fig/6666666.474 865.peg.1507	Autolysin precursor	sle1	0.748	0.398	-2.02	-2.37	0.402	0.803	0.00798	0.00331
fig/6666666.474 865.peg.2214	Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-)		0.489	0.398	0.422	0.331	0.15	0.432	0.126	0.227
fig/6666666.474 865.peg.230	Hypothetical protein YfkK		-0.977	0.397	-3.19	-1.81	0.0456	0.581	1.88E-06	0.000354

fig/6666666.474 865.peg.2642	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) / Transpeptidase, Penicillin binding protein transpeptidase domain	pbp3	0.0757	0.397	-0.153	0.168	0.789	0.323	0.473	0.422
fig/6666666.474 865.peg.1684	Teichoic acid export ATP-binding protein TagH (EC 3.6.3.40)		-0.152	0.396	-0.422	0.126	0.674	0.419	0.108	0.648
fig/6666666.474 865.peg.519	PTS system, mannitol-specific IIA component		-0.415	0.396	-0.126	0.685	0.351	0.538	0.765	0.0578
fig/6666666.474 865.peg.654	Hypothetical protein SAV2296		-0.664	0.396	0.0278	1.09	0.39	0.77	0.967	0.0756
fig/6666666.474 865.peg.803	FIG01107870: hypothetical protein		-0.00842	0.39	0.192	0.59	0.984	0.536	0.604	0.0845
fig/6666666.474 865.peg.2200	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)		-0.327	0.386	-0.752	-0.0385	0.258	0.397	0.00467	0.885
fig/6666666.474 865.peg.9	Porphobilinogen deaminase (EC 2.5.1.61)		0.326	0.386	-0.48	-0.42	0.109	0.217	0.00746	0.0164
fig/6666666.474 865.peg.1508	FIG01108237: hypothetical protein		-0.368	0.385	0.484	1.24	0.229	0.417	0.0539	0.000225
fig/6666666.474 865.peg.1924	D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13)		-0.165	0.383	-0.79	-0.242	0.693	0.506	0.016	0.443
fig/6666666.474 865.peg.766	Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)		0.0231	0.382	-2.53	-2.17	0.974	0.716	0.000198	0.000919
fig/6666666.474 865.peg.2052	FIG01108206: hypothetical protein		0.259	0.381	2.13	2.25	0.812	0.831	0.0117	0.00901
fig/6666666.474 865.peg.386	Hypothetical SAV2027 homolog in superantigen-encoding pathogenicity islands SaPI		-1.74	0.379	-2.45	-0.33	0.0304	0.78	0.00113	0.615
fig/6666666.474 865.peg.1796	6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I		0.627	0.378	-0.209	-0.459	0.0723	0.458	0.469	0.101
fig/6666666.474 865.peg.2080	FIG01108691: hypothetical protein		-0.479	0.375	-0.817	0.0372	0.125	0.422	0.00407	0.891
fig/6666666.474 865.peg.809	Hypothetical protein, similar to glucose epimerase		-0.043	0.374	0.429	0.845	0.952	0.621	0.28	0.039
fig/6666666.474 865.peg.200	Fumarate hydratase class II (EC 4.2.1.2)		-0.682	0.371	-0.952	0.102	0.191	0.664	0.0302	0.834
fig/6666666.474 865.peg.2431	Cold shock protein CspA		0.0962	0.369	-0.814	-0.542	0.658	0.217	9.93E-05	0.00288
fig/6666666.474 865.peg.442	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D- alanyl-D-alanine ligase (EC 6.3.2.10)		0.0281	0.368	0.716	1.06	0.893	0.167	9.60E-05	6.21E-06
fig/6666666.474 865.peg.1898	Methionine ABC transporter ATP-binding protein		0.171	0.367	-0.346	-0.15	0.728	0.595	0.356	0.707
fig/6666666.474 865.peg.1915	Lipoate synthase		0.476	0.357	-0.454	-0.573	0.342	0.653	0.258	0.154
fig/6666666.474 865.peg.1828	Tripeptide aminopeptidase (EC 3.4.11.4)		-0.725	0.352	-0.368	0.709	0.453	0.841	0.66	0.351
fig/6666666.474 865.peg.1928	NADH dehydrogenase (EC 1.6.99.3)		0.343	0.35	-0.529	-0.521	0.222	0.419	0.0255	0.0296
fig/6666666.474 865.peg.550	Putative oxidoreductase YncB		-0.0411	0.348	-0.21	0.179	0.901	0.399	0.332	0.418

fig 6666666.474 865.peg.958	2-dehydropantoate 2-reductase (EC 1.1.1.169)		-0.103	0.348	0.773	1.22	0.832	0.586	0.0285	0.00233
fig 6666666.474 865.peg.2426	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89)		0.888	0.346	-0.87	-1.41	0.423	0.864	0.31	0.101
fig 6666666.474 865.peg.496	HmrA protein involved in methicillin resistance / amidohydrolase of M40 family		-0.247	0.345	0.2	0.792	0.562	0.559	0.567	0.0203
fig 6666666.474 865.peg.1597	L-threonine 3-dehydrogenase (EC 1.1.1.103)		-0.501	0.342	-0.492	0.352	0.118	0.467	0.0608	0.175
fig 6666666.474 865.peg.2241	Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)		0.0866	0.339	-0.103	0.149	0.721	0.323	0.592	0.409
fig 6666666.474 865.peg.2733	Holliday junction DNA helicase RuvA		-0.344	0.338	-0.0378	0.645	0.732	0.851	0.964	0.404
fig 6666666.474 865.peg.2455	hypothetical protein		-0.287	0.337	-0.0452	0.578	0.27	0.399	0.859	0.0118
fig 6666666.474 865.peg.461	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)		-0.0248	0.337	0.944	1.31	0.962	0.529	0.00398	0.000473
fig 6666666.474 865.peg.2065	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)		-0.0147	0.335	-0.497	-0.148	0.963	0.339	0.0124	0.432
fig 6666666.474 865.peg.1833	FIG000605: protein co-occurring with transport systems (COG1739)		0.455	0.334	0.248	0.127	0.643	0.841	0.768	0.875
fig 6666666.474 865.peg.2715	Flavin-utilizing monooxygenase		0.19	0.334	-0.351	-0.206	0.907	0.906	0.78	0.868
fig 6666666.474 865.peg.1200	Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)	adhE	1.76	0.331	0.227	-1.2	0.0137	0.774	0.708	0.0296
fig 6666666.474 865.peg.2047	N-acetyl-L,L-diaminopimelate aminotransferase (EC 2.6.1.-)		-0.44	0.329	-0.987	-0.218	0.657	0.842	0.164	0.777
fig 6666666.474 865.peg.1095	Prophage LambdaSa2, replicative DNA helicase		-0.349	0.328	-0.444	0.232	0.719	0.844	0.565	0.766
fig 6666666.474 865.peg.1779	FIG01108024: hypothetical protein		-0.0972	0.328	-0.711	-0.285	0.909	0.796	0.207	0.627
fig 6666666.474 865.peg.32	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)		-0.102	0.323	-0.0245	0.4	0.704	0.399	0.921	0.0494
fig 6666666.474 865.peg.2605	FIG01226417: hypothetical protein		0.0989	0.321	-0.568	-0.346	0.691	0.364	0.00549	0.0632
fig 6666666.474 865.peg.362	Acetylmithine deacetylase (EC 3.5.1.16)		-0.427	0.321	-0.195	0.553	0.627	0.826	0.797	0.394
fig 6666666.474 865.peg.2498	Nucleoside diphosphate kinase (EC 2.7.4.6)		0.396	0.316	-0.847	-0.928	0.15	0.433	0.0015	0.000943
fig 6666666.474 865.peg.2197	Dihydroorotase (EC 3.5.2.3)		-0.139	0.315	-0.84	-0.386	0.564	0.369	0.000297	0.0405
fig 6666666.474 865.peg.1634	Diphosphomevalonate decarboxylase (EC 4.1.1.33)		-0.337	0.314	-0.0664	0.584	0.514	0.699	0.891	0.141
fig 6666666.474 865.peg.659	D-octopine dehydrogenase		-0.342	0.314	-0.273	0.383	0.0645	0.247	0.0646	0.0152
fig 6666666.474 865.peg.1120	Cassette chromosome recombinase A		-0.275	0.313	-0.854	-0.266	0.772	0.845	0.213	0.72

fig/6666666.474 865.peg.1238	Nicotinamidase/isochorismatase family protein		-0.896	0.311	-0.343	0.864	0.0259	0.596	0.277	0.0115
fig/6666666.474 865.peg.221	Teichoic acid export ATP-binding protein TagH (EC 3.6.3.40)		-0.937	0.31	0.153	1.4	0.128	0.774	0.796	0.00997
fig/6666666.474 865.peg.684	Hypothetical protein SAV2325		-1.23	0.309	-1.22	0.312	0.259	0.898	0.17	0.749
fig/6666666.474 865.peg.486	Transcriptional regulator, HxlR family		1.65	0.307	1.92	0.582	0.000242	0.537	7.58E-06	0.0392
fig/6666666.474 865.peg.898	PTS system, glucose-specific IIC component (EC 2.7.1.69) / PTS system, glucose-specific IIB component (EC 2.7.1.69) / PTS system, glucose-specific IIA component (EC 2.7.1.69)		-0.79	0.305	-0.508	0.587	0.118	0.708	0.215	0.151
fig/6666666.474 865.peg.1926	NifU-like domain protein		0.817	0.301	-0.101	-0.617	0.0117	0.497	0.714	0.0158
fig/6666666.474 865.peg.2735	GTP-binding protein Obg		0.0966	0.301	-0.265	-0.0612	0.658	0.323	0.0949	0.721
fig/6666666.474 865.peg.1584	LSU ribosomal protein L7/L12 (P1/P2)		0.426	0.3	-0.154	-0.281	0.0456	0.339	0.364	0.0947
fig/6666666.474 865.peg.949	Dihydroorotate dehydrogenase (EC 1.3.3.1)		-0.605	0.3	-0.822	0.0833	0.0723	0.538	0.00584	0.777
fig/6666666.474 865.peg.845	Short-chain dehydrogenase/reductase SDR		-0.172	0.299	-0.123	0.348	0.502	0.419	0.566	0.0804
fig/6666666.474 865.peg.256	ATP-dependent DNA helicase UvrD/PcrA		0.0864	0.298	0.113	0.324	0.728	0.399	0.577	0.0829
fig/6666666.474 865.peg.2067	Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit (EC 6.3.5.3)		-0.248	0.297	-1.03	-0.49	0.468	0.537	0.00113	0.0676
fig/6666666.474 865.peg.229	Aminopeptidase S (Leu, Val, Phe, Tyr preference) (EC 3.4.11.24)		-0.102	0.297	0.0964	0.496	0.643	0.323	0.577	0.00555
fig/6666666.474 865.peg.2497	Chorismate synthase (EC 4.2.3.5)		0.0642	0.296	-0.0926	0.14	0.901	0.664	0.822	0.703
fig/6666666.474 865.peg.2626	Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2)		0.456	0.293	-0.553	-0.716	0.0669	0.422	0.01	0.00225
fig/6666666.474 865.peg.1395	FIG01108269: hypothetical protein		0.187	0.291	1.01	1.12	0.85	0.861	0.146	0.11
fig/6666666.474 865.peg.2653	ATP/GTP-binding protein, SA1392 homolog		0.14	0.29	0.422	0.573	0.85	0.806	0.427	0.268
fig/6666666.474 865.peg.1817	Ribonucleotide reductase of class Ib (aerobic), beta subunit (EC 1.17.4.1)		-0.472	0.289	-0.636	0.125	0.0344	0.389	0.00185	0.485
fig/6666666.474 865.peg.2015	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase (EC 6.3.2.7)	murE	-0.0387	0.289	0.359	0.687	0.926	0.539	0.17	0.0146
fig/6666666.474 865.peg.399	Fructokinase (EC 2.7.1.4)		0.162	0.288	0.0914	0.217	0.792	0.773	0.865	0.648
fig/6666666.474 865.peg.425	RNA polymerase sigma factor SigB		0.516	0.288	-0.782	-1.01	0.715	0.918	0.465	0.335
fig/6666666.474 865.peg.491	DNA-directed RNA polymerase delta subunit (EC 2.7.7.6)		0.293	0.285	-0.158	-0.166	0.238	0.433	0.448	0.419

fig/6666666.474 865.peg.1645	Oxidoreductase ion channel		-0.118	0.282	-0.19	0.21	0.812	0.699	0.628	0.571
fig/6666666.474 865.peg.700	Aldose 1-epimerase (EC 5.1.3.3)		-1.33	0.281	-0.924	0.689	0.225	0.906	0.301	0.447
fig/6666666.474 865.peg.2199	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)		-0.148	0.279	-1.04	-0.616	0.469	0.356	1.47E-05	0.00135
fig/6666666.474 865.peg.283	ABC transporter ATP-binding protein		-0.526	0.279	-0.071	0.734	0.0788	0.529	0.803	0.00614
fig/6666666.474 865.peg.2155	FIG01108519: hypothetical protein		-1.15	0.278	-0.101	1.33	0.518	0.943	0.955	0.338
fig/6666666.474 865.peg.2263	COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination		-0.184	0.277	-1.28	-0.824	0.843	0.861	0.0538	0.208
fig/6666666.474 865.peg.2661	Phosphate starvation-inducible protein PhoH, predicted ATPase		-0.219	0.276	0.345	0.84	0.243	0.339	0.0292	0.000107
fig/6666666.474 865.peg.469	ATP synthase B chain (EC 3.6.3.14)		-0.21	0.276	-1.04	-0.552	0.232	0.323	6.05E-06	0.00139
fig/6666666.474 865.peg.19	Translation initiation factor 3	infC	0.802	0.273	-0.543	-1.07	0.0137	0.537	0.0293	0.000552
fig/6666666.474 865.peg.1633	Mevalonate kinase (EC 2.7.1.36)		0.0948	0.272	0.35	0.527	0.926	0.861	0.628	0.428
fig/6666666.474 865.peg.180	Protoporphyrinogen IX oxidase, aerobic, HemY (EC 1.3.3.4)		-0.181	0.269	-0.0958	0.354	0.781	0.803	0.865	0.464
fig/6666666.474 865.peg.409	TsaD/Kae1/Qri7 protein, required for threonylcarbamoyladenosine t(6)A37 formation in tRNA		0.477	0.267	-0.135	-0.345	0.594	0.864	0.865	0.621
fig/6666666.474 865.peg.952	PhnB protein; putative DNA binding 3-demethylubiquinone-9 3-methyltransferase domain protein		0.363	0.265	1.18	1.08	0.116	0.432	1.92E-05	6.13E-05
fig/6666666.474 865.peg.2207	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)		0.0737	0.263	-0.307	-0.118	0.781	0.458	0.112	0.56
fig/6666666.474 865.peg.2579	Osmosensitive K ⁺ channel histidine kinase KdpD (EC 2.7.3.-)		-0.596	0.263	-0.188	0.671	0.247	0.774	0.695	0.112
fig/6666666.474 865.peg.853	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)		-0.768	0.261	-0.965	0.0629	0.0197	0.574	0.00125	0.826
fig/6666666.474 865.peg.187	Hypothetical protein SAV1839		-0.231	0.259	-1.18	-0.69	0.449	0.542	0.000144	0.00811
fig/6666666.474 865.peg.815	Osmotically activated L-carnitine/choline ABC transporter, ATP-binding protein OpuCA		-1.42	0.257	-1.78	-0.108	0.0258	0.82	0.00206	0.848
fig/6666666.474 865.peg.2675	Translation elongation factor LepA		0.122	0.256	-0.0409	0.0926	0.521	0.364	0.817	0.544
fig/6666666.474 865.peg.2503	Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)		-0.169	0.255	-0.152	0.271	0.555	0.529	0.508	0.212
fig/6666666.474 865.peg.2193	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)		1.01	0.254	-0.0448	-0.801	0.000966	0.48	0.849	0.00103
fig/6666666.474 865.peg.1614	D-arabino-3-hexulose 6-phosphate formaldehyde lyase		0.0357	0.253	-0.262	-0.0452	0.909	0.506	0.202	0.847
fig/6666666.474 865.peg.1943	FIG01107890: hypothetical protein		-0.065	0.248	-0.181	0.132	0.832	0.536	0.415	0.562

fig/6666666.474 865.peg.520	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)		-0.832	0.247	-0.74	0.34	0.0265	0.683	0.0169	0.244
fig/6666666.474 865.peg.1558	Dihydropteroate synthase (EC 2.5.1.15)		-0.225	0.246	-0.338	0.133	0.382	0.513	0.0957	0.526
fig/6666666.474 865.peg.1576	23S rRNA (guanosine-2'-O-) -methyltransferase rlmB (EC 2.1.1.-)		0.569	0.246	0.0517	-0.272	0.00341	0.339	0.745	0.0504
fig/6666666.474 865.peg.36	6-phosphofructokinase (EC 2.7.1.11)		0.103	0.243	0.025	0.165	0.678	0.458	0.915	0.373
fig/6666666.474 865.peg.858	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)		-0.326	0.243	-1.14	-0.567	0.15	0.467	2.60E-05	0.00612
fig/6666666.474 865.peg.2231	Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)		-0.106	0.241	-0.2	0.147	0.685	0.495	0.296	0.447
fig/6666666.474 865.peg.1304	Glycosyl transferase family protein, putative		0.118	0.24	0.655	0.777	0.529	0.389	0.000317	0.000117
fig/6666666.474 865.peg.1077	GTPase and tRNA-U34 5-formylation enzyme TrmE		-0.145	0.239	0.0186	0.402	0.646	0.571	0.95	0.0801
fig/6666666.474 865.peg.1946	Putative NADH-dependent flavin oxidoreductase		-0.33	0.238	-0.0746	0.494	0.137	0.462	0.72	0.0114
fig/6666666.474 865.peg.2267	tRNA pseudouridine synthase B (EC 4.2.1.70)		-0.122	0.238	-0.187	0.172	0.84	0.806	0.697	0.707
fig/6666666.474 865.peg.2145	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)		-0.0868	0.237	-0.846	-0.522	0.726	0.49	0.000317	0.0101
fig/6666666.474 865.peg.2229	Ribonuclease III (EC 3.1.26.3)		0.291	0.236	-0.474	-0.528	0.382	0.651	0.0723	0.0488
fig/6666666.474 865.peg.2073	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)		0.12	0.235	-0.528	-0.413	0.677	0.537	0.0169	0.0529
fig/6666666.474 865.peg.1804	COG0488: ATPase components of ABC transporters with duplicated ATPase domains		0.0576	0.234	0.0684	0.245	0.953	0.859	0.921	0.676
fig/6666666.474 865.peg.49	Adenine-specific methyltransferase (EC 2.1.1.72)		-0.886	0.234	-0.86	0.261	0.322	0.904	0.231	0.738
fig/6666666.474 865.peg.2494	TPR-repeat-containing protein, putative component of Menaquinone-cytochrome C reductase		-0.578	0.233	-0.116	0.695	0.437	0.864	0.865	0.225
fig/6666666.474 865.peg.2669	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)		0.0323	0.233	0.483	0.684	0.967	0.855	0.374	0.2
fig/6666666.474 865.peg.38	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)		0.522	0.232	0.71	0.42	0.0127	0.419	0.000297	0.012
fig/6666666.474 865.peg.1522	FIG000557: hypothetical protein co-occurring with RecR		-0.254	0.23	-0.307	0.177	0.428	0.629	0.217	0.485
fig/6666666.474 865.peg.225	ThiJ/PfpI family protein		-0.496	0.23	-0.788	-0.0621	0.187	0.708	0.0153	0.862
fig/6666666.474 865.peg.928	Acyltransferase		0.156	0.228	0.569	0.641	0.893	0.908	0.466	0.404
fig/6666666.474 865.peg.1687	Teichoic acid biosynthesis protein X		-0.568	0.227	-0.437	0.357	0.59	0.914	0.607	0.67
fig/6666666.474 865.peg.1696	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), dihydroxyacetone binding subunit DhaK		-1.05	0.227	-0.128	1.15	0.0193	0.757	0.749	0.00344

fig 6666666.474 865.peg.44	FIG002379: metal-dependent hydrolase		-0.144	0.227	-0.355	0.0162	0.694	0.69	0.194	0.955
fig 6666666.474 865.peg.255	DNA ligase (EC 6.5.1.2)		-0.0895	0.226	0.0198	0.336	0.681	0.433	0.921	0.0407
fig 6666666.474 865.peg.2406	tRNA-dependent lipid II-GlyGlyGly--glycine ligase @ tRNA-dependent lipid II-GlyGlyGlyGly--glycine ligase @ FemB, factor involved in methicillin resistance	femB	0.104	0.223	1.22	1.34	0.737	0.618	9.93E-05	7.30E-05
fig 6666666.474 865.peg.1581	LSU ribosomal protein L11p (L12e)		0.792	0.221	-0.331	-0.902	0.00999	0.598	0.141	0.0011
fig 6666666.474 865.peg.951	FIG053235: Diacylglycerol hydrolase like		-0.121	0.22	-2.4	-2.06	0.911	0.907	0.00336	0.00894
fig 6666666.474 865.peg.1948	NAD-specific glutamate dehydrogenase (EC 1.4.1.2)		-0.28	0.217	-0.538	-0.0403	0.19	0.503	0.00561	0.841
fig 6666666.474 865.peg.1526	protein from nitrogen regulatory protein P-II (GLNB) family, ortholog YAAQ B. subtilis		-0.392	0.216	-0.389	0.218	0.196	0.664	0.116	0.388
fig 6666666.474 865.peg.2627	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)		0.63	0.214	-0.938	-1.35	0.475	0.906	0.17	0.052
fig 6666666.474 865.peg.758	Two-component response regulator		-0.636	0.214	-1.17	-0.318	0.0941	0.727	0.0012	0.296
fig 6666666.474 865.peg.882	Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-) / Dihydropteridine reductase (EC 1.5.1.34)		-0.438	0.214	-0.49	0.163	0.0723	0.542	0.0172	0.412
fig 6666666.474 865.peg.400	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)		0.179	0.212	0.139	0.171	0.489	0.57	0.515	0.404
fig 6666666.474 865.peg.1097	Two-component response regulator SA14-24	walR	-1.16	0.209	-0.962	0.41	0.00499	0.727	0.004	0.164
fig 6666666.474 865.peg.1594	2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)		0.157	0.209	-0.17	-0.118	0.481	0.513	0.325	0.504
fig 6666666.474 865.peg.2429	Diaminopimelate decarboxylase (EC 4.1.1.20)		0.0708	0.209	0.898	1.04	0.861	0.708	0.00406	0.00173
fig 6666666.474 865.peg.2227	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)		-0.124	0.207	-0.151	0.18	0.517	0.433	0.304	0.217
fig 6666666.474 865.peg.2687	GTP-binding protein YqeH, required for biogenesis of 30S ribosome subunit		-0.205	0.205	0.221	0.632	0.331	0.513	0.192	0.00182
fig 6666666.474 865.peg.1603	HMP-PP hydrolase (pyridoxal phosphatase) Cof, detected in genetic screen for thiamin metabolic genes (PMID:15292217)		0.0191	0.204	-0.383	-0.199	0.962	0.653	0.0949	0.394
fig 6666666.474 865.peg.247	RNA methyltransferase, TrmA family		-0.309	0.203	-0.063	0.449	0.461	0.774	0.87	0.167
fig 6666666.474 865.peg.242	proposed amino acid ligase found clustered with an amidotransferase		0.11	0.198	0.32	0.408	0.763	0.708	0.23	0.127
fig 6666666.474 865.peg.2607	Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)		0.186	0.197	0.188	0.199	0.27	0.432	0.17	0.147
fig 6666666.474 865.peg.1413	Single-stranded DNA-binding protein		0.157	0.196	-0.74	-0.701	0.691	0.756	0.0166	0.0229
fig 6666666.474 865.peg.1445	FIG01108125: hypothetical protein		0.42	0.192	-0.52	-0.748	0.116	0.653	0.0208	0.00282

fig/6666666.474 865.peg.516	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)		0.388	0.192	0.363	0.166	0.0283	0.437	0.0139	0.225
fig/6666666.474 865.peg.527	Scaffold protein for [4Fe-4S] cluster assembly ApbC, MRP-like		-0.208	0.192	-0.561	-0.16	0.408	0.598	0.00887	0.424
fig/6666666.474 865.peg.1085	DNA gyrase subunit A (EC 5.99.1.3)		-0.0725	0.191	0.26	0.523	0.733	0.522	0.105	0.00421
fig/6666666.474 865.peg.186	Histidine triad (HIT) nucleotide-binding protein, similarity with At5g48545 and yeast YDL125C (HNT1)		0.0297	0.189	0.0379	0.197	0.924	0.613	0.871	0.324
fig/6666666.474 865.peg.711	putative esterase		-0.717	0.188	-1.48	-0.576	0.382	0.914	0.0267	0.38
fig/6666666.474 865.peg.462	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)		-0.0475	0.185	0.04	0.273	0.782	0.422	0.787	0.0357
fig/6666666.474 865.peg.571	Acetolactate synthase, catabolic (EC 2.2.1.6)		-0.357	0.185	-0.333	0.209	0.0544	0.497	0.0283	0.155
fig/6666666.474 865.peg.1536	SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)		-0.00551	0.184	-0.303	-0.113	0.983	0.655	0.146	0.607
fig/6666666.474 865.peg.91	Beta-lactamase (EC 3.5.2.6)		-0.0954	0.182	2.8	3.08	0.544	0.419	5.30E-11	1.47E-11
fig/6666666.474 865.peg.2239	50S ribosomal subunit maturation GTPase RbgA (B. subtilis Y1qF)		0.354	0.182	-0.00981	-0.182	0.144	0.629	0.964	0.358
fig/6666666.474 865.peg.1060	N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118)		-0.247	0.179	1.21	1.63	0.658	0.853	0.0067	0.00105
fig/6666666.474 865.peg.1889	Organic hydroperoxide resistance protein		-0.882	0.179	-1.17	-0.106	0.0748	0.846	0.00729	0.814
fig/6666666.474 865.peg.2205	Guanylate kinase (EC 2.7.4.8)		0.0106	0.179	-0.554	-0.386	0.967	0.652	0.0102	0.057
fig/6666666.474 865.peg.859	Fibronectin binding protein FnBA		0.254	0.179	0.152	0.0772	0.787	0.926	0.853	0.917
fig/6666666.474 865.peg.2107	GTP-binding protein TypA/BipA		0.162	0.177	-0.106	-0.0902	0.203	0.377	0.307	0.394
fig/6666666.474 865.peg.2470	Uncharacterized protein Bsub YpbR		0.155	0.173	0.478	0.496	0.689	0.775	0.0917	0.0794
fig/6666666.474 865.peg.1544	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)		-0.0903	0.172	-0.287	-0.0245	0.613	0.467	0.0319	0.87
fig/6666666.474 865.peg.2356	FIG01108654: hypothetical protein		-0.706	0.172	-0.0984	0.78	0.0456	0.774	0.765	0.0102
fig/6666666.474 865.peg.426	Serine-protein kinase RsbW (EC 2.7.11.1)		-0.156	0.167	-0.676	-0.353	0.463	0.588	0.00076	0.0385
fig/6666666.474 865.peg.487	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	murZ	0.962	0.164	2.13	1.34	0.000114	0.536	3.22E-09	1.12E-06
fig/6666666.474 865.peg.2091	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)		-0.229	0.164	-0.0632	0.33	0.153	0.503	0.667	0.0183
fig/6666666.474 865.peg.2365	Catalase (EC 1.11.1.6)		-0.156	0.164	-0.887	-0.566	0.598	0.708	0.000852	0.0159
fig/6666666.474 865.peg.2071	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)		-0.0177	0.161	-0.98	-0.801	0.967	0.806	0.00291	0.0104

fig/6666666.474 865.peg.941	Predicted hydrolase/acyltransferase		-0.477	0.16	-0.36	0.276	0.231	0.827	0.263	0.399
fig/6666666.474 865.peg.2068	Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3)		-0.201	0.159	-0.56	-0.2	0.182	0.479	0.000309	0.103
fig/6666666.474 865.peg.1093	Phosphoesterase, DHH family protein		-1.21	0.157	0.0883	1.46	0.183	0.943	0.923	0.0533
fig/6666666.474 865.peg.1788	oxidoreductase of aldo/keto reductase family, subgroup 1		-0.223	0.157	-0.358	0.0228	0.366	0.699	0.0706	0.915
fig/6666666.474 865.peg.431	Alanine racemase (EC 5.1.1.1)		-0.241	0.155	0.0369	0.433	0.533	0.82	0.921	0.143
fig/6666666.474 865.peg.1850	Hypothetical ATP-binding protein UPF0042, contains P-loop		-0.387	0.154	1.04	1.58	0.203	0.774	0.000633	3.47E-05
fig/6666666.474 865.peg.288	Aspartate aminotransferase (EC 2.6.1.1)		-0.225	0.154	-0.0856	0.292	0.238	0.596	0.611	0.062
fig/6666666.474 865.peg.568	HMP-PP hydrolase (pyridoxal phosphatase) Cof, detected in genetic screen for thiamin metabolic genes (PMID:15292217)		-0.858	0.154	-0.244	0.768	0.254	0.933	0.732	0.21
fig/6666666.474 865.peg.2064	Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)		-0.193	0.151	-0.559	-0.215	0.27	0.57	0.00112	0.133
fig/6666666.474 865.peg.667	Formate dehydrogenase related protein		-0.607	0.151	-1.18	-0.419	0.0917	0.82	0.000757	0.145
fig/6666666.474 865.peg.254	Putative pheromone cAM373 precursor lipoprotein CamS		0.658	0.15	-0.0806	-0.589	0.0684	0.82	0.817	0.0466
fig/6666666.474 865.peg.1970	Phospholipid-binding protein		-0.86	0.149	-1.36	-0.352	0.447	0.947	0.119	0.71
fig/6666666.474 865.peg.2254	Uridine monophosphate kinase (EC 2.7.4.22)		0.0812	0.145	0.285	0.349	0.755	0.708	0.136	0.07
fig/6666666.474 865.peg.406	ABC transporter ATP-binding protein uup		-1.18	0.145	-0.825	0.498	0.0588	0.912	0.0949	0.319
fig/6666666.474 865.peg.485	Aldehyde dehydrogenase (EC 1.2.1.3)		0.0118	0.144	0.0117	0.144	0.966	0.694	0.957	0.419
fig/6666666.474 865.peg.1539	PurR: transcription regulator associated with purine metabolism		-0.31	0.142	0.23	0.683	0.232	0.752	0.277	0.00453
fig/6666666.474 865.peg.2447	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	murG	-0.0149	0.141	0.00778	0.164	0.962	0.69	0.967	0.339
fig/6666666.474 865.peg.1894	Glycine cleavage system H protein		0.103	0.14	-0.651	-0.614	0.666	0.699	0.0015	0.00249
fig/6666666.474 865.peg.2722	Histidyl-tRNA synthetase (EC 6.1.1.21)		0.209	0.14	-0.261	-0.33	0.48	0.776	0.255	0.15
fig/6666666.474 865.peg.424	Transcription accessory protein (S1 RNA-binding domain)		0.11	0.14	-0.282	-0.252	0.661	0.707	0.119	0.164
fig/6666666.474 865.peg.1925	Poly(glycerophosphate chain) D-alanine transfer protein DltD		-0.0531	0.139	-0.412	-0.22	0.871	0.776	0.0718	0.339
fig/6666666.474 865.peg.523	Phosphoglucosamine mutase (EC 5.4.2.10) / FemD, factor involved in methicillin resistance		-0.0754	0.137	-0.262	-0.0493	0.643	0.529	0.0302	0.699

fig/6666666.474 865.peg.210	Peroxide stress regulator PerR, FUR family		-0.319	0.136	-0.172	0.284	0.536	0.898	0.703	0.483
fig/6666666.474 865.peg.2063	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)		-0.351	0.135	-1.03	-0.542	0.15	0.747	9.99E-05	0.0117
fig/6666666.474 865.peg.1303	Putative polyribitolphosphotransferase		-0.0569	0.133	0.149	0.339	0.83	0.727	0.434	0.0699
fig/6666666.474 865.peg.1762	FIG01107934: hypothetical protein		-0.202	0.133	-1.21	-0.877	0.431	0.757	2.79E-05	0.000562
fig/6666666.474 865.peg.966	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases, YtcI homolog		-0.326	0.133	-0.212	0.246	0.0838	0.66	0.16	0.103
fig/6666666.474 865.peg.2221	FIG001802: Putative alkaline-shock protein		0.036	0.131	-0.109	-0.0141	0.897	0.731	0.589	0.941
fig/6666666.474 865.peg.2738	LSU ribosomal protein L21p		0.505	0.13	-0.131	-0.506	0.0141	0.681	0.398	0.00395
fig/6666666.474 865.peg.40	DNA polymerase III alpha subunit (EC 2.7.7.7)		1.29	0.13	1.02	-0.14	0.231	0.956	0.244	0.885
fig/6666666.474 865.peg.2651	RNA polymerase sigma factor RpoD		0.216	0.128	-0.12	-0.208	0.437	0.79	0.605	0.338
fig/6666666.474 865.peg.1962	FIG002540: Haloacid dehalogenase-like hydrolase		0.193	0.127	0.486	0.419	0.216	0.592	0.0013	0.00399
fig/6666666.474 865.peg.1784	1-phosphofructokinase (EC 2.7.1.56)		-0.214	0.126	-0.682	-0.342	0.419	0.775	0.00347	0.0947
fig/6666666.474 865.peg.2393	4-oxalocrotonate tautomerase (EC 5.3.2.-)		0.378	0.125	-1.85	-2.1	0.282	0.855	1.64E-05	1.05E-05
fig/6666666.474 865.peg.549	Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Similar to arginate lyase		-1.39	0.123	-1.25	0.269	0.0941	0.946	0.0625	0.707
fig/6666666.474 865.peg.2566	Phage protein		-0.376	0.122	0.629	1.13	0.736	0.956	0.47	0.179
fig/6666666.474 865.peg.1821	Iron compound ABC uptake transporter substrate-binding protein		0.203	0.121	-0.591	-0.672	0.602	0.861	0.0439	0.0262
fig/6666666.474 865.peg.2283	FIG01107999: hypothetical protein		-0.861	0.121	-1.42	-0.443	0.0729	0.906	0.0016	0.246
fig/6666666.474 865.peg.238	Methionine aminopeptidase (EC 3.4.11.18)		-0.41	0.121	-0.534	-0.0027	0.116	0.799	0.016	0.991
fig/6666666.474 865.peg.2489	Glycosyl transferase, group 1 family protein		0.0335	0.121	0.434	0.522	0.938	0.845	0.102	0.0533
fig/6666666.474 865.peg.2031	FIG01108706: hypothetical protein		-0.607	0.12	-1.08	-0.358	0.00341	0.693	4.79E-06	0.0198
fig/6666666.474 865.peg.2175	rRNA small subunit methyltransferase H		-0.445	0.12	0.0484	0.614	0.0815	0.796	0.845	0.0069
fig/6666666.474 865.peg.2242	Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)		-0.13	0.12	-0.572	-0.321	0.544	0.712	0.00255	0.0533
fig/6666666.474 865.peg.1599	Hydrolase, haloacid dehalogenase-like family		-0.326	0.119	-0.626	-0.181	0.165	0.774	0.00403	0.355

fig/6666666.474 865.peg.1555	Cell division protein FtsH (EC 3.4.24.-)		0.224	0.118	0.404	0.298	0.15	0.624	0.00434	0.0246
fig/6666666.474 865.peg.2058	quinol oxidase polypeptide II QoxA (EC:1.9.3.-)		-0.379	0.118	-1.3	-0.804	0.102	0.773	7.77E-06	0.000621
fig/6666666.474 865.peg.1716	FIG007491: hypothetical protein YeeN		-0.3	0.117	-0.768	-0.351	0.121	0.708	0.000166	0.0318
fig/6666666.474 865.peg.2643	Manganese superoxide dismutase (EC 1.15.1.1); Superoxide dismutase		-0.105	0.117	0.634	0.856	0.719	0.811	0.00699	0.0011
fig/6666666.474 865.peg.129	Hypothetical protein SAV1789		-0.213	0.116	-0.236	0.0921	0.33	0.761	0.177	0.615
fig/6666666.474 865.peg.2189	Isoleucyl-tRNA synthetase (EC 6.1.1.5)		0.0646	0.116	-0.0522	-0.00099	0.672	0.57	0.673	0.993
fig/6666666.474 865.peg.2380	Aconitate hydratase (EC 4.2.1.3)		0.262	0.116	-0.403	-0.549	0.176	0.712	0.0157	0.00282
fig/6666666.474 865.peg.2266	Ribosome-binding factor A		0.113	0.113	-0.116	-0.116	0.701	0.82	0.628	0.612
fig/6666666.474 865.peg.117	Autolysin (EC 3.5.1.28)		0.289	0.112	0.749	0.571	0.395	0.861	0.00975	0.039
fig/6666666.474 865.peg.2069	Amidophosphoribosyltransferase (EC 2.4.2.14)		0.059	0.111	-0.536	-0.484	0.777	0.714	0.00236	0.00486
fig/6666666.474 865.peg.502	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1)		-0.0438	0.11	0.496	0.649	0.868	0.779	0.0113	0.00233
fig/6666666.474 865.peg.110	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)		0.419	0.105	0.287	-0.0266	0.0432	0.77	0.078	0.884
fig/6666666.474 865.peg.1161	Oleate hydratase (EC 4.2.1.53)		-0.512	0.105	-0.685	-0.0688	0.554	0.953	0.299	0.92
fig/6666666.474 865.peg.2438	Nitric oxide reductase activation protein NorQ		-0.119	0.105	0.288	0.512	0.545	0.735	0.0581	0.00327
fig/6666666.474 865.peg.730	Malate:quinone oxidoreductase (EC 1.1.5.4)		-0.216	0.105	-0.862	-0.541	0.408	0.82	0.000587	0.0138
fig/6666666.474 865.peg.2135	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)		0.0896	0.104	-0.165	-0.151	0.726	0.814	0.396	0.436
fig/6666666.474 865.peg.1678	Manganese ABC transporter, periplasmic-binding protein SitA		-1.41	0.102	-1.96	-0.452	0.000125	0.836	8.07E-07	0.0406
fig/6666666.474 865.peg.7	Porphobilinogen synthase (EC 4.2.1.24)		-0.404	0.102	-0.729	-0.223	0.175	0.861	0.00653	0.368
fig/6666666.474 865.peg.2259	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type		0.359	0.101	1.21	0.955	0.0607	0.756	2.45E-06	3.53E-05
fig/6666666.474 865.peg.1845	HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)		-0.184	0.1	0.24	0.524	0.247	0.703	0.0657	0.00105
fig/6666666.474 865.peg.2457	Thymidylate synthase (EC 2.1.1.45)		-0.0648	0.1	-0.413	-0.247	0.8	0.814	0.0304	0.181
fig/6666666.474 865.peg.1797	Queuosine Biosynthesis QueC ATPase		0.615	0.0994	-0.0719	-0.588	0.232	0.937	0.888	0.162
fig/6666666.474 865.peg.2125	Cell surface receptor IsdB for hemoglobin and hemoglobin-haptoglobin complexes		0.186	0.0983	-0.191	-0.278	0.716	0.926	0.645	0.468

fig/6666666.474 865.peg.2414	Oligoendopeptidase F (EC 3.4.24.-)		-0.326	0.098	0.941	1.37	0.134	0.806	8.29E-05	6.21E-06
fig/6666666.474 865.peg.2421	ABC transporter ATP-binding protein uup		-0.289	0.0954	-0.63	-0.246	0.0691	0.708	0.000153	0.057
fig/6666666.474 865.peg.2070	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)		-0.0284	0.095	-0.824	-0.7	0.893	0.735	3.00E-05	0.000184
fig/6666666.474 865.peg.2572	Phage repressor		-0.342	0.0948	-1.22	-0.787	0.241	0.865	0.00011	0.00395
fig/6666666.474 865.peg.1766	FIG01108121: hypothetical protein		-0.166	0.0943	0.0397	0.3	0.478	0.82	0.854	0.0993
fig/6666666.474 865.peg.620	tRNA-dependent lipid II--glycine ligase (FmhB)		-0.0104	0.0932	-0.271	-0.168	0.962	0.674	0.0179	0.125
fig/6666666.474 865.peg.1582	LSU ribosomal protein L1p (L10Ac)		0.184	0.0931	-0.0447	-0.136	0.183	0.693	0.732	0.225
fig/6666666.474 865.peg.1839	Peptide chain release factor 2; programmed frameshift-containing		-0.443	0.0927	-0.647	-0.112	0.322	0.926	0.0724	0.776
fig/6666666.474 865.peg.1907	Putative iron-sulfur cluster assembly scaffold protein for SUF system, SufE2		-0.17	0.0924	-0.388	-0.126	0.658	0.903	0.161	0.67
fig/6666666.474 865.peg.2287	FIG01108320: hypothetical protein		-1.67	0.0915	-1.21	0.558	0.0172	0.947	0.0276	0.296
fig/6666666.474 865.peg.504	Hypothetical protein SAV2141		-0.8	0.0915	-0.18	0.711	0.0244	0.903	0.536	0.0154
fig/6666666.474 865.peg.1834	FIG005590: DegV family protein		-0.345	0.091	-0.614	-0.178	0.313	0.903	0.0297	0.532
fig/6666666.474 865.peg.2182	Cell division protein FtsZ (EC 3.4.24.-)		-0.0336	0.0898	-0.104	0.0199	0.832	0.699	0.362	0.875
fig/6666666.474 865.peg.643	Ferrichrome-binding periplasmic protein precursor (TC 3.A.1.14.3)		0.383	0.0897	-0.194	-0.488	0.22	0.895	0.458	0.0575
fig/6666666.474 865.peg.608	LSU ribosomal protein L4p (L1e)		0.431	0.0896	-0.506	-0.848	0.116	0.864	0.0268	0.0015
fig/6666666.474 865.peg.1786	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)		-0.564	0.0888	-0.107	0.546	0.0172	0.827	0.582	0.00618
fig/6666666.474 865.peg.2448	Acetyltransferase (GNAT) family		-0.214	0.0888	0.382	0.685	0.618	0.915	0.224	0.0356
fig/6666666.474 865.peg.2405	tRNA-dependent lipid II-Gly--glycine ligase @ tRNA-dependent lipid II-GlyGly--glycine ligase @ FemA, factor essential for methicillin resistance	femA	0.221	0.0885	0.732	0.599	0.15	0.727	3.62E-05	0.000284
fig/6666666.474 865.peg.971	FIG009707: Betaine operon transcriptional regulator		0.787	0.0881	-0.444	-1.14	0.0967	0.941	0.241	0.0067
fig/6666666.474 865.peg.1302	Xylitol dehydrogenase		0.158	0.0872	0.426	0.355	0.461	0.82	0.0157	0.039
fig/6666666.474 865.peg.466	ATP synthase gamma chain (EC 3.6.3.14)		-0.213	0.0871	-0.172	0.129	0.258	0.806	0.264	0.412
fig/6666666.474 865.peg.696	FIG01108370: hypothetical protein		0.557	0.0865	-0.085	-0.556	0.109	0.906	0.798	0.0516

fig 6666666.474 865.peg.594	LSU ribosomal protein L6p (L9e)		0.0884	0.0842	0.0252	0.021	0.526	0.699	0.845	0.867
fig 6666666.474 865.peg.1816	Ribonucleotide reductase of class Ib (aerobic), alpha subunit (EC 1.17.4.1)		-0.493	0.0841	-0.538	0.0395	0.00152	0.695	9.88E-05	0.721
fig 6666666.474 865.peg.2721	Aspartyl-tRNA synthetase (EC 6.1.1.12)		-0.316	0.0839	-0.274	0.126	0.0197	0.695	0.0129	0.221
fig 6666666.474 865.peg.547	Hypothetical protein SAV2184		0.272	0.0839	-0.639	-0.827	0.627	0.943	0.115	0.047
fig 6666666.474 865.peg.673	Sialic acid utilization regulator, RpiR family		0.344	0.0833	-0.216	-0.477	0.533	0.943	0.645	0.257
fig 6666666.474 865.peg.1691	nucleoside transport protein		0.232	0.0815	1.85	1.7	0.783	0.959	0.00665	0.0115
fig 6666666.474 865.peg.1647	hypothetical fig 282458.1.peg.579 homolog		-0.901	0.0814	-0.512	0.47	0.19	0.956	0.368	0.41
fig 6666666.474 865.peg.2740	Rod shape-determining protein MreC		0.00249	0.0806	0.28	0.358	0.991	0.89	0.205	0.105
fig 6666666.474 865.peg.2368	GMP reductase (EC 1.7.1.7)		0.501	0.08	0.314	-0.107	0.0137	0.819	0.0406	0.487
fig 6666666.474 865.peg.1055	Collagen binding protein Cna		1.29	0.0788	-1.46	-2.67	0.0432	0.953	0.00774	0.000129
fig 6666666.474 865.peg.2702	Transcription elongation factor GreA		0.282	0.0784	-0.0741	-0.278	0.109	0.807	0.633	0.053
fig 6666666.474 865.peg.2458	FIG01226173: hypothetical protein		-0.362	0.0765	-0.565	-0.126	0.187	0.902	0.0168	0.589
fig 6666666.474 865.peg.2660	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly		-0.299	0.0753	-0.757	-0.383	0.725	0.964	0.229	0.56
fig 6666666.474 865.peg.1705	Two-component response regulator BceR		-0.204	0.0747	-0.247	0.0316	0.446	0.891	0.233	0.89
fig 6666666.474 865.peg.1888	FIG01108288: hypothetical protein		-0.257	0.0742	-0.144	0.187	0.58	0.943	0.721	0.608
fig 6666666.474 865.peg.183	Uncharacterized protein, homolog of B.subtilis yhgC		0.0963	0.0728	0.819	0.796	0.658	0.844	0.000104	0.000216
fig 6666666.474 865.peg.1583	LSU ribosomal protein L10p (P0)		0.183	0.0725	-0.465	-0.575	0.435	0.864	0.0155	0.00493
fig 6666666.474 865.peg.353	Phage repressor		0.243	0.0725	-0.465	-0.635	0.232	0.855	0.00973	0.0015
fig 6666666.474 865.peg.427	Anti-sigma F factor antagonist (spoIIAA-2); Anti-sigma B factor antagonist RsbV		-0.249	0.0724	-0.813	-0.492	0.36	0.903	0.00152	0.0307
fig 6666666.474 865.peg.2	Valyl-tRNA synthetase (EC 6.1.1.9)		-0.0339	0.0716	-0.0188	0.0868	0.798	0.708	0.87	0.377
fig 6666666.474 865.peg.2179	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	murD	0.156	0.0714	0.809	0.724	0.544	0.89	0.000739	0.00198
fig 6666666.474 865.peg.2072	IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)		-0.343	0.0711	-0.892	-0.478	0.0668	0.836	3.22E-05	0.00469

fig 6666666.474 865.peg.354	DNA helicase, phage-associated		-0.43	0.0709	-1.46	-0.956	0.278	0.943	0.000334	0.00749
fig 6666666.474 865.peg.2474	FIG001721: Predicted N6-adenine-specific DNA methylase		0.374	0.0706	0.387	0.0836	0.0669	0.856	0.0226	0.623
fig 6666666.474 865.peg.2093	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)		-0.113	0.0696	0.119	0.302	0.429	0.774	0.283	0.0118
fig 6666666.474 865.peg.2225	Phosphate:acyl-ACP acyltransferase PlsX		0.129	0.0696	0.00756	-0.0522	0.461	0.823	0.962	0.722
fig 6666666.474 865.peg.2247	tRNA:m(5)U-54 MTase gid		-0.705	0.0694	-1.38	-0.61	0.0207	0.912	3.58E-05	0.0153
fig 6666666.474 865.peg.916	Maltose O-acetyltransferase (EC 2.3.1.79)		0.355	0.0693	-1.12	-1.4	0.482	0.947	0.00887	0.00233
fig 6666666.474 865.peg.453	Hydroxyethylthiazole kinase (EC 2.7.1.50)		-0.338	0.0692	0.38	0.787	0.15	0.891	0.0516	0.00097
fig 6666666.474 865.peg.838	FIG01108532: hypothetical protein		-0.107	0.0686	0.372	0.547	0.84	0.946	0.315	0.14
fig 6666666.474 865.peg.1770	Transcriptional regulator MgrA (Regulator of autolytic activity)	mgrA	0.0451	0.0681	-0.54	-0.517	0.83	0.842	0.00167	0.00255
fig 6666666.474 865.peg.1900	Methionine ABC transporter substrate-binding protein		0.402	0.0667	-0.206	-0.541	0.231	0.934	0.466	0.0517
fig 6666666.474 865.peg.2388	UPF0118 membrane protein YrrI		0.247	0.065	2.96	2.78	0.782	0.969	0.000321	0.000705
fig 6666666.474 865.peg.2619	Translation elongation factor P		0.104	0.0642	-0.243	-0.283	0.643	0.865	0.132	0.0804
fig 6666666.474 865.peg.1554	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)		0.0596	0.0641	-0.0978	-0.0933	0.78	0.861	0.561	0.564
fig 6666666.474 865.peg.605	SSU ribosomal protein S19p (S15e)		0.48	0.0641	0.386	-0.0296	0.00573	0.82	0.00542	0.835
fig 6666666.474 865.peg.2420	S1 RNA binding domain		0.144	0.0632	-0.0439	-0.125	0.383	0.831	0.776	0.343
fig 6666666.474 865.peg.2587	ADP-ribose pyrophosphatase (EC 3.6.1.13)		-0.987	0.0631	-0.529	0.521	0.222	0.969	0.432	0.433
fig 6666666.474 865.peg.1299	Putative polyribitolphosphotransferase		-0.518	0.0622	0.231	0.811	0.191	0.946	0.499	0.0188
fig 6666666.474 865.peg.2726	Adenine phosphoribosyltransferase (EC 2.4.2.7)		0.0464	0.062	0.403	0.419	0.928	0.946	0.223	0.203
fig 6666666.474 865.peg.441	DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)		0.238	0.062	0.0802	-0.096	0.088	0.807	0.49	0.397
fig 6666666.474 865.peg.475	Serine hydroxymethyltransferase (EC 2.1.2.1)		-0.0638	0.0608	-0.181	-0.0562	0.755	0.864	0.23	0.729
fig 6666666.474 865.peg.28	DNA polymerase I (EC 2.7.7.7)		-0.11	0.0603	0.177	0.348	0.453	0.82	0.119	0.00628
fig 6666666.474 865.peg.764	Respiratory nitrate reductase alpha chain (EC 1.7.99.4)		-0.289	0.0596	-0.899	-0.551	0.156	0.891	7.99E-05	0.00395
fig 6666666.474 865.peg.2613	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)		-1.4	0.0583	-2.53	-1.07	0.00125	0.943	9.60E-07	0.00164

fig 6666666.474 865.peg.2087	Ribonuclease J1 (endonuclease and 5' exonuclease)		-0.183	0.0581	0.000467	0.242	0.313	0.865	0.997	0.0985
fig 6666666.474 865.peg.2284	FIG006542: Phosphoesterase		-0.252	0.0581	-1.04	-0.727	0.243	0.903	3.58E-05	0.000901
fig 6666666.474 865.peg.816	DUF1801 domain-containing protein		-0.55	0.0581	-0.213	0.394	0.0393	0.918	0.307	0.062
fig 6666666.474 865.peg.574	SSU ribosomal protein S9p (S16e)		0.0943	0.0576	-0.743	-0.78	0.726	0.914	0.0016	0.00135
fig 6666666.474 865.peg.2611	Arginine pathway regulatory protein ArgR, repressor of arg regulon		0.271	0.0575	0.348	0.134	0.258	0.914	0.0782	0.506
fig 6666666.474 865.peg.1412	SSU ribosomal protein S6p		-0.0573	0.057	-0.442	-0.328	0.807	0.903	0.0138	0.0547
fig 6666666.474 865.peg.533	N-acetylglucosamine-1-phosphate uridyltransferase eukaryotic (EC 2.7.7.23)		0.415	0.0569	0.602	0.244	0.0207	0.861	0.000441	0.0777
fig 6666666.474 865.peg.78	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)		-0.102	0.0564	0.298	0.456	0.676	0.906	0.0922	0.0157
fig 6666666.474 865.peg.1905	Iron-sulfur cluster assembly protein SufD		0.239	0.0555	0.32	0.136	0.0967	0.831	0.01	0.232
fig 6666666.474 865.peg.781	L-Cystine ABC transporter, periplasmic cystine-binding protein TcyA		0.3	0.0554	-0.00277	-0.248	0.0755	0.863	0.988	0.0695
fig 6666666.474 865.peg.582	LSU ribosomal protein L17p		0.259	0.0548	-0.325	-0.529	0.111	0.861	0.0181	0.00105
fig 6666666.474 865.peg.915	Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)		0.421	0.0539	0.342	-0.0247	0.0481	0.906	0.047	0.891
fig 6666666.474 865.peg.1846	Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	lgt	0.108	0.0515	2.76	2.7	0.78	0.947	4.75E-07	9.29E-07
fig 6666666.474 865.peg.1591	Translation elongation factor G		0.00525	0.0512	-0.139	-0.0936	0.967	0.809	0.132	0.319
fig 6666666.474 865.peg.619	RND multidrug efflux transporter; Acriflavin resistance protein		-0.231	0.0492	-0.605	-0.325	0.54	0.947	0.0388	0.255
fig 6666666.474 865.peg.194	Hypothetical protein SAV1845		-0.532	0.049	-0.972	-0.391	0.00602	0.898	8.68E-06	0.0104
fig 6666666.474 865.peg.735	Alcohol dehydrogenase (EC 1.1.1.1)		0.27	0.0484	-0.245	-0.467	0.0967	0.883	0.0608	0.00225
fig 6666666.474 865.peg.2147	Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.15)		-0.345	0.0482	-0.659	-0.266	0.201	0.943	0.00668	0.225
fig 6666666.474 865.peg.1549	possible tetrapyrrole methyltransferase domain / Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)		-0.39	0.0471	-0.194	0.244	0.16	0.943	0.401	0.286
fig 6666666.474 865.peg.2637	Glucokinase (EC 2.7.1.2)		-0.118	0.0453	0.561	0.724	0.691	0.943	0.016	0.00406
fig 6666666.474 865.peg.2092	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)		0.00411	0.0431	0.0127	0.0517	0.98	0.898	0.932	0.699
fig 6666666.474 865.peg.1164	Protein A, von Willebrand factor binding protein Spa	spa	-0.408	0.0422	-1.79	-1.34	0.00781	0.882	1.34E-09	9.21E-08
fig 6666666.474 865.peg.1186	Predicted cell-wall-anchored protein SasD (LPXAG motif)		-2.93	0.0422	-2.32	0.654	0.00499	0.985	0.00516	0.389

fig 6666666.474 865.peg.1564	Pyridoxine biosynthesis glutamine amidotransferase, glutaminase subunit (EC 2.4.2.-)		-0.171	0.0417	0.0243	0.237	0.563	0.946	0.928	0.294
fig 6666666.474 865.peg.97	Hypothetical protein SAV1752		-0.509	0.0401	-1	-0.453	0.13	0.956	0.00169	0.0974
fig 6666666.474 865.peg.732	Putative glycosyl/glycerophosphate transferase in teichoic acid biosynthesis		-0.506	0.0399	0.0686	0.614	0.161	0.956	0.846	0.0431
fig 6666666.474 865.peg.595	SSU ribosomal protein S8p (S15Ae)		0.135	0.0392	-0.491	-0.587	0.427	0.911	0.00151	0.000506
fig 6666666.474 865.peg.2602	Peptidase T (EC 3.4.11.4)		-0.382	0.0383	-0.179	0.241	0.0223	0.912	0.164	0.0631
fig 6666666.474 865.peg.1561	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)		-0.0684	0.0369	0.158	0.263	0.643	0.899	0.14	0.0201
fig 6666666.474 865.peg.688	Dehydrogenase		-1.43	0.0366	-3.62	-2.15	0.144	0.985	0.000306	0.012
fig 6666666.474 865.peg.1301	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)		0.109	0.0363	0.977	0.904	0.726	0.954	0.000642	0.00139
fig 6666666.474 865.peg.102	Rhodanese-like domain protein		-0.244	0.0357	-1.02	-0.742	0.232	0.943	2.62E-05	0.000526
fig 6666666.474 865.peg.1931	NADH dehydrogenase (EC 1.6.99.3)		0.242	0.0355	0.261	0.0544	0.15	0.926	0.0578	0.711
fig 6666666.474 865.peg.2460	FIG01108403: hypothetical protein		0.00548	0.0355	-0.401	-0.371	0.98	0.943	0.022	0.034
fig 6666666.474 865.peg.1955	Signal peptidase I (EC 3.4.21.89)		0.893	0.0346	1.66	0.805	0.00999	0.956	1.52E-05	0.00494
fig 6666666.474 865.peg.989	Transcriptional regulator, MarR family		-0.318	0.0337	0.71	1.06	0.773	0.985	0.38	0.179
fig 6666666.474 865.peg.1185	Manganese superoxide dismutase (EC 1.15.1.1); Superoxide dismutase		-0.501	0.0331	-1.08	-0.541	0.0315	0.947	3.59E-05	0.00744
fig 6666666.474 865.peg.1109	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)		-0.463	0.0327	-1.04	-0.544	0.726	0.986	0.296	0.6
fig 6666666.474 865.peg.26	Dephospho-CoA kinase (EC 2.7.1.24)		-0.0101	0.0327	0.245	0.288	0.966	0.943	0.1	0.057
fig 6666666.474 865.peg.1616	Phosphoglycolate phosphatase (EC 3.1.3.18)		0.609	0.0323	-1.76	-2.33	0.526	0.985	0.0218	0.00493
fig 6666666.474 865.peg.2222	Dihydroxyacetone kinase family protein		-0.144	0.0317	-0.0813	0.0947	0.433	0.943	0.599	0.519
fig 6666666.474 865.peg.82	FIG009688: Thioredoxin		-0.183	0.0314	-0.534	-0.32	0.547	0.956	0.0264	0.167
fig 6666666.474 865.peg.1168	Siderophore staphylobactin ABC transporter, substrate-binding protein SirA		-0.0438	0.0313	-1.09	-1.02	0.84	0.943	6.62E-06	2.49E-05
fig 6666666.474 865.peg.205	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)		-0.797	0.03	-1.2	-0.371	0.46	0.985	0.152	0.677
fig 6666666.474 865.peg.1403	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14)		0.171	0.0296	-0.147	-0.289	0.868	0.985	0.859	0.699
fig 6666666.474 865.peg.2235	16S rRNA processing protein RimM		0.102	0.0293	-0.53	-0.602	0.789	0.969	0.0578	0.0357

fig/6666666.474 865.peg.1080	Chromosomal replication initiator protein DnaA		0.193	0.0276	-0.399	-0.565	0.436	0.956	0.0416	0.00783
fig/6666666.474 865.peg.443	D-alanine--D-alanine ligase (EC 6.3.2.4)		0.0587	0.0271	0.804	0.772	0.776	0.947	7.99E-05	0.000173
fig/6666666.474 865.peg.996	Arginine deiminase (EC 3.5.3.6)		-2.63	0.0267	0.0738	2.73	0.00245	0.985	0.921	0.000453
fig/6666666.474 865.peg.1861	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)		-0.166	0.0243	-0.305	-0.114	0.382	0.951	0.0451	0.451
fig/6666666.474 865.peg.1631	Phosphate acetyltransferase (EC 2.3.1.8)		0.00895	0.0241	-0.62	-0.605	0.962	0.937	2.60E-05	5.25E-05
fig/6666666.474 865.peg.1823	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	murB	-0.109	0.0241	-0.0681	0.0646	0.685	0.962	0.768	0.764
fig/6666666.474 865.peg.587	Translation initiation factor 1		-0.156	0.024	-0.973	-0.793	0.567	0.964	0.000245	0.0015
fig/6666666.474 865.peg.492	spermine/spermidine acetyltransferase blt		-0.354	0.0229	-0.255	0.122	0.471	0.985	0.529	0.768
fig/6666666.474 865.peg.428	Serine phosphatase RsbU, regulator of sigma subunit		-0.0908	0.0228	0.329	0.443	0.798	0.971	0.202	0.0868
fig/6666666.474 865.peg.467	ATP synthase alpha chain (EC 3.6.3.14)		-0.0856	0.0218	-0.0281	0.0793	0.54	0.943	0.827	0.466
fig/6666666.474 865.peg.468	ATP synthase delta chain (EC 3.6.3.14)		0.325	0.0208	0.228	-0.0757	0.162	0.969	0.23	0.712
fig/6666666.474 865.peg.13	ATP-dependent Clp protease ATP-binding subunit ClpX		0.0608	0.0205	-0.0208	-0.061	0.716	0.948	0.89	0.636
fig/6666666.474 865.peg.22	Helicase loader DnaI		0.196	0.0197	0.66	0.485	0.563	0.979	0.0155	0.0624
fig/6666666.474 865.peg.583	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)		0.0955	0.0193	-0.0853	-0.161	0.518	0.947	0.468	0.154
fig/6666666.474 865.peg.1908	Iron-sulfur cluster assembly protein SufB		0.01	0.0185	0.3	0.308	0.962	0.951	0.0133	0.012
fig/6666666.474 865.peg.609	LSU ribosomal protein L3p (L3e)		0.0119	0.0184	-0.507	-0.501	0.963	0.964	0.00405	0.00469
fig/6666666.474 865.peg.2246	DNA topoisomerase I (EC 5.99.1.2)		0.384	0.0179	-0.133	-0.498	0.108	0.969	0.508	0.0148
fig/6666666.474 865.peg.2188	Cell division initiation protein DivIVA		-0.404	0.0171	-0.736	-0.315	0.126	0.976	0.00277	0.14
fig/6666666.474 865.peg.2485	Asparaginyl-tRNA synthetase (EC 6.1.1.22)		-0.1	0.017	-0.0967	0.0204	0.489	0.956	0.396	0.872
fig/6666666.474 865.peg.662	Glyoxylate reductase (EC 1.1.1.79) / Glyoxylate reductase (EC 1.1.1.26) / Hydroxypyruvate reductase (EC 1.1.1.81)		-0.217	0.017	-0.126	0.109	0.13	0.956	0.277	0.355
fig/6666666.474 865.peg.21	Threonyl-tRNA synthetase (EC 6.1.1.3)		-0.315	0.0169	-0.444	-0.112	0.0456	0.956	0.00224	0.377
fig/6666666.474 865.peg.2590	3-oxoacyl-[acyl-carrier protein] reductase paralog (EC 1.1.1.100)		1.29	0.0159	0.21	-1.06	0.111	0.987	0.787	0.103
fig/6666666.474 865.peg.54	Septation ring formation regulator EzrA		-0.349	0.0155	-1.06	-0.695	0.0258	0.96	1.24E-06	7.30E-05

fig/6666666.474 865.peg.2270	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)		0.152	0.0154	0.18	0.0438	0.352	0.964	0.169	0.761
fig/6666666.474 865.peg.1453	FIG01108201: hypothetical protein		-0.0119	0.015	-0.928	-0.901	0.975	0.985	0.00425	0.00549
fig/6666666.474 865.peg.1454	Xanthine phosphoribosyltransferase (EC 2.4.2.22)		0.423	0.0144	0.0855	-0.324	0.0257	0.969	0.59	0.034
fig/6666666.474 865.peg.539	Heme ABC type transporter HtsABC, heme-binding protein		1.57	0.0132	-0.723	-2.28	0.15	0.993	0.428	0.0168
fig/6666666.474 865.peg.1922	D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13)		0.121	0.0128	-0.376	-0.484	0.489	0.969	0.0101	0.00233
fig/6666666.474 865.peg.2053	Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily F2 (as in PMID19099556)		0.299	0.0128	1.05	0.768	0.243	0.985	0.000132	0.002
fig/6666666.474 865.peg.1076	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA		0.463	0.0115	0.595	0.144	0.108	0.985	0.0148	0.55
fig/6666666.474 865.peg.2252	SSU ribosomal protein S2p (SAe)		0.188	0.0112	-0.0372	-0.214	0.153	0.969	0.771	0.0517
fig/6666666.474 865.peg.2304	Glutamine synthetase type I (EC 6.3.1.2)	glnA	-0.132	0.0107	-0.142	0.000434	0.338	0.969	0.199	0.996
fig/6666666.474 865.peg.1521	DNA polymerase III subunits gamma and tau (EC 2.7.7.7)		0.796	0.0091	0.219	-0.567	0.15	0.99	0.66	0.203
fig/6666666.474 865.peg.1375	FIG01108282: hypothetical protein		-0.388	0.00898	-0.352	0.0448	0.0781	0.985	0.0494	0.824
fig/6666666.474 865.peg.1600	Deoxyadenosine kinase (EC 2.7.1.76) / Deoxyguanosine kinase (EC 2.7.1.113)		-0.102	0.00828	0.319	0.429	0.792	0.987	0.259	0.131
fig/6666666.474 865.peg.50	Thiol peroxidase, Tpx-type (EC 1.11.1.15)		0.0341	0.00756	0.0574	0.0309	0.893	0.985	0.768	0.87
fig/6666666.474 865.peg.182	Uroporphyrinogen III decarboxylase (EC 4.1.1.37)		-0.093	0.0071	-0.468	-0.368	0.643	0.985	0.00409	0.0172
fig/6666666.474 865.peg.2435	Tellurite resistance protein		0.21	0.00635	1.07	0.87	0.187	0.985	1.88E-06	2.49E-05
fig/6666666.474 865.peg.1285	L-lactate dehydrogenase (EC 1.1.1.27)		0.412	0.00612	0.271	-0.135	0.0202	0.985	0.0499	0.326
fig/6666666.474 865.peg.545	alkaline shock protein 23		-0.0799	0.00594	-0.696	-0.61	0.812	0.987	0.00794	0.0172
fig/6666666.474 865.peg.204	Hypothetical protein SAV1854		-0.0978	0.00465	-0.369	-0.267	0.678	0.987	0.0348	0.12
fig/6666666.474 865.peg.252	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7)		-0.156	0.00461	-1.17	-1.01	0.504	0.987	1.54E-05	7.93E-05
fig/6666666.474 865.peg.2082	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)		-0.108	0.00392	-0.222	-0.11	0.448	0.985	0.0476	0.323
fig/6666666.474 865.peg.2019	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)		0.973	0.00366	-0.283	-1.25	0.108	0.998	0.59	0.0157
fig/6666666.474 865.peg.546	Hypothetical protein SAV2183		-1.6	0.00056	0.00847	1.61	0.113	0.999	0.995	0.0522
fig/6666666.474 865.peg.2703	Uridine kinase (EC 2.7.1.48) [C1]		0.503	-0.00042	0.342	-0.162	0.185	0.999	0.268	0.617

fig 6666666.474 865.peg.2074	Transmembrane component YkoC of energizing module of thiamin-regulated ECF transporter for HydroxyMethylPyrimidine		0.366	-0.00044	1.66	1.29	0.687	0.999	0.0174	0.0547
fig 6666666.474 865.peg.196	HTH domain protein SA1665, binds to mecA promoter region		-0.0935	-0.00072	0.19	0.283	0.738	0.999	0.375	0.179
fig 6666666.474 865.peg.281	Thioredoxin		0.0298	-0.00141	0.682	0.651	0.926	0.998	0.00359	0.00502
fig 6666666.474 865.peg.683	Transcriptional regulator, RpiR family		-0.664	-0.00146	0.872	1.54	0.183	0.999	0.0351	0.00164
fig 6666666.474 865.peg.1587	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)		0.0222	-0.00151	-0.34	-0.363	0.868	0.992	0.0016	0.00118
fig 6666666.474 865.peg.2251	GTP-sensing transcriptional pleiotropic repressor codY	codY	0.398	-0.00196	0.374	-0.0258	0.0456	0.994	0.0226	0.884
fig 6666666.474 865.peg.264	NAD synthetase (EC 6.3.1.5)		-0.226	-0.00407	-0.36	-0.138	0.232	0.987	0.0242	0.377
fig 6666666.474 865.peg.2081	Phosphocarrier protein of PTS system		-0.343	-0.00457	-0.277	0.0611	0.24	0.99	0.245	0.823
fig 6666666.474 865.peg.2268	Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)		-0.0113	-0.00585	0.843	0.849	0.965	0.985	7.96E-05	0.000108
fig 6666666.474 865.peg.2453	Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)	mrsB	1.13	-0.00718	3.56	2.42	0.000364	0.985	3.76E-10	9.21E-08
fig 6666666.474 865.peg.1592	Translation elongation factor Tu		0.0245	-0.00739	0.0128	-0.0191	0.868	0.98	0.921	0.868
fig 6666666.474 865.peg.610	SSU ribosomal protein S10p (S20e)		0.601	-0.00938	-0.432	-1.04	0.0456	0.985	0.07	0.000564
fig 6666666.474 865.peg.1918	BH3430 unknown conserved protein		-0.694	-0.00942	-0.56	0.125	0.0972	0.987	0.0949	0.729
fig 6666666.474 865.peg.1973	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.180)		-0.154	-0.00963	-0.113	0.0314	0.536	0.985	0.584	0.884
fig 6666666.474 865.peg.179	Hypothetical protein SAV1831		-0.0398	-0.00969	0.0236	0.0537	0.936	0.986	0.954	0.877
fig 6666666.474 865.peg.213	Thiol peroxidase, Bcp-type (EC 1.11.1.15)		-0.356	-0.0102	-0.0523	0.294	0.102	0.985	0.801	0.0914
fig 6666666.474 865.peg.1995	Oligoendopeptidase F (EC 3.4.24.-)		-0.0109	-0.0114	0.219	0.219	0.962	0.969	0.0626	0.0635
fig 6666666.474 865.peg.2581	Ribosomal large subunit pseudouridine synthase B (EC 4.2.1.70)		0.728	-0.0119	0.0355	-0.705	0.0684	0.985	0.927	0.034
fig 6666666.474 865.peg.1661	Staphylococcal accessory regulator A (SarA)	sarA	0.599	-0.0121	0.954	0.343	0.00862	0.98	4.73E-05	0.0448
fig 6666666.474 865.peg.259	Adenylosuccinate lyase (EC 4.3.2.2)		-0.142	-0.0122	0.294	0.424	0.313	0.969	0.0144	0.00172
fig 6666666.474 865.peg.2024	Lipoate-protein ligase A		-0.317	-0.0128	0.42	0.725	0.156	0.98	0.0265	0.00118
fig 6666666.474 865.peg.2670	Chaperone protein DnaJ		0.0202	-0.0134	0.212	0.178	0.962	0.985	0.332	0.421
fig 6666666.474 865.peg.1611	FIG013761: LmbE family protein		1.02	-0.0148	0.373	-0.664	0.0294	0.985	0.309	0.0721

fig 6666666.474 865.peg.17	LSU ribosomal protein L20p		0.114	-0.0153	-0.847	-0.975	0.774	0.985	0.00714	0.00327
fig 6666666.474 865.peg.1190	Deoxyribose-phosphate aldolase (EC 4.1.2.4)		-0.451	-0.0164	-0.143	0.291	0.016	0.964	0.307	0.0434
fig 6666666.474 865.peg.653	Transcriptional regulator SarR (Staphylococcal accessory regulator R)		-0.514	-0.0174	-1.32	-0.819	0.0258	0.969	5.55E-06	0.000434
fig 6666666.474 865.peg.1543	N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)	glmU	-0.352	-0.0184	-0.728	-0.395	0.27	0.98	0.00987	0.131
fig 6666666.474 865.peg.2657	GTP-binding protein Era		-0.461	-0.0192	0.157	0.599	0.0657	0.969	0.443	0.00674
fig 6666666.474 865.peg.613	DNA topoisomerase III (EC 5.99.1.2)		-0.0583	-0.0197	0.104	0.143	0.871	0.976	0.714	0.574
fig 6666666.474 865.peg.2655	Glycyl-tRNA synthetase (EC 6.1.1.14)		-0.231	-0.0199	0.711	0.923	0.118	0.948	3.40E-05	6.21E-06
fig 6666666.474 865.peg.2296	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)		-0.231	-0.0201	1.02	1.23	0.331	0.969	8.79E-05	3.41E-05
fig 6666666.474 865.peg.597	LSU ribosomal protein L5p (L11e)		0.186	-0.0213	-0.351	-0.559	0.166	0.946	0.00451	0.000203
fig 6666666.474 865.peg.39	NADP-dependent malic enzyme (EC 1.1.1.40)		-0.0657	-0.0227	-0.229	-0.186	0.732	0.953	0.111	0.194
fig 6666666.474 865.peg.2710	Alanyl-tRNA synthetase (EC 6.1.1.7)		-0.304	-0.0228	-0.305	-0.0243	0.0645	0.947	0.0241	0.87
fig 6666666.474 865.peg.2624	Rhodanese-like domain protein		0.139	-0.0231	-0.727	-0.889	0.643	0.969	0.00347	0.000989
fig 6666666.474 865.peg.2647	Endonuclease IV (EC 3.1.21.2)		0.0334	-0.0237	0.237	0.179	0.938	0.971	0.38	0.513
fig 6666666.474 865.peg.192	DNA double-strand break repair Rad50 ATPase		-0.182	-0.024	-0.795	-0.637	0.39	0.956	0.000214	0.00153
fig 6666666.474 865.peg.2181	Cell division protein FtsA		0.0116	-0.0243	0.618	0.582	0.962	0.946	0.000192	0.000447
fig 6666666.474 865.peg.1545	LSU ribosomal protein L25p		0.0886	-0.0244	0.489	0.376	0.598	0.943	0.00107	0.0067
fig 6666666.474 865.peg.1893	Arsenate reductase (EC 1.20.4.1)		0.0151	-0.0253	0.532	0.492	0.94	0.943	0.000478	0.0011
fig 6666666.474 865.peg.1590	SSU ribosomal protein S7p (S5e)		0.645	-0.0263	-0.445	-1.12	0.0116	0.956	0.0226	5.59E-05
fig 6666666.474 865.peg.1586	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)		0.00294	-0.0267	-0.52	-0.55	0.981	0.918	7.99E-05	7.30E-05
fig 6666666.474 865.peg.465	ATP synthase beta chain (EC 3.6.3.14)		-0.102	-0.0284	-0.139	-0.0655	0.342	0.904	0.107	0.456
fig 6666666.474 865.peg.241	Putative amidotransferase similar to cobyric acid synthase		0.444	-0.0299	0.713	0.239	0.0432	0.947	7.00E-04	0.164
fig 6666666.474 865.peg.906	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)		0.05	-0.0299	-0.043	-0.123	0.724	0.914	0.723	0.235
fig 6666666.474 865.peg.1081	DNA polymerase III beta subunit (EC 2.7.7.7)		-0.0283	-0.0302	0.177	0.176	0.893	0.943	0.199	0.202

fig 6666666.474 865.peg.2133	FIG011178: rRNA methylase		-0.994	-0.0307	-0.967	-0.00356	0.338	0.985	0.246	0.996
fig 6666666.474 865.peg.1859	Phosphoglycerate kinase (EC 2.7.2.3)		-0.0265	-0.0312	0.0578	0.0531	0.866	0.912	0.617	0.632
fig 6666666.474 865.peg.1006	Isochorismatase (EC 3.3.2.1)		-0.37	-0.0315	0.115	0.453	0.187	0.956	0.649	0.052
fig 6666666.474 865.peg.1813	NADPH dependent preQ0 reductase (EC 1.7.1.13)		-2.03	-0.0321	-0.568	1.43	0.102	0.986	0.595	0.148
fig 6666666.474 865.peg.1284	Flavohepotein (Hemoglobin-like protein) (Flavohepotein) (Nitric oxide dioxygenase) (EC 1.14.12.17)		-0.762	-0.0329	-0.136	0.592	0.0025	0.946	0.45	0.00339
fig 6666666.474 865.peg.2233	Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)		-0.181	-0.0334	-0.0332	0.115	0.455	0.947	0.884	0.56
fig 6666666.474 865.peg.46	Alanine dehydrogenase (EC 1.4.1.1)		-0.922	-0.0334	-0.978	-0.089	0.191	0.985	0.0925	0.89
fig 6666666.474 865.peg.1096	Adenylosuccinate synthetase (EC 6.3.4.4)		-0.164	-0.0337	-0.669	-0.539	0.293	0.925	8.79E-05	0.000693
fig 6666666.474 865.peg.1443	phosphoglycerate mutase family protein		-0.247	-0.0344	0.247	0.46	0.554	0.969	0.45	0.148
fig 6666666.474 865.peg.248	Transcription regulator [contains diacylglycerol kinase catalytic domain]		-0.24	-0.0353	-0.517	-0.312	0.423	0.956	0.0302	0.177
fig 6666666.474 865.peg.2601	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)		0.0271	-0.0358	0.449	0.386	0.873	0.908	0.0013	0.00408
fig 6666666.474 865.peg.570	Alpha-acetolactate decarboxylase (EC 4.1.1.5)		-0.621	-0.0363	-0.0552	0.53	0.0258	0.948	0.831	0.0203
fig 6666666.474 865.peg.243	Ferritin-like protein 2		-0.573	-0.037	-0.477	0.0593	0.0172	0.943	0.0138	0.766
fig 6666666.474 865.peg.73	Catabolite control protein A		-0.138	-0.0374	-0.0588	0.0417	0.476	0.933	0.734	0.805
fig 6666666.474 865.peg.2582	Segregation and condensation protein B	scpB	0.706	-0.0385	1.55	0.807	0.298	0.98	0.00905	0.141
fig 6666666.474 865.peg.490	CTP synthase (EC 6.3.4.2)		0.113	-0.0396	0.168	0.0162	0.554	0.921	0.246	0.918
fig 6666666.474 865.peg.2272	Cell division protein FtsK		0.121	-0.04	-0.0962	-0.258	0.893	0.981	0.892	0.684
fig 6666666.474 865.peg.2385	Topoisomerase IV subunit A (EC 5.99.1.-)		-0.28	-0.04	0.116	0.356	0.459	0.956	0.733	0.221
fig 6666666.474 865.peg.1222	FIG01108032: hypothetical protein		0.378	-0.0402	0.133	-0.285	0.55	0.975	0.819	0.568
fig 6666666.474 865.peg.1785	PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)		0.112	-0.0409	0.133	-0.0203	0.691	0.943	0.548	0.925
fig 6666666.474 865.peg.1457	GMP synthase		0.0548	-0.042	0.201	0.104	0.691	0.861	0.0503	0.306
fig 6666666.474 865.peg.2281	RecA protein		-0.118	-0.0434	-0.47	-0.395	0.433	0.884	0.00087	0.00335

fig/6666666.474 865.peg.1851	FIG002813: LPPG:FO 2-phospho-L-lactate transferase like, CofD-like		-0.142	-0.0436	0.66	0.759	0.68	0.947	0.0138	0.0067
fig/6666666.474 865.peg.707	Isopentenyl-diphosphate delta-isomerase, FMN-dependent (EC 5.3.3.2)		-0.162	-0.0441	-0.0133	0.105	0.587	0.943	0.961	0.659
fig/6666666.474 865.peg.2580	Staphylococcal respiratory response protein SrrA	srrA	-0.224	-0.0444	-0.45	-0.27	0.384	0.943	0.0304	0.179
fig/6666666.474 865.peg.1450	L-cystine uptake protein TcyP		-0.54	-0.0445	-0.379	0.117	0.192	0.959	0.263	0.755
fig/6666666.474 865.peg.2104	FIG01108286: hypothetical protein		-0.136	-0.047	0.342	0.43	0.643	0.943	0.108	0.048
fig/6666666.474 865.peg.2262	Transcription termination protein NusA		0.101	-0.0476	0.271	0.123	0.639	0.906	0.078	0.428
fig/6666666.474 865.peg.2186	Cell division protein YlmG/Ycf19 (putative), YggT family		0.176	-0.0484	1.74	1.52	0.812	0.971	0.00393	0.00929
fig/6666666.474 865.peg.2679	dCMP deaminase (EC 3.5.4.12); Late competence protein ComEB		-0.515	-0.0487	0.332	0.798	0.27	0.96	0.39	0.0415
fig/6666666.474 865.peg.2249	ATP-dependent protease HslV (EC 3.4.25.-)	clpQ	0.712	-0.049	0.674	-0.0872	0.0456	0.947	0.022	0.777
fig/6666666.474 865.peg.2615	Transcription termination protein NusB		0.331	-0.0495	1.25	0.87	0.287	0.943	0.000152	0.00296
fig/6666666.474 865.peg.2111	Pyruvate carboxylase (EC 6.4.1.1)		-0.554	-0.0496	-0.534	-0.0303	0.0458	0.943	0.0204	0.898
fig/6666666.474 865.peg.1534	Putative deoxyribonuclease YcfH		-0.235	-0.0506	-0.433	-0.248	0.351	0.933	0.036	0.218
fig/6666666.474 865.peg.2508	Thioredoxin reductase (EC 1.8.1.9)		0.188	-0.0508	0.534	0.295	0.443	0.925	0.0096	0.122
fig/6666666.474 865.peg.80	Phenylalanyl-tRNA synthetase domain protein (Bsu YtpR)		0.217	-0.0508	0.284	0.0163	0.323	0.914	0.107	0.929
fig/6666666.474 865.peg.2017	Peptide chain release factor 3		0.0415	-0.0512	-0.213	-0.305	0.812	0.861	0.089	0.0201
fig/6666666.474 865.peg.474	Uracil phosphoribosyltransferase (EC 2.4.2.9)		-0.204	-0.0513	-0.477	-0.324	0.321	0.906	0.00792	0.0528
fig/6666666.474 865.peg.96	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases		-0.372	-0.0517	-0.373	-0.0528	0.0565	0.903	0.0209	0.755
fig/6666666.474 865.peg.2265	Translation initiation factor 2		-0.059	-0.0518	0.351	0.359	0.716	0.855	0.00714	0.0067
fig/6666666.474 865.peg.64	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)		0.345	-0.0524	2.18	1.78	0.016	0.831	1.29E-10	2.67E-09
fig/6666666.474 865.peg.524	Uncharacterized secreted protein associated with spyDAC		-0.00564	-0.053	-0.458	-0.506	0.982	0.926	0.0286	0.0189
fig/6666666.474 865.peg.2274	FIG001621: Zinc protease		0.185	-0.0531	0.0343	-0.204	0.658	0.947	0.927	0.513
fig/6666666.474 865.peg.1506	Methionine ABC transporter substrate-binding protein		0.547	-0.0535	-1.55	-2.16	0.108	0.943	4.79E-05	5.48E-06
fig/6666666.474 865.peg.1808	Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57)		0.238	-0.054	0.338	0.0465	0.442	0.943	0.159	0.868

fig/6666666.474 865.peg.2253	Translation elongation factor Ts		0.0556	-0.0541	-0.126	-0.235	0.668	0.802	0.183	0.0188
fig/6666666.474 865.peg.995	Ornithine carbamoyltransferase (EC 2.1.3.3)		-2.05	-0.0549	0.235	2.23	0.00175	0.962	0.629	0.000217
fig/6666666.474 865.peg.1448	Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)		-0.149	-0.0552	-0.618	-0.524	0.27	0.826	5.87E-05	0.000314
fig/6666666.474 865.peg.592	SSU ribosomal protein S5p (S2e)		0.276	-0.0552	-0.553	-0.884	0.304	0.93	0.0158	0.000985
fig/6666666.474 865.peg.2617	Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)		0.174	-0.0554	0.271	0.0414	0.428	0.904	0.11	0.832
fig/6666666.474 865.peg.1533	Methionyl-tRNA synthetase (EC 6.1.1.10)		-0.128	-0.0564	0.217	0.288	0.475	0.864	0.117	0.0431
fig/6666666.474 865.peg.2488	tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)		0.423	-0.0566	0.469	-0.0101	0.697	0.98	0.59	0.991
fig/6666666.474 865.peg.392	Nitroreductase family protein		-0.897	-0.0577	-1.27	-0.431	0.00602	0.934	8.01E-05	0.0696
fig/6666666.474 865.peg.1782	Cys-tRNA(Pro) deacylase YbaK		-0.17	-0.0579	0.459	0.572	0.772	0.956	0.278	0.176
fig/6666666.474 865.peg.2323	FIG01108053: hypothetical protein		0.318	-0.058	-1.22	-1.59	0.714	0.971	0.0578	0.0183
fig/6666666.474 865.peg.2506	Cytidylate kinase (EC 2.7.4.25)		-0.0383	-0.058	-0.624	-0.643	0.835	0.851	0.000206	0.000243
fig/6666666.474 865.peg.2440	FIG01107869: hypothetical protein		-0.771	-0.0593	-1.23	-0.515	0.000242	0.844	5.21E-07	0.0011
fig/6666666.474 865.peg.2050	Bifunctional autolysin Atl / N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)/ endo-beta-N-acetylglucosaminidase (EC 3.2.1.96)		-0.0406	-0.0606	-1	-1.02	0.933	0.943	0.00385	0.00359
fig/6666666.474 865.peg.2042	Naphthoate synthase (EC 4.1.3.36)		0.139	-0.0614	-0.128	-0.329	0.288	0.799	0.227	0.0057
fig/6666666.474 865.peg.2608	Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)		0.133	-0.0627	0.211	0.0156	0.482	0.861	0.153	0.92
fig/6666666.474 865.peg.499	Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)		-0.351	-0.0632	-0.439	-0.152	0.0393	0.838	0.00374	0.252
fig/6666666.474 865.peg.2713	tRNA-specific 2-thiouridylase MnmA		-0.22	-0.0635	-0.0886	0.0683	0.591	0.943	0.809	0.847
fig/6666666.474 865.peg.2088	Protein of unknown function DUF1447		0.0435	-0.064	-0.174	-0.282	0.897	0.914	0.45	0.207
fig/6666666.474 865.peg.1902	FIG01108089: hypothetical protein		-0.445	-0.0641	-2.29	-1.91	0.661	0.972	0.0053	0.0158
fig/6666666.474 865.peg.273	Aldehyde dehydrogenase (EC 1.2.1.3)		-0.147	-0.0649	0.701	0.783	0.691	0.937	0.0157	0.0092
fig/6666666.474 865.peg.1911	Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9)		0.0717	-0.0652	0.17	0.0334	0.897	0.947	0.677	0.929
fig/6666666.474 865.peg.2141	Thioredoxin		0.0507	-0.0657	-0.238	-0.355	0.792	0.842	0.0917	0.0177
fig/6666666.474 865.peg.2456	Dihydrofolate reductase (EC 1.5.1.3)		0.164	-0.0657	-0.0439	-0.273	0.527	0.903	0.853	0.167

fig/6666666.474 865.peg.483	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-independent		0.00584	-0.0669	-0.457	-0.53	0.975	0.846	0.00554	0.00234
fig/6666666.474 865.peg.1552	S1 RNA binding domain protein		0.418	-0.0673	-0.603	-1.09	0.173	0.925	0.021	0.000621
fig/6666666.474 865.peg.991	Clumping factor ClfB, fibrinogen binding protein	clfB	-1.52	-0.0677	-0.471	0.981	0.288	0.985	0.727	0.406
fig/6666666.474 865.peg.2226	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)		-0.032	-0.068	-0.187	-0.223	0.855	0.806	0.122	0.0687
fig/6666666.474 865.peg.2648	DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)		0.583	-0.0682	0.529	-0.122	0.0193	0.891	0.00975	0.534
fig/6666666.474 865.peg.1447	Alkyl hydroperoxide reductase protein F (EC 1.6.4.-)		-0.0429	-0.0688	-0.366	-0.392	0.824	0.824	0.012	0.00864
fig/6666666.474 865.peg.251	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)		0.0758	-0.0694	0.358	0.213	0.576	0.749	0.00246	0.0422
fig/6666666.474 865.peg.2286	2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3)		0.0568	-0.0696	-0.107	-0.233	0.873	0.915	0.707	0.352
fig/6666666.474 865.peg.1540	Bona fide RidA/YjgF/TdcF/RutC subgroup		-0.465	-0.0699	-0.418	-0.0226	0.0472	0.882	0.0293	0.913
fig/6666666.474 865.peg.185	ABC transporter, ATP-binding protein EcsA		-0.475	-0.0703	0.656	1.06	0.437	0.956	0.168	0.0327
fig/6666666.474 865.peg.2206	DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)		0.21	-0.0714	-1.96	-2.25	0.763	0.956	0.00119	0.000557
fig/6666666.474 865.peg.965	Malate:quinone oxidoreductase (EC 1.1.5.4)		-0.279	-0.0718	-0.402	-0.196	0.0244	0.708	0.00062	0.0459
fig/6666666.474 865.peg.2208	Helicase PriA essential for oriC/DnaA-independent DNA replication		-0.348	-0.0719	-1.23	-0.955	0.723	0.969	0.0904	0.183
fig/6666666.474 865.peg.602	LSU ribosomal protein L16p (L10e)		0.344	-0.0727	0.000925	-0.416	0.15	0.882	0.996	0.0374
fig/6666666.474 865.peg.1401	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)		-0.11	-0.0729	0.629	0.666	0.704	0.903	0.00748	0.0057
fig/6666666.474 865.peg.2275	FIG009210: peptidase, M16 family		0.566	-0.0747	0.328	-0.313	0.0258	0.882	0.0962	0.113
fig/6666666.474 865.peg.1792	FIG01108426: hypothetical protein	saeQ	-1.08	-0.0763	1.92	2.92	0.146	0.96	0.00434	0.000262
fig/6666666.474 865.peg.83	Glutamyl aminopeptidase (EC 3.4.11.7); Deblocking aminopeptidase		-0.122	-0.0769	0.121	0.166	0.63	0.861	0.533	0.373
fig/6666666.474 865.peg.454	Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7)		-0.322	-0.078	0.375	0.619	0.431	0.934	0.235	0.0536
fig/6666666.474 865.peg.604	LSU ribosomal protein L22p (L17e)		0.175	-0.0783	-0.12	-0.373	0.395	0.832	0.477	0.0286
fig/6666666.474 865.peg.1853	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)		-0.165	-0.0793	0.505	0.59	0.431	0.831	0.00516	0.00212
fig/6666666.474 865.peg.1300	CDP-ribitol:poly(ribitol phosphate) ribitol phosphotransferase		0.442	-0.0796	0.673	0.151	0.161	0.906	0.0143	0.571
fig/6666666.474 865.peg.2729	Preprotein translocase subunit YajC (TC 3.A.5.1.1)		1.86	-0.0797	1.56	-0.377	0.211	0.982	0.198	0.776

fig/6666666.474 865.peg.1904	Iron-sulfur cluster assembly ATPase protein SufC		-0.0418	-0.0809	0.257	0.218	0.823	0.774	0.0531	0.0974
fig/6666666.474 865.peg.1440	FIG01108790: hypothetical protein		-0.51	-0.081	-1.3	-0.869	0.288	0.943	0.0035	0.0329
fig/6666666.474 865.peg.2452	PTS system, glucose-specific IIA component (EC 2.7.1.69)		0.906	-0.0824	2.15	1.16	1.60E-05	0.704	1.29E-10	2.50E-07
fig/6666666.474 865.peg.651	Urease accessory protein UreG		-0.451	-0.083	0.579	0.946	0.15	0.904	0.0285	0.00193
fig/6666666.474 865.peg.1654	Vitamin B12 ABC transporter, B12-binding component BtuF		0.243	-0.0835	-0.867	-1.19	0.492	0.908	0.00477	0.000621
fig/6666666.474 865.peg.2075	Duplicated ATPase component YkoD of energizing module of thiamin-regulated ECF transporter for HydroxyMethylPyrimidine		-0.318	-0.0853	-0.433	-0.201	0.13	0.826	0.0158	0.233
fig/6666666.474 865.peg.1866	3'-to-5' exoribonuclease RNase R		0.413	-0.0858	0.605	0.106	0.258	0.914	0.0472	0.745
fig/6666666.474 865.peg.1906	Cysteine desulfurase (EC 2.8.1.7), SufS subfamily		-0.189	-0.0868	0.664	0.766	0.351	0.818	0.000766	0.000335
fig/6666666.474 865.peg.607	LSU ribosomal protein L23p (L23Ae)		0.969	-0.0878	0.0185	-1.04	0.0116	0.906	0.957	0.00199
fig/6666666.474 865.peg.1787	Magnesium and cobalt efflux protein CorC		-0.186	-0.0882	-0.196	-0.0988	0.732	0.943	0.667	0.833
fig/6666666.474 865.peg.2194	Uracil phosphoribosyltransferase (EC 2.4.2.9) / Pyrimidine operon regulatory protein PyrR		-0.264	-0.0894	-0.554	-0.379	0.223	0.824	0.00486	0.0379
fig/6666666.474 865.peg.1838	Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1)		0.143	-0.091	0.539	0.305	0.241	0.637	7.82E-05	0.00596
fig/6666666.474 865.peg.1574	Cysteinyl-tRNA synthetase (EC 6.1.1.16)		-0.0493	-0.0921	0.225	0.182	0.826	0.796	0.154	0.244
fig/6666666.474 865.peg.48	Acetate kinase (EC 2.7.2.1)		-0.231	-0.0925	-0.821	-0.683	0.109	0.699	7.09E-06	5.83E-05
fig/6666666.474 865.peg.1368	FIG01108623: hypothetical protein		-0.239	-0.0927	-0.11	0.0363	0.408	0.862	0.661	0.885
fig/6666666.474 865.peg.663	Salicylate hydroxylase (EC 1.14.13.1)		-0.301	-0.0953	-0.438	-0.232	0.27	0.859	0.0528	0.301
fig/6666666.474 865.peg.1932	Cytosol aminopeptidase PepA (EC 3.4.11.1)		-0.458	-0.096	0.129	0.491	0.0834	0.846	0.577	0.0271
fig/6666666.474 865.peg.455	Thiaminase II (EC 3.5.99.2)		-0.256	-0.0981	1.1	1.26	0.329	0.842	9.66E-05	5.25E-05
fig/6666666.474 865.peg.2714	Cysteine desulfurase (EC 2.8.1.7)		-0.396	-0.0994	0.0811	0.378	0.313	0.906	0.831	0.227
fig/6666666.474 865.peg.488	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)		-0.0749	-0.0999	-0.151	-0.176	0.681	0.708	0.257	0.183
fig/6666666.474 865.peg.35	Pyruvate kinase (EC 2.7.1.40)		-0.228	-0.1	-0.266	-0.139	0.0668	0.588	0.0123	0.162
fig/6666666.474 865.peg.2507	L-asparaginase (EC 3.5.1.1)		-0.16	-0.101	-0.12	-0.0607	0.78	0.934	0.809	0.891
fig/6666666.474 865.peg.1862	Enolase (EC 4.2.1.11)		0.00838	-0.102	0.0413	-0.0694	0.963	0.595	0.73	0.513

fig/6666666.474 865.peg.405	Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)		-0.0274	-0.102	0.934	0.859	0.924	0.806	0.000113	0.000336
fig/6666666.474 865.peg.763	Respiratory nitrate reductase beta chain (EC 1.7.99.4)		-0.151	-0.102	-1.08	-1.03	0.926	0.969	0.308	0.338
fig/6666666.474 865.peg.124	Transaldolase (EC 2.2.1.2)		-0.378	-0.104	-0.323	-0.0483	0.0323	0.708	0.0247	0.749
fig/6666666.474 865.peg.1361	N-acetylneuraminate lyase (EC 4.1.3.3)		0.531	-0.105	0.452	-0.184	0.429	0.943	0.392	0.746
fig/6666666.474 865.peg.484	Transcription termination factor Rho		-0.124	-0.107	-0.387	-0.37	0.466	0.695	0.00735	0.0101
fig/6666666.474 865.peg.1268	Pyruvate formate-lyase (EC 2.3.1.54)		-0.966	-0.109	-1.6	-0.743	0.00161	0.818	2.92E-06	0.00212
fig/6666666.474 865.peg.1074	Chromosome (plasmid) partitioning protein ParB		0.0736	-0.109	0.0758	-0.107	0.907	0.925	0.876	0.82
fig/6666666.474 865.peg.2731	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)		0.336	-0.109	-0.241	-0.685	0.32	0.864	0.38	0.0174
fig/6666666.474 865.peg.2216	Serine/threonine protein kinase PrkC, regulator of stationary phase		0.0494	-0.11	0.0329	-0.127	0.893	0.842	0.914	0.61
fig/6666666.474 865.peg.2500	2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163)		-0.205	-0.11	0.229	0.324	0.351	0.774	0.194	0.0683
fig/6666666.474 865.peg.644	Butyryl-CoA dehydrogenase (EC 1.3.99.2)		-0.746	-0.111	-1.27	-0.631	0.00568	0.802	1.50E-05	0.00414
fig/6666666.474 865.peg.1598	Branched-chain amino acid aminotransferase (EC 2.6.1.42)		-0.101	-0.114	0.204	0.191	0.519	0.621	0.0929	0.113
fig/6666666.474 865.peg.1919	Hypothetical NagD-like phosphatase		-0.0608	-0.114	-0.108	-0.161	0.808	0.773	0.578	0.377
fig/6666666.474 865.peg.957	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)		-0.282	-0.115	0.151	0.318	0.118	0.699	0.299	0.0351
fig/6666666.474 865.peg.1541	Protein of unknown function identified by role in sporulation (SpoVG)	spoV G	-0.381	-0.116	-1.08	-0.811	0.0451	0.703	6.42E-06	0.000108
fig/6666666.474 865.peg.130	S-adenosylmethionine synthetase (EC 2.5.1.6)		0.535	-0.118	0.451	-0.202	0.0244	0.771	0.0188	0.269
fig/6666666.474 865.peg.2586	Ferric uptake regulation protein FUR		0.0132	-0.119	-0.244	-0.377	0.974	0.881	0.448	0.225
fig/6666666.474 865.peg.542	Uncharacterized siderophore biosynthesis protein near heme transporter HtsABC @ Siderophore synthetase superfamily, group B		-0.355	-0.119	-0.0364	0.2	0.475	0.906	0.94	0.621
fig/6666666.474 865.peg.231	FIG133424: Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)		1.41	-0.12	-0.605	-2.13	0.0535	0.943	0.296	0.00193
fig/6666666.474 865.peg.1219	Aldehyde dehydrogenase B (EC 1.2.1.22)		-0.361	-0.12	0.0527	0.294	0.263	0.845	0.867	0.265
fig/6666666.474 865.peg.1790	Sensor histidine protein kinase SaeS (EC 2.7.13.3) (exoprotein expression protein S)	saeS	-0.486	-0.122	0.365	0.73	0.0259	0.727	0.0361	0.000696
fig/6666666.474 865.peg.2094	Dihydropyridine dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)		-0.16	-0.122	-0.121	-0.0828	0.259	0.57	0.299	0.487
fig/6666666.474 865.peg.2730	tRNA-guanine transglycosylase (EC 2.4.2.29)		-0.288	-0.122	-0.143	0.0221	0.331	0.82	0.578	0.929

fig/6666666.474 865.peg.1710	Probable low-affinity inorganic phosphate transporter		-0.724	-0.123	0.513	1.11	0.502	0.956	0.572	0.179
fig/6666666.474 865.peg.263	FIG01225759: possible membrane protein		0.89	-0.123	-0.206	-1.22	0.489	0.962	0.865	0.221
fig/6666666.474 865.peg.271	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)		0.0705	-0.124	0.414	0.22	0.691	0.613	0.00435	0.0899
fig/6666666.474 865.peg.2481	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-) / Penicillin-binding protein 1A/1B (PBP1)	pbp2	0.808	-0.125	1.26	0.322	0.000725	0.693	1.88E-06	0.0398
fig/6666666.474 865.peg.1652	Arginyl-tRNA synthetase (EC 6.1.1.19)		-0.208	-0.126	-0.159	-0.0768	0.189	0.601	0.22	0.568
fig/6666666.474 865.peg.56	SSU ribosomal protein S4p (S9e)		0.395	-0.126	0.228	-0.293	0.0503	0.7	0.155	0.0695
fig/6666666.474 865.peg.1858	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)		-0.0682	-0.127	-0.0516	-0.11	0.684	0.573	0.714	0.375
fig/6666666.474 865.peg.65	Tyrosyl-tRNA synthetase (EC 6.1.1.1)		-0.0589	-0.128	-0.505	-0.574	0.729	0.59	0.00101	0.000491
fig/6666666.474 865.peg.214	Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)		-0.0996	-0.129	0.451	0.421	0.663	0.703	0.0117	0.0174
fig/6666666.474 865.peg.1451	FIG01108085: hypothetical protein		0.0209	-0.131	-0.144	-0.296	0.962	0.816	0.586	0.221
fig/6666666.474 865.peg.1952	Glucose-6-phosphate isomerase (EC 5.3.1.9)		-0.127	-0.131	0.568	0.563	0.389	0.537	0.000165	0.000262
fig/6666666.474 865.peg.269	cell wall surface anchor family protein		-0.195	-0.131	0.576	0.64	0.789	0.933	0.274	0.221
fig/6666666.474 865.peg.1891	Putative nitroreductase family protein SACOL0874		0.466	-0.132	1.17	0.57	0.626	0.946	0.093	0.419
fig/6666666.474 865.peg.2066	Phosphoribosylformylglycinamide synthase, PurS subunit (EC 6.3.5.3)		-0.299	-0.133	-0.581	-0.414	0.216	0.752	0.00711	0.0406
fig/6666666.474 865.peg.274	6-phosphogluconolactonase (EC 3.1.1.31)		-0.237	-0.137	0.281	0.381	0.291	0.708	0.122	0.042
fig/6666666.474 865.peg.585	SSU ribosomal protein S13p (S18e)		0.249	-0.137	-0.321	-0.708	0.166	0.626	0.0331	0.000288
fig/6666666.474 865.peg.1563	Pyridoxine biosynthesis glutamine amidotransferase, synthase subunit (EC 2.4.2.-)		-0.103	-0.138	-0.213	-0.248	0.478	0.508	0.0615	0.0342
fig/6666666.474 865.peg.1974	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)		-0.165	-0.138	-0.129	-0.103	0.35	0.596	0.364	0.473
fig/6666666.474 865.peg.95	D-alanine aminotransferase (EC 2.6.1.21)		-0.107	-0.138	0.566	0.536	0.639	0.681	0.00276	0.00414
fig/6666666.474 865.peg.2623	Lipoate-protein ligase A		-0.185	-0.139	0.181	0.226	0.437	0.708	0.33	0.218
fig/6666666.474 865.peg.481	Thymidine kinase (EC 2.7.1.21)		-0.155	-0.139	-0.0525	-0.0358	0.453	0.664	0.782	0.847
fig/6666666.474 865.peg.588	Adenylate kinase (EC 2.7.4.3)		0.224	-0.139	-0.377	-0.74	0.15	0.542	0.00697	6.13E-05
fig/6666666.474 865.peg.2449	Carboxyl-terminal protease (EC 3.4.21.102)		0.198	-0.14	1.2	0.863	0.615	0.831	0.000668	0.00701

fig/6666666.474 865.peg.2502	DNA-binding protein HBSu		-0.058	-0.14	-0.778	-0.86	0.826	0.708	0.000635	0.000383
fig/6666666.474 865.peg.1957	ATP-dependent nuclease, subunit A		-1.14	-0.143	-0.365	0.629	0.0456	0.906	0.429	0.162
fig/6666666.474 865.peg.784	Phosphoglycerate mutase (EC 5.4.2.1)		-1.36	-0.144	-1.48	-0.257	3.41E-05	0.699	1.90E-06	0.154
fig/6666666.474 865.peg.1525	Thymidylate kinase (EC 2.7.4.9)		0.206	-0.144	0.117	-0.233	0.543	0.806	0.689	0.375
fig/6666666.474 865.peg.2718	Iron-sulfur cluster regulator IscR		0.206	-0.144	0.204	-0.146	0.363	0.699	0.259	0.425
fig/6666666.474 865.peg.1572	Glutamyl-tRNA synthetase (EC 6.1.1.17) @ Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)		-0.221	-0.145	-0.313	-0.237	0.102	0.458	0.00774	0.034
fig/6666666.474 865.peg.584	SSU ribosomal protein S11p (S14e)		0.311	-0.148	-0.339	-0.798	0.461	0.846	0.301	0.021
fig/6666666.474 865.peg.388	Heat shock protein 60 family chaperone GroEL		-0.0317	-0.149	0.354	0.237	0.832	0.432	0.00316	0.0308
fig/6666666.474 865.peg.1650	Alcohol dehydrogenase (EC 1.1.1.1)		-1.17	-0.15	-2.37	-1.35	0.00223	0.803	8.70E-07	0.000182
fig/6666666.474 865.peg.1961	CoA-disulfide reductase (EC 1.8.1.14)		-0.0261	-0.151	0.421	0.297	0.897	0.536	0.00425	0.0307
fig/6666666.474 865.peg.1965	ClpB protein		-0.0292	-0.151	0.257	0.136	0.897	0.588	0.0861	0.372
fig/6666666.474 865.peg.6	Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)		-0.315	-0.154	-0.399	-0.238	0.0665	0.537	0.00752	0.0818
fig/6666666.474 865.peg.2057	quinol oxidase polypeptide I QoxB (EC:1.9.3.-)		-0.317	-0.155	-0.34	-0.178	0.211	0.708	0.0997	0.395
fig/6666666.474 865.peg.2372	FIG01108406: hypothetical protein		0.00139	-0.156	-2.91	-3.07	0.998	0.904	2.84E-05	3.41E-05
fig/6666666.474 865.peg.14	Cell division trigger factor (EC 5.2.1.8)		0.131	-0.157	0.0544	-0.234	0.504	0.578	0.764	0.125
fig/6666666.474 865.peg.1410	GTP-binding and nucleic acid-binding protein YchF		0.505	-0.157	0.566	-0.0953	0.00499	0.508	0.000393	0.465
fig/6666666.474 865.peg.1681	Mn-dependent transcriptional regulator MntR		-0.171	-0.158	-0.628	-0.615	0.691	0.826	0.0509	0.0555
fig/6666666.474 865.peg.1764	Lysine decarboxylase family		0.432	-0.158	0.573	-0.0165	0.109	0.713	0.013	0.941
fig/6666666.474 865.peg.1569	ATP-dependent Clp protease, ATP-binding subunit ClpC / Negative regulator of genetic competence clcC/mecB		-0.0294	-0.159	0.192	0.0626	0.842	0.419	0.0652	0.562
fig/6666666.474 865.peg.276	FIG01108203: hypothetical protein		-0.324	-0.159	-0.97	-0.805	0.22	0.708	0.000325	0.00172
fig/6666666.474 865.peg.895	Esterase/lipase (EC 3.1.1.-)		0.0941	-0.159	0.201	-0.0514	0.723	0.695	0.304	0.819
fig/6666666.474 865.peg.1239	Pyruvate decarboxylase (EC 4.1.1.1); Alpha-keto-acid decarboxylase (EC 4.1.1.-)		-0.311	-0.162	-0.165	-0.016	0.15	0.638	0.356	0.929
fig/6666666.474 865.peg.1709	FIG01107977: hypothetical protein		0.202	-0.163	0.302	-0.062	0.33	0.598	0.0708	0.729

fig/6666666.474 865.peg.2271	Ribonuclease J2 (endoribonuclease in RNA processing)		-0.178	-0.163	0.164	0.179	0.324	0.537	0.259	0.215
fig/6666666.474 865.peg.494	Hypothetical protein SAV2131		0.929	-0.164	-0.473	-1.56	0.0244	0.82	0.137	0.000247
fig/6666666.474 865.peg.601	LSU ribosomal protein L29p (L35e)		-0.467	-0.164	-1.25	-0.949	0.0535	0.673	1.52E-05	0.000237
fig/6666666.474 865.peg.2672	Heat shock protein GrpE		0.0143	-0.165	0.285	0.105	0.966	0.699	0.171	0.629
fig/6666666.474 865.peg.1865	Carboxylesterase (EC 3.1.1.1)		0.182	-0.166	0.0505	-0.297	0.749	0.87	0.923	0.493
fig/6666666.474 865.peg.2505	SSU ribosomal protein S1p		-0.132	-0.166	0.478	0.444	0.461	0.519	0.0028	0.00479
fig/6666666.474 865.peg.1456	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)		0.0858	-0.167	-0.105	-0.358	0.507	0.389	0.294	0.00232
fig/6666666.474 865.peg.1791	Response regulator SaeR (Staphylococcus exoprotein expression protein R)	saeR	-0.881	-0.167	-0.0133	0.701	0.0137	0.774	0.964	0.0142
fig/6666666.474 865.peg.748	FIG01108504: hypothetical protein		-0.0662	-0.167	-1.26	-1.36	0.897	0.829	0.00156	0.00106
fig/6666666.474 865.peg.1860	Triosephosphate isomerase (EC 5.3.1.1)		0.138	-0.169	-0.144	-0.451	0.449	0.519	0.307	0.00484
fig/6666666.474 865.peg.2501	Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)		-0.182	-0.169	-0.116	-0.103	0.576	0.742	0.674	0.699
fig/6666666.474 865.peg.2250	ATP-dependent hsl protease ATP-binding subunit HslU		0.0834	-0.172	-0.141	-0.396	0.716	0.581	0.408	0.0246
fig/6666666.474 865.peg.2384	Topoisomerase IV subunit B (EC 5.99.1.-)		-0.0953	-0.172	-0.314	-0.391	0.68	0.581	0.0634	0.0266
fig/6666666.474 865.peg.2509	Elastin binding protein EbpS		-0.197	-0.173	-0.0924	-0.0685	0.614	0.779	0.785	0.834
fig/6666666.474 865.peg.2593	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)		-0.101	-0.173	0.823	0.751	0.615	0.525	5.91E-05	0.000193
fig/6666666.474 865.peg.265	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)		-0.248	-0.173	-0.132	-0.0572	0.146	0.497	0.338	0.699
fig/6666666.474 865.peg.1991	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)		0.345	-0.174	-0.11	-0.628	0.13	0.621	0.582	0.00318
fig/6666666.474 865.peg.45	Proline dipeptidase (EC 3.4.13.9)		-0.226	-0.176	0.395	0.445	0.22	0.525	0.0136	0.0074
fig/6666666.474 865.peg.880	acetyltransferase (GNAT) family protein		-1.61	-0.177	-2.84	-1.4	0.116	0.943	0.00285	0.0908
fig/6666666.474 865.peg.2504	GTP-binding protein EngA		0.12	-0.178	0.225	-0.0736	0.581	0.543	0.17	0.676
fig/6666666.474 865.peg.779	Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)		-0.0804	-0.178	-0.174	-0.272	0.64	0.432	0.158	0.034
fig/6666666.474 865.peg.747	General stress protein 26		0.415	-0.179	-2.03	-2.63	0.732	0.943	0.0297	0.00875
fig/6666666.474 865.peg.103	Leucyl-tRNA synthetase (EC 6.1.1.4)		-0.32	-0.18	-0.112	0.0278	0.0456	0.432	0.38	0.847

fig 6666666.474 865.peg.107	Repressor of toxins Rot	rot	-0.193	-0.181	-0.753	-0.741	0.5	0.694	0.00303	0.00359
fig 6666666.474 865.peg.181	Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1)		-0.098	-0.183	0.24	0.155	0.745	0.695	0.288	0.502
fig 6666666.474 865.peg.2011	2H phosphoesterase superfamily protein Bsu1186 (yjcG)		0.119	-0.183	-0.722	-1.02	0.64	0.59	0.000971	7.93E-05
fig 6666666.474 865.peg.2363	FIG01108419: hypothetical protein		-0.645	-0.183	-0.554	-0.092	0.0173	0.653	0.0122	0.676
fig 6666666.474 865.peg.501	Purine nucleoside phosphorylase (EC 2.4.2.1)		0.119	-0.185	0.629	0.325	0.493	0.455	0.000269	0.0228
fig 6666666.474 865.peg.1585	Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.52)		-0.45	-0.186	-0.298	-0.0341	0.109	0.691	0.186	0.89
fig 6666666.474 865.peg.1958	Fumarylacetoacetate hydrolase family protein		0.0431	-0.186	0.248	0.0186	0.8	0.419	0.0492	0.89
fig 6666666.474 865.peg.2591	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)		-0.423	-0.186	0.0364	0.274	0.239	0.773	0.921	0.357
fig 6666666.474 865.peg.1556	Chaperonin (heat shock protein 33)		0.145	-0.189	-0.0714	-0.405	0.539	0.57	0.732	0.0308
fig 6666666.474 865.peg.2664	DUF1432 domain-containing protein		-0.243	-0.193	0.00179	0.0518	0.142	0.432	0.994	0.721
fig 6666666.474 865.peg.1094	LSU ribosomal protein L9p		0.425	-0.194	-0.914	-1.53	0.304	0.798	0.0108	0.000403
fig 6666666.474 865.peg.590	LSU ribosomal protein L15p (L27Ae)		0.394	-0.194	-0.476	-1.06	0.131	0.636	0.0289	0.000215
fig 6666666.474 865.peg.16	FIG01108166: hypothetical protein		0.46	-0.196	0.323	-0.333	0.0379	0.537	0.0645	0.0576
fig 6666666.474 865.peg.75	Chorismate mutase I (EC 5.4.99.5) / 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)		-0.247	-0.196	-0.296	-0.245	0.122	0.419	0.0267	0.0601
fig 6666666.474 865.peg.964	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)		-0.267	-0.196	-1.02	-0.95	0.108	0.422	3.49E-06	1.31E-05
fig 6666666.474 865.peg.899	Pyruvate oxidase [ubiquinone, cytochrome] (EC 1.2.2.2) @ Pyruvate oxidase, CidC		-0.161	-0.197	0.391	0.355	0.251	0.369	0.00299	0.00573
fig 6666666.474 865.peg.2032	Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52)		-0.56	-0.198	0.0288	0.39	0.0912	0.708	0.928	0.14
fig 6666666.474 865.peg.1559	Dihydroneopterin aldolase (EC 4.1.2.25)		0.197	-0.204	0.46	0.0582	0.64	0.753	0.129	0.868
fig 6666666.474 865.peg.2597	Glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein		0.308	-0.206	1.18	0.661	0.527	0.808	0.00478	0.0776
fig 6666666.474 865.peg.1557	Cysteine synthase (EC 2.5.1.47)		-0.187	-0.207	-0.129	-0.149	0.22	0.389	0.299	0.225
fig 6666666.474 865.peg.41	FIG146085: 3'-to-5' oligoribonuclease A, Bacillus type		-0.256	-0.207	0.103	0.152	0.547	0.773	0.787	0.659
fig 6666666.474 865.peg.1179	2,3-butanediol dehydrogenase, S-alcohol forming, (R)-acetoin-specific (EC 1.1.1.4) / Acetoin (diacetyl) reductase (EC 1.1.1.5)		-0.373	-0.21	-0.375	-0.211	0.0588	0.458	0.0216	0.176
fig 6666666.474 865.peg.2373	Transketolase (EC 2.2.1.1)		-0.0826	-0.211	0.00275	-0.126	0.481	0.223	0.98	0.167

fig/6666666.474 865.peg.831	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)		-1.33	-0.214	-2.58	-1.46	0.108	0.904	0.00114	0.0342
fig/6666666.474 865.peg.603	SSU ribosomal protein S3p (S3e)		0.281	-0.215	0.204	-0.292	0.162	0.473	0.217	0.0775
fig/6666666.474 865.peg.657	Secretory antigen precursor SsaA	ssaA	-0.766	-0.215	-0.721	-0.17	0.0668	0.771	0.0341	0.625
fig/6666666.474 865.peg.666	Hypothetical protein YrhD		-1.41	-0.217	-2.53	-1.33	0.00905	0.811	1.84E-05	0.00345
fig/6666666.474 865.peg.43	Universal stress protein family		-0.167	-0.217	-0.963	-1.01	0.229	0.323	1.41E-06	1.43E-06
fig/6666666.474 865.peg.2184	Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC		-0.109	-0.219	-0.093	-0.203	0.859	0.82	0.853	0.648
fig/6666666.474 865.peg.956	Pantoate--beta-alanine ligase (EC 6.3.2.1)		-0.336	-0.219	0.719	0.836	0.33	0.699	0.0146	0.0067
fig/6666666.474 865.peg.780	L-Cystine ABC transporter, permease protein TcyB		0.38	-0.22	2.58	1.98	0.764	0.937	0.00984	0.0385
fig/6666666.474 865.peg.1580	Transcription antitermination protein NusG		0.331	-0.22	0.26	-0.291	0.0788	0.43	0.0864	0.0572
fig/6666666.474 865.peg.2292	DNA mismatch repair protein MutL		0.769	-0.22	0.749	-0.24	0.109	0.803	0.0545	0.55
fig/6666666.474 865.peg.1630	Hemoprotein HemQ, essential component of heme biosynthetic pathway in Gram-positive bacteria		-0.166	-0.223	0.39	0.332	0.394	0.43	0.0159	0.0359
fig/6666666.474 865.peg.1288	Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)		-0.293	-0.225	0.216	0.284	0.384	0.681	0.428	0.286
fig/6666666.474 865.peg.2620	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)		-0.5	-0.226	0.033	0.307	0.00732	0.389	0.839	0.0301
fig/6666666.474 865.peg.753	Molecular chaperone, small heat shock protein		0.218	-0.227	2.02	1.58	0.576	0.703	8.93E-06	0.000117
fig/6666666.474 865.peg.1241	PTS system, glucose-specific IIC component (EC 2.7.1.69) / PTS system, glucose-specific IIB component (EC 2.7.1.69) / PTS system, glucose-specific IIA component (EC 2.7.1.69)		-0.269	-0.227	-0.396	-0.354	0.136	0.415	0.0116	0.0213
fig/6666666.474 865.peg.1944	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)		0.552	-0.228	-0.069	-0.849	0.00175	0.323	0.592	1.31E-05
fig/6666666.474 865.peg.464	ATP synthase epsilon chain (EC 3.6.3.14)		-0.0733	-0.229	1.71	1.56	0.962	0.926	0.0542	0.0777
fig/6666666.474 865.peg.2001	NAD kinase (EC 2.7.1.23)		0.0202	-0.23	0.439	0.189	0.961	0.542	0.0393	0.375
fig/6666666.474 865.peg.2237	LSU ribosomal protein L19p		-0.15	-0.23	0.21	0.13	0.598	0.543	0.32	0.555
fig/6666666.474 865.peg.250	Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7)		0.0446	-0.231	0.273	-0.00223	0.773	0.276	0.0199	0.987
fig/6666666.474 865.peg.2671	Chaperone protein DnaK		-0.151	-0.232	0.261	0.18	0.238	0.225	0.0172	0.0838
fig/6666666.474 865.peg.1697	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), ADP-binding subunit DhaL		-0.266	-0.237	1.65	1.68	0.777	0.898	0.0199	0.0192

fig 6666666.474 865.peg.1414	SSU ribosomal protein S18p @ SSU ribosomal protein S18p, zinc-independent		-0.272	-0.237	-0.481	-0.446	0.298	0.537	0.0276	0.0405
fig 6666666.474 865.peg.1570	DNA repair protein RadA		1.32	-0.238	1.74	0.185	0.106	0.889	0.0124	0.798
fig 6666666.474 865.peg.1807	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1) / Osmotic adaptation		-0.848	-0.239	0.706	1.31	0.502	0.934	0.489	0.177
fig 6666666.474 865.peg.2255	Ribosome recycling factor		-0.0117	-0.239	-0.987	-1.22	0.967	0.495	9.88E-05	3.41E-05
fig 6666666.474 865.peg.2606	Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)		0.48	-0.242	0.487	-0.235	0.0838	0.543	0.0323	0.293
fig 6666666.474 865.peg.79	Cell division protein FtsK		0.243	-0.243	-0.0288	-0.515	0.414	0.57	0.921	0.033
fig 6666666.474 865.peg.1837	Ribosomal subunit interface protein		-0.176	-0.245	-0.00822	-0.0778	0.341	0.389	0.962	0.615
fig 6666666.474 865.peg.2486	DinG family ATP-dependent helicase YoaA		-0.213	-0.246	0.908	0.875	0.554	0.652	0.00359	0.00484
fig 6666666.474 865.peg.920	D-specific D-2-hydroxyacid dehydrogenase ddh homolog (EC 1.1.1.28)		-0.765	-0.247	-0.469	0.0492	0.0208	0.604	0.0671	0.868
fig 6666666.474 865.peg.1084	DNA gyrase subunit B (EC 5.99.1.3)		0.163	-0.249	0.24	-0.173	0.561	0.529	0.259	0.425
fig 6666666.474 865.peg.199	Similar to ribosomal large subunit pseudouridine synthase D, Bacillus subtilis YhcT type		0.659	-0.249	0.371	-0.536	0.0409	0.596	0.141	0.0394
fig 6666666.474 865.peg.497	S-ribosylhomocysteine lyase (EC 4.4.1.21) / Autoinducer-2 production protein LuxS		0.15	-0.25	0.0669	-0.333	0.667	0.597	0.827	0.187
fig 6666666.474 865.peg.873	ABC transporter ATP-binding protein		-1.38	-0.251	-3.38	-2.25	0.149	0.904	0.00044	0.00837
fig 6666666.474 865.peg.2230	Chromosome partition protein smc		-0.565	-0.251	-0.203	0.112	0.183	0.718	0.589	0.767
fig 6666666.474 865.peg.2300	Glutathione peroxidase family protein		0.495	-0.253	0.323	-0.425	0.256	0.727	0.371	0.229
fig 6666666.474 865.peg.1568	Putative ATP:guanido phosphotransferase YacI (EC 2.7.3.-)		0.136	-0.254	0.562	0.172	0.926	0.921	0.577	0.87
fig 6666666.474 865.peg.63	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)		-0.191	-0.259	-0.697	-0.765	0.508	0.529	0.00499	0.00309
fig 6666666.474 865.peg.1930	probable iron binding protein from the HesB_IscA_SufA family		0.459	-0.26	-0.0276	-0.746	0.311	0.727	0.954	0.0454
fig 6666666.474 865.peg.2307	FIG01108533: hypothetical protein		-0.44	-0.26	-1.33	-1.14	0.68	0.903	0.091	0.142
fig 6666666.474 865.peg.733	hypothetical protein similar to TpgX		-0.213	-0.261	-1.02	-1.07	0.594	0.66	0.00277	0.00222
fig 6666666.474 865.peg.908	ATP-dependent protease ATP-binding subunit clpL		-0.995	-0.265	-0.618	0.112	0.000242	0.399	0.00158	0.511
fig 6666666.474 865.peg.2288	tRNA-i(6)A37 methyltransferase		-0.164	-0.267	-0.0773	-0.18	0.604	0.536	0.78	0.447
fig 6666666.474 865.peg.905	Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)		-0.116	-0.27	-0.337	-0.491	0.666	0.437	0.0852	0.0177

fig 6666666.474 865.peg.2146	Glutamate racemase (EC 5.1.1.3)	murI	-0.226	-0.274	0.515	0.467	0.245	0.369	0.00406	0.00781
fig 6666666.474 865.peg.266	Nitric oxide synthase oxygenase (EC 1.-.-.-)		-0.498	-0.274	-1.2	-0.975	0.35	0.772	0.00936	0.0288
fig 6666666.474 865.peg.449	Cardiolipin synthetase (EC 2.7.8.-)		0.185	-0.276	0.394	-0.0665	0.658	0.637	0.191	0.847
fig 6666666.474 865.peg.2728	Protein-export membrane protein SecD (TC 3.A.5.1.1) / Protein-export membrane protein SecF (TC 3.A.5.1.1)		0.526	-0.281	0.174	-0.634	0.0696	0.513	0.469	0.0118
fig 6666666.474 865.peg.631	Molybdopterin biosynthesis protein MoeA		-1	-0.282	-1.27	-0.552	0.00245	0.506	6.30E-05	0.0222
fig 6666666.474 865.peg.1892	Thioredoxin		0.118	-0.285	-0.0895	-0.492	0.647	0.419	0.668	0.0145
fig 6666666.474 865.peg.2089	Peptide deformylase (EC 3.5.1.88)		0.0509	-0.289	0.681	0.341	0.812	0.323	0.000407	0.0338
fig 6666666.474 865.peg.1754	Cadmium-transporting ATPase (EC 3.6.3.3)		-0.0455	-0.29	0.204	-0.0403	0.967	0.89	0.831	0.962
fig 6666666.474 865.peg.236	Transporter associated with VraSR	vraT	1.18	-0.294	3.88	2.41	0.15	0.853	4.07E-05	0.00224
fig 6666666.474 865.peg.222	Transcription regulator CDS_ID OB0894		0.033	-0.294	-0.00524	-0.332	0.967	0.82	0.995	0.572
fig 6666666.474 865.peg.451	Inner membrane protein translocase component YidC, short form Oxal-like	yidC	0.712	-0.295	1.62	0.609	0.0745	0.635	0.00013	0.0598
fig 6666666.474 865.peg.2496	3-dehydroquinate synthase (EC 4.2.3.4)		-0.391	-0.295	0.316	0.412	0.615	0.82	0.611	0.482
fig 6666666.474 865.peg.883	D-lactate dehydrogenase (EC 1.1.1.28)		-0.59	-0.295	-0.154	0.142	0.0197	0.419	0.438	0.471
fig 6666666.474 865.peg.2362	HMP-PP hydrolase (pyridoxal phosphatase) Cof, detected in genetic screen for thiamin metabolic genes (PMID:15292217)		-0.294	-0.297	-0.507	-0.51	0.137	0.324	0.00468	0.00486
fig 6666666.474 865.peg.1795	Queuosine Biosynthesis QueE Radical SAM		-0.894	-0.3	-0.686	-0.0923	0.0657	0.703	0.0766	0.834
fig 6666666.474 865.peg.190	Foldase protein PrsA precursor (EC 5.2.1.8) @ Foldase clustered with pyrimidine conversion	prsA	1.1	-0.302	2.64	1.24	2.08E-05	0.225	1.69E-10	1.43E-06
fig 6666666.474 865.peg.2212	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	fmt	-1.06	-0.302	-1.13	-0.373	0.313	0.891	0.181	0.68
fig 6666666.474 865.peg.2234	SSU ribosomal protein S16p		0.0578	-0.302	0.00182	-0.358	0.916	0.687	0.996	0.326
fig 6666666.474 865.peg.290	Extracellular adherence protein of broad specificity Eap/Map	eap/map	-2.35	-0.305	-2.02	0.0277	0.0137	0.859	0.00887	0.973
fig 6666666.474 865.peg.2689	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)		-0.637	-0.311	0.0734	0.4	0.0024	0.245	0.645	0.0109
fig 6666666.474 865.peg.232	FIG010063: hypothetical protein		-0.176	-0.316	-1.44	-1.58	0.849	0.831	0.0304	0.0209
fig 6666666.474 865.peg.1589	SSU ribosomal protein S12p (S23e)		0.194	-0.317	-0.133	-0.644	0.777	0.773	0.825	0.193
fig 6666666.474 865.peg.1230	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)		-0.492	-0.318	1.86	2.04	0.544	0.82	0.00649	0.00406

fig/6666666.474 865.peg.2256	Undecaprenyl diphosphate synthase (EC 2.5.1.31)		0.672	-0.318	1.68	0.688	0.13	0.653	0.000252	0.0578
fig/6666666.474 865.peg.1088	Seryl-tRNA synthetase (EC 6.1.1.11)		-0.325	-0.322	-0.85	-0.846	0.0315	0.167	6.62E-06	1.31E-05
fig/6666666.474 865.peg.2213	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		0.0608	-0.322	0.505	0.122	0.832	0.401	0.0183	0.566
fig/6666666.474 865.peg.2291	DNA mismatch repair protein MutS		-0.191	-0.322	0.0736	-0.0569	0.726	0.699	0.879	0.896
fig/6666666.474 865.peg.506	Mannose-6-phosphate isomerase, class I (EC 5.3.1.8)		-0.0988	-0.326	-0.668	-0.895	0.724	0.401	0.00409	0.000621
fig/6666666.474 865.peg.1793	FIG01107853: hypothetical protein	saeP	-1.07	-0.327	0.268	1.01	0.00175	0.433	0.249	0.000621
fig/6666666.474 865.peg.234	Two component transcriptional regulator VraR	vraR	0.479	-0.328	2.85	2.04	0.0619	0.399	6.63E-09	5.89E-07
fig/6666666.474 865.peg.2396	Deblocking aminopeptidase (EC 3.4.11.-)		0.204	-0.329	0.204	-0.328	0.492	0.432	0.38	0.154
fig/6666666.474 865.peg.2476	Cell division protein GpsB, coordinates the switch between cylindrical and septal cell wall synthesis by re-localization of PBP1		-0.379	-0.331	-0.658	-0.61	0.382	0.604	0.0566	0.0757
fig/6666666.474 865.peg.1593	N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)		-1.98	-0.332	-1.38	0.269	0.0173	0.82	0.0322	0.692
fig/6666666.474 865.peg.606	LSU ribosomal protein L2p (L8e)		8.77E-05	-0.332	0.086	-0.246	0.999	0.29	0.636	0.138
fig/6666666.474 865.peg.960	L-lactate dehydrogenase (EC 1.1.1.27)		-0.667	-0.332	-1.12	-0.783	0.0258	0.432	0.000198	0.00344
fig/6666666.474 865.peg.591	LSU ribosomal protein L30p (L7e)		0.146	-0.336	-0.419	-0.901	0.699	0.519	0.135	0.00469
fig/6666666.474 865.peg.1364	N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)		-0.298	-0.34	0.373	0.331	0.691	0.776	0.527	0.568
fig/6666666.474 865.peg.76	MaebI		-0.269	-0.341	-0.487	-0.558	0.324	0.417	0.0304	0.0172
fig/6666666.474 865.peg.1191	Phosphopentomutase (EC 5.4.2.7)		-0.19	-0.342	0.025	-0.127	0.211	0.167	0.865	0.312
fig/6666666.474 865.peg.1305	Nitric oxide-dependent regulator DnrN or NorA	scdA	-0.588	-0.345	-1.38	-1.14	0.0457	0.422	3.58E-05	0.000262
fig/6666666.474 865.peg.2121	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)		-0.753	-0.35	0.186	0.589	0.395	0.826	0.825	0.406
fig/6666666.474 865.peg.1849	Thioredoxin reductase (EC 1.8.1.9)		-0.194	-0.354	-0.154	-0.314	0.211	0.167	0.223	0.0192
fig/6666666.474 865.peg.2374	UPF0154 membrane protein YoxG		-0.0435	-0.355	0.467	0.156	0.915	0.46	0.0805	0.571
fig/6666666.474 865.peg.855	Phosphoglucosamine mutase (EC 5.4.2.10) / Phosphomannomutase (EC 5.4.2.8)		-0.182	-0.365	-0.32	-0.503	0.643	0.48	0.259	0.0775
fig/6666666.474 865.peg.1165	staphylococcal accessory regulator A homologue	sarS	-0.401	-0.371	-0.547	-0.517	0.157	0.399	0.0232	0.0328
fig/6666666.474 865.peg.2711	RecD-like DNA helicase YrrC		-0.864	-0.373	-0.4	0.0918	0.232	0.774	0.524	0.889

fig/6666666.474 865.peg.2379	Glycine betaine transporter OpuD		0.344	-0.378	0.696	-0.0259	0.395	0.525	0.033	0.938
fig/6666666.474 865.peg.47	Universal stress protein family		-0.281	-0.383	-0.292	-0.394	0.138	0.201	0.0594	0.0164
fig/6666666.474 865.peg.719	Teicoplanin-resistance associated HTH-type transcriptional regulator TcaR		0.0982	-0.383	-0.109	-0.59	0.725	0.324	0.631	0.0092
fig/6666666.474 865.peg.389	Heat shock protein 60 family co-chaperone GroES		-0.147	-0.388	0.508	0.266	0.691	0.432	0.0625	0.33
fig/6666666.474 865.peg.1801	Allophanate hydrolase 2 subunit 1 (EC 3.5.1.54)		0.278	-0.39	1.29	0.626	0.677	0.699	0.0127	0.194
fig/6666666.474 865.peg.2736	LSU ribosomal protein L27p		0.506	-0.396	-0.766	-1.67	0.421	0.695	0.115	0.00314
fig/6666666.474 865.peg.1993	Negative regulator of genetic competence MecA	trfa	-0.299	-0.396	0.81	0.713	0.336	0.399	0.00407	0.0092
fig/6666666.474 865.peg.2005	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)		0.167	-0.399	0.852	0.286	0.42	0.201	8.79E-05	0.0765
fig/6666666.474 865.peg.77	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)		-0.369	-0.401	-0.519	-0.551	0.139	0.303	0.0154	0.0118
fig/6666666.474 865.peg.1802	Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)		-0.167	-0.41	0.211	-0.032	0.661	0.422	0.464	0.915
fig/6666666.474 865.peg.575	LSU ribosomal protein L13p (L13Ae)		0.302	-0.41	0.363	-0.349	0.277	0.339	0.108	0.124
fig/6666666.474 865.peg.1	Dihydrofolate synthase (EC 6.3.2.12) / Folylpolyglutamate synthase (EC 6.3.2.17)		-0.175	-0.415	-0.747	-0.987	0.68	0.459	0.021	0.00486
fig/6666666.474 865.peg.2381	4-hydroxybenzoyl-CoA thioesterase family active site		0.0712	-0.416	0.573	0.0859	0.962	0.831	0.525	0.923
fig/6666666.474 865.peg.712	FIG01108339: hypothetical protein		-0.509	-0.417	0.395	0.486	0.502	0.727	0.527	0.416
fig/6666666.474 865.peg.731	L-lactate permease		0.0513	-0.418	0.525	0.0559	0.924	0.503	0.118	0.884
fig/6666666.474 865.peg.514	HMP-PP hydrolase (pyridoxal phosphatase) Cof, detected in genetic screen for thiamin metabolic genes (PMID:15292217)		-0.193	-0.42	0.271	0.0438	0.517	0.335	0.237	0.868
fig/6666666.474 865.peg.589	Preprotein translocase secY subunit (TC 3.A.5.1.1)		0.842	-0.422	3.2	1.93	0.256	0.735	9.37E-05	0.00486
fig/6666666.474 865.peg.2724	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.6.1.n1)		0.0154	-0.422	0.248	-0.19	0.967	0.364	0.307	0.441
fig/6666666.474 865.peg.1280	FIG01108038: hypothetical protein		-0.499	-0.435	-0.618	-0.554	0.15	0.419	0.0323	0.0533
fig/6666666.474 865.peg.2727	Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)		-0.459	-0.435	0.871	0.894	0.466	0.653	0.0766	0.0695
fig/6666666.474 865.peg.1610	GTP cyclohydrolase I (EC 3.5.4.16) type 2		0.17	-0.436	1.28	0.67	0.64	0.389	0.000166	0.0161
fig/6666666.474 865.peg.1623	Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7)		0.232	-0.439	0.124	-0.547	0.173	0.113	0.38	0.00124
fig/6666666.474 865.peg.2389	FmtC (MrpF) protein involved in methicillin resistance / L-lysine modification of phosphatidylglycerol		0.21	-0.446	0.0031	-0.653	0.822	0.749	0.996	0.325

fig/6666666.474 865.peg.918	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)		-0.72	-0.452	-0.146	0.123	0.331	0.708	0.839	0.86
fig/6666666.474 865.peg.1812	Di/tripeptide permease YjdL		-0.361	-0.456	2.09	2	0.552	0.596	0.000325	0.000635
fig/6666666.474 865.peg.773	Candidate zinc-binding lipoprotein ZinT		0.442	-0.459	-1.06	-1.96	0.527	0.673	0.0503	0.002
fig/6666666.474 865.peg.2487	Biotin operon repressor / Biotin-protein ligase (EC 6.3.4.15)		0.222	-0.465	0.952	0.266	0.672	0.508	0.0172	0.494
fig/6666666.474 865.peg.1434	Hypothetical SAV0801 homolog in superantigen-encoding pathogenicity islands SaPI		0.0689	-0.466	-0.494	-1.03	0.871	0.399	0.0929	0.00262
fig/6666666.474 865.peg.1297	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)		-0.394	-0.468	-0.426	-0.5	0.691	0.772	0.59	0.504
fig/6666666.474 865.peg.2666	SSU ribosomal protein S21p		-0.0517	-0.469	-1.79	-2.2	0.966	0.774	0.0228	0.00816
fig/6666666.474 865.peg.2173	BH2577 unknown conserved protein in B. subtilis		0.0749	-0.471	-0.0235	-0.569	0.791	0.225	0.927	0.0111
fig/6666666.474 865.peg.2382	FIG01108262: hypothetical protein		0.107	-0.479	2.24	1.66	0.849	0.511	4.85E-05	0.000771
fig/6666666.474 865.peg.818	Carboxylesterase type B (EC 3.1.1.-)		-1.16	-0.484	0.272	0.945	0.306	0.819	0.802	0.302
fig/6666666.474 865.peg.1827	Glycerate kinase (EC 2.7.1.31)		0.489	-0.489	0.675	-0.303	0.118	0.323	0.0127	0.227
fig/6666666.474 865.peg.746	AraC family regulatory protein		0.0816	-0.489	1.76	1.19	0.962	0.82	0.0634	0.204
fig/6666666.474 865.peg.2324	FIG01107943: hypothetical protein		0.219	-0.49	-1.98	-2.69	0.799	0.703	0.00473	0.000674
fig/6666666.474 865.peg.128	oxidoreductase of aldo/keto reductase family, subgroup 1		0.0184	-0.494	0.506	-0.00722	0.965	0.323	0.0503	0.98
fig/6666666.474 865.peg.637	Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)		-2.35	-0.496	-3.91	-2.06	0.016	0.749	8.34E-05	0.00997
fig/6666666.474 865.peg.411	TsaB protein, required for threonylcarbamoyladenosine (t(6)A) formation in tRNA		-0.192	-0.502	0.571	0.261	0.744	0.536	0.195	0.568
fig/6666666.474 865.peg.681	Hypothetical protein SAV2322		2.38	-0.507	7.48	4.6	0.0197	0.77	5.21E-07	5.83E-05
fig/6666666.474 865.peg.1446	FIG01109315: hypothetical protein		-2.13	-0.511	-0.551	1.07	0.0366	0.772	0.513	0.179
fig/6666666.474 865.peg.393	Aliphatic amidase AmiE (EC 3.5.1.4)		-0.624	-0.52	0.191	0.294	0.11	0.389	0.577	0.357
fig/6666666.474 865.peg.633	Molybdenum cofactor biosynthesis protein MoaB		-1.78	-0.523	-2	-0.745	0.00152	0.433	7.99E-05	0.0498
fig/6666666.474 865.peg.993	Carbamate kinase (EC 2.7.2.2)		-3.32	-0.523	-0.13	2.67	0.00499	0.774	0.901	0.00494
fig/6666666.474 865.peg.576	tRNA pseudouridine synthase A (EC 4.2.1.70)		0.148	-0.523	0.0498	-0.621	0.909	0.774	0.961	0.472
fig/6666666.474 865.peg.1806	Glycine betaine ABC transport system, ATP-binding protein OpuAA (EC 3.6.3.32)		-0.13	-0.528	-0.0813	-0.478	0.691	0.225	0.774	0.0504

fig/6666666.474 865.peg.2285	2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3)		-0.716	-0.537	-1.68	-1.51	0.672	0.855	0.17	0.218
fig/6666666.474 865.peg.836	Oxidoreductase, short chain dehydrogenase/reductase family		0.477	-0.542	0.0921	-0.928	0.674	0.761	0.927	0.257
fig/6666666.474 865.peg.2126	Cell surface protein IsdA, transfers heme from hemoglobin to apo-IsdC		-0.332	-0.547	-0.184	-0.399	0.734	0.708	0.835	0.607
fig/6666666.474 865.peg.2454	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)	msrA1	1.59	-0.556	4.9	2.76	0.00808	0.491	9.16E-08	3.53E-05
fig/6666666.474 865.peg.599	LSU ribosomal protein L14p (L23e)		-0.0609	-0.559	0.338	-0.161	0.893	0.323	0.257	0.608
fig/6666666.474 865.peg.1441	FIG01107864: hypothetical protein		-2.53	-0.56	-1.21	0.754	0.000966	0.537	0.0194	0.129
fig/6666666.474 865.peg.184	ABC transporter, permease protein EscB		0.0445	-0.567	2.07	1.46	0.967	0.718	0.013	0.0632
fig/6666666.474 865.peg.503	Hypothetical protein SAV2140		0.0137	-0.572	0.718	0.132	0.967	0.225	0.00877	0.615
fig/6666666.474 865.peg.1637	Putative Dihydropolipoamide dehydrogenase (EC 1.8.1.4); Mercuric ion reductase (EC 1.16.1.1); PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase		-0.356	-0.58	0.551	0.327	0.193	0.181	0.0192	0.145
fig/6666666.474 865.peg.598	LSU ribosomal protein L24p (L26e)		0.18	-0.595	-1.03	-1.81	0.794	0.525	0.0439	0.00229
fig/6666666.474 865.peg.759	Sensor protein DegS		-0.15	-0.596	1.42	0.974	0.901	0.708	0.0777	0.221
fig/6666666.474 865.peg.1430	ORF007		0.0447	-0.601	-1.65	-2.3	0.971	0.77	0.0766	0.0193
fig/6666666.474 865.peg.2103	Manganese transport protein MntH		0.383	-0.606	3.48	2.49	0.481	0.432	1.88E-06	5.83E-05
fig/6666666.474 865.peg.2641	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-dependent		-0.105	-0.607	-0.218	-0.72	0.726	0.167	0.33	0.00463
fig/6666666.474 865.peg.718	Teicoplanin resistance associated membrane protein TcaA	tcaA	1.41	-0.613	3.42	1.39	0.0451	0.538	2.51E-05	0.0177
fig/6666666.474 865.peg.751	FIG01108216: hypothetical protein		0.0691	-0.618	0.606	-0.0813	0.871	0.26	0.0424	0.805
fig/6666666.474 865.peg.235	Sensor histidine kinase VraS	vraS	1.43	-0.631	5.39	3.33	0.0197	0.458	7.53E-08	1.31E-05
fig/6666666.474 865.peg.978	Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)		-0.0119	-0.638	1.59	0.966	0.984	0.497	0.00479	0.059
fig/6666666.474 865.peg.2390	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)	msrA2	-0.663	-0.649	-0.287	-0.274	0.0258	0.167	0.215	0.233
fig/6666666.474 865.peg.158	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-dependent		-0.519	-0.659	0.473	0.333	0.0323	0.0751	0.0179	0.0805
fig/6666666.474 865.peg.1992	Regulatory protein spx	spx	-0.174	-0.661	-2.2	-2.68	0.749	0.397	7.82E-05	2.60E-05
fig/6666666.474 865.peg.2280	N-terminal domain of CinA protein, COG1058		-0.458	-0.665	-0.0594	-0.266	0.691	0.702	0.956	0.774

fig/6666666.474 865.peg.1496	FIG01108316: hypothetical protein		-0.349	-0.684	0.703	0.368	0.453	0.323	0.0542	0.312
fig/6666666.474 865.peg.2101	FIG01108899: hypothetical protein		0.316	-0.693	1.78	0.767	0.685	0.512	0.0051	0.177
fig/6666666.474 865.peg.1157	hypothetical protein		0.457	-0.7	-0.00749	-1.16	0.721	0.708	0.996	0.214
fig/6666666.474 865.peg.1547	Transcription-repair coupling factor	mfd	0.596	-0.706	1.4	0.0936	0.187	0.323	0.00138	0.824
fig/6666666.474 865.peg.535	Hypothetical protein SAV2173		-0.561	-0.758	-0.84	-1.04	0.39	0.422	0.102	0.0486
fig/6666666.474 865.peg.593	LSU ribosomal protein L18p (L5e)		-0.28	-0.78	-0.734	-1.23	0.723	0.459	0.208	0.0401
fig/6666666.474 865.peg.1263	FIG01107841: hypothetical protein		-0.0348	-0.812	1.31	0.534	0.967	0.503	0.0485	0.421
fig/6666666.474 865.peg.2732	Holliday junction DNA helicase RuvB		-0.452	-0.836	-0.157	-0.542	0.394	0.29	0.745	0.19
fig/6666666.474 865.peg.919	Copper(I) chaperone CopZ		0.161	-0.839	0.0348	-0.965	0.828	0.399	0.957	0.0641
fig/6666666.474 865.peg.1729	Arsenate reductase (EC 1.20.4.1)		0.743	-0.903	1.02	-0.63	0.644	0.704	0.392	0.608
fig/6666666.474 865.peg.907	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)		-0.23	-0.903	-0.7	-1.37	0.773	0.415	0.227	0.0243
fig/6666666.474 865.peg.2378	Large-conductance mechanosensitive channel		0.66	-0.929	0.895	-0.694	0.626	0.619	0.367	0.488
fig/6666666.474 865.peg.786	IgG-binding protein SBI	sbi	-2.68	-0.94	-1.97	-0.232	0.0057	0.458	0.00905	0.762
fig/6666666.474 865.peg.2468	Alanine dehydrogenase (EC 1.4.1.1)		-3.02	-0.956	-5.02	-2.96	0.00718	0.525	2.51E-05	0.00212
fig/6666666.474 865.peg.2467	Threonine dehydratase, catabolic (EC 4.3.1.19)		-3.41	-0.978	-5.75	-3.32	0.00492	0.536	1.20E-05	0.00137
fig/6666666.474 865.peg.360	Leukocidin LukF-PV		-1.32	-1	-1.44	-1.13	0.15	0.458	0.0556	0.132
fig/6666666.474 865.peg.2588	Oxidoreductase, aldo/keto reductase family protein		-0.245	-1.06	0.382	-0.437	0.576	0.106	0.246	0.182
fig/6666666.474 865.peg.2269	SSU ribosomal protein S15p (S13e)		-0.461	-1.11	1.32	0.673	0.719	0.525	0.159	0.485
fig/6666666.474 865.peg.478	TsaC protein (YrdC-Sua5 domains) required for threonylcarbamoyladenine t(6)A37 modification in tRNA		0.084	-1.11	0.104	-1.1	0.953	0.433	0.92	0.167
fig/6666666.474 865.peg.806	Na ⁺ /H ⁺ antiporter		1.22	-1.46	3.13	0.449	0.421	0.503	0.013	0.722

Table S2. List of identified metabolites in the intracellular metabolite analysis.

Metabolite	log2 fold change (MRSA with oxacillin / MSSA with oxacillin)	log2 fold change (MRSA/MSSA)	log2 fold change (MRSA with oxacillin/ MRSA)	log2 fold change (MSSA with oxacillin/MSSA)	adjusted p-value (MRSA with oxacillin/MSSA with oxacillin)	adjusted p-value (MRSA/MSSA)	adjusted p-value (MRSA with oxacillin/ MRSA)	adjusted p-value (MSSA with oxacillin/MSSA)
Valine	-0.11332	-0.00967	-1.7512	0.50119	0.02877	0.46962	0.020075	0.029431
UTP	-0.12371	-0.24225	0.85572	-0.04843	0.37908	0.049887	0.24468	1
Uridine	-0.02306	0.060758	-2.371	1.5785	1	0.049887	0.020075	0.029431
Uracil	0.043418	0.075147	-2.0625	1.839	0.71109	0.14379	0.020075	0.029431
UMP	-0.11024	-1.1841	4.0145	-0.08042	0.070818	0.053354	0.023174	0.91309
UDP	-0.12391	0.052907	-1.0112	-0.19161	0.02877	0.19955	0.020075	0.51014
TTP	0.005331	-0.02923	0.34684	-0.07189	1	0.83235	0.44365	1
Tryptophan	-0.09319	-0.0317	-1.2096	0.6458	0.02877	0.058201	0.020075	0.048714
Threonine	0.59925	-0.46875	0.21548	1.7718	0.60431	0.19955	0.87168	0.059358
Thiamine-phosphate	ND	-0.18079	ND	0.5407	ND	0.56495	ND	0.60823
Taurine	-0.25238	ND	ND	-1.3111	0.60431	ND	ND	0.60823
Succinyl-CoA	0.1856	-0.16785	-0.53064	0.47444	1	1	0.51323	0.78785
Succinic acid	-0.33729	0.007495	-2.6189	0.33158	0.02877	0.94912	0.020075	0.085618
s-Adenosyl-methionine	-1.1363	-0.12077	-3.5835	0.56918	0.033759	0.049887	0.023174	0.048714
Riboflavin	1.1426	1.0657	-0.88859	2.932	0.068974	0.053354	0.020075	0.60823
Reduced glutathione	ND	-0.55856	ND	2.5519	ND	0.32947	ND	0.35543
Quinolate	-0.35852	-0.7164	1.6854	1.1744	0.6738	0.17601	0.51323	1
Pyridoxine	-0.02741	0.25234	0.60246	-1.5796	0.8229	0.19955	0.17427	0.029431
PRPP	0.058086	-0.27601	1.6257	0.86527	0.8229	0.058201	0.034127	0.78785
Propionyl-CoA	-0.09455	0.11623	0.16432	-0.92752	0.51786	1	0.62794	0.13363
Proline	-0.0329	0.002882	-2.1033	1.6199	0.070818	1	0.020075	0.029431
Phenylalanine	-0.06038	-0.00992	-0.77881	0.18122	0.02877	0.29489	0.020075	0.30501
Orotate	0.1832	-0.03064	-1.0981	2.4973	0.070818	0.94912	0.32392	0.029431
O-phosphoserine	-0.08201	-0.1053	-0.54159	-0.86474	1	0.94799	1	0.89808
Nicotinamide	0.06396	0.12652	0.50256	-0.88473	0.18413	0.049887	0.24468	0.048714

N-acetyl glutamine	-0.07331	-0.01551	-0.93842	0.48169	0.070818	0.56495	0.020075	0.13363
Methionine	-0.11421	-0.02816	-1.555	0.69625	0.02877	0.14379	0.020075	0.029431
Lysine	-0.21619	-0.0752	-3.5143	2.1614	0.02877	0.049887	0.020075	0.029431
Leucine	-0.07899	0.001647	-1.79	0.70191	0.02877	1	0.020075	0.029431
Lactic acid	-0.34444	-0.0712	-2.7698	0.83575	0.02877	0.14379	0.020075	0.085618
ITP	-0.04697	-0.07534	-0.43172	0.26758	1	0.46962	0.74226	0.70635
Inosine	-0.18073	-0.10768	-2.8056	2.512	0.02877	0.46962	0.020075	0.029431
IDP	0.003709	-0.14521	0.27032	1.1174	1	0.36897	0.74226	0.78785
Hypoxathine	0.029684	0.05517	-0.60626	0.36731	0.18413	0.049887	0.020075	0.13363
Homoserine	-0.01627	-0.27621	0.41059	0.39186	0.8229	0.093122	0.51323	0.20674
Histidine	-0.11467	-0.08637	-1.3505	1.1615	0.02877	0.058201	0.020075	0.029431
Guanosine	0.087641	0.047485	-0.68733	1.0028	0.044547	0.093122	0.065004	0.029431
Guanine	-0.00582	0.087038	0.57287	-1.3056	0.96303	0.19955	0.034127	0.029431
GTP	-0.08545	0.050399	-0.69339	-0.17393	0.71109	0.56495	0.32392	0.70635
GMP	-0.07392	-0.58697	3.7629	-1.8576	0.11789	0.16834	0.025256	0.029431
Glutamine	-0.44365	-0.08842	-4.3965	1.9154	0.02877	0.049887	0.020075	0.029431
Glutamate	-0.07992	-0.00327	-1.5945	0.59273	0.02877	0.94912	0.020075	0.029431
GDP	0.022825	0.02895	0.69113	-1.5253	0.96303	1	0.17427	1
Fumaric acid	-0.16616	0.002625	-0.59365	-0.24616	0.070818	1	0.51323	0.70635
Fuctose-1,6-bisphosphate	-0.2833	-0.00711	-0.66883	-0.57013	0.37908	1	0.6794	0.70635
Folate	0.02577	-0.37303	1.6611	0.88933	0.71109	0.14379	0.24468	0.91309
FAD	-0.53103	-0.50101	-0.62064	0.24025	0.037053	0.055233	0.51323	0.30501
Dihydrofolic acid	0.14765	-0.44075	0.18765	1.2104	1	0.38437	0.46822	0.20674
dGTP	-0.10377	-0.0738	-0.12283	-0.28127	0.27913	0.69841	0.74226	0.78785
dGMP	-0.07144	0.11811	0.53985	0.55627	0.96303	0.83235	0.87168	0.91309
D-glucose-6-phosphate	-0.24273	-0.08448	0.39989	-0.20246	1	0.94912	0.74226	1
dGDP	0.03618	-0.22579	0.12913	0.32519	0.60431	0.56495	0.24468	0.78785
Deoxyguanosine	ND	0.027863	-6.7824	5.6871	ND	0.19955	0.020075	0.029431
Deoxyadenosine	0.074216	0.030835	-1.1305	1.5112	0.070818	0.093122	0.020075	0.029431

dCTP	-0.0772	-0.04414	0.24272	-0.77861	0.71109	0.69841	0.51323	0.60823
dCDP	-0.51584	-0.55258	0.86267	0.25979	0.36309	0.055233	1	0.70635
dAMP	-0.88392	-0.75817	2.5309	-1.7325	0.035958	0.30214	0.52637	0.042454
D2-phosphoglyceric acid	-0.31893	-0.30898	-1.5941	0.90994	0.60054	0.56495	0.59353	0.60823
Cytosine	0.047119	0.10307	-2.8565	2.2624	0.27913	0.049887	0.020075	0.029431
Cystathionine	-0.06469	0.008875	-0.58216	-0.14301	0.02877	0.83235	0.020075	0.78785
Cyclic-AMP	-0.54107	-0.62288	-2.2145	1.8006	0.14569	0.24312	0.51323	0.50668
CTP	-0.00314	-0.09165	0.72443	0.041959	0.8229	0.36897	0.62794	1
CoA	0.14085	-0.00932	0.96912	0.10252	1	0.56495	0.24468	1
CMP	-0.11214	-1.5549	6.947	-0.25197	0.02877	0.049887	0.020075	0.13363
Citrulline	-0.29266	-0.09926	-2.2161	0.43546	0.02877	0.058201	0.020075	0.41204
Citrate	-0.12545	-0.06981	-0.7303	0.38307	0.02877	0.093122	0.020075	0.20674
Choline	-0.02082	0.011793	-3.4056	2.9267	0.60431	0.36897	0.020075	0.029431
Carnitine	-0.1444	-0.13502	0.65976	-0.83978	0.02877	0.049887	0.10859	0.029431
Biotin	-0.25494	ND	ND	-1.34	0.60431	ND	ND	0.60823
ATP	-0.01878	-0.0249	-0.08303	0.041911	1	1	1	0.78785
Aspartate	-0.08858	-0.01969	-0.77688	0.11569	0.02877	0.29489	0.020075	0.51014
Asparagine	-0.36524	-0.07809	-3.0831	1.1799	0.02877	0.058201	0.020075	0.029431
Arginine	-0.04457	-0.00448	-1.8186	1.4839	0.070818	0.46962	0.020075	0.029431
AMP	-0.19109	-1.3953	6.3848	-0.6493	0.02877	0.055233	0.025256	0.048714
Ammonium persulfate APS	0.11315	-0.3506	1.2348	-0.80726	1	0.59189	0.24468	0.76118
alpha-ketoglutarate	-0.87294	-1.5254	4.8686	-0.42862	0.035958	0.049887	0.27115	0.085618
ADP-d-glucose	-0.23662	0.013075	-2.5834	0.53492	0.60431	1	0.27115	0.76118
ADP	-0.16443	0.038613	-1.8453	0.22765	0.02877	0.36897	0.020075	0.41204
Adenosine	0.052482	0.034748	-1.474	1.6658	0.044547	0.049887	0.020075	0.029431
Adenine	0.009166	0.051672	-0.69641	0.19633	0.71109	0.049887	0.020075	0.51014
Aconitate	-0.50719	-0.35898	-0.29103	0.31105	0.078616	0.049887	0.51323	0.70635
Acetylphosphate	-0.37634	0.44373	-0.8388	-1.8367	0.56882	0.51685	0.48066	0.42598
Acetyl-CoA	-0.31081	-0.1405	-1.0883	0.85485	0.044547	0.19955	0.10859	0.30501

Acetoacetyl-CoA	0.0883	-0.17311	1.6792	-0.45887	0.8229	1	0.17427	0.41204
Acetoacetate	-0.15014	ND	ND	-0.42329	0.60431	ND	ND	0.60823
6-phospho-D-gluconate	-0.19865	-0.90048	2.0094	1.3541	0.7769	0.085867	0.51323	0.42598
5-Methyl-THF	-0.51504	0.15172	-5.9369	1.162	0.14569	0.75479	0.053215	0.20674
3-Hydroxy-3-methylglutary-CoA	-0.24359	-0.1544	-0.33173	0.057544	0.02877	0.36897	0.87168	0.70635
2-keto-D-gluconic acid	0.002625	-0.25102	ND	1.1401	0.98174	0.56495	ND	0.60823