Suplemental Table 1: List of all proteins detected by 1D-SDS-PAGE and LC-MS/MS in three biological replicates of cells grown on oxalate including previously published acetate and methanol samples.

Gene number	description (gene name)	spectral counts (‰)									average spectral counts (‰)			fold change	p value	fold change	p value
		acetate S1	acetate S2	acetate S3	methanol S1	methanol S2	methanol S3	oxalate S1	oxalate S2	oxalate S2	acetate	methanol	oxalate	oxalate vs acetate		oxalat vs methanol	
META1_0001	DNA replication initiator protein, transcriptional regulat	0.000	0.340	0.346	0.000	0.665	0.567	0.428	0.406	0.377	0.263	0.524	0.403	2.07	0.40	1.15	0.31
META1_0002	DNA polymerase III, beta-subunit	1.051	1.020	0.990	0.676	0.903	0.851	0.836	0.850	0.754	1.016	0.847	0.813	1.08	0.01	1.44	0.92
META1_0003	putative RecF protein	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_0010	phosphoribosylformylglycinamide synthetase	0.740	0.725	0.742	1.217	1.021	1.016	1.393	1.198	0.953	0.735	1.048	1.176	2.16	0.01	1.68	0.57
META1_0012	glutaredoxin-like protein	0.234	0.385	0.346	0.406	0.594	0.520	0.386	0.251	0.536	0.336	0.534	0.390	1.57	0.56	1.09	0.30
META1_0016	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.000	0.040	0.000	0.000	0.060	n.d.	0.12	n.d.	0.12
META1_0017	putative sensor hybrid histidine kinase with PAS/PAC m	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.000	0.060	0.000	0.020	0.040	n.d.	0.12	3.00	0.53
META1_0018	conserved protein of unknown function, ATP-binding do	0.195	0.408	0.322	0.135	0.404	0.354	0.343	0.251	0.278	0.327	0.343	0.289	1.19	0.93	1.26	0.85
META1_0020	putative Short-chain dehydrogenase/reductase SDR	0.078	0.136	0.148	0.000	0.000	0.000	0.000	0.058	0.040	0.127	0.000	0.034	0.36	0.51	n.d.	0.12
META1_0025	malonate decarboxylase, beta-subunit	0.000	0.113	0.000	0.000	0.000	0.047	0.150	0.213	0.139	0.045	0.020	0.168	5.00	0.13	12.50	0.18
META1_0026	Malonate decarboxylase, gamma subunit	0.000	0.045	0.074	0.000	0.071	0.118	0.236	0.290	0.198	0.045	0.081	0.242	7.20	0.60	4.50	0.53
META1_0049	tryptophan synthase, beta protein	0.545	0.861	0.693	0.406	0.855	0.780	0.643	0.657	0.377	0.726	0.756	0.558	1.04	0.35	1.11	0.58
META1_0051	conserved protein of unknown function; putative expor	0.156	0.000	0.000	0.135	0.000	0.000	0.150	0.155	0.198	0.036	0.020	0.168	6.25	0.12	12.50	0.13
META1_0052	integration host factor (IHF), beta subunit, site-specific	0.117	0.136	0.173	0.000	0.119	0.142	0.107	0.135	0.139	0.145	0.111	0.128	1.19	0.50	1.73	0.37
META1_0053	putative peptidase	0.506	0.725	0.718	0.406	0.048	0.284	0.557	0.522	0.437	0.671	0.202	0.504	1.01	0.15	3.75	0.19
META1_0054	protein of unknown function	0.000	0.000	0.000	0.000	0.119	0.047	0.000	0.116	0.079	0.000	0.071	0.067	n.d.	0.12	1.43	0.97
META1_0055	30S ribosomal subunit protein S1	6.503	6.548	7.794	6.628	7.601	6.308	7.327	6.901	6.808	6.994	6.904	7.003	1.35	0.86	1.52	0.68
META1_0057	rRNA methylase	0.389	0.476	0.495	0.744	0.095	0.189	0.450	0.406	0.377	0.463	0.232	0.410	1.20	0.35	2.65	0.42
META1_0063	conserved protein of unknown function	0.000	0.000	0.000	0.271	0.285	0.118	0.129	0.097	0.079	0.000	0.212	0.101	n.d.	0.00	0.71	0.08
META1_0064	conserved exported protein of unknown function	0.584	0.657	0.569	0.947	0.713	0.732	0.793	0.831	0.675	0.608	0.756	0.766	1.70	0.04	1.52	0.77
META1_0070	membrane protein of unknown function	0.000	0.091	0.099	0.000	0.143	0.118	0.043	0.058	0.000	0.073	0.111	0.034	0.63	0.93	0.45	0.89
META1_0071	protein of unknown function; putative exported protein	0.273	0.249	0.173	0.000	0.285	0.213	0.129	0.174	0.119	0.227	0.212	0.141	0.84	0.05	1.00	0.29
META1_0072	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0074	protein of unknown function	0.000	0.340	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.154	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_0076	Pirin-like protein	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.000	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_0083	putative ATP-binding protein with two ATPase domains	0.000	0.068	0.247	0.203	0.356	0.189	0.129	0.213	0.218	0.118	0.262	0.188	2.15	0.43	1.08	0.36
META1_0086	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0087	conserved protein of unknown function; putative hydro	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.040	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_0090	Glycosyl transferase group 1	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.040	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_0096	putative methyltransferase, putative O-methyltransfera	0.000	0.000	0.074	0.000	0.071	0.189	0.064	0.058	0.079	0.027	0.111	0.067	3.33	0.11	0.91	0.30
META1_0105	D-3-phosphoglycerate dehydrogenase	3.660	2.606	2.672	0.473	1.045	1.465	1.178	1.527	1.151	2.876	1.139	1.290	0.61	0.00	1.70	0.37
META1_0106	Putative oxidoreductase (automated annotation called	0.389	0.906	0.594	0.000	0.356	0.213	0.257	0.329	0.258	0.671	0.242	0.282	0.57	0.04	1.75	0.38
META1_0119	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_0120	RNA polymerase sigma factor	0.000	0.000	0.000	0.000	0.048	0.000	0.086	0.077	0.079	0.000	0.020	0.081	n.d.	0.00	6.00	0.14
META1_0121	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.129	0.097	0.060	0.000	0.000	0.094	n.d.	0.00	n.d.	0.00
META1_0122	putative catalase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_0130	Potassium-transporting ATPase B chain (Potassium- tra	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0162	putative resolvase	0.000	0.000	0.074	0.000	0.048	0.047	0.107	0.116	0.119	0.027	0.040	0.114	5.67	0.14	4.25	0.50
META1_0165	recombination protein	0.000	0.000	0.000	0.000	0.190	0.165	0.150	0.193	0.079	0.000	0.151	0.141	n.d.	0.00	1.40	0.33
META1_0166	putative Zn dependent carboxypeptidase	0.857	1.020	0.965	0.338	0.831	0.756	0.407	0.503	0.675	0.962	0.726	0.531	0.75	0.02	1.10	0.68
META1_0167	molecular chaperone, HSP70 class	0.117	0.227	0.223	0.135	0.808	0.543	0.428	0.406	0.397	0.200	0.595	0.410	2.77	0.02	1.03	0.93
META1_0168	Pseudouridine synthase, RluD	0.000	0.113	0.099	0.000	0.166	0.189	0.129	0.251	0.179	0.082	0.151	0.188	3.11	0.46	1.87	0.38
META1_0169	putative haloacid dehalogenase family hydrolase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0170	conserved protein of unknown function; putative doma	0.000	0.000	0.000	0.135	0.000	0.118	0.236	0.155	0.159	0.000	0.071	0.181	n.d.	0.00	3.86	0.43
META1_0172	propionyl-CoA carboxylase beta chain	2.842	2.538	3.810	2.435	2.898	3.402	1.971	2.165	1.985	3.075	3.044	2.043	0.90	0.03	1.01	0.03
META1_0173	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.077	0.000	0.000	0.000	0.074	n.d.	0.12	n.d.	0.12
META1_0174	transcriptional regulator TetR family	0.000	0.091	0.099	0.000	0.166	0.284	0.279	0.406	0.298	0.073	0.192	0.329	6.13	0.58	2.58	0.44
META1_0175	ketol-acid reductoisomerase	2.025	1.020	1.534	2.841	2.922	3.544	3.214	2.571	3.136	1.442	3.175	2.964	2.77	0.03	1.40	0.69
META1_0176	putative pyridoxamine 5'-phosphate oxidase-related	0.000	0.204	0.272	0.271	0.238	0.425	0.257	0.406	0.258	0.181	0.323	0.309	2.30	0.41	1.44	0.98
META1_0178	crotonyl-CoA carboxylase/reductase	3.660	2.538	2.474	3.517	3.064	3.071	1.542	1.546	1.449	2.776	3.135	1.512	0.74	0.01	0.72	0.00
META1_0179	catalase (hydroperoxidase II)	2.219	1.473	1.856	0.000	0.119	0.000	0.171	0.097	0.159	1.787	0.050	0.141	0.11	0.00	4.20	0.12
META1_0180	ethylmalonyl-CoA mutase	1.519	1.903	2.400	2.435	3.159	2.693	1.992	2.107	1.925	1.996	2.853	2.009	1.36	0.72	1.06	0.02
META1_0181	conserved protein of unknown function	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0182	Short-chain dehydrogenase/reductase SDR	0.000	0.136	0.297	0.406	0.404	0.496	0.536	0.329	0.278	0.163	0.443	0.376	3.11	0.48	1.27	0.46
META1_0184	Tryptophanyl tRNA synthetase	0.389	0.793	0.594	0.271	0.665	0.638	0.836	0.657	0.615	0.626	0.595	0.699	1.51	0.42	1.76	0.31
META1_0186	Isopropylmalate dehydratase small subunit/isopropylm	0.078	0.385	0.297	0.609	0.665	0.803	0.536	0.657	0.456	0.281	0.716	0.551	2.65	0.13	1.15	0.15
META1_0187	putative pyrrolidone-carboxylate peptidase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0188	methylmalonyl-CoA mutase accessory protein	0.000	0.227	0.124	0.406	0.261	0.236	0.257	0.251	0.218	0.136	0.272	0.242	2.40	0.43	1.33	0.33
META1_0189	conserved protein of unknown function; putative expor	0.000	0.068	0.049	0.000	0.000	0.047	0.086	0.039	0.040	0.045	0.020	0.054	1.60	0.36	4.00	0.12
META1_0190	conserved protein of unknown function	0.467	0.295	0.346	0.406	0.333	0.331	0.407	0.367	0.337	0.354	0.343	0.370	1.41	0.90	1.62	0.66
META1_0191	putative Acylaminoacyl-peptidase	0.857	0.884	0.817	0.812	0.570	0.118	0.771	0.580	0.576	0.853	0.413	0.638	1.01	0.04	2.32	0.44
META1_0192	conserved protein of unknown function precursor, ErfK	0.467	0.295	0.346	0.947	0.285	0.591	0.428	0.657	0.675	0.354	0.514	0.591	2.26	0.08	1.73	0.88
META1_0195	Nuclease sbcCD subunit C	0.000	0.068	0.074	0.000	0.261	0.118	0.086	0.174	0.198	0.054	0.161	0.155	3.83	0.48	1.44	0.35
META1_0198	conserved exported protein of unknown function	0.000	0.045	0.049	0.000	0.000	0.000	0.000	0.000	0.040	0.036	0.000	0.013	0.50	0.53	n.d.	0.37
META1_0199	conserved protein of unknown function; putative SAM-	0.000	0.113	0.099	0.000	0.048	0.000	0.150	0.155	0.119	0.082	0.020	0.141	2.33	0.42	10.50	0.17
META1_0200	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.018	0.000	0.013	1.00	1.00	n.d.	0.37
META1_0201	conserved protein of unknown function	0.000	0.181	0.124	0.000	0.000	0.000	0.064	0.077	0.079	0.118	0.000	0.074	0.85	0.28	n.d.	0.00
META1_0202	putative mutator MutT protein precursor; putative NTP	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_0203	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.039	0.000	0.000	0.040	0.013	n.d.	0.37	0.50	0.53
META1_0204	glutamate N-acetyltransferase/amino-acid acetyltransfe	0.584	0.657	0.520	0.947	0.641	0.567	0.771	0.831	0.754	0.590	0.655	0.786	1.80	0.02	1.80	0.51
META1_0207	putative glutathione peroxidase	0.000	0.068	0.000	0.000	0.048	0.000	0.000	0.000	0.060	0.027	0.020	0.020	1.00	0.99	1.50	0.99
META1_0212	conserved protein of unknown function; putative expor	0.000	0.385	0.396	0.000	0.380	0.165	0.471	0.348	0.397	0.299	0.232	0.403	1.82	0.38	2.61	0.46
META1_0213	protein of unknown function; putative exported protein	0.000	0.091	0.099	0.000	0.000	0.000	0.043	0.000	0.000	0.073	0.000	0.013	0.25	0.57	n.d.	0.37
META1_0214	DNA-dependent ATPase I and helicase II	0.000	0.068	0.272	0.609	0.309	0.378	0.493	0.290	0.218	0.127	0.383	0.329	3.50	0.52	1.29	0.43
META1_0215	putative phosphate starvation induced PhoH-like prote	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.018	0.000	0.027	2.00	0.51	n.d.	0.12
META1_0219	Glutamate-ammonia-ligase adenylyltransferase ([Gluta	0.273	0.612	0.520	0.473	0.570	0.425	0.728	0.793	0.814	0.499	0.494	0.780	2.11	0.09	2.37	0.01
META1_0222	putative sensor histidine kinase; putative membrane pr	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.060	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_0223	response regulator in two-component regulatory syster	0.000	0.113	0.000	0.000	0.071	0.095	0.150	0.135	0.079	0.045	0.071	0.121	3.60	0.12	2.57	0.43
META1_0224	conserved protein of unknown function; putative OsmC	0.467	0.884	0.544	0.947	0.570	0.378	0.600	0.638	0.834	0.662	0.544	0.692	1.41	0.62	1.91	0.63
META1_0225	alkanesulfonate transport protein (ABC superfamily, atp	0.000	0.000	0.000	0.000	0.000	0.047	0.086	0.077	0.099	0.000	0.020	0.087	n.d.	0.00	6.50	0.14
META1_0226	alkanesulfonate transporter subunit ; membrane compo	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0228	sulfonate transport system substrate-binding protein	0.467	0.680	0.693	0.947	0.333	0.756	0.471	0.657	0.556	0.635	0.605	0.565	1.20	0.64	1.40	0.76
META1_0229	[Protein-PII] uridylyltransferase (PII uridylyl- transferase	0.273	0.453	0.619	0.541	0.760	0.732	0.536	0.619	0.536	0.472	0.716	0.565	1.62	0.31	1.18	0.21
META1_0230	putative heat shock protein (HSP-70 COFACTOR), grpE	0.584	0.227	0.421	0.676	0.736	0.732	0.343	0.580	0.516	0.381	0.726	0.484	1.71	0.56	1.00	0.06
META1_0232	putative Prephenate dehydratase	0.195	0.068	0.173	0.135	0.166	0.354	0.257	0.251	0.278	0.136	0.242	0.262	2.60	0.11	1.63	0.41
META1_0233	3-deoxy-manno-octulosonate cytidylyltransferase	0.195	0.136	0.148	0.135	0.000	0.142	0.043	0.116	0.139	0.154	0.081	0.101	0.88	0.20	1.88	0.32
META1_0234	Putative cytochrome c, class I	1.558	1.677	1.262	0.609	1.496	1.654	1.028	1.102	0.754	1.497	1.431	0.961	0.87	0.04	1.01	0.61
META1_0235	putative ABC transporter, periplasmic protein precurso	1.051	1.405	1.831	0.676	0.713	0.260	0.321	0.599	0.516	1.479	0.514	0.484	0.44	0.01	1.41	0.85
META1_0236	putative ABC transporter, periplasmic protein precurso	0.273	0.702	0.841	0.271	0.404	0.095	0.214	0.232	0.198	0.653	0.252	0.215	0.44	0.06	1.28	0.97
META1_0237	putative ABC transporter, permease	0.117	0.113	0.148	0.000	0.000	0.000	0.000	0.039	0.060	0.127	0.000	0.034	0.36	0.52	n.d.	0.12
META1_0238	putative acyltransferase with acyl-CoA N-acyltransferas	0.000	0.000	0.049	0.000	0.119	0.071	0.107	0.116	0.198	0.018	0.081	0.141	10.50	0.17	2.63	0.43
META1_0239	putative Long-chain acyl-CoA synthetase	0.000	0.113	0.124	0.000	0.071	0.095	0.129	0.000	0.000	0.091	0.071	0.040	0.60	0.51	0.86	0.49
META1_0240	putative lipopolysaccharide core biosynthesis glycosyl t	0.000	0.113	0.099	0.000	0.000	0.095	0.150	0.135	0.139	0.082	0.040	0.141	2.33	0.42	5.25	0.13
META1_0251	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0269	transposase of ISMex3, IS256 family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_0277	conserved protein of unknown function, DUF883; putat	0.117	0.317	0.322	0.000	0.071	0.095	0.150	0.174	0.159	0.272	0.071	0.161	0.80	0.36	3.43	0.48
META1_0278	conserved protein of unknown function; putative memb	0.234	0.113	0.148	0.135	0.071	0.071	0.064	0.155	0.079	0.154	0.081	0.101	0.88	0.19	1.88	0.89
META1_0280	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0281	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.058	0.079	0.000	0.020	0.067	n.d.	0.00	5.00	0.13
META1_0284	ApaG domain protein	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_0286	2'-deoxycytidine 5'-triphosphate deaminase	0.156	0.204	0.247	0.203	0.238	0.354	0.257	0.232	0.218	0.209	0.282	0.235	1.52	0.30	1.25	0.63
META1_0287	putative transport protein	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_0288	putative Molybdopterin binding, CinA-related	0.000	0.272	0.569	0.338	0.166	0.142	0.193	0.251	0.258	0.318	0.181	0.235	1.00	0.30	1.94	0.62
META1_0290	putative Methyltransferase FkbM	0.234	0.249	0.247	0.203	0.143	0.284	0.257	0.251	0.238	0.245	0.212	0.249	1.37	0.51	1.76	0.35
META1_0291	putative alpha/beta hydrolase	0.662	0.431	0.445	0.541	0.071	0.260	0.450	0.503	0.456	0.490	0.222	0.470	1.30	0.65	3.18	0.26
META1_0293	putative ABC-2 transporter, permease	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_0294	putative ABC transporter, ATPase	0.350	0.249	0.346	0.203	0.048	0.118	0.279	0.232	0.198	0.308	0.101	0.235	1.03	0.13	3.50	0.14
META1_0295	4Fe-4S ferredoxin, iron-sulfur binding	0.000	0.000	0.000	0.000	0.190	0.165	0.214	0.193	0.179	0.000	0.151	0.195	n.d.	0.00	1.93	0.39
META1_0296	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.079	0.000	0.000	0.081	n.d.	0.00	n.d.	0.00
META1_0298	conserved protein of unknown function	0.000	0.045	0.074	0.000	0.143	0.142	0.236	0.193	0.139	0.045	0.121	0.188	5.60	0.56	2.33	0.41
META1_0301	Cytoplasmic chaperone TorD	0.000	0.136	0.099	0.135	0.238	0.284	0.300	0.213	0.198	0.091	0.242	0.235	3.50	0.49	1.46	0.69
META1_0303	formate dehydrogenase alpha subunit precursor (tat pa	0.000	0.340	0.544	0.338	1.211	1.063	0.707	0.696	0.675	0.336	1.018	0.692	2.78	0.46	1.02	0.83
META1_0304	Formate dehydrogenase iron-sulfur (beta) subunit	0.000	0.000	0.000	0.000	0.190	0.142	0.150	0.135	0.119	0.000	0.141	0.134	n.d.	0.00	1.43	0.35
META1_0305	Formate dehydrogenase gamma (cytochrome) subunit	0.000	0.091	0.099	0.000	0.048	0.095	0.043	0.077	0.000	0.073	0.060	0.040	0.75	0.94	1.00	0.98
META1_0306	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.119	0.071	0.000	0.000	0.040	0.000	0.081	0.013	n.d.	0.37	0.25	0.57
META1_0307	conserved protein of unknown function; putative expor	0.000	0.045	0.000	0.000	0.166	0.189	0.171	0.097	0.139	0.018	0.151	0.134	10.00	0.17	1.33	0.33
META1_0310	putative TetR family transcriptional regulatory protein	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.058	0.000	0.000	0.020	0.020	n.d.	0.37	1.50	0.99

META1_0312	efflux transporter (AcrB/AcrD/AcrF family multidrug eff	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.097	0.000	0.000	0.020	0.034	n.d.	0.37	2.50	0.96
META1_0314	Heat-inducible transcription repressor HrcA	0.000	0.204	0.198	0.135	0.166	0.189	0.214	0.155	0.099	0.154	0.171	0.155	1.35	0.33	1.35	0.74
META1_0317	Ribonuclease PH (RNase PH) (tRNA nucleotidyltransfera	0.389	0.317	0.346	0.473	0.166	0.402	0.257	0.329	0.377	0.345	0.312	0.323	1.26	0.48	1.55	0.99
META1_0318	non-canonical purine NTP pyrophosphatase, RdgB/HAM	0.000	0.068	0.074	0.203	0.166	0.189	0.107	0.232	0.139	0.054	0.181	0.161	4.00	0.49	1.33	0.43
META1_0320	putative extracellular ligand-binding receptor precursor	0.117	0.045	0.074	0.135	0.119	0.236	0.129	0.058	0.079	0.073	0.171	0.087	1.63	0.72	0.76	0.12
META1_0321	putative methyltransferase	0.117	0.136	0.124	0.135	0.119	0.165	0.107	0.077	0.119	0.127	0.141	0.101	1.07	0.17	1.07	0.11
META1_0323	Response regulator receiver protein	0.156	0.181	0.272	0.271	0.190	0.189	0.321	0.193	0.218	0.209	0.202	0.242	1.57	0.45	1.80	0.60
META1_0328	Peptidyl-dipeptidase	0.000	0.000	0.049	0.000	0.095	0.000	0.171	0.174	0.099	0.018	0.040	0.148	11.00	0.17	5.50	0.14
META1_0329	formate-tetrahydrofolate ligase (formyltetrahydrofolate	1.363	1.473	1.237	4.058	4.513	3.709	3.706	3.595	3.890	1.361	4.102	3.730	3.70	0.00	1.36	0.21
META1_0330	putative copper ion binding protein; putative heavy me	0.078	0.068	0.049	0.000	0.143	0.000	0.000	0.039	0.060	0.064	0.060	0.034	0.71	0.41	0.83	0.45
META1_0331	conserved protein of unknown function; putative EAL d	0.000	0.000	0.000	0.000	0.071	0.071	0.064	0.058	0.040	0.000	0.060	0.054	n.d.	0.00	1.33	0.34
META1_0333	conserved protein of unknown function, chemotaxis pr	0.000	0.000	0.000	0.000	0.119	0.000	0.150	0.097	0.119	0.000	0.050	0.121	n.d.	0.00	3.60	0.12
META1_0334	putative response regulator receiver (CheY-like protein)	0.156	0.249	0.124	0.879	0.428	0.591	0.450	0.367	0.595	0.181	0.564	0.470	3.50	0.02	1.25	0.34
META1_0335	putative riboflavin biosynthesis protein ribF [Includes: F	0.156	0.136	0.173	0.203	0.143	0.189	0.150	0.174	0.119	0.154	0.171	0.148	1.29	0.69	1.29	0.29
META1_0336	putative 2-hydroxyacid dehydrogenase	0.973	0.838	0.668	1.014	0.903	0.827	0.814	0.812	0.953	0.807	0.887	0.860	1.44	0.71	1.45	0.48
META1_0337	conserved protein of unknown function precursor	0.234	0.227	0.124	0.406	0.238	0.189	0.214	0.290	0.179	0.191	0.242	0.228	1.62	0.52	1.42	0.57
META1_0338	Putative ferric uptake regulator family	0.000	0.204	0.198	0.338	0.143	0.047	0.107	0.000	0.179	0.154	0.131	0.094	0.82	0.95	1.08	0.38
META1_0339	Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase	0.623	0.612	0.495	0.473	0.499	0.260	0.600	0.657	0.615	0.572	0.393	0.625	1.48	0.35	2.38	0.10
META1_0340	3-oxoacyl-[acyl-carrier-protein] synthase I	1.947	0.770	0.891	0.879	1.140	1.158	1.221	0.928	0.834	1.089	1.109	0.988	1.23	0.73	1.34	0.66
META1_0342	Enoyl-[acyl-carrier-protein] reductase (NADH)	0.389	0.249	0.272	0.541	0.095	0.213	0.364	0.290	0.298	0.290	0.212	0.316	1.47	0.73	2.24	0.53
META1_0344	conserved protein of unknown function, putative inner	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0346	protein of unknown function; putative exported protein	0.000	0.045	0.074	0.473	0.119	0.000	0.129	0.193	0.179	0.045	0.121	0.168	5.00	0.53	2.08	0.33
META1_0347	Peptidase S9, prolyl oligopeptidase	0.818	1.178	1.212	1.082	1.259	1.110	1.093	0.947	0.794	1.107	1.169	0.941	1.15	0.50	1.21	0.12
META1_0348	Transcriptional regulatory protein mucR	0.740	0.521	0.322	0.947	0.760	0.543	0.793	0.715	0.814	0.499	0.695	0.773	2.09	0.15	1.67	0.76
META1_0349	protein of unknown function	0.195	0.136	0.099	0.000	0.000	0.000	0.086	0.039	0.060	0.136	0.000	0.060	0.60	0.05	n.d.	0.00
META1_0351	putative sulfur acceptor protein sufE	0.000	0.000	0.000	0.000	0.119	0.047	0.064	0.039	0.000	0.000	0.071	0.034	n.d.	0.12	0.71	0.96
META1_0352	protein of unknown function; putative sensor protein; s	0.156	0.113	0.049	0.000	0.071	0.095	0.086	0.000	0.000	0.100	0.071	0.027	0.36	0.12	0.57	0.52
META1_0357	protein of unknown function; putative PYP-like sensor d	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0358	conserved protein of unknown function	0.078	0.091	0.173	0.000	0.000	0.000	0.086	0.058	0.040	0.118	0.000	0.060	0.69	0.14	n.d.	0.00
META1_0359	putative lactoylglutathione lyase	0.623	0.453	0.173	0.338	0.095	0.189	0.171	0.116	0.298	0.390	0.171	0.195	0.67	0.21	1.71	0.99
META1_0360	protein of unknown function	0.078	0.181	0.099	0.000	0.000	0.118	0.236	0.232	0.139	0.127	0.050	0.202	2.14	0.14	6.00	0.14
META1_0361	aminopeptidase N, a cysteinylglycinase, (alpha-aminoac	0.506	0.884	0.866	0.541	0.618	0.402	0.450	0.638	0.635	0.789	0.514	0.578	0.99	0.31	1.69	0.58
META1_0363	arginase (arginine amidinase)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0364	Glucose-6-phosphate 1-dehydrogenase (G6PD)	0.273	0.702	0.495	0.203	0.356	0.473	0.407	0.387	0.377	0.526	0.383	0.390	1.00	0.60	1.53	0.50
META1_0366	protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.107	0.058	0.119	0.000	0.040	0.094	n.d.	0.00	3.50	0.11
META1_0368	copper binding protein, copper sensitivity	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0369	putative inorganic polyphosphate/ATP-NAD kinase (Pol	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.060	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00
META1_0371	16S rRNA m5C967 methyltransferase, S-adenosyl-L-met	0.000	0.068	0.124	0.135	0.190	0.189	0.086	0.155	0.139	0.073	0.181	0.128	2.38	0.42	1.06	0.20
META1_0376	malonyl-CoA-[acyl-carrier-protein] transacylase	0.779	0.498	0.569	0.879	0.380	0.992	0.900	1.005	1.111	0.590	0.716	1.008	2.31	0.03	2.11	0.30
META1_0377	3-oxoacyl-[acyl-carrier-protein] reductase	0.973	0.589	0.742	1.014	0.499	1.276	0.836	0.870	0.635	0.735	0.907	0.780	1.43	0.89	1.29	0.73
META1_0379	3-oxoacyl-[acyl-carrier-protein] synthase II	0.506	0.249	0.223	0.000	0.380	0.378	0.279	0.290	0.218	0.299	0.323	0.262	1.18	0.60	1.22	0.32
META1_0380	conserved protein of unknown function	0.000	0.295	0.223	0.338	0.190	0.284	0.193	0.174	0.179	0.200	0.252	0.181	1.23	0.32	1.08	0.10
META1_0384	putative membrane protein, component of efflux syste	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0387	D-xylulose 5-phosphate/D-fructose 6-phosphate phosp	0.117	0.181	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.163	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_0390	putative sulfate/thiosulfate transporter subunit ; ATP-b	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_0391	ABC transporter, periplasmic protein precursor, putativ	1.674	1.133	0.940	1.217	0.428	0.331	0.364	0.445	0.357	1.188	0.504	0.390	0.44	0.00	1.16	0.42
META1_0396	putative flavin containing amine oxidase	0.000	0.000	0.000	0.000	0.095	0.071	0.000	0.039	0.040	0.000	0.071	0.027	n.d.	0.12	0.57	0.92
META1_0397	putative cyclic nucleotide-binding domain	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_0398	protein of unknown function	0.078	0.091	0.000	0.000	0.000	0.000	0.000	0.058	0.119	0.054	0.000	0.060	1.50	1.00	n.d.	0.12
META1_0403	ABC transporter, periplasmic protein, putative sulfate/t	0.350	0.702	0.668	1.014	0.808	0.874	0.364	0.715	0.377	0.608	0.867	0.491	1.09	0.61	0.85	0.04
META1_0405	ABC transporter, permease, putative sulfate/thiosulfate	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0406	ABC transporter, ATPase, putative sulfate/thiosulfate tr	0.000	0.204	0.049	0.203	0.736	0.614	0.407	0.329	0.258	0.100	0.605	0.329	4.45	0.57	0.82	0.48
META1_0412	phosphoribosylaminoimidazole-succinocarboxamide sy	0.935	1.337	1.188	1.217	0.713	0.992	1.007	1.546	1.111	1.188	0.907	1.230	1.40	0.77	2.03	0.32
META1_0414	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0416	conserved protein of unknown function; putative expor	0.156	0.181	0.297	0.744	0.285	0.236	0.064	0.271	0.119	0.218	0.333	0.155	0.96	0.37	0.70	0.12
META1_0417	protein of unknown function	0.195	0.181	0.173	0.000	0.095	0.165	0.043	0.058	0.000	0.181	0.111	0.034	0.25	0.58	0.45	0.90
META1_0419	intracellular PHB depolymerase	0.506	0.091	0.124	0.000	0.309	0.142	0.171	0.329	0.298	0.200	0.192	0.269	1.82	0.56	2.11	0.41
META1_0420	two component sensor histidine kinase, RegS	0.000	0.136	0.148	0.000	0.000	0.000	0.043	0.039	0.079	0.109	0.000	0.054	0.67	0.25	n.d.	0.00
META1_0421	two-component transcriptional regulator RegR, Fis fami	0.078	0.159	0.074	0.203	0.143	0.331	0.257	0.348	0.238	0.109	0.232	0.282	3.50	0.02	1.83	0.38
META1_0423	Phosphoribosylformylglycinamidine synthetase PurS	0.234	0.249	0.346	0.271	0.404	0.307	0.107	0.213	0.179	0.281	0.343	0.168	0.81	0.09	0.74	0.04
META1_0424	phosphoribosylformylglycinamidine synthase I	0.350	0.181	0.099	0.338	0.166	0.213	0.214	0.290	0.139	0.191	0.212	0.215	1.52	0.82	1.52	0.73
META1_0425	adenine phosphoribosyltransferase	0.623	0.476	0.470	0.338	0.333	0.378	0.364	0.290	0.456	0.508	0.353	0.370	0.98	0.09	1.57	0.78
META1_0426	inositol monophosphatase	0.740	0.748	0.619	0.879	0.356	0.614	0.557	0.812	0.516	0.699	0.544	0.632	1.22	0.45	1.74	0.84
META1_0427	thiamine-phosphate pyrophosphorylase (TMP pyropho	0.000	0.000	0.000	0.000	0.048	0.000	0.107	0.058	0.000	0.000	0.020	0.054	n.d.	0.12	4.00	0.55
META1_0428	thiazole synthase	0.156	0.181	0.198	0.000	0.000	0.118	0.386	0.348	0.456	0.181	0.050	0.397	2.95	0.00	11.80	0.18
META1_0430	glycine oxidase	0.000	0.000	0.000	0.000	0.000	0.047	0.086	0.155	0.159	0.000	0.020	0.134	n.d.	0.00	10.00	0.17
META1_0431	putative Adenylate/Guanylate cyclase	0.000	0.000	0.074	0.000	0.143	0.047	0.129	0.135	0.099	0.027	0.081	0.121	6.00	0.14	2.25	0.43
META1_0432	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.018	0.030	0.000	0.00	0.37	0.00	0.37
META1_0436	DNA primase	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.040	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_0437	Gluconolactonase (D-glucono-delta-lactone lactonohyd	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0439	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase sub	0.156	0.227	0.049	0.541	0.618	0.378	0.407	0.367	0.437	0.145	0.504	0.403	3.75	0.06	1.20	0.23
META1_0440	carbamoyl phosphate synthetase, glutamine amidotran	0.350	0.136	0.173	0.338	0.808	0.756	0.321	0.503	0.397	0.200	0.716	0.410	2.77	0.09	0.86	0.27
META1_0442	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.107	0.097	0.060	0.000	0.030	0.087	n.d.	0.00	4.33	0.12
META1_0447	flagellar biosynthesis; cell-distal portion of basal-body r	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.058	0.040	0.000	0.030	0.054	n.d.	0.00	2.67	0.10
META1_0448	flagella basal body P-ring protein	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_0449	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.099	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_0450	flagellar L-ring protein FlgH	0.000	0.000	0.000	0.000	0.071	0.165	0.150	0.077	0.139	0.000	0.101	0.121	n.d.	0.00	1.80	0.39
META1_0452	flagellar biosynthesis protein FliP	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.000	0.040	0.000	0.060	0.013	n.d.	0.37	0.33	0.55
META1_0459	fragment of conserved protein of unknown function (C-	0.000	0.045	0.049	0.000	0.048	0.000	0.043	0.000	0.000	0.036	0.020	0.013	0.50	0.52	1.00	0.99
META1_0461	Two-component response regulator	0.000	0.000	0.000	0.000	0.048	0.000	0.107	0.135	0.079	0.000	0.020	0.108	n.d.	0.00	8.00	0.15
META1_0464	flagellar motor switch protein FliG	0.000	0.000	0.000	0.000	0.071	0.095	0.150	0.097	0.099	0.000	0.071	0.114	n.d.	0.00	2.43	0.42
META1_0465	flagellar motor switch protein fliN	0.000	0.000	0.000	0.000	0.143	0.095	0.064	0.097	0.060	0.000	0.101	0.074	n.d.	0.00	1.10	0.31
META1_0466	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_0467	protein of unknown function	0.000	0.113	0.124	0.000	0.095	0.142	0.000	0.077	0.179	0.091	0.101	0.087	1.30	1.00	1.30	1.00
META1_0468	Flagellar motor switch protein FliM	0.000	0.045	0.049	0.000	0.285	0.213	0.236	0.213	0.238	0.036	0.212	0.228	8.50	0.63	1.62	0.36
META1_0469	Chemotaxis protein MotA (Motility protein A)	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0470	ATP-dependent protease hslV	0.117	0.136	0.173	0.000	0.285	0.165	0.129	0.232	0.298	0.145	0.192	0.222	2.06	0.23	1.74	0.37
META1_0471	ATP-dependent hsl protease ATP-binding subunit hslU	0.312	0.589	0.520	0.271	0.285	0.378	0.364	0.483	0.576	0.499	0.323	0.477	1.29	0.94	2.22	0.07
META1_0473	Beta-lactamase-like	0.000	0.159	0.099	0.000	0.071	0.095	0.086	0.077	0.119	0.100	0.071	0.094	1.27	0.33	2.00	0.39
META1_0474	putative rieske 2Fe-2S family protein	0.000	0.068	0.000	0.000	0.000	0.071	0.043	0.077	0.000	0.027	0.030	0.040	2.00	0.51	2.00	0.51
META1_0475	protein of unknown function	0.000	0.091	0.000	0.000	0.190	0.095	0.086	0.116	0.159	0.036	0.121	0.121	4.50	0.13	1.50	0.36
META1_0476	conserved protein of unknown function	0.195	0.091	0.173	0.000	0.119	0.118	0.107	0.000	0.079	0.145	0.101	0.060	0.56	0.44	0.90	0.97
META1_0477	signal recognition particle protein, GTPase	0.195	0.363	0.767	0.744	1.306	1.229	1.093	0.889	1.012	0.472	1.189	0.995	2.85	0.07	1.25	0.75
META1_0478	putative chorismate mutase	0.000	0.159	0.124	0.000	0.238	0.260	0.086	0.097	0.099	0.109	0.212	0.094	1.17	0.32	0.67	0.25
META1_0479	ribosomal protein S16	0.545	0.181	0.322	0.879	0.641	0.614	1.071	0.735	1.052	0.318	0.665	0.948	4.03	0.03	2.14	0.16
META1_0480	putative 16S rRNA processing protein	0.117	0.249	0.124	0.271	0.190	0.142	0.193	0.232	0.218	0.172	0.181	0.215	1.68	0.25	1.78	0.64
META1_0481	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0484	tRNA (guanine)-methyltransferase	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.000	0.060	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_0485	phosphoserine aminotransferase	0.156	0.181	0.272	0.473	0.475	0.520	0.193	0.232	0.337	0.209	0.494	0.255	1.65	0.39	0.78	0.02
META1_0486	phosphoglycerate dehydrogenase	0.000	0.295	0.247	0.271	0.475	0.165	0.300	0.271	0.278	0.209	0.312	0.282	1.83	0.38	1.35	0.95
META1_0488	5-methylthioribose-1-phosphate isomerase	0.078	0.227	0.173	0.000	0.333	0.402	0.343	0.290	0.278	0.172	0.312	0.302	2.37	0.09	1.45	0.34
META1_0491	ABC transporter, fused ATPase and permease domains	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0492	putative rRNA methylase	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.000	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META1_0493	putative methyl-accepting chemotaxis sensory transduc	0.000	0.113	0.000	0.000	0.000	0.000	0.086	0.000	0.000	0.045	0.000	0.027	0.80	0.98	n.d.	0.37
META1_0494	conserved protein of unknown function	0.078	0.159	0.124	0.000	0.095	0.047	0.000	0.000	0.139	0.127	0.060	0.047	0.50	0.11	1.17	0.47
META1_0497	putative TonB-dependent siderophore receptor	0.350	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.082	0.030	0.000	0.00	0.37	0.00	0.37
META1_0498	Coproporphyrinogen III oxidase, aerobic (Coproporphyr	0.000	0.113	0.074	0.203	0.048	0.284	0.321	0.174	0.278	0.073	0.171	0.255	4.75	0.54	2.24	0.37
META1_0499	Exodeoxyribonuclease V	0.000	0.000	0.000	0.000	0.048	0.071	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_0500	conserved protein of unknown function; putative amino	1.168	0.997	1.361	0.947	2.019	2.032	0.964	1.353	0.873	1.170	1.865	1.069	1.23	0.53	0.86	0.23
META1_0502	putative flagellin (flaA-like; flaB-like)	0.000	0.159	0.322	0.473	1.425	1.512	0.321	0.735	0.496	0.181	1.320	0.524	3.90	0.51	0.60	0.18
META1_0508	flagellar hook protein FlgE	0.000	0.000	0.000	0.000	0.095	0.095	0.129	0.077	0.099	0.000	0.081	0.101	n.d.	0.00	1.88	0.38
META1_0511	Flagellar protein FlaF	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_0512	flagellum biosynthesis repressor protein FlbT	0.000	0.045	0.000	0.000	0.190	0.095	0.043	0.174	0.218	0.018	0.121	0.148	11.00	0.17	1.83	0.36
META1_0513	FlgD (BASAL-BODY ROD MODIFICATION PROTEIN)/hook	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_0519	conserved protein of unknown function	0.000	0.068	0.049	0.000	0.071	0.095	0.000	0.000	0.060	0.045	0.071	0.020	0.60	0.52	0.43	0.54
META1_0520	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.039	0.000	0.000	0.040	0.013	n.d.	0.37	0.50	0.53
META1_0521	putative dihydrodipicolinate synthase (dapA-like)	0.000	0.091	0.074	0.135	0.071	0.142	0.129	0.155	0.159	0.064	0.111	0.148	3.14	0.46	2.00	0.29
META1_0522	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.058	0.000	0.000	0.020	0.040	n.d.	0.12	3.00	0.53
META1_0535	AMP nucleosidase	0.000	0.113	0.223	0.000	0.190	0.236	0.107	0.174	0.159	0.127	0.181	0.148	1.57	0.36	1.22	0.32
META1_0536	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.071	0.086	0.058	0.139	0.000	0.071	0.094	n.d.	0.00	2.00	0.39
META1_0543	protein of unknown function, putative chaperone-like p	0.000	0.000	0.124	0.000	0.000	0.047	0.086	0.097	0.099	0.045	0.020	0.094	2.80	0.10	7.00	0.15
META1_0553	conserved protein of unknown function	0.117	0.091	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.064	0.020	0.000	0.00	0.12	0.00	0.37
META1_0555	conserved protein of unknown function (DUF589)	0.000	0.045	0.000	0.000	0.071	0.047	0.129	0.058	0.060	0.018	0.050	0.081	6.00	0.14	2.40	0.41
META1_0556	glycerol-3-phosphate dehydrogenase (NAD+)	0.000	0.181	0.198	0.271	0.214	0.142	0.300	0.251	0.119	0.145	0.192	0.222	2.06	0.39	1.74	0.93

META1_0558	O-sialoglycoprotein endopeptidase, with actin-like ATPa	0.195	0.295	0.297	0.338	0.214	0.354	0.386	0.329	0.298	0.272	0.292	0.336	1.67	0.17	1.72	0.51
META1_0559	putative uroporphyrinogen III synthase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0561	conserved protein of unknown function; two putative n	2.025	1.903	2.351	1.894	1.520	1.630	1.907	1.527	1.191	2.096	1.623	1.532	0.99	0.10	1.42	0.54
META1_0562	conserved protein of unknown function; putative expor	1.558	1.292	1.188	1.217	0.831	0.567	0.664	0.580	0.734	1.315	0.776	0.659	0.68	0.00	1.27	0.36
META1_0572	putative chemoreceptor y4sI (Methyl-accepting chemot	0.000	0.000	0.000	0.000	0.214	0.189	0.279	0.174	0.179	0.000	0.171	0.208	n.d.	0.00	1.82	0.38
META1_0574	conserved protein of unknown function; putative ATP-d	0.000	0.227	0.223	0.000	0.190	0.142	0.257	0.271	0.218	0.172	0.141	0.249	1.95	0.39	2.64	0.44
META1_0580	ABC-type polysaccharide/polyol phosphate transport sy	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.058	0.000	0.000	0.020	0.020	n.d.	0.37	1.50	0.99
META1_0581	putative Capsule polysaccharide export inner-membran	0.000	0.000	0.049	0.000	0.119	0.142	0.000	0.039	0.000	0.018	0.111	0.013	1.00	0.99	0.18	0.60
META1_0582	conserved protein of unknown function	0.078	0.091	0.049	0.000	0.000	0.000	0.043	0.000	0.040	0.073	0.000	0.027	0.50	0.45	n.d.	0.12
META1_0585	putative methyl-accepting chemotaxis receptor/sensor	0.000	0.000	0.000	0.000	0.214	0.000	0.107	0.097	0.119	0.000	0.091	0.108	n.d.	0.00	1.78	0.09
META1_0588	conserved protein of unknown function, putative flagell	0.000	0.045	0.000	0.135	0.214	0.095	0.150	0.135	0.278	0.018	0.151	0.188	14.00	0.19	1.87	0.50
META1_0590	Cell cycle transcriptional regulator ctrA (Response regul	0.078	0.204	0.173	0.338	0.309	0.449	0.450	0.425	0.258	0.163	0.373	0.376	3.11	0.05	1.51	0.94
META1_0592	conserved protein of unknown function	0.000	0.136	0.198	0.271	0.071	0.118	0.129	0.135	0.179	0.127	0.121	0.148	1.57	0.36	1.83	0.81
META1_0594	NAD-dependent malic enzyme	4.711	5.801	5.345	1.488	1.568	1.465	2.528	2.551	1.965	5.380	1.512	2.345	0.59	0.00	2.33	0.01
META1_0597	protein of unknown function	0.000	0.068	0.074	0.000	0.000	0.047	0.043	0.058	0.119	0.054	0.020	0.074	1.83	0.37	5.50	0.13
META1_0598	putative glycosyl transferase	0.000	0.045	0.049	0.000	0.095	0.000	0.107	0.097	0.079	0.036	0.040	0.094	3.50	0.47	3.50	0.12
META1_0599	protein of unknown function	0.000	0.000	0.099	0.000	0.000	0.071	0.064	0.097	0.000	0.036	0.030	0.054	2.00	0.50	2.67	0.53
META1_0600	protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.058	0.000	0.018	0.000	0.020	1.50	0.99	n.d.	0.37
META1_0601	peptidase	0.584	0.612	0.520	0.203	0.641	0.449	0.321	0.387	0.278	0.572	0.494	0.329	0.78	0.01	1.00	0.65
META1_0603	oxidoreductase, FAD-binding subunit; putative molybdo	0.000	0.476	0.148	0.000	0.214	0.213	0.214	0.174	0.139	0.245	0.181	0.175	0.96	0.32	1.44	0.34
META1_0604	oxidoreductase, molybdopterin-binding subunit	0.000	0.453	0.124	0.000	0.166	0.142	0.279	0.251	0.159	0.227	0.131	0.228	1.36	0.37	2.62	0.43
META1_0610	Putative transcriptional regulator, MarR family	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_0611	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.039	0.000	0.000	0.060	0.013	n.d.	0.37	0.33	0.56
META1_0612	alpha-D-glucose-1-phosphate cytidylyltransferase	0.000	0.113	0.099	0.000	0.048	0.095	0.129	0.174	0.040	0.082	0.060	0.114	1.89	0.37	2.83	0.43
META1_0613	cdp-glucose 4,6-dehydratase	0.000	0.091	0.074	0.000	0.143	0.165	0.043	0.077	0.060	0.064	0.131	0.060	1.29	0.33	0.69	0.25
META1_0614	putative Methyltransferase	0.117	0.113	0.099	0.000	0.166	0.142	0.150	0.116	0.119	0.109	0.131	0.128	1.58	0.19	1.46	0.35
META1_0615	dTDP-4-dehydrorhamnose 3,5-epimerase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_0616	putative CDP-4-dehydro-6-deoxy-D-gulose 4-reductase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_0617	Putative response regulator receiver	0.000	0.204	0.099	0.000	0.048	0.000	0.064	0.058	0.060	0.118	0.020	0.060	0.69	0.27	4.50	0.13
META1_0619	7,8-diaminopelargonic acid synthetase, PLP-dependent	0.000	0.000	0.000	0.000	0.095	0.118	0.064	0.039	0.000	0.000	0.091	0.034	n.d.	0.12	0.56	0.92
META1_0620	glycine decarboxylase, PLP-dependent, subunit (protein	4.361	3.082	4.083	0.000	0.190	0.142	4.477	4.136	3.731	3.747	0.141	4.106	1.48	0.55	43.64	0.92
META1_0622	glycine cleavage complex protein T, aminomethyltransf	0.389	1.110	1.410	0.203	0.000	0.000	2.399	1.933	2.243	1.052	0.030	2.184	2.80	0.08	108.33	0.31
META1_0624	7-keto-8-aminopelargonic acid synthetase (8-amino-7-c	0.000	0.000	0.000	0.000	0.143	0.165	0.129	0.116	0.119	0.000	0.131	0.121	n.d.	0.00	1.38	0.34
META1_0625	conserved protein of unknown function; putative NLP/P	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.058	0.079	0.000	0.020	0.067	n.d.	0.00	5.00	0.13
META1_0626	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0629	MxaR-like protein, an ATPase	0.000	0.091	0.074	0.203	0.428	0.331	0.364	0.329	0.377	0.064	0.353	0.356	7.57	0.62	1.51	0.53
META1_0630	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.077	0.079	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00
META1_0631	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_0632	conserved protein of unknown function containing a vo	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0639	conserved protein of unknown function	0.273	0.340	0.322	0.000	0.000	0.071	0.000	0.000	0.000	0.318	0.030	0.000	0.00	0.00	0.00	0.37
META1_0640	protein of unknown function	0.973	0.838	0.940	0.609	0.618	0.662	0.686	0.522	0.556	0.907	0.635	0.585	0.87	0.01	1.38	0.44
META1_0641	methionine sulfoxide reductase (Peptide- methionine (F	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.018	0.000	0.020	1.50	0.99	n.d.	0.37
META1_0643	putative SENSORY TRANSDUCTION HISTIDINE KINASE o	0.000	0.045	0.099	0.000	0.309	0.284	0.236	0.213	0.337	0.054	0.252	0.262	6.50	0.59	1.56	0.35
META1_0644	malonyl CoA synthetase	0.467	0.816	0.643	0.135	0.641	0.614	0.578	0.677	0.695	0.671	0.554	0.652	1.31	0.85	1.76	0.35
META1_0646	protein of unknown function; putative exported protein	0.273	0.227	0.223	0.473	0.380	0.284	0.236	0.232	0.159	0.236	0.353	0.208	1.19	0.35	0.89	0.04
META1_0647	conserved protein of unknown function; putative FAD/N	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_0650	General stress protein, putative intracellular proteinase	0.195	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_0652	conserved protein of unknown function; putative memb	0.312	0.000	0.000	0.000	0.071	0.095	0.000	0.039	0.040	0.073	0.071	0.027	0.50	0.40	0.57	0.92
META1_0653	protein of unknown function	0.000	0.113	0.099	0.000	0.048	0.000	0.000	0.000	0.000	0.082	0.020	0.000	0.00	0.12	0.00	0.37
META1_0654	major cold shock protein	0.389	0.453	0.371	0.609	0.261	0.236	0.428	0.309	0.734	0.408	0.302	0.491	1.62	0.64	2.43	0.46
META1_0656	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0657	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.119	0.047	0.043	0.077	0.099	0.000	0.071	0.074	n.d.	0.00	1.57	0.37
META1_0659	Putative ABC transporter, permease	0.000	0.068	0.099	0.000	0.000	0.071	0.000	0.000	0.000	0.064	0.030	0.000	0.00	0.12	0.00	0.37
META1_0660	putative ABC transporter, ATPase	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.058	0.079	0.018	0.000	0.047	3.50	0.54	n.d.	0.12
META1_0661	putative ABC transporter, periplasmic protein	0.000	0.113	0.074	0.135	0.166	0.260	0.064	0.077	0.099	0.073	0.202	0.081	1.50	0.35	0.60	0.02
META1_0662	putative uncharacterized ABC-transporter auxiliary com	0.000	0.000	0.049	0.000	0.190	0.095	0.064	0.000	0.060	0.018	0.121	0.040	3.00	0.53	0.50	0.91
META1_0667	protein of unknown function precursor; putative export	0.000	0.068	0.074	0.203	0.166	0.118	0.107	0.135	0.159	0.054	0.151	0.134	3.33	0.47	1.33	0.40
META1_0669	conserved protein of unknown function	0.117	0.113	0.148	0.135	0.143	0.142	0.171	0.232	0.139	0.127	0.141	0.181	1.93	0.12	1.93	0.19
META1_0670	putative L-asparaginase (ansA-like)	0.195	0.159	0.148	0.135	0.285	0.378	0.171	0.213	0.179	0.163	0.302	0.188	1.56	0.33	0.93	0.44
META1_0671	gamma-glutamylcysteine synthetase	0.000	0.045	0.124	0.000	0.190	0.213	0.193	0.271	0.218	0.064	0.171	0.228	4.86	0.55	2.00	0.39
META1_0674	putative NUDIX hydrolase	0.000	0.000	0.099	0.135	0.095	0.071	0.107	0.039	0.079	0.036	0.091	0.074	2.75	0.10	1.22	0.39
META1_0676	conserved protein of unknown function	0.156	0.204	0.148	0.000	0.190	0.000	0.000	0.000	0.119	0.172	0.081	0.040	0.32	0.13	0.75	0.97
META1_0677	protein of unknown function; putative exported protein	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0678	conserved protein of unknown function; putative memb	0.117	0.000	0.000	0.000	0.190	0.142	0.086	0.077	0.119	0.027	0.141	0.094	4.67	0.11	1.00	0.30
META1_0681	Cobalamin synthase	0.000	0.045	0.000	0.000	0.095	0.047	0.043	0.058	0.040	0.018	0.060	0.047	3.50	0.12	1.17	0.33
META1_0682	Nicotinate-nucleotide--dimethylbenzimidazole phospho	0.117	0.113	0.148	0.271	0.451	0.354	0.150	0.174	0.218	0.127	0.383	0.181	1.93	0.06	0.71	0.02
META1_0686	putative sensory histidine kinase, putative methyltransf	0.000	0.045	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.018	0.020	0.000	0.00	0.37	0.00	0.37
META1_0687	Amidase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0688	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.203	0.000	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_0689	conserved protein of unknown function precursor	0.234	0.136	0.099	0.000	0.261	0.071	0.129	0.058	0.119	0.145	0.141	0.101	0.94	0.30	1.07	0.33
META1_0690	Ribonuclease T2	0.234	0.136	0.148	0.203	0.000	0.118	0.043	0.155	0.060	0.163	0.081	0.087	0.72	0.12	1.63	0.28
META1_0691	putative DNA (exogenous) processing protein, yhiR	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0692	conserved protein of unknown function	0.078	0.045	0.000	0.000	0.000	0.000	0.000	0.039	0.060	0.036	0.000	0.034	1.25	0.98	n.d.	0.12
META1_0693	conserved protein of unknown function; putative expor	0.117	0.068	0.074	0.000	0.000	0.047	0.000	0.039	0.000	0.082	0.020	0.013	0.22	0.15	1.00	0.99
META1_0694	putative glycolate oxidase (glcD-like), FAD-linked subun	0.078	0.340	0.124	0.000	0.356	0.260	0.193	0.155	0.139	0.200	0.262	0.161	1.09	0.87	0.92	0.28
META1_0695	Cytochrome c2 precursor	0.584	0.997	1.163	1.014	0.903	0.827	0.643	0.561	0.893	0.962	0.887	0.699	0.98	0.38	1.18	0.13
META1_0696	transcriptional regulator, MarR family	0.117	0.068	0.074	0.203	0.214	0.142	0.129	0.116	0.198	0.082	0.181	0.148	2.44	0.08	1.22	0.31
META1_0697	conserved protein of unknown function; putative expor	0.000	0.091	0.000	0.000	0.095	0.047	0.000	0.097	0.060	0.036	0.060	0.054	2.00	0.51	1.33	0.99
META1_0698	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.047	0.043	0.058	0.000	0.000	0.040	0.034	n.d.	0.12	1.25	0.99
META1_0699	putative penicillin-binding protein	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_0705	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.071	0.071	0.107	0.058	0.060	0.018	0.060	0.074	5.50	0.14	1.83	0.38
META1_0706	AFG1-like ATPase	0.000	0.227	0.173	0.000	0.380	0.213	0.257	0.348	0.278	0.154	0.252	0.296	2.59	0.44	1.76	0.38
META1_0708	Ribonuclease H (RNase H)	0.156	0.181	0.124	0.203	0.095	0.213	0.171	0.232	0.179	0.154	0.161	0.195	1.71	0.18	1.81	0.55
META1_0711	conserved protein of unknown function precursor	0.117	0.068	0.124	0.203	0.190	0.142	0.129	0.116	0.119	0.100	0.171	0.121	1.64	0.37	1.06	0.03
META1_0712	glutathione synthetase	0.078	0.204	0.173	0.338	0.404	0.473	0.300	0.290	0.318	0.163	0.423	0.302	2.50	0.06	1.07	0.05
META1_0715	N-acetylmuramoyl-L-alanine amidase (AGR_C_3833p)	0.000	0.000	0.000	0.000	0.048	0.047	0.086	0.077	0.040	0.000	0.040	0.067	n.d.	0.00	2.50	0.42
META1_0716	DnaJ-like protein	0.000	0.000	0.000	0.000	0.095	0.095	0.064	0.135	0.079	0.000	0.081	0.094	n.d.	0.00	1.75	0.37
META1_0717	conserved protein of unknown function	1.674	0.317	0.866	0.744	2.565	3.308	0.279	0.232	0.734	0.835	2.611	0.417	0.67	0.28	0.24	0.05
META1_0719	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.047	0.043	0.000	0.060	0.036	0.020	0.034	1.25	0.48	2.50	0.52
META1_0720	tRNA-dihydrouridine synthase A	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0722	putative response regulator receiver (CheY-like protein)	0.000	0.159	0.099	0.271	0.261	0.142	0.279	0.271	0.318	0.100	0.212	0.289	3.91	0.51	2.05	0.25
META1_0723	protein of unknown function; putative domain: Sensors	0.000	0.000	0.000	0.000	0.071	0.095	0.064	0.039	0.040	0.000	0.071	0.047	n.d.	0.00	1.00	0.30
META1_0727	conserved protein of unknown function	0.234	0.884	1.089	0.947	0.879	0.473	0.686	0.619	0.834	0.807	0.716	0.712	1.19	0.77	1.49	0.89
META1_0728	protein-(glutamine-N5) methyltransferase, release facto	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_0729	peptide chain release factor RF-1	0.156	0.340	0.247	0.203	0.570	0.449	0.193	0.251	0.218	0.263	0.464	0.222	1.14	0.78	0.72	0.17
META1_0730	conserved protein of unknown function	0.000	0.045	0.099	0.000	0.071	0.118	0.064	0.116	0.000	0.054	0.081	0.060	1.50	0.97	1.13	0.99
META1_0731	phosphoenolpyruvate-protein phosphotransferase	0.117	0.317	0.346	0.203	0.333	0.213	0.578	0.387	0.377	0.281	0.262	0.444	2.13	0.17	2.54	0.05
META1_0732	aspartate kinase	0.740	0.589	0.569	0.271	1.211	1.040	0.814	0.850	0.794	0.617	0.998	0.820	1.79	0.04	1.23	0.75
META1_0733	putative UbiG: ubiquinone biosynthesis O-methyltransf	0.000	0.068	0.124	0.135	0.095	0.047	0.150	0.116	0.099	0.073	0.081	0.121	2.25	0.41	2.25	0.35
META1_0734	conserved protein of unknown function	0.156	0.113	0.074	0.000	0.000	0.000	0.000	0.039	0.000	0.109	0.000	0.013	0.17	0.17	n.d.	0.37
META1_0735	Zn-binding quinone oxidoreductase	0.234	0.363	0.173	0.338	0.523	0.449	0.536	0.329	0.318	0.263	0.464	0.390	2.00	0.18	1.26	0.61
META1_0737	RuvC; Holliday junction nuclease	0.000	0.000	0.000	0.000	0.071	0.142	0.107	0.116	0.119	0.000	0.091	0.114	n.d.	0.00	1.89	0.39
META1_0738	polyprenyl-pyrophosphate binding protein	0.273	0.317	0.173	0.203	0.214	0.284	0.129	0.116	0.119	0.254	0.242	0.121	0.64	0.02	0.75	0.00
META1_0740	conserved protein of unknown function;	0.000	0.045	0.000	0.000	0.048	0.071	0.107	0.058	0.099	0.018	0.050	0.087	6.50	0.14	2.60	0.43
META1_0745	transcriptional regulator, rrf2 family	0.000	0.000	0.000	0.000	0.071	0.000	0.043	0.000	0.040	0.000	0.030	0.027	n.d.	0.12	1.33	0.49
META1_0746	bifunctional: nitric oxide dioxygenase (N-terminal); dihy	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0750	protein of unknown function	0.117	0.113	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_0751	subunit of cysteine synthase A and O-acetylserine sulfh	2.570	1.835	1.534	1.758	2.755	2.835	2.721	2.300	3.215	1.896	2.641	2.742	1.95	0.13	1.56	0.52
META1_0753	protein of unknown function	0.234	0.272	0.148	0.541	0.238	0.354	0.300	0.387	0.377	0.218	0.333	0.356	2.21	0.06	1.61	0.96
META1_0754	protein of unknown function	0.000	0.136	0.099	0.000	0.000	0.000	0.086	0.097	0.060	0.091	0.000	0.081	1.20	0.32	n.d.	0.00
META1_0755	putative FAD-dependent pyridine nucleotide-disulphide	0.000	0.159	0.124	0.000	0.095	0.071	0.064	0.116	0.000	0.109	0.071	0.060	0.75	0.94	1.29	0.99
META1_0756	LysR-type regulator of assimilatory C1 metabolism	0.117	0.159	0.074	0.000	0.309	0.165	0.150	0.174	0.139	0.118	0.202	0.155	1.77	0.23	1.15	0.32
META1_0757	fructose-1,6-bisphosphatase	1.441	1.042	0.965	1.150	0.808	1.158	1.007	0.966	0.873	1.107	1.008	0.948	1.16	0.24	1.41	0.57
META1_0758	phosphoribulokinase	0.000	0.181	0.148	0.203	0.000	0.118	0.364	0.251	0.278	0.127	0.081	0.296	3.14	0.47	5.50	0.48
META1_0760	conserved protein with domain of unknown function DI	0.506	0.385	0.396	0.271	0.071	0.354	0.364	0.367	0.417	0.417	0.222	0.383	1.24	0.33	2.59	0.23
META1_0763	protein of unknown function precursor	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.039	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_0765	conserved protein of unknown function	0.000	0.091	0.074	0.000	0.095	0.118	0.064	0.058	0.060	0.064	0.091	0.060	1.29	0.33	1.00	0.30
META1_0767	aloacid dehalogenase-like hydrolase	0.000	0.181	0.148	0.000	0.119	0.260	0.193	0.193	0.139	0.127	0.161	0.175	1.86	0.38	1.63	0.37
META1_0768	D-ribulose-5-phosphate 3-epimerase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.000	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_0769	phophinothricin N-acetyltransferase	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_0770	ornithine decarboxylase	0.350	0.385	0.544	0.744	0.689	0.827	0.793	0.677	0.417	0.435	0.756	0.625	1.94	0.19	1.24	0.35
META1_0772	molybdopterin biosynthesis protein B	0.273	0.340	0.247	0.000	0.285	0.189	0.257	0.309	0.298	0.290	0.202	0.289	1.34	0.93	2.15	0.41
META1_0773	adenylosuccinate lyase	2.142	1.790	2.227	0.676	1.544	1.512	1.200	1.121	1.131	2.032	1.401	1.149	0.76	0.00	1.23	0.97
META1_0774	Putative D-amino-acid transaminase (D-alanine aminot	0.662	0.589	0.495	0.473	0.214	0.591	0.621	0.599	0.675	0.572	0.413	0.632	1.49	0.39	2.29	0.20

META1_0775	conserved protein of unknown function; putative expor	0.078	0.068	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_0776	adenylosuccinate synthetase	1.830	1.835	1.757	1.014	1.188	1.370	1.050	1.218	0.834	1.805	1.240	1.035	0.77	0.01	1.25	0.36
META1_0777	conserved protein of unknown function	0.117	0.453	0.495	0.541	0.285	0.260	0.300	0.213	0.218	0.390	0.312	0.242	0.84	0.68	1.16	0.24
META1_0778	RNA polymerase sigma-32 (sigma H) factor	0.000	0.159	0.173	0.000	0.309	0.165	0.236	0.116	0.179	0.127	0.202	0.175	1.86	0.38	1.30	0.33
META1_0779	putative diguanylate cyclase/phosphodiesterase, GGDE	0.000	0.000	0.074	0.000	0.048	0.000	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META1_0783	ribosomal large subunit pseudouridine synthase D (Pse	0.000	0.000	0.000	0.000	0.071	0.142	0.086	0.077	0.040	0.000	0.091	0.067	n.d.	0.00	1.11	0.32
META1_0788	Peptidase M23B	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_0790	putative glutamyl-tRNA synthetase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0791	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.000	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_0793	chaperone Hsp90, heat shock protein C 62.5	4.244	5.189	5.988	4.802	5.677	4.749	4.585	4.368	4.168	5.262	5.151	4.368	1.12	0.21	1.27	0.08
META1_0795	putative gamma-glutamyltranspeptidase	1.635	1.065	1.039	0.609	1.235	0.992	0.771	0.677	0.734	1.188	1.038	0.726	0.82	0.03	1.05	0.36
META1_0796	Dihydroxyacetone kinase (Glycerone kinase)	0.078	0.566	0.668	0.271	0.143	0.165	0.171	0.232	0.119	0.490	0.171	0.175	0.48	0.44	1.53	0.73
META1_0797	Putative methyltransferase	0.584	0.544	0.322	0.473	0.071	0.213	0.236	0.232	0.337	0.472	0.192	0.269	0.77	0.06	2.11	0.61
META1_0799	Precorrin-6Y C(5,15)-methyltransferase [decarboxylatin	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.058	0.000	0.000	0.020	0.040	n.d.	0.12	3.00	0.53
META1_0800	putative cobalamin biosynthesis protein	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_0804	Precorrin-4 C(11)-methyltransferase (Precorrin-3 methy	0.078	0.113	0.148	0.135	0.190	0.095	0.150	0.251	0.159	0.118	0.141	0.188	2.15	0.11	2.00	0.31
META1_0805	cobyrinic acid a,c-diamide synthase	0.000	0.000	0.000	0.000	0.119	0.071	0.107	0.077	0.079	0.000	0.081	0.087	n.d.	0.00	1.63	0.37
META1_0806	putative transcriptional regulator, XRE family	0.078	0.227	0.173	0.541	0.333	0.213	0.536	0.541	0.536	0.172	0.312	0.538	4.21	0.02	2.58	0.16
META1_0807	conserved protein of unknown function	0.156	0.272	0.000	0.135	0.190	0.307	0.236	0.193	0.198	0.145	0.232	0.208	1.94	0.38	1.35	0.86
META1_0810	putative transcriptional regulator, Fur family; zinc uptak	0.078	0.000	0.049	0.000	0.048	0.000	0.086	0.116	0.079	0.036	0.020	0.094	3.50	0.43	7.00	0.15
META1_0813	ABC transporter, ATP-binding protein	0.000	0.045	0.000	0.000	0.119	0.095	0.064	0.058	0.060	0.018	0.091	0.060	4.50	0.13	1.00	0.30
META1_0816	DNA polymerase III, alpha subunit	0.000	0.000	0.049	0.000	0.166	0.047	0.171	0.174	0.159	0.018	0.091	0.168	12.50	0.18	2.78	0.47
META1_0817	putative membrane bound lytic murein transglycosylase	1.207	1.156	0.841	1.894	0.736	1.087	0.964	1.121	0.933	1.052	1.058	1.008	1.29	0.71	1.43	0.65
META1_0822	DNA topoisomerase IV subunitA	0.078	0.091	0.173	0.000	0.641	0.638	0.407	0.483	0.377	0.118	0.544	0.423	4.85	0.01	1.17	0.31
META1_0823	translation initiation factor if-1 (infA)	0.195	0.431	0.396	0.271	0.451	0.425	0.321	0.309	0.417	0.363	0.413	0.349	1.30	0.80	1.27	0.71
META1_0826	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.071	0.150	0.135	0.079	0.000	0.050	0.121	n.d.	0.00	3.60	0.48
META1_0827	conserved protein of unknown function	0.000	0.068	0.049	0.000	0.048	0.047	0.043	0.077	0.040	0.045	0.040	0.054	1.60	0.36	2.00	0.38
META1_0830	putative Formyl transferase (fmt-like)	0.117	0.136	0.173	0.000	0.000	0.071	0.129	0.058	0.139	0.145	0.030	0.108	1.00	0.34	5.33	0.13
META1_0834	protein of unknown function; putative membrane prote	0.000	0.000	0.000	0.000	0.095	0.071	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.12
META1_0835	outer membrane-specific lipoprotein transporter subun	0.078	0.317	0.322	0.271	0.214	0.354	0.450	0.367	0.238	0.263	0.282	0.349	1.79	0.35	1.86	0.41
META1_0836	putative Lipoprotein releasing system, transmembrane	0.000	0.136	0.148	0.000	0.119	0.189	0.064	0.097	0.000	0.109	0.131	0.054	0.67	0.93	0.62	0.93
META1_0837	proline-tRNA ligase	0.701	1.042	1.089	0.879	0.499	0.496	0.643	0.599	0.615	0.980	0.554	0.618	0.85	0.05	1.67	0.89
META1_0839	ethylmalonyl-CoA/methylmalonyl-CoA epimerase	0.234	0.408	0.322	0.338	0.238	0.331	0.214	0.232	0.298	0.336	0.292	0.249	1.00	0.27	1.28	0.27
META1_0840	putative hydrolase, metallo-beta-lactamase superfamily	0.857	1.156	1.039	0.338	1.211	0.803	0.921	1.024	1.032	1.043	0.907	0.995	1.29	0.86	1.64	0.39
META1_0841	putative biotin-protein ligase (birA-like)	0.000	0.091	0.049	0.000	0.000	0.000	0.086	0.039	0.040	0.054	0.000	0.054	1.33	0.34	n.d.	0.00
META1_0842	NADH-quinone oxidoreductase chain N (NADH dehydro	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.039	0.000	0.000	0.030	0.013	n.d.	0.37	0.67	0.97
META1_0843	NADH-quinone oxidoreductase chain M (NADH dehydro	0.000	0.181	0.124	0.000	0.071	0.165	0.129	0.135	0.159	0.118	0.101	0.141	1.62	0.36	2.10	0.41
META1_0844	NADH-quinone oxidoreductase chain L (NADH dehydrog	0.195	0.544	0.470	0.338	0.451	0.473	0.450	0.290	0.298	0.435	0.443	0.343	1.06	0.83	1.16	0.31
META1_0846	NADH-quinone oxidoreductase chain J (NADH dehydrog	0.312	0.363	0.223	0.000	0.190	0.213	0.536	0.367	0.576	0.299	0.171	0.491	2.21	0.07	4.29	0.53
META1_0847	NADH-quinone oxidoreductase subunit I (NADH dehydr	0.156	0.249	0.223	0.203	0.285	0.118	0.386	0.348	0.437	0.218	0.202	0.390	2.42	0.02	2.90	0.05
META1_0849	NADH-quinone oxidoreductase chain G (NADH dehydro	1.635	2.900	2.697	2.299	1.971	1.465	2.121	2.223	1.806	2.531	1.804	2.050	1.09	0.52	1.70	0.60
META1_0850	NADH-quinone oxidoreductase chain F (NADH dehydro	0.623	1.065	0.866	0.473	0.713	0.662	0.985	1.082	0.774	0.889	0.655	0.948	1.44	0.55	2.17	0.05
META1_0851	NADH-quinone oxidoreductase chain E (NADH dehydro	0.818	0.974	1.014	0.676	0.926	0.425	1.007	0.908	1.131	0.953	0.675	1.015	1.44	0.42	2.25	0.13
META1_0852	NADH-quinone oxidoreductase chain D (NADH dehydro	0.935	0.929	0.841	0.338	0.831	0.827	0.771	0.793	0.456	0.898	0.756	0.672	1.01	0.15	1.33	0.87
META1_0853	NADH-quinone oxidoreductase chain C (NADH dehydro	0.857	1.020	0.495	0.609	0.546	0.827	0.707	0.870	0.496	0.789	0.675	0.692	1.18	0.69	1.54	0.87
META1_0854	NADH-quinone oxidoreductase chain B (NADH dehydro	0.350	0.340	0.124	0.473	0.214	0.165	0.407	0.309	0.318	0.263	0.232	0.343	1.76	0.40	2.22	0.43
META1_0856	putative SCP-like extracellular protein	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0857	pseudoazurin	1.285	0.634	1.014	0.406	0.095	0.047	0.150	0.135	0.179	0.925	0.121	0.155	0.23	0.00	1.92	0.74
META1_0858	carbamoyl phosphate synthase, large subunit	1.713	2.243	2.920	4.937	3.967	3.355	3.085	2.938	3.453	2.368	3.850	3.159	1.80	0.10	1.23	0.11
META1_0860	protein of unknown function; putative exported protein	0.195	0.000	0.000	0.135	0.143	0.142	0.000	0.000	0.000	0.045	0.141	0.000	0.00	0.37	0.00	0.00
META1_0861	conserved protein of unknown function	0.156	0.204	0.223	0.000	0.285	0.236	0.193	0.232	0.179	0.200	0.222	0.202	1.36	0.77	1.36	0.34
META1_0863	putative transcriptional regulator, LysR family	0.584	0.702	0.767	0.541	0.095	0.331	0.514	0.638	0.576	0.699	0.262	0.578	1.12	0.17	3.31	0.20
META1_0864	3-dehydroquinate dehydratase (3-dehydroquinase) (Typ	0.000	0.159	0.074	0.000	0.119	0.071	0.043	0.077	0.079	0.091	0.081	0.067	1.00	0.31	1.25	0.33
META1_0865	acetyl-CoA carboxylase, biotin carboxyl carrier protein s	0.000	0.159	0.074	0.203	0.333	0.354	0.214	0.271	0.298	0.091	0.323	0.262	3.90	0.52	1.22	0.62
META1_0866	acetyl CoA carboxylase, biotin carboxylase subunit	0.584	0.476	0.569	0.406	0.665	0.685	0.514	0.522	0.456	0.535	0.635	0.497	1.25	0.33	1.17	0.48
META1_0868	putative transcriptional regulator, TetR family	0.000	0.068	0.000	0.000	0.143	0.142	0.043	0.077	0.060	0.027	0.121	0.060	3.00	0.11	0.75	0.26
META1_0870	conserved protein of unknown function; putative expor	0.078	0.113	0.000	0.000	0.119	0.095	0.086	0.097	0.060	0.064	0.091	0.081	1.71	0.35	1.33	0.34
META1_0871	NADH:ubiquinone oxidoreductase 17.2 kD subunit	0.312	0.181	0.049	0.203	0.166	0.047	0.300	0.290	0.278	0.163	0.121	0.289	2.39	0.26	3.58	0.12
META1_0872	ribonucleoside-diphosphate reductase, adenosylcobala	0.935	1.065	0.990	1.961	1.924	1.654	1.478	1.643	1.945	1.007	1.814	1.694	2.27	0.00	1.40	0.39
META1_0887	conserved protein of unknown function	0.000	0.091	0.148	0.000	0.000	0.000	0.043	0.039	0.040	0.091	0.000	0.040	0.60	0.25	n.d.	0.00
META1_0891	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.039	0.000	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META1_0930	transcriptional regulator, LysR family	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.039	0.060	0.000	0.020	0.054	n.d.	0.00	4.00	0.12
META1_0938	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_0943	ABC transporter, ATPase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.116	0.000	0.000	0.000	0.040	n.d.	0.37	n.d.	0.37
META1_0945	ABC transporter, periplasmic protein	0.000	0.091	0.000	0.000	0.000	0.000	0.171	0.097	0.198	0.036	0.000	0.155	5.75	0.14	n.d.	0.00
META1_0946	Acyl-CoA dehydrogenase	0.000	0.000	0.000	0.000	0.048	0.071	0.150	0.097	0.060	0.000	0.050	0.101	n.d.	0.00	3.00	0.45
META1_0947	putative alkanesulfonate monooxygenase	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.097	0.139	0.000	0.000	0.114	n.d.	0.00	n.d.	0.00
META1_0948	ABC transporter, substrate-binding protein, aliphatic su	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0954	eshA	0.350	1.156	0.866	0.947	1.378	1.583	1.221	1.063	1.389	0.862	1.401	1.223	1.92	0.21	1.31	0.81
META1_0955	putative cysteine desulfurase	0.000	0.113	0.074	0.135	0.261	0.118	0.257	0.251	0.238	0.073	0.181	0.249	4.63	0.54	2.06	0.15
META1_0960	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_0962	cold shock DNA binding protein CspA	0.701	0.521	0.767	0.541	0.404	0.284	0.214	0.309	0.576	0.653	0.373	0.370	0.76	0.10	1.49	0.66
META1_0965	protein of unknown function	0.117	0.091	0.124	0.000	0.000	0.000	0.086	0.097	0.179	0.109	0.000	0.121	1.50	0.88	n.d.	0.00
META1_0966	conserved protein of unknown function; putative expor	0.000	0.340	0.099	0.135	0.285	0.000	0.214	0.290	0.139	0.172	0.141	0.215	1.68	0.40	2.29	0.38
META1_0967	putative periplasmic binding protein; improves cobalt u	0.000	0.000	0.000	0.203	0.095	0.071	0.171	0.232	0.099	0.000	0.101	0.168	n.d.	0.00	2.50	0.43
META1_0968	putative histidine kinase of the HWE family	0.000	0.068	0.000	0.000	0.071	0.000	0.107	0.135	0.159	0.027	0.030	0.134	6.67	0.15	6.67	0.15
META1_0969	conserved protein of unknown function	0.117	0.113	0.173	0.000	0.071	0.000	0.107	0.058	0.099	0.136	0.030	0.087	0.87	0.14	4.33	0.12
META1_0975	urease gamma (N-terminal) and beta (C-terminal) subun	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0981	putative TonB-dependent porin receptor	0.078	0.000	0.000	0.000	0.119	0.142	0.000	0.000	0.000	0.018	0.111	0.000	0.00	0.37	0.00	0.12
META1_0984	conserved protein of unknown function	0.000	0.181	0.074	0.135	0.000	0.000	0.321	0.309	0.318	0.100	0.020	0.316	4.27	0.54	23.50	0.16
META1_0985	conserved protein of unknown function; putative OsmC	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.077	0.159	0.000	0.000	0.114	n.d.	0.00	n.d.	0.00
META1_0987	conserved protein of unknown function, PAS domain S-	0.000	0.000	0.000	0.000	0.000	0.000	0.193	0.232	0.238	0.000	0.000	0.222	n.d.	0.00	n.d.	0.00
META1_0988	formyl-CoA transferase, NAD(P)-binding	0.000	0.000	0.000	0.000	0.000	0.000	11.376	11.656	11.531	0.000	0.000	11.526	n.d.	0.00	n.d.	0.00
META1_0989	Phospholipase/Carboxylesterase	0.000	0.000	0.000	0.000	0.000	0.000	0.386	0.483	0.377	0.000	0.000	0.417	n.d.	0.00	n.d.	0.00
META1_0990	putative oxalyl-CoA decarboxylase (oxc, yfdU)	0.000	0.000	0.000	0.000	0.000	0.000	11.676	11.578	11.571	0.000	0.000	11.606	n.d.	0.00	n.d.	0.00
META1_0992	oxalate/formate antiporter	0.000	0.000	0.000	0.000	0.000	0.000	0.578	0.735	0.675	0.000	0.000	0.665	n.d.	0.00	n.d.	0.00
META1_0993	oxalate/formate antiporter	0.000	0.000	0.000	0.000	0.000	0.000	1.071	1.179	0.973	0.000	0.000	1.075	n.d.	0.00	n.d.	0.00
META1_0994	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_0995	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.174	0.198	0.000	0.000	0.155	n.d.	0.00	n.d.	0.00
META1_0999	formyl-CoA transferase, NAD(P)-binding	0.000	0.000	0.000	0.000	0.000	0.000	1.435	1.759	1.211	0.000	0.000	1.472	n.d.	0.00	n.d.	0.00
META1_1001	transcriptional regulator, GntR family	0.312	0.295	0.272	0.473	0.285	0.473	1.050	1.218	0.714	0.290	0.393	0.995	4.63	0.00	3.79	0.02
META1_1002	putative GTPase, putative cobalamin biosynthesis prote	0.000	0.113	0.223	0.135	0.214	0.236	0.279	0.155	0.060	0.127	0.212	0.161	1.71	0.36	1.14	0.53
META1_1003	serine-type D-alanyl-D-alanine carboxypeptidase precur	0.000	0.068	0.000	0.000	0.095	0.236	0.150	0.000	0.119	0.027	0.141	0.087	4.33	0.56	0.93	0.99
META1_1004	conserved protein of unknown function	0.078	0.068	0.074	0.000	0.095	0.095	0.064	0.116	0.000	0.073	0.081	0.060	1.13	0.35	1.13	0.99
META1_1009	putative 6-pyruvol tetrahydrobiopterin synthase	0.000	0.136	0.198	0.000	0.048	0.142	0.129	0.097	0.119	0.127	0.081	0.114	1.21	0.32	2.13	0.42
META1_1010	Putative regulator, ATP-binding.	0.000	0.068	0.000	0.203	0.119	0.118	0.086	0.077	0.079	0.027	0.131	0.081	4.00	0.12	0.92	0.04
META1_1011	putative LmbE-like protein	0.273	0.227	0.247	0.203	0.190	0.260	0.321	0.309	0.278	0.245	0.222	0.302	1.67	0.05	2.05	0.03
META1_1012	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.060	0.000	0.000	0.054	n.d.	0.00	n.d.	0.00
META1_1016	putative glycosyl transferase; putative UDP-N-acetylglu	0.000	0.000	0.000	0.000	0.071	0.000	0.129	0.039	0.079	0.000	0.030	0.081	n.d.	0.00	4.00	0.12
META1_1017	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.095	0.189	0.107	0.174	0.179	0.000	0.121	0.155	n.d.	0.00	1.92	0.39
META1_1018	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.119	0.142	0.193	0.058	0.040	0.000	0.111	0.094	n.d.	0.00	1.27	0.31
META1_1019	putative Phosphoryl transfer system, HPr	0.117	0.159	0.198	0.000	0.095	0.118	0.107	0.155	0.119	0.163	0.091	0.128	1.06	0.33	2.11	0.40
META1_1020	putative PTS system subfamily mannose/fructose-speci	0.195	0.295	0.297	0.000	0.261	0.284	0.257	0.213	0.337	0.272	0.232	0.269	1.33	0.90	1.74	0.37
META1_1022	integral membrane sensor signal transduction histidine	0.000	0.068	0.099	0.000	0.143	0.000	0.064	0.058	0.079	0.064	0.060	0.067	1.43	0.35	1.67	0.09
META1_1023	Two-component response regulator ChvI	0.389	0.476	0.322	0.000	0.285	0.449	0.450	0.522	0.397	0.399	0.312	0.457	1.55	0.34	2.19	0.41
META1_1024	conserved protein of unknown function; putative pyride	0.000	0.136	0.198	0.000	0.000	0.047	0.150	0.251	0.159	0.127	0.020	0.188	2.00	0.39	14.00	0.19
META1_1025	GTP-binding protein lepA	0.545	1.292	1.311	1.014	1.330	0.756	1.221	1.256	1.131	1.125	1.038	1.203	1.44	0.51	1.74	0.35
META1_1027	Heavy metal efflux pump CzcA	0.000	0.159	0.099	0.000	0.333	0.118	0.000	0.097	0.119	0.100	0.192	0.074	1.00	0.98	0.58	0.93
META1_1029	protein of unknown function; putative exported protein	0.195	0.249	0.173	0.000	0.261	0.118	0.150	0.213	0.139	0.209	0.161	0.168	1.09	0.28	1.56	0.37
META1_1030	putative bifunctional N-terminal transglycosylase/C-ter	0.000	0.181	0.148	0.000	0.095	0.000	0.043	0.039	0.060	0.127	0.040	0.047	0.50	0.22	1.75	0.09
META1_1031	conserved protein of unknown function; putative Flagel	0.000	0.068	0.049	0.338	0.214	0.189	0.129	0.155	0.099	0.045	0.222	0.128	3.80	0.49	0.86	0.04
META1_1032	conserved protein of unknown function; putative Flagel	0.000	0.431	0.520	0.812	0.641	0.662	0.450	0.464	0.456	0.363	0.675	0.457	1.70	0.37	1.01	0.00
META1_1033	putative flagellar FlbT family protein	0.078	0.091	0.049	0.203	0.214	0.284	0.236	0.135	0.179	0.073	0.242	0.181	3.38	0.02	1.13	0.25
META1_1035	Acyltransferase 3 family	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_1042	conserved protein of unknown function	0.000	0.045	0.000	0.135	0.048	0.047	0.000	0.097	0.060	0.018	0.060	0.054	4.00	0.55	1.33	0.36
META1_1045	taurine transport protein (ABC superfamily, atp_bind)	0.000	0.000	0.000	0.000	0.166	0.000	0.043	0.000	0.000	0.000	0.071	0.013	n.d.	0.37	0.29	0.92
META1_1047	Extracellular solute-binding protein, family 3 precursor	0.078	0.181	0.124	0.676	0.000	0.284	0.171	0.155	0.139	0.136	0.222	0.155	1.53	0.38	1.05	0.23
META1_1048	septum site-determining protein	0.078	0.136	0.198	0.203	0.071	0.165	0.171	0.174	0.179	0.145	0.131	0.175	1.63	0.32	2.00	0.45
META1_1050	GTP-binding elongation factor family protein with P-loo	1.986	2.470	2.920	3.855	3.159	2.906	2.528	2.416	2.580	2.522	3.155	2.507	1.34	0.79	1.19	0.04
META1_1051	putative methyl-accepting chemotaxis sensory transduc	0.000	0.340	0.148	0.000	0.356	0.095	0.193	0.135	0.198	0.191	0.192	0.175	1.24	0.34	1.37	0.37
META1_1052	putative septum site-determining protein minC	0.000	0.159	0.223	0.338	0.285	0.307	0.279	0.251	0.198	0.145	0.302	0.242	2.25	0.41	1.20	0.09
META1_1053	membrane ATPase of the MinC-MinD-MinE system	0.234	0.657	0.817	0.947	0.404	0.898	0.557	0.657	0.476	0.617	0.695	0.565	1.24	0.80	1.22	0.48
META1_1054	cell division topological specificity factor	0.078	0.159	0.198	0.203	0.190	0.189	0.064	0.058	0.040	0.154	0.192	0.054	0.47	0.04	0.42	0.00
META1_1055	putative cytochrome P450 family enzyme	0.000	0.113	0.000	0.000	0.095	0.095	0.064	0.097	0.079	0.045	0.081	0.081	2.40	0.10	1.50	0.35

META1_1076	TonB-dependent outer membrane transporter associat	0.000	0.000	0.000	0.676	0.000	0.000	0.000	0.000	0.000	0.000	0.101	0.000	n.d.	n.d.	0.00	0.37
META1_1077	periplasmic binding protein associated to improved cob	0.078	0.136	0.074	1.623	0.261	0.142	0.386	0.309	0.179	0.100	0.413	0.289	3.91	0.02	1.05	0.68
META1_1102	Transcriptional regulator, LysR family	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.018	0.000	0.013	1.00	1.00	n.d.	0.37
META1_1103	short-chain dehydrogenase/reductase	0.117	0.227	0.148	0.000	0.071	0.000	0.107	0.116	0.139	0.172	0.030	0.121	0.95	0.26	6.00	0.14
META1_1109	conserved protein of unknown function precursor	0.312	0.453	0.346	0.609	0.190	0.142	0.279	0.232	0.298	0.381	0.232	0.269	0.95	0.08	1.74	0.91
META1_1116	phosphoglyceromutase	0.000	0.000	0.000	0.135	0.095	0.071	0.086	0.174	0.079	0.000	0.091	0.114	n.d.	0.00	1.89	0.79
META1_1122	putative short-chain dehydrogenase/reductase SDR	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.097	0.000	0.027	0.000	0.034	1.67	0.98	n.d.	0.37
META1_1123	conserved protein of unknown function	0.000	0.091	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.073	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1124	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1132	putative tRNA delta(2)-isopentenylpyrophosphate trans	0.117	0.000	0.049	0.000	0.000	0.047	0.064	0.058	0.000	0.045	0.020	0.040	1.20	0.98	3.00	0.53
META1_1135	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.058	0.040	0.000	0.020	0.034	n.d.	0.12	2.50	0.52
META1_1136	conserved protein of unknown function; putative expor	0.156	0.113	0.272	0.000	0.214	0.260	0.064	0.116	0.079	0.181	0.202	0.087	0.65	0.09	0.65	0.24
META1_1137	Putative cytochrome c550	0.195	0.204	0.198	0.338	0.071	0.071	0.171	0.213	0.198	0.200	0.111	0.195	1.32	0.69	2.64	0.41
META1_1138	conserved protein of unknown function, periplasmic bi	0.701	0.657	0.718	0.473	0.238	0.402	0.150	0.425	0.337	0.689	0.343	0.309	0.61	0.05	1.35	0.55
META1_1139	Quinoprotein ethanol dehydrogenase precursor (QEDH	0.156	0.068	0.445	0.000	0.333	0.189	0.214	0.271	0.238	0.227	0.222	0.242	1.44	0.55	1.64	0.37
META1_1141	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_1142	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1145	protein of unknown function; putative exported protei	0.078	0.136	0.173	0.000	0.095	0.000	0.000	0.000	0.000	0.136	0.040	0.000	0.00	0.00	0.00	0.37
META1_1149	putative peptidase	0.000	0.068	0.223	0.000	0.119	0.000	0.000	0.097	0.099	0.109	0.050	0.067	0.83	0.97	2.00	0.51
META1_1151	conserved protein of unknown function, Cupin barrel d	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1152	Short-chain dehydrogenase/reductase SDR	0.000	0.045	0.074	0.000	0.000	0.000	0.000	0.000	0.040	0.045	0.000	0.013	0.40	0.54	n.d.	0.37
META1_1154	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.000	0.071	0.086	0.077	0.079	0.091	0.030	0.081	1.20	0.33	4.00	0.12
META1_1155	conserved protein of unknown function, putative unive	0.389	0.612	0.520	0.000	0.000	0.118	0.257	0.135	0.119	0.526	0.050	0.168	0.43	0.01	5.00	0.13
META1_1156	putative cytochrome c, class I	0.000	0.159	0.099	0.000	0.095	0.071	0.043	0.000	0.060	0.100	0.071	0.034	0.45	0.90	0.71	0.95
META1_1157	transcriptional regulator, Crp/Fnr family	0.078	0.272	0.198	0.135	0.000	0.142	0.150	0.193	0.159	0.200	0.081	0.168	1.14	0.94	3.13	0.40
META1_1160	cytochrome d terminal oxidase, polypeptide subunit I	0.078	0.408	0.322	0.000	0.095	0.142	0.043	0.116	0.060	0.299	0.101	0.074	0.33	0.12	1.10	0.30
META1_1163	transcriptional regulator, DeoR family	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.077	0.000	0.000	0.020	0.027	n.d.	0.37	2.00	0.97
META1_1167	Cellulose synthase (UDP-forming)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1169	Putative cellulase, endoglucanase (celC)	0.000	0.113	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.045	0.020	0.000	0.00	0.37	0.00	0.37
META1_1170	Conserved protein of unknown function; putative expor	0.000	0.045	0.099	0.000	0.071	0.000	0.000	0.000	0.000	0.054	0.030	0.000	0.00	0.12	0.00	0.37
META1_1175	putative NADH dehydrogenase (ubiquinone) 1 alpha su	1.869	2.379	1.955	1.488	1.496	1.677	1.521	1.237	1.310	2.105	1.572	1.351	0.87	0.01	1.29	0.13
META1_1178	Primosome factor N' (replication factor Y)	0.000	0.091	0.124	0.000	0.143	0.165	0.236	0.116	0.099	0.082	0.131	0.148	2.44	0.42	1.69	0.36
META1_1179	conserved protein of unknown function	0.506	0.634	0.693	0.609	0.665	0.638	0.664	0.406	0.536	0.626	0.645	0.531	1.14	0.45	1.23	0.25
META1_1186	Short-chain dehydrogenase/reductase SDR	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1189	putative ubiquinone biosynthesis protein	0.000	0.363	0.272	0.271	0.238	0.260	0.321	0.271	0.337	0.245	0.252	0.309	1.70	0.37	1.84	0.07
META1_1201	putative thioredoxin domain protein precursor	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_1203	conserved protein of unknown function; putative expor	0.078	0.181	0.000	0.135	0.143	0.095	0.000	0.077	0.099	0.091	0.121	0.060	0.90	0.96	0.75	0.42
META1_1207	beta-lactamase domain protein, putative hydroxyacylgl	0.000	0.045	0.074	0.000	0.071	0.071	0.086	0.097	0.060	0.045	0.060	0.081	2.40	0.42	2.00	0.39
META1_1208	rhodanese domain protein, putative sulfur transferase	0.000	0.045	0.000	0.000	0.095	0.189	0.129	0.077	0.099	0.018	0.121	0.101	7.50	0.15	1.25	0.33
META1_1224	Putative oxidoreductase, molybdopterin binding subunit	0.156	0.295	0.297	0.000	0.095	0.071	0.086	0.097	0.040	0.263	0.071	0.074	0.38	0.02	1.57	0.35
META1_1225	putative sulfite:cytochrome c oxidoreductase subunit B	0.000	0.181	0.124	0.000	0.071	0.047	0.000	0.000	0.000	0.118	0.050	0.000	0.00	0.12	0.00	0.12
META1_1226	conserved protein of unknown function	0.156	0.363	0.223	0.000	0.048	0.142	0.343	0.309	0.198	0.263	0.081	0.282	1.45	0.59	5.25	0.58
META1_1229	Transcriptional regulator, LysR family	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_1231	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1233	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.193	0.135	0.099	0.000	0.020	0.141	n.d.	0.00	10.50	0.17
META1_1235	40-residue YVTN beta-propeller repeat family protein	0.078	0.249	0.173	0.000	0.095	0.071	0.257	0.251	0.218	0.181	0.071	0.242	1.80	0.24	5.14	0.55
META1_1238	putative Cyclic nucleotide-binding protein	0.000	0.068	0.000	0.000	0.071	0.071	0.129	0.116	0.099	0.027	0.060	0.114	5.67	0.14	2.83	0.44
META1_1240	Thioredoxin-related	0.000	0.227	0.099	0.000	0.048	0.047	0.107	0.077	0.079	0.127	0.040	0.087	0.93	0.30	3.25	0.46
META1_1255	protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_1258	putative glycosyl transferase	1.558	1.971	2.177	2.367	1.948	1.441	1.457	1.740	1.866	1.950	1.794	1.694	1.17	0.40	1.42	0.52
META1_1259	protein of unknown function, putative methyltransfera	0.000	0.091	0.124	0.338	0.190	0.142	0.086	0.116	0.198	0.082	0.192	0.134	2.22	0.40	1.05	0.22
META1_1262	putative Peptidoglycan-binding protein	0.312	0.272	0.297	0.473	0.499	0.260	0.321	0.367	0.337	0.290	0.393	0.343	1.59	0.05	1.31	0.54
META1_1264	conserved protein of unknown function precursor; puta	0.428	0.431	0.346	0.135	0.428	0.260	0.321	0.387	0.298	0.399	0.312	0.336	1.14	0.16	1.61	0.43
META1_1265	conserved protein of unknown function; putative expor	0.234	0.181	0.124	0.000	0.190	0.095	0.150	0.251	0.198	0.172	0.121	0.202	1.58	0.64	2.50	0.43
META1_1266	conserved protein of unknown function	0.156	0.113	0.000	0.000	0.048	0.071	0.000	0.000	0.000	0.082	0.050	0.000	0.00	0.12	0.00	0.12
META1_1271	transcriptional regulator, GntR family	0.000	0.000	0.000	0.000	0.000	0.000	0.129	0.000	0.000	0.000	0.000	0.040	n.d.	0.37	n.d.	0.37
META1_1272	putative tripartite ATP-independent periplasmic transp	0.195	0.113	0.124	0.271	0.000	0.071	0.321	0.329	0.437	0.136	0.071	0.363	3.60	0.01	7.71	0.54
META1_1273	putative tripartite ATP-independent periplasmic transp	0.078	0.113	0.074	0.000	0.095	0.071	0.150	0.174	0.198	0.091	0.071	0.175	2.60	0.01	3.71	0.49
META1_1278	Cysteine synthase	0.350	0.317	0.371	0.473	0.380	0.425	0.343	0.290	0.337	0.345	0.413	0.323	1.26	0.38	1.17	0.03
META1_1280	conserved protein of unknown function precursor	0.000	0.068	0.074	0.000	0.000	0.071	0.107	0.077	0.079	0.054	0.030	0.087	2.17	0.40	4.33	0.13
META1_1282	conserved protein of unknown function (large extracell	1.674	1.722	1.633	0.947	1.021	0.803	0.643	0.773	0.834	1.678	0.917	0.753	0.61	0.00	1.23	0.12
META1_1285	conserved protein of unknown function; putative trans	0.000	0.113	0.074	0.000	0.000	0.071	0.129	0.155	0.119	0.073	0.030	0.134	2.50	0.43	6.67	0.15
META1_1288	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_1291	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.095	0.118	0.043	0.000	0.000	0.000	0.091	0.013	n.d.	0.37	0.22	0.58
META1_1292	cytochrome c-type biogenesis protein CycL precursor	0.000	0.000	0.049	0.000	0.000	0.047	0.000	0.097	0.000	0.018	0.020	0.034	2.50	0.96	2.50	0.96
META1_1293	cytochrome c-type biogenesis protein CycK; heme lyase	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1294	cytochrome c-type biogenesis protein CycJ; periplasmic	0.117	0.000	0.099	0.271	0.143	0.000	0.086	0.135	0.198	0.064	0.101	0.141	3.00	0.41	2.10	0.32
META1_1295	cytochrome c-type biogenesis protein CycH	0.000	0.000	0.000	0.000	0.119	0.000	0.107	0.155	0.099	0.000	0.050	0.121	n.d.	0.00	3.60	0.12
META1_1296	integral membrane sensor signal transduction histidine	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1298	putative phoP: DNA-binding response regulator in two-	0.234	0.272	0.198	0.271	0.143	0.165	0.236	0.290	0.198	0.236	0.171	0.242	1.38	0.87	2.12	0.32
META1_1316	putative Peptidase S1 and S6, chymotrypsin/Hap [Precu	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.000	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_1317	putative peptidase	0.156	0.204	0.148	0.135	0.000	0.165	0.236	0.155	0.119	0.172	0.091	0.168	1.32	0.91	2.78	0.39
META1_1324	Precorrin-3B C(17)-methyltransferase (Precorrin-3 meth	0.117	0.091	0.173	0.203	0.143	0.165	0.150	0.271	0.159	0.127	0.161	0.195	2.07	0.19	1.81	0.67
META1_1325	Precorrin-2 C(20)-methyltransferase (S-adenosyl-L- met	0.078	0.000	0.000	0.000	0.000	0.118	0.193	0.232	0.139	0.018	0.050	0.188	14.00	0.16	5.60	0.14
META1_1326	Precorrin-8X methylmutase (Precorrin isomerase) (HBA	0.506	0.204	0.148	0.203	0.356	0.307	0.343	0.348	0.397	0.254	0.312	0.363	1.93	0.37	1.74	0.22
META1_1327	precorrin-3B synthase	0.000	0.000	0.000	0.000	0.095	0.000	0.043	0.000	0.000	0.000	0.040	0.013	n.d.	0.37	0.50	0.96
META1_1328	putative cobaltochelatase, CobN subunit	0.000	0.045	0.074	0.135	0.333	0.000	0.150	0.058	0.060	0.045	0.161	0.087	2.60	0.42	0.81	0.25
META1_1329	conserved protein of unknown function	0.234	0.000	0.099	0.000	0.190	0.165	0.086	0.077	0.119	0.091	0.151	0.094	1.40	0.31	0.93	0.29
META1_1330	cobalamin biosynthesis protein CobW	1.090	0.295	0.346	0.609	0.594	0.638	0.279	0.232	0.179	0.499	0.615	0.228	0.62	0.15	0.56	0.00
META1_1331	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.095	0.095	0.000	0.000	0.060	0.054	0.081	0.020	0.50	0.53	0.38	0.55
META1_1335	transcriptional regulator, MarR family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1337	Cob(I)yrinic acid a,c-diamide adenosyltransferase (Cob(	0.195	0.249	0.223	0.000	0.261	0.189	0.150	0.174	0.179	0.227	0.192	0.168	1.00	0.04	1.32	0.33
META1_1338	fumarase C	0.117	0.295	0.148	0.000	0.190	0.260	0.000	0.000	0.000	0.200	0.192	0.000	0.00	0.00	0.00	0.12
META1_1339	formaldehyde activating enzyme homolog	0.584	0.317	0.322	0.947	0.974	0.732	0.836	0.986	0.754	0.381	0.867	0.860	3.05	0.02	1.49	0.83
META1_1340	protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1341	protein of unknown function; putative exported protei	0.117	0.000	0.000	0.000	0.119	0.071	0.000	0.039	0.000	0.027	0.081	0.013	0.67	0.94	0.25	0.57
META1_1342	putative alpha/beta hydrolase, putative epoxide hydrol	0.000	0.159	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1343	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1348	conserved protein of unknown function; putative mem	0.195	0.227	0.297	0.000	0.190	0.165	0.043	0.097	0.060	0.245	0.151	0.067	0.37	0.01	0.67	0.25
META1_1349	conserved protein of unknown function; putative doub	0.117	0.204	0.371	0.000	0.214	0.071	0.129	0.155	0.099	0.245	0.121	0.128	0.70	0.23	1.58	0.38
META1_1350	conserved protein of unknown function (DUF58)	0.000	0.068	0.049	0.000	0.000	0.000	0.086	0.058	0.099	0.045	0.000	0.081	2.40	0.42	n.d.	0.00
META1_1351	putative ATPase, MoxR-like protein	0.740	0.566	0.544	0.203	0.523	0.567	0.557	0.483	0.397	0.599	0.494	0.477	1.08	0.14	1.45	0.61
META1_1352	conserved protein of unknown function; putative Thioe	0.000	0.091	0.000	0.000	0.048	0.000	0.086	0.058	0.060	0.036	0.020	0.067	2.50	0.10	5.00	0.13
META1_1353	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.119	0.071	0.129	0.174	0.139	0.091	0.081	0.148	2.20	0.41	2.75	0.44
META1_1356	putative nucleotidyl transferase/polymerase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1357	ATP synthase F1 sector epsilon subunit	0.740	0.544	0.371	1.217	0.689	0.756	0.471	0.561	0.873	0.526	0.796	0.638	1.64	0.62	1.20	0.26
META1_1358	protein of unknown function; putative exported protei	0.000	0.000	0.000	0.000	0.048	0.047	0.043	0.000	0.000	0.000	0.040	0.013	n.d.	0.37	0.50	0.52
META1_1359	ATP synthase F1 sector subunit beta	6.658	4.781	5.790	6.154	5.724	6.356	5.784	5.663	6.688	5.588	6.058	6.048	1.46	0.63	1.50	0.91
META1_1360	ATP synthase F1 sector gamma subunit	1.752	1.314	1.435	2.367	1.496	2.103	1.435	1.430	1.290	1.461	1.885	1.384	1.28	0.47	1.10	0.07
META1_1361	ATP synthase F1 sector subunit alpha	6.152	4.396	6.211	5.005	4.727	6.072	4.499	4.774	4.704	5.470	5.342	4.664	1.15	0.21	1.31	0.21
META1_1362	putative ATP synthase delta chain (atpH)	1.207	1.201	1.014	0.947	1.449	1.205	1.114	1.024	1.032	1.134	1.270	1.055	1.26	0.31	1.25	0.42
META1_1363	Ferrochelatase (Protoheme ferro-lyase) (Heme syntheta	0.273	0.113	0.148	0.271	0.333	0.260	0.214	0.251	0.198	0.163	0.292	0.222	1.83	0.35	1.14	0.06
META1_1364	Putative methyltransferase	0.312	0.272	0.346	0.744	0.451	0.378	0.407	0.445	0.357	0.308	0.464	0.403	1.76	0.05	1.30	0.35
META1_1366	Uracil-DNA glycosylase (UDG)	0.234	0.317	0.247	0.135	0.095	0.095	0.171	0.193	0.179	0.272	0.101	0.181	0.90	0.02	2.70	0.01
META1_1367	conserved protein of unknown function, ChrB-like dom	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.077	0.079	0.000	0.000	0.067	n.d.	0.00	n.d.	0.00
META1_1370	putative cell-binding factor 2 precursor (Major antigen	1.363	0.929	1.089	0.879	0.689	1.181	0.643	0.812	0.834	1.089	0.927	0.766	0.95	0.05	1.24	0.40
META1_1371	preprotein translocase subunit, ATPase	2.336	2.855	2.845	2.638	3.800	2.646	2.357	3.189	2.957	2.731	3.135	2.850	1.41	0.66	1.36	0.72
META1_1378	DNA polymerase III epsilon subunit	0.000	0.068	0.124	0.000	0.119	0.142	0.064	0.097	0.079	0.073	0.111	0.081	1.50	0.35	1.09	0.31
META1_1379	dephospho-CoA kinase (dephosphocoenzyme A kinase)	0.000	0.045	0.099	0.000	0.048	0.000	0.086	0.058	0.000	0.054	0.020	0.047	1.17	0.99	3.50	0.54
META1_1380	putative shikimate 5-dehydrogenase (aroE)	0.117	0.045	0.148	0.541	0.000	0.165	0.236	0.213	0.179	0.100	0.151	0.208	2.82	0.09	2.07	0.32
META1_1382	Maf-like protein	0.117	0.204	0.247	0.338	0.238	0.118	0.150	0.251	0.198	0.200	0.202	0.202	1.36	0.78	1.50	0.83
META1_1384	conserved protein of unknown function, UPF0085 prote	0.195	0.295	0.371	0.000	0.000	0.118	0.300	0.290	0.238	0.299	0.050	0.276	1.24	0.97	8.20	0.16
META1_1385	uroporphyrinogen decarboxylase	0.350	0.408	0.322	0.676	0.451	0.402	0.407	0.387	0.357	0.363	0.464	0.383	1.43	0.44	1.24	0.18
META1_1388	conserved protein of unknown function, putative expor	0.000	0.136	0.049	0.000	0.000	0.000	0.064	0.000	0.000	0.073	0.000	0.020	0.38	0.53	n.d.	0.37
META1_1389	ATP phosphoribosyltransferase	0.156	0.317	0.223	0.473	0.333	0.473	0.428	0.387	0.417	0.245	0.413	0.410	2.26	0.04	1.49	0.85
META1_1390	putative histidyl-tRNA synthetase (hisS)	0.195	0.431	0.396	0.271	0.570	0.520	0.386	0.348	0.377	0.363	0.504	0.370	1.38	0.61	1.10	0.55
META1_1391	putative haloacid dehalogenase-like hydrolase, HAD-su	0.156	0.227	0.198	0.338	0.095	0.284	0.343	0.232	0.218	0.200	0.212	0.262	1.77	0.17	1.86	0.64
META1_1392	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1393	putative bifunctional protein (aas-like) : 2-acylglycerol	0.000	0.363	0.396	0.338	0.784	0.473	0.450	0.464	0.437	0.290	0.585	0.450	2.09	0.40	1.16	0.69
META1_1396	protein of unknown function; putative exported protei	0.234	0.340	0.346	0.338	0.285	0.213	0.107	0.271	0.159	0.318	0.262	0.181	0.77	0.12	1.04	0.17
META1_1397	conserved protein of unknown function; putative mem	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.079	0.000	0.020	0.027	n.d.	0.37	2.00	0.97
META1_1398	conserved protein of unknown function	0.156	0.227	0.049	0.000	0.190	0.236	0.214	0.232	0.179	0.145	0.181	0.208	1.94	0.31	1.72	0.37
META1_1399	molybdopterin synthase, large subunit	0.000	0.068	0.099	0.000	0.166	0.142	0.257	0.232	0.278	0.064	0.131	0.255	5.43	0.56	2.92	0.45
META1_1400	conserved protein of unknown function, putative perm	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37

META1_1401	malate dehydrogenase, FAD/NAD(P)-binding domain (t	0.779	0.816	0.891	0.271	0.285	0.213	0.043	0.097	0.099	0.835	0.252	0.081	0.13	0.00	0.48	0.01
META1_1403	conserved protein of unknown function	0.000	0.000	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1404	conserved protein of unknown function	0.350	0.272	0.520	0.203	0.285	0.236	0.279	0.367	0.179	0.381	0.252	0.276	0.98	0.30	1.64	0.70
META1_1405	putative ABC superfamily protein	1.752	1.609	1.188	1.217	0.665	0.709	1.007	1.121	0.814	1.488	0.766	0.981	0.89	0.05	1.92	0.50
META1_1406	conserved protein of unknown function	0.195	0.363	0.520	0.000	0.238	0.142	0.214	0.290	0.298	0.381	0.161	0.269	0.95	0.50	2.50	0.43
META1_1407	conserved protein of unknown function, putative zinc i	0.078	0.181	0.198	0.135	0.095	0.071	0.214	0.232	0.238	0.163	0.091	0.228	1.89	0.18	3.78	0.01
META1_1408	glucose-6-phosphate 1-dehydrogenase (G6PD)	0.000	0.204	0.198	0.000	0.000	0.000	0.086	0.000	0.040	0.154	0.000	0.040	0.35	0.86	n.d.	0.12
META1_1411	orotidine 5'-phosphate decarboxylase	0.234	0.295	0.272	0.203	0.285	0.378	0.257	0.445	0.278	0.272	0.312	0.329	1.63	0.39	1.58	0.64
META1_1412	conserved protein of unknown function (DUF1330)	0.156	0.113	0.124	0.203	0.095	0.000	0.150	0.193	0.099	0.127	0.071	0.148	1.57	0.69	3.14	0.38
META1_1417	Putative mutator protein MutT/NUDIX-family hydrolase	0.195	0.249	0.099	0.203	0.095	0.071	0.150	0.077	0.099	0.181	0.101	0.108	0.80	0.23	1.60	0.88
META1_1418	putative carbonic anhydrase domain	1.129	0.884	0.841	0.947	0.570	0.992	0.750	1.044	0.635	0.925	0.806	0.813	1.19	0.37	1.51	0.92
META1_1419	putative CysQ protein (PAPS (adenosine 3'-phosphate 5	0.000	0.000	0.049	0.000	0.071	0.047	0.043	0.058	0.000	0.018	0.050	0.034	2.50	0.52	1.00	0.98
META1_1420	conserved protein of unknown function	0.350	0.385	0.322	0.473	0.071	0.567	0.428	0.445	0.556	0.354	0.343	0.477	1.82	0.04	2.09	0.44
META1_1421	signal transduction histidine kinase with N-terminal pho	0.000	0.770	0.619	1.150	1.639	0.945	1.221	1.643	1.766	0.535	1.270	1.552	3.92	0.54	1.83	0.31
META1_1422	Chemotaxis signal transduction/oligomerization protei	0.000	0.181	0.000	0.338	0.238	0.213	0.150	0.193	0.099	0.073	0.242	0.148	2.75	0.11	0.92	0.07
META1_1423	Chemotaxis response regulator receiver	0.000	0.113	0.000	0.271	0.119	0.095	0.086	0.097	0.139	0.045	0.131	0.108	3.20	0.11	1.23	0.41
META1_1424	Chemotaxis response regulator protein-glutamate meth	0.000	0.045	0.074	0.000	0.119	0.095	0.064	0.039	0.119	0.045	0.091	0.074	2.20	0.40	1.22	0.32
META1_1425	glutamate methyltransferase, chemotactic response re	0.000	0.045	0.000	0.000	0.048	0.000	0.064	0.000	0.000	0.018	0.020	0.020	1.50	0.98	1.50	0.98
META1_1429	conserved protein of unknown function; putative memb	0.000	0.136	0.124	0.000	0.166	0.000	0.086	0.135	0.139	0.100	0.071	0.121	1.64	0.36	2.57	0.10
META1_1431	conserved protein of unknown function	0.312	0.340	0.247	0.000	0.048	0.047	0.000	0.000	0.000	0.299	0.040	0.000	0.00	0.00	0.00	0.12
META1_1432	conserved protein of unknown function; putative expor	0.662	0.363	0.421	0.812	0.333	0.378	0.343	0.251	0.318	0.454	0.423	0.302	0.90	0.10	1.07	0.21
META1_1433	cobalamin adenosyltransferase, methylmalonyl-CoA mu	0.234	0.408	0.247	0.744	0.285	0.165	0.257	0.271	0.397	0.308	0.302	0.309	1.35	0.83	1.53	0.87
META1_1434	Electron transfer flavoprotein subunit beta (Beta-ETF) (	1.713	1.110	1.336	2.435	0.760	1.536	0.793	0.986	0.576	1.334	1.341	0.786	0.80	0.05	0.88	0.17
META1_1435	electron transfer flavoprotein, NAD/FAD-binding domai	2.064	1.631	1.683	2.976	1.330	1.890	1.157	0.889	1.032	1.751	1.814	1.022	0.79	0.01	0.84	0.06
META1_1436	3-hydroxybutyryl-CoA dehydrogenase	0.584	0.612	0.643	0.609	0.594	0.473	0.450	0.425	0.456	0.617	0.544	0.444	0.97	0.00	1.22	0.06
META1_1437	protein of unknown function	0.389	0.136	0.173	0.000	0.095	0.000	0.150	0.077	0.139	0.209	0.040	0.121	0.78	0.20	4.50	0.13
META1_1438	putative NADPH quinone oxidoreductase	0.312	0.431	0.297	0.406	0.404	0.473	0.514	0.367	0.456	0.354	0.433	0.444	1.69	0.17	1.53	0.76
META1_1439	uracil phosphoribosyltransferase	0.195	0.000	0.000	0.203	0.261	0.378	0.343	0.541	0.437	0.045	0.302	0.444	13.20	0.16	2.20	0.11
META1_1440	glycosyl hydrolase (Debranching enzyme)	0.000	0.091	0.074	0.000	0.000	0.000	0.000	0.000	0.060	0.064	0.000	0.020	0.43	0.54	n.d.	0.37
META1_1441	alpha,alpha-trehalose-phosphate synthase (UDP-formin	0.273	0.431	0.272	0.000	0.143	0.189	0.343	0.290	0.238	0.336	0.141	0.289	1.16	0.62	3.07	0.47
META1_1442	conserved protein of unknown function	0.350	0.816	0.668	0.473	0.238	0.189	0.257	0.193	0.357	0.653	0.252	0.269	0.56	0.06	1.60	0.86
META1_1444	protein of unknown function	0.234	0.317	0.124	0.000	0.095	0.142	0.171	0.135	0.179	0.227	0.101	0.161	0.96	0.41	2.40	0.42
META1_1445	protein of unknown function	0.701	0.725	0.520	0.271	0.214	0.307	0.236	0.290	0.298	0.644	0.262	0.276	0.58	0.00	1.58	0.74
META1_1446	histidyl-tRNA synthetase	0.389	0.589	0.495	0.338	0.618	0.685	0.536	0.522	0.576	0.508	0.605	0.544	1.45	0.40	1.35	0.87
META1_1447	Secretion chaperone protein	0.000	0.068	0.000	0.203	0.000	0.071	0.129	0.077	0.079	0.027	0.060	0.094	4.67	0.13	2.33	0.34
META1_1450	protein-export protein SecB	0.740	0.544	0.445	0.812	0.736	0.402	0.750	0.715	0.814	0.553	0.605	0.759	1.85	0.12	1.88	0.42
META1_1451	conserved protein of unknown function, putative memb	0.896	0.929	0.619	0.473	0.404	0.449	0.536	0.464	0.476	0.807	0.433	0.491	0.82	0.02	1.70	0.17
META1_1452	putative membrane-bound lytic murein transglycosylas	0.000	0.000	0.000	0.000	0.143	0.142	0.000	0.000	0.040	0.000	0.121	0.013	n.d.	0.37	0.17	0.60
META1_1453	putative Smr protein/MutS2 C-terminal, damaged DNA	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1454	transcription termination factor Rho; polarity suppresso	0.584	1.042	1.262	1.285	1.876	1.961	1.050	1.237	1.131	1.016	1.824	1.142	1.52	0.41	0.94	0.05
META1_1455	poxB; pyruvate dehydrogenase/oxidase: FAD- and thiam	0.000	0.453	0.173	0.000	0.095	0.000	0.000	0.039	0.060	0.245	0.040	0.034	0.19	0.80	1.25	0.48
META1_1457	Membrane protein, TerC family	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_1458	putative diacylglycerol kinase.	0.000	0.045	0.074	0.000	0.095	0.047	0.129	0.097	0.060	0.045	0.060	0.094	2.80	0.44	2.33	0.42
META1_1459	protein of unknown function; putative exported protein	0.078	0.000	0.000	0.000	0.000	0.071	0.043	0.000	0.000	0.018	0.030	0.013	1.00	0.97	0.67	0.97
META1_1460	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.058	0.079	0.000	0.020	0.047	n.d.	0.12	3.50	0.54
META1_1461	Putative acid phosphatase	0.000	0.045	0.049	0.000	0.000	0.000	0.129	0.097	0.060	0.036	0.000	0.094	3.50	0.47	n.d.	0.00
META1_1462	conserved protein of unknown function	0.117	0.113	0.173	0.000	0.000	0.047	0.150	0.213	0.218	0.136	0.020	0.195	1.93	0.11	14.50	0.19
META1_1463	DNA-binding protein, putative transcriptional regulator	0.000	0.068	0.074	0.000	0.095	0.095	0.107	0.039	0.119	0.054	0.081	0.087	2.17	0.39	1.63	0.35
META1_1465	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltran	1.207	0.929	0.767	0.812	0.333	0.803	0.793	1.024	0.853	0.934	0.605	0.894	1.29	0.66	2.22	0.27
META1_1467	Putative two-component transcriptional regulator, wing	0.000	0.227	0.000	0.338	0.095	0.236	0.193	0.174	0.179	0.091	0.192	0.181	2.70	0.11	1.42	0.85
META1_1468	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1469	putative enzyme with PLP-binding domain, putative ala	0.195	0.498	0.470	0.203	0.000	0.189	0.300	0.445	0.278	0.417	0.111	0.343	1.11	0.85	4.64	0.46
META1_1470	leucine tRNA synthetase	1.441	1.359	1.658	1.217	1.473	1.110	1.071	1.102	0.953	1.488	1.280	1.042	0.95	0.01	1.22	0.11
META1_1471	tRNA modification GTPase trmE	0.000	0.091	0.000	0.000	0.143	0.095	0.000	0.058	0.060	0.036	0.101	0.040	1.50	0.49	0.60	0.92
META1_1474	tRNA uridine 5-carboxymethylaminomethyl modificatio	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_1475	Methyltransferase gidB (Glucose-inhibited division prot	0.000	0.000	0.049	0.000	0.000	0.095	0.043	0.097	0.000	0.018	0.040	0.047	3.50	0.54	1.75	0.50
META1_1476	chromosome partitioning protein, ATP-binding, nucleot	0.000	0.000	0.074	0.000	0.000	0.071	0.107	0.135	0.139	0.027	0.030	0.128	6.33	0.14	6.33	0.14
META1_1477	chromosome-partitioning protein parB	0.623	0.498	0.421	0.609	0.546	0.780	0.557	0.425	0.377	0.499	0.655	0.450	1.22	0.48	1.03	0.09
META1_1478	putative DNA polymerase III, delta subunit, holA	0.000	0.068	0.000	0.000	0.048	0.118	0.043	0.058	0.060	0.027	0.071	0.054	2.67	0.11	1.14	0.33
META1_1479	conserved protein of unknown function; putative expor	0.273	0.068	0.099	0.338	0.238	0.095	0.064	0.039	0.179	0.127	0.192	0.094	1.00	0.48	0.74	0.18
META1_1481	protein of unknown function	0.195	0.272	0.247	0.541	0.285	0.284	0.129	0.329	0.298	0.245	0.323	0.255	1.41	0.97	1.19	0.32
META1_1483	protein of unknown function	0.000	0.068	0.074	0.000	0.048	0.047	0.000	0.058	0.079	0.054	0.040	0.047	1.17	0.99	1.75	0.96
META1_1484	protein of unknown function	0.389	0.385	0.247	0.203	0.404	0.543	0.321	0.329	0.278	0.336	0.433	0.309	1.24	0.65	1.07	0.66
META1_1485	putative cyclohexadienyl dehydrogenase (tyrC-like)	0.078	0.068	0.074	0.000	0.285	0.118	0.214	0.155	0.119	0.073	0.171	0.161	3.00	0.01	1.41	0.35
META1_1486	histidinol-phosphate aminotransferase	0.273	0.521	0.421	0.473	0.594	0.496	0.364	0.367	0.516	0.426	0.534	0.417	1.32	0.84	1.17	0.15
META1_1487	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.095	0.000	0.086	0.077	0.139	0.000	0.040	0.101	n.d.	0.00	3.75	0.12
META1_1488	putative TonB-dependent siderophore receptor (putativ	1.207	0.000	0.297	0.609	0.475	0.378	0.086	0.077	0.079	0.390	0.454	0.081	0.28	0.15	0.27	0.00
META1_1489	potassium uptake protein Kup	0.000	0.000	0.000	0.000	0.261	0.165	0.193	0.213	0.238	0.000	0.181	0.215	n.d.	0.00	1.78	0.38
META1_1490	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.935	1.201	1.485	1.150	1.829	1.748	1.264	1.566	1.092	1.243	1.693	1.311	1.42	0.64	1.16	0.38
META1_1491	conserved protein of unknown function (putative phosp	0.467	0.136	0.148	0.000	0.214	0.142	0.107	0.232	0.099	0.218	0.151	0.148	0.92	0.41	1.47	0.34
META1_1492	conserved protein of unknown function; putative bifun	0.000	0.068	0.099	0.000	0.095	0.118	0.171	0.155	0.159	0.064	0.091	0.161	3.43	0.48	2.67	0.44
META1_1493	5,10-methylenetetrahydrofolate reductase	0.000	0.317	0.247	0.338	0.095	0.213	0.279	0.290	0.258	0.218	0.181	0.276	1.71	0.37	2.28	0.37
META1_1494	B12-dependent homocysteine-N5-methyltetrahydrofola	0.506	0.929	1.386	2.705	2.447	1.890	2.035	1.759	1.747	0.998	2.248	1.841	2.49	0.06	1.23	0.12
META1_1495	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.039	0.060	0.000	0.020	0.034	n.d.	0.12	2.50	0.52
META1_1496	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.040	0.000	0.030	0.013	n.d.	0.37	0.67	0.97
META1_1498	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_1500	putative cytochrome c oxidase assembly protein	0.000	0.000	0.000	0.135	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_1503	Thiamine biosynthesis protein thiC	0.467	0.612	1.064	0.541	1.164	0.803	1.757	1.604	1.489	0.744	0.917	1.613	2.93	0.02	2.64	0.04
META1_1504	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1505	putative flagellar protein FlaF	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_1508	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.039	0.000	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META1_1510	putative TonB family C-terminal domain protein	0.350	0.000	0.074	0.000	0.071	0.000	0.000	0.039	0.040	0.109	0.030	0.027	0.33	0.84	1.33	0.48
META1_1511	uptake of enterobactin; tonB-dependent uptake of B co	0.467	0.091	0.173	0.338	0.190	0.142	0.214	0.193	0.238	0.209	0.192	0.215	1.39	0.85	1.68	0.92
META1_1512	membrane spanning protein in TonB-ExbB-ExbD comple	0.623	0.272	0.198	0.473	0.166	0.118	0.107	0.155	0.139	0.327	0.192	0.134	0.56	0.07	1.05	0.34
META1_1513	conserved protein of unknown function; putative expor	0.973	0.363	0.371	0.879	0.546	0.425	0.728	0.599	0.615	0.508	0.544	0.645	1.71	0.51	1.78	0.70
META1_1516	conserved protein of unknown function	0.000	0.159	0.000	0.000	0.000	0.000	0.086	0.174	0.079	0.064	0.000	0.114	2.43	0.10	n.d.	0.00
META1_1517	putative glycosyl transferase	0.000	0.136	0.000	0.000	0.143	0.071	0.086	0.097	0.040	0.054	0.091	0.074	1.83	0.09	1.22	0.33
META1_1518	Translation initiation factor IF-3	0.273	0.227	0.346	1.082	0.475	0.614	0.664	0.831	0.516	0.281	0.625	0.672	3.23	0.01	1.61	0.91
META1_1519	conserved protein of unknown function, putative glycos	1.558	1.224	1.237	1.150	0.594	0.638	1.028	0.966	0.774	1.306	0.695	0.921	0.95	0.03	1.99	0.45
META1_1520	putative glycosyl transferase	0.000	0.091	0.000	0.000	0.095	0.142	0.386	0.155	0.278	0.036	0.101	0.269	10.00	0.17	4.00	0.50
META1_1521	50S ribosomal protein L35	0.156	0.272	0.322	0.609	0.261	0.354	0.343	0.251	0.496	0.263	0.353	0.363	1.86	0.27	1.54	0.78
META1_1522	50S ribosomal protein L20	0.740	0.521	0.322	0.676	1.164	0.945	0.964	0.812	0.953	0.499	0.998	0.907	2.45	0.07	1.36	1.00
META1_1523	phenylalanine tRNA synthetase, alpha-subunit	0.467	0.227	0.297	0.473	0.831	0.992	0.386	0.425	0.377	0.308	0.847	0.397	1.74	0.35	0.70	0.05
META1_1524	phenylalanine tRNA synthetase, beta-subunit	1.908	1.382	1.732	2.232	2.518	2.339	2.292	2.165	1.866	1.633	2.399	2.104	1.74	0.11	1.32	0.17
META1_1525	protein of unknown function	0.195	0.385	0.520	0.609	0.190	0.496	0.343	0.367	0.417	0.390	0.383	0.376	1.30	0.75	1.47	0.94
META1_1526	molybdopterin synthase sulfurylase	0.000	0.068	0.074	0.000	0.048	0.142	0.064	0.097	0.099	0.054	0.081	0.087	2.17	0.40	1.63	0.38
META1_1527	N-succinyl-diaminopimelate deacylase (dapE)	0.000	0.091	0.049	0.000	0.095	0.118	0.000	0.193	0.040	0.054	0.091	0.081	2.00	0.97	1.33	0.98
META1_1529	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-fo	0.000	0.159	0.049	0.000	0.000	0.047	0.150	0.135	0.198	0.082	0.020	0.161	2.67	0.47	12.00	0.18
META1_1530	peptide deformylase	0.195	0.181	0.198	0.203	0.214	0.118	0.150	0.174	0.179	0.191	0.171	0.168	1.19	0.09	1.47	0.88
META1_1532	recombination protein recR	0.000	0.091	0.000	0.000	0.071	0.071	0.043	0.097	0.060	0.036	0.060	0.067	2.50	0.10	1.67	0.36
META1_1533	phosphoenolpyruvate carboxykinase	1.402	1.065	1.683	0.000	0.000	0.000	0.000	0.077	0.040	1.370	0.000	0.040	0.04	0.98	n.d.	0.12
META1_1534	putative Fe-S containing enzyme (yfgB)	0.000	0.385	0.297	0.000	0.760	0.567	0.193	0.309	0.278	0.263	0.564	0.262	1.34	0.33	0.70	0.24
META1_1535	bifunctional shikimate kinase (N-terminal) / dehydroqu	0.273	0.498	0.495	0.135	0.618	0.614	0.300	0.464	0.337	0.445	0.544	0.370	1.12	0.64	1.02	0.96
META1_1536	putative transcriptional regulator (helix-turn-helix struc	0.117	0.181	0.247	0.135	0.190	0.331	0.300	0.251	0.218	0.191	0.242	0.255	1.81	0.18	1.58	0.47
META1_1537	malate dehydrogenase	4.867	3.376	3.291	1.826	2.185	2.315	1.521	1.682	1.985	3.692	2.187	1.734	0.63	0.01	1.19	0.13
META1_1538	succinyl-CoA synthetase, beta subunit	4.595	3.285	3.786	1.826	1.758	2.292	1.500	1.527	1.012	3.774	1.996	1.344	0.48	0.00	1.01	0.07
META1_1539	succinyl-CoA synthetase, alpha subunit	3.193	1.813	2.351	1.691	1.235	1.630	1.007	1.005	1.330	2.331	1.472	1.116	0.65	0.01	1.14	0.09
META1_1540	2-oxoglutarate dehydrogenase complex, E1 component	5.996	5.098	5.468	2.299	2.067	1.843	2.421	2.435	2.421	5.443	2.006	2.426	0.60	0.00	1.81	0.06
META1_1541	dihydrolipoamide succinyltransferase component of 2-o	3.777	3.489	3.142	0.406	1.211	1.252	1.114	1.198	1.231	3.429	1.109	1.183	0.47	0.00	1.60	0.43
META1_1542	dihydrolipoamide dehydrogenase, FAD/NAD(P)-binding	2.648	2.991	2.425	0.338	0.808	0.969	0.643	0.773	0.913	2.703	0.806	0.780	0.39	0.00	1.45	0.63
META1_1544	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1553	putative gamma-glutamylmethylamide synthetase; glut	0.000	0.000	0.074	0.000	0.143	0.000	0.064	0.135	0.099	0.027	0.060	0.101	5.00	0.13	2.50	0.10
META1_1558	protein of unknown function	0.000	0.091	0.099	0.000	0.261	0.165	0.129	0.077	0.139	0.073	0.181	0.114	2.13	0.40	0.94	0.29
META1_1570	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.119	0.071	0.000	0.000	0.040	0.000	0.081	0.013	n.d.	0.37	0.25	0.57
META1_1572	conserved protein of unknown function	0.000	0.136	0.074	0.000	0.071	0.071	0.193	0.251	0.198	0.082	0.060	0.215	3.56	0.49	5.33	0.55
META1_1584	zinc-containing alcohol dehydrogenase	0.156	0.136	0.124	0.000	0.000	0.047	0.043	0.058	0.000	0.136	0.020	0.034	0.33	0.53	2.50	0.52
META1_1585	putative Short-chain dehydrogenase/reductase SDR	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1590	SENSORY TRANSDUCTION HISTIDINE KINASE	0.000	0.045	0.099	0.000	0.000	0.000	0.107	0.077	0.159	0.054	0.000	0.114	2.83	0.45	n.d.	0.00
META1_1598	Transcriptional regulator, XRE family	0.000	0.000	0.074	0.000	0.048	0.000	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META1_1609	conserved protein of unknown function	0.000	0.000	0.074	0.203	0.071	0.000	0.129	0.116	0.079	0.027	0.060	0.108	5.33	0.13	2.67	0.36
META1_1610	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.000	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META1_1611	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_1613	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.071	0.047	0.107	0.039	0.079	0.018	0.050	0.074	5.50	0.13	2.20	0.40
META1_1621	putative ubiE/COQ5 methyltransferase family enzyme	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.

META1_1623	protein of unknown function	0.000	0.363	0.569	0.879	0.926	0.591	1.264	1.450	1.528	0.354	0.776	1.418	5.41	0.61	2.74	0.02
META1_1624	putative sensor hybrid histidine kinase with PAS and tw	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.097	0.000	0.000	0.000	0.054	n.d.	0.12	n.d.	0.12
META1_1625	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1627	putative bacterial luciferase family oxidoreductase	0.000	0.000	0.000	0.000	0.000	0.095	0.086	0.097	0.000	0.000	0.040	0.060	n.d.	0.12	2.25	0.52
META1_1628	conserved protein of unknown function; putative meml	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_1656	conserved protein of unknown function; putative expor	0.117	0.045	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.073	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_1665	putative transcriptional regulator, TetR/AcrR family	0.000	0.045	0.000	0.000	0.000	0.000	0.086	0.077	0.060	0.018	0.000	0.074	5.50	0.14	n.d.	0.00
META1_1667	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1669	Transcriptional regulator, LysR family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1670	conserved protein of unknown function; putative xylan	0.000	0.045	0.000	0.000	0.048	0.000	0.086	0.135	0.099	0.018	0.020	0.108	8.00	0.16	8.00	0.15
META1_1671	conserved protein of unknown function	0.000	0.068	0.049	0.000	0.071	0.000	0.064	0.077	0.139	0.045	0.030	0.094	2.80	0.43	4.67	0.13
META1_1673	conserved protein of unknown function	0.234	0.136	0.297	0.406	0.000	0.071	0.107	0.155	0.159	0.218	0.091	0.141	0.88	0.18	2.33	0.35
META1_1675	putative diguanylate cyclase with GGDEF motif; putativ	0.000	0.045	0.074	0.000	0.000	0.000	0.000	0.058	0.000	0.045	0.000	0.020	0.60	0.52	n.d.	0.37
META1_1676	putative outer membrane protein, OmpW family	0.000	0.000	0.000	0.000	0.048	0.071	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_1682	gamma-glutamyltranspeptidase	0.117	0.113	0.000	0.000	0.048	0.000	0.086	0.058	0.139	0.073	0.020	0.094	1.75	0.34	7.00	0.14
META1_1685	putative 1-acylglycerol-3-phosphate O-acyltransferase (	0.000	0.159	0.198	0.000	0.143	0.118	0.257	0.406	0.298	0.136	0.111	0.323	3.20	0.47	4.36	0.52
META1_1688	MetW (putative cysthationine synthase)	0.078	0.204	0.148	0.135	0.071	0.095	0.171	0.155	0.179	0.154	0.091	0.168	1.47	0.46	2.78	0.04
META1_1689	homoserine O-acetyltransferase	0.000	0.249	0.173	0.271	0.428	0.354	0.300	0.174	0.179	0.163	0.373	0.215	1.78	0.38	0.86	0.09
META1_1690	methionine sulfoxide reductase (Peptide- methionine (F	0.000	0.113	0.074	0.000	0.048	0.047	0.043	0.077	0.000	0.073	0.040	0.040	0.75	0.95	1.50	0.98
META1_1691	Peptide methionine sulfoxide reductase msrA (Protein-	0.000	0.000	0.000	0.203	0.143	0.095	0.000	0.039	0.000	0.000	0.131	0.013	n.d.	0.37	0.15	0.18
META1_1692	bacterioferritin, an iron storage homoprotein	0.584	1.042	0.792	0.879	1.116	0.827	0.900	0.831	1.052	0.844	0.958	0.927	1.48	0.42	1.45	0.93
META1_1694	conserved protein of unknown function	0.467	0.181	0.297	0.473	0.000	0.284	0.343	0.329	0.298	0.290	0.192	0.323	1.50	0.75	2.53	0.35
META1_1696	protein of unknown function; putative exported protein	1.752	0.906	0.569	0.000	0.285	0.260	0.300	0.406	0.119	0.980	0.232	0.276	0.38	0.05	1.78	0.36
META1_1698	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_1700	50S ribosomal subunit protein L33	0.350	0.385	0.371	0.271	0.570	0.614	0.771	0.503	0.695	0.372	0.544	0.652	2.37	0.01	1.80	0.30
META1_1701	3-methyl-2-oxobutanoate hydroxymethyltransferase, p	0.312	0.295	0.371	0.000	0.285	0.307	0.300	0.387	0.337	0.327	0.252	0.343	1.42	0.67	2.04	0.40
META1_1702	thioredoxin-related	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1703	conserved protein of unknown function; putative expor	0.195	0.159	0.099	0.000	0.071	0.047	0.064	0.058	0.099	0.145	0.050	0.074	0.69	0.05	2.20	0.40
META1_1704	conserved protein of unknown function; putative expor	0.000	0.068	0.074	0.000	0.048	0.000	0.064	0.155	0.000	0.054	0.020	0.074	1.83	0.96	5.50	0.57
META1_1705	Putative metallo-hydrolase/oxidoreductase	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1706	Transcriptional regulator, TetR family	0.000	0.045	0.074	0.000	0.190	0.213	0.129	0.155	0.119	0.045	0.171	0.134	4.00	0.50	1.18	0.32
META1_1709	putative GTPase, putative CobW-like cobalamin biosynt	0.234	0.227	0.322	0.000	0.238	0.213	0.214	0.309	0.179	0.263	0.192	0.235	1.21	0.57	1.84	0.38
META1_1713	protein of unknown function	0.000	0.091	0.049	0.000	0.119	0.000	0.000	0.155	0.119	0.054	0.050	0.094	2.33	0.92	2.80	0.53
META1_1714	conserved protein of unknown function	0.000	0.045	0.074	0.000	0.214	0.047	0.107	0.116	0.139	0.045	0.111	0.121	3.60	0.48	1.64	0.40
META1_1715	conserved protein of unknown function, putative meml	0.156	0.204	0.173	0.203	0.261	0.213	0.321	0.135	0.179	0.181	0.232	0.208	1.55	0.69	1.35	0.67
META1_1716	protein of unknown function; putative exported protein	0.234	0.136	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.136	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_1717	conserved protein of unknown function	0.117	0.363	0.148	0.203	0.261	0.213	0.279	0.309	0.417	0.227	0.232	0.336	2.00	0.19	2.17	0.05
META1_1718	diaminopimelate decarboxylase	0.234	0.113	0.124	0.000	0.380	0.402	0.257	0.193	0.099	0.145	0.333	0.181	1.69	0.73	0.82	0.26
META1_1719	protein of unknown function; putative exported protein	0.312	0.000	0.000	0.000	0.119	0.142	0.193	0.116	0.159	0.073	0.111	0.155	2.88	0.09	2.09	0.40
META1_1720	protein of unknown function	0.000	0.091	0.124	0.000	0.095	0.047	0.000	0.058	0.000	0.082	0.060	0.020	0.33	0.56	0.50	0.53
META1_1721	protein of unknown function	0.000	0.000	0.074	0.000	0.000	0.118	0.107	0.193	0.099	0.027	0.050	0.134	6.67	0.14	4.00	0.12
META1_1722	conserved protein of unknown function	0.078	0.091	0.074	0.203	0.143	0.118	0.129	0.097	0.318	0.082	0.141	0.181	3.00	0.14	1.93	0.91
META1_1726	serine-glyoxylate aminotransferase (SGAT)	1.674	1.427	1.262	9.401	10.190	12.404	5.656	5.103	5.240	1.424	11.017	5.323	5.04	0.00	0.72	0.00
META1_1727	Hydroxypyruvate reductase, NAD(P)H-dependent.	0.623	0.566	0.297	2.367	1.971	2.930	1.542	1.604	1.469	0.481	2.439	1.539	4.32	0.01	0.95	0.02
META1_1728	NADP-dependent methylene-tetrahydromethanopterin	0.935	0.770	0.767	5.208	2.684	6.450	3.706	4.175	3.870	0.807	4.667	3.925	6.56	0.00	1.26	0.64
META1_1729	methenyl tetrahydrofolate cyclohydrolase	0.156	0.498	0.371	2.773	1.829	2.056	0.878	1.121	1.627	0.372	2.066	1.216	4.41	0.03	0.88	0.05
META1_1730	Malate thiokinase, large subunit	0.350	0.816	0.619	4.531	5.154	5.505	2.314	2.532	2.342	0.635	5.211	2.399	5.10	0.00	0.69	0.00
META1_1731	Malate thiokinase, small subunit	0.234	0.249	0.198	2.976	2.565	3.544	1.585	1.256	1.131	0.227	3.044	1.317	7.84	0.00	0.65	0.00
META1_1732	phosphoenolpyruvate carboxylase	0.273	0.227	0.198	4.058	3.705	3.568	2.292	2.068	2.104	0.227	3.699	2.151	12.80	0.00	0.87	0.00
META1_1733	malyl-CoA lyase/beta-methylmalyl-CoA lyase	2.025	1.835	1.509	11.633	7.815	10.443	3.792	3.827	3.890	1.760	9.505	3.837	2.94	0.00	0.61	0.00
META1_1735	putative carboxymethylenebutenolidase precursor (die	0.584	0.521	0.247	0.271	0.333	0.449	0.300	0.213	0.179	0.435	0.373	0.228	0.71	0.11	0.92	0.12
META1_1736	putative transcriptional coactivator/pterin dehydratase	0.156	0.204	0.099	0.135	0.071	0.047	0.171	0.155	0.218	0.154	0.071	0.181	1.59	0.43	3.86	0.06
META1_1737	ABC transporter substrate binding protein (subunit A).	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.099	0.000	0.000	0.087	n.d.	0.00	n.d.	0.00
META1_1740	XoxF, PQQ-linked dehydrogenase of unknown function.	0.428	0.363	0.569	0.338	0.689	0.425	0.964	0.986	0.933	0.454	0.524	0.961	2.86	0.00	2.75	0.03
META1_1741	Cytochrome c	0.000	0.159	0.124	0.000	0.618	0.307	0.279	0.348	0.536	0.109	0.393	0.390	4.83	0.54	1.49	0.35
META1_1743	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine p	0.000	0.113	0.099	0.000	0.095	0.118	0.129	0.174	0.238	0.082	0.091	0.181	3.00	0.45	3.00	0.45
META1_1744	dihydroneopterin aldolase	0.000	0.068	0.000	0.000	0.095	0.118	0.086	0.039	0.139	0.027	0.091	0.087	4.33	0.12	1.44	0.33
META1_1745	7,8-dihydropteroate synthase (dihydropteroate synthas	0.389	0.317	0.421	0.406	0.143	0.378	0.536	0.464	0.456	0.372	0.282	0.484	1.76	0.06	2.57	0.18
META1_1746	Orf3, putative exported protein	0.000	0.000	0.000	0.000	0.071	0.095	0.064	0.000	0.079	0.000	0.071	0.047	n.d.	0.12	1.00	0.98
META1_1747	Orf4	0.117	0.227	0.074	0.135	0.238	0.189	0.321	0.445	0.357	0.145	0.202	0.376	3.50	0.03	2.80	0.02
META1_1748	Pyrroloquinoline quinone (PQQ) biosynthesis protein E.	0.234	0.476	0.322	0.135	0.238	0.165	0.450	0.425	0.357	0.363	0.192	0.410	1.53	0.38	3.21	0.01
META1_1749	bifunctional coenzyme pyrroloquinoline quinone (PQQ)	1.674	1.133	1.212	0.947	0.855	0.803	1.071	1.430	1.151	1.288	0.847	1.223	1.28	0.58	2.17	0.03
META1_1750	Pyrroloquinoline quinone (PQQ) biosynthesis protein B	0.389	0.385	0.099	0.000	0.000	0.118	0.343	0.425	0.397	0.281	0.050	0.390	1.87	0.38	11.60	0.18
META1_1752	two-component transcriptional regulator, response reg	0.506	0.725	0.643	0.541	0.309	0.496	0.364	0.619	0.417	0.644	0.423	0.470	0.99	0.18	1.67	0.87
META1_1753	two-component transcriptional regulator, sensor kinase	0.000	0.295	0.272	0.135	0.190	0.213	0.300	0.193	0.278	0.218	0.192	0.255	1.58	0.36	2.00	0.13
META1_1755	formyltransferase/hydrolase complex Fhc subunit C	0.428	0.748	0.470	0.744	0.499	0.921	0.686	0.889	0.595	0.572	0.716	0.726	1.71	0.23	1.52	0.93
META1_1756	formyltransferase/hydrolase complex Fhc subunit D	0.584	0.408	0.470	0.744	0.641	0.945	0.471	0.425	0.576	0.472	0.786	0.491	1.40	0.95	0.94	0.03
META1_1757	formyltransferase/hydrolase complex Fhc subunit A	0.506	1.088	0.866	0.947	1.140	0.827	0.728	0.850	1.012	0.871	0.978	0.867	1.34	0.73	1.33	0.43
META1_1758	Formyltransferase/hydrolase complex Fhc subunit B	0.545	0.816	0.990	1.353	1.069	1.181	0.664	0.812	0.814	0.816	1.159	0.766	1.27	1.00	0.99	0.01
META1_1760	ribofuranosylaminobenzene 5'-phosphate (RFAP) synth	0.000	0.204	0.124	0.000	0.261	0.284	0.107	0.097	0.099	0.127	0.232	0.101	1.07	0.31	0.65	0.24
META1_1761	NAD(P)-dependent methylene tetrahydromethanopteri	1.168	0.861	0.693	0.812	0.523	1.087	0.707	0.870	0.774	0.871	0.806	0.786	1.22	0.48	1.46	0.96
META1_1763	N(5),N(10)-methenyltetrahydromethanopterin cyclohyd	1.752	1.337	1.237	2.908	1.520	1.796	1.200	1.179	1.270	1.397	1.845	1.216	1.18	0.21	0.99	0.06
META1_1764	Orf5. Involved in biosynthesis of tetrahydromethanopte	0.000	0.000	0.000	0.000	0.000	0.095	0.043	0.077	0.119	0.000	0.040	0.081	n.d.	0.00	3.00	0.11
META1_1765	Orf7. Involved in tetrahydromethanopterin-linked form	0.000	0.000	0.000	0.135	0.095	0.047	0.043	0.058	0.040	0.000	0.081	0.047	n.d.	0.00	0.88	0.14
META1_1766	formaldehyde-activating enzyme	4.088	4.124	3.192	7.101	5.772	6.048	2.014	2.455	3.771	3.774	6.088	2.762	0.99	0.16	0.68	0.01
META1_1768	Orf9, involved in biosynthesis of tetrahydromethanopte	0.000	0.091	0.074	0.000	0.356	0.213	0.236	0.232	0.198	0.064	0.242	0.222	4.71	0.53	1.38	0.34
META1_1770	conserved protein of unknown function, homolog of M	0.000	0.068	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1771	conserved exported protein of unknown function, hom	1.051	1.020	0.718	1.285	1.021	0.543	0.814	0.793	0.794	0.916	0.857	0.800	1.18	0.33	1.40	0.69
META1_1772	conserved protein of unknown function, homolog of M	0.000	0.045	0.049	0.000	0.000	0.000	0.043	0.000	0.000	0.036	0.000	0.013	0.50	0.52	n.d.	0.37
META1_1773	Orf19. Involved in biosynthesis of tetrahydromethanop	0.195	0.068	0.000	0.000	0.071	0.095	0.193	0.232	0.198	0.073	0.071	0.208	3.88	0.47	4.43	0.52
META1_1774	Orf20. Involved in biosynthesis of tetrahydromethanop	0.000	0.068	0.000	0.000	0.119	0.071	0.171	0.097	0.079	0.027	0.081	0.114	5.67	0.14	2.13	0.40
META1_1775	Orf21. Involved in biosynthesis of tetrahydromethanop	0.000	0.000	0.000	0.000	0.048	0.071	0.043	0.097	0.000	0.000	0.050	0.047	n.d.	0.12	1.40	0.99
META1_1776	Orf22. Involved in biosynthesis of tetrahydromethanop	0.000	0.000	0.000	0.000	0.214	0.260	0.150	0.251	0.119	0.000	0.202	0.175	n.d.	0.00	1.30	0.32
META1_1777	conserved protein of unknown function; putative expor	0.000	0.136	0.049	0.000	0.143	0.071	0.171	0.193	0.238	0.073	0.091	0.202	3.75	0.51	3.33	0.48
META1_1778	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.097	0.000	0.000	0.000	0.054	n.d.	0.12	n.d.	0.12
META1_1779	conserved protein of unknown function; putative expor	0.195	0.181	0.124	0.203	0.214	0.189	0.129	0.290	0.179	0.163	0.202	0.202	1.67	0.64	1.50	0.79
META1_1780	conserved protein of unknown function; putative expor	0.000	0.068	0.000	0.000	0.166	0.047	0.064	0.058	0.040	0.027	0.091	0.054	2.67	0.11	0.89	0.31
META1_1781	conserved protein of unknown function; putative expor	0.000	0.045	0.074	0.000	0.048	0.047	0.000	0.000	0.000	0.045	0.040	0.000	0.00	0.12	0.00	0.12
META1_1782	putative ABC transporter, ATPase	0.156	0.113	0.148	0.135	0.143	0.142	0.214	0.213	0.099	0.136	0.141	0.175	1.73	0.54	1.86	0.55
META1_1784	conserved protein of unknown function; putative expor	0.273	0.159	0.148	0.135	0.143	0.165	0.236	0.290	0.258	0.181	0.151	0.262	1.95	0.17	2.60	0.00
META1_1785	putative TonB-dependent receptor:IMP dehydrogenase	1.558	0.431	0.866	6.425	2.399	2.670	1.178	0.773	1.191	0.853	3.115	1.042	1.65	0.63	0.50	0.02
META1_1787	protein of unknown function; putative exported protein	0.117	0.068	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_1788	putative glycosyl transferase	0.000	0.159	0.173	0.000	0.309	0.165	0.279	0.290	0.238	0.127	0.202	0.269	2.86	0.45	2.00	0.40
META1_1789	glycosyl transferase	0.000	0.068	0.000	0.135	0.119	0.071	0.043	0.000	0.000	0.027	0.101	0.013	0.67	0.98	0.20	0.16
META1_1790	putative polysaccharide export protein	0.273	0.000	0.000	0.000	0.071	0.071	0.171	0.116	0.119	0.064	0.060	0.134	2.86	0.09	3.33	0.47
META1_1791	putative succinoglycan biosynthesis transport protein e	0.000	0.000	0.000	0.000	0.143	0.142	0.064	0.039	0.060	0.000	0.121	0.054	n.d.	0.00	0.67	0.25
META1_1793	UPF0133 protein	0.000	0.113	0.124	0.000	0.095	0.118	0.129	0.116	0.179	0.091	0.091	0.141	2.10	0.40	2.33	0.41
META1_1794	DNA polymerase III, tau and gamma subunits	0.000	0.476	0.544	0.135	0.499	0.284	0.300	0.406	0.258	0.390	0.353	0.323	1.12	0.30	1.37	0.70
META1_1795	protein of unknown function; putative exported protein	0.078	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1798	putative glutathione S-transferase	0.117	0.045	0.000	0.000	0.000	0.047	0.000	0.097	0.139	0.045	0.020	0.081	2.40	0.95	6.00	0.58
META1_1799	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.043	0.000	0.060	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META1_1800	putative sensor and regulator, histidine kinase and Che	0.000	0.045	0.000	0.000	0.048	0.071	0.064	0.039	0.119	0.018	0.050	0.074	5.50	0.13	2.20	0.39
META1_1803	thioesterase/thiol ester dehydrase-isomerase domain p	0.156	0.181	0.198	0.000	0.048	0.000	0.129	0.135	0.099	0.181	0.020	0.121	0.90	0.03	9.00	0.16
META1_1804	alpha/beta hydrolase protein precursor	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_1806	putative molybdopterin oxidoreductase	0.000	0.045	0.074	0.000	0.000	0.000	0.557	0.445	0.417	0.045	0.000	0.470	14.00	0.74	n.d.	0.00
META1_1807	oligopeptide transport protein (ABC superfamily, atp_b	0.078	0.227	0.247	0.000	0.285	0.118	0.150	0.155	0.139	0.200	0.171	0.148	1.00	0.80	1.29	0.34
META1_1808	phosphopentomutase	0.000	0.068	0.074	0.000	0.000	0.000	0.000	0.039	0.040	0.054	0.000	0.027	0.67	0.94	n.d.	0.12
META1_1809	putative ATP-binding protein with two ATPase domains	1.168	1.427	1.534	1.285	1.686	1.134	1.435	1.179	1.171	1.406	1.391	1.257	1.21	0.46	1.36	0.62
META1_1814	putative dihydroflavonol-4-reductase (Dihydrokaempfe	0.156	0.181	0.124	0.609	0.238	0.331	0.364	0.290	0.218	0.154	0.333	0.289	2.53	0.03	1.30	0.48
META1_1815	putative phytoene synthase	0.156	0.295	0.322	0.406	0.071	0.473	0.428	0.503	0.476	0.272	0.292	0.470	2.33	0.05	2.41	0.33
META1_1816	putative phytoene synthase	0.195	0.295	0.173	0.406	0.333	0.449	0.514	0.290	0.298	0.227	0.393	0.363	2.16	0.11	1.38	0.64
META1_1817	putative oxidoreductase, putative amine oxidase	0.467	0.453	0.470	0.135	0.641	0.378	0.214	0.290	0.298	0.463	0.454	0.269	0.78	0.01	0.89	0.70
META1_1818	squalene-hopene-cyclase	0.000	0.476	0.594	0.541	0.855	0.473	0.621	0.561	0.516	0.408	0.645	0.565	1.87	0.38	1.31	0.74
META1_1819	conserved protein of unknown function; putative sperm	0.000	0.000	0.049	0.000	0.119	0.189	0.171	0.174	0.119	0.018	0.131	0.155	11.50	0.17	1.77	0.38
META1_1820	acyltransferase (wcbT-like, rkpG-like)	0.273	0.702	0.619	0.406	0.760	0.638	0.514	0.638	0.536	0.572	0.655	0.565	1.33	0.69	1.29	0.86
META1_1821	putative fatty acid synthase multidomain protein (rkpA-	1.674	1.745	2.153	8.048	3.515	4.395	4.028	3.151	3.652	1.878	4.566	3.595	2.58	0.00	1.18	0.27
META1_1822	UDP-glucose-6-dehydrogenase	0.428	0.408	0.594	0.406	0.618	0.543	0.321	0.503	0.397	0.481	0.554	0.410	1.15	0.41	1.11	0.23
META1_1823	putative glycosyl transferase	0.000	0.136	0.124	0.000	0.071	0.118	0.129	0.077	0.099	0.100	0.081	0.101	1.36	0.34	1.88	0.39
META1_1824	protein of unknown function	0.000	0.113	0.099	0.000	0.143	0.118	0.086	0.077	0.079	0.082	0.111	0.081	1.33	0.34	1.09	0.31
META1_1826	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.060	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_1827	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_1829	protein of unknown function	0.000	0.000	0.074	0.000	0.071	0.118	0.064	0.058	0.040	0.027	0.081	0.054	2.67	0.10	1.00	0.31
META1_1832	Transcriptional regulatory protein fixJ	1.129	1.246	1.212	1.014	0.451	0.567	0.536	0.928	0.595	1.207	0.585	0.692	0.77	0.03	1.78	0.89
META1_1833	PAS/PAC sensor signal transduction histidine kinase (fra	0.623	1.450	1.509	0.541	0.641	0.307	0.471	0.445	0.556	1.279	0.484	0.491	0.52	0.05	1.52	0.91

META1_1838	conserved protein of unknown function	0.389	0.521	0.594	0.338	0.546	0.425	0.450	0.425	0.238	0.517	0.464	0.370	0.96	0.25	1.20	0.50
META1_1839	conserved protein of unknown function	0.000	0.068	0.124	0.135	0.095	0.095	0.043	0.058	0.099	0.073	0.101	0.067	1.25	0.33	1.00	0.12
META1_1841	conserved protein of unknown function	0.234	0.295	0.000	0.000	0.285	0.165	0.214	0.309	0.278	0.172	0.192	0.269	2.11	0.38	2.11	0.41
META1_1843	protein of unknown function	0.000	0.113	0.074	0.000	0.000	0.000	0.043	0.000	0.060	0.073	0.000	0.034	0.63	0.93	n.d.	0.12
META1_1845	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1846	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_1847	conserved protein of unknown function	0.117	0.113	0.124	0.000	0.000	0.000	0.000	0.000	0.000	0.118	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_1849	conserved protein of unknown function	1.246	1.042	1.237	0.947	0.380	0.449	0.514	0.483	0.437	1.161	0.494	0.477	0.55	0.00	1.45	0.67
META1_1852	protein of unknown function	0.156	0.091	0.099	0.000	0.095	0.071	0.064	0.058	0.119	0.109	0.071	0.081	1.00	0.24	1.71	0.37
META1_1855	Copper resistance protein A precursor	1.363	0.295	0.520	1.082	0.760	0.756	0.514	0.309	0.258	0.626	0.806	0.356	0.77	0.33	0.66	0.02
META1_1856	Copper resistance protein CopB precursor	0.779	0.091	0.247	0.203	0.166	0.402	0.193	0.174	0.179	0.308	0.272	0.181	0.79	0.60	1.00	0.37
META1_1857	conserved protein of unknown function	0.273	0.295	0.099	0.000	0.000	0.000	0.064	0.058	0.139	0.218	0.000	0.087	0.54	0.11	n.d.	0.00
META1_1858	Putative glucoamylase, (GLUCAN 1,4-ALPHA-GLUCOSID	0.195	0.431	0.297	0.000	0.048	0.000	0.107	0.039	0.099	0.327	0.020	0.081	0.33	0.03	6.00	0.14
META1_1859	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.043	0.000	0.079	0.036	0.000	0.040	1.50	0.49	n.d.	0.12
META1_1860	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_1861	transketolase	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1862	putative Transaldolase Phosphoglucose isomerase	0.000	0.227	0.099	0.000	0.071	0.000	0.000	0.097	0.000	0.127	0.030	0.034	0.36	0.55	1.67	0.98
META1_1863	6-phosphogluconate dehydrogenase	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.027	0.000	0.020	1.00	0.99	n.d.	0.37
META1_1865	Hydrolase (HAD superfamily)	0.156	0.363	0.198	0.135	0.000	0.071	0.150	0.135	0.079	0.254	0.050	0.121	0.64	0.11	3.60	0.40
META1_1866	6-phosphogluconolactonase	0.000	0.045	0.000	0.000	0.000	0.000	0.064	0.039	0.000	0.018	0.000	0.034	2.50	0.52	n.d.	0.12
META1_1867	gluconate kinase 2 ; gluconate transport, GNT I system	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.018	0.000	0.013	1.00	1.00	n.d.	0.37
META1_1871	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.077	0.099	0.000	0.020	0.060	n.d.	0.12	4.50	0.56
META1_1872	protein of unknown function	0.273	0.340	0.396	0.744	0.190	0.142	0.279	0.271	0.238	0.345	0.252	0.262	1.03	0.11	1.56	0.95
META1_1875	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.058	0.099	0.000	0.000	0.101	n.d.	0.00	n.d.	0.00
META1_1879	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.039	0.079	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_1880	putative plasmid stabilization protein (PilT)	0.000	0.068	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.027	0.030	0.000	0.00	0.37	0.00	0.37
META1_1881	putative Prevent-host-death family protein	0.000	0.068	0.074	0.000	0.048	0.000	0.000	0.000	0.079	0.054	0.020	0.027	0.67	0.51	2.00	0.97
META1_1889	cation transporting P-type ATPase	0.156	0.317	0.198	0.000	0.071	0.047	0.129	0.058	0.060	0.236	0.050	0.081	0.46	0.04	2.40	0.41
META1_1890	conserved protein of unknown function; putative alpha	0.000	0.136	0.124	0.000	0.048	0.071	0.000	0.000	0.079	0.100	0.050	0.027	0.36	0.55	0.80	0.50
META1_1891	putative acetate kinase, propionate kinase	0.000	0.068	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_1893	Phosphate acetyltransferase	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1907	protein of unknown function; putative exported protein	0.156	0.181	0.099	0.000	0.000	0.047	0.000	0.000	0.000	0.145	0.020	0.000	0.00	0.00	0.00	0.37
META1_1912	protein of unknown function; putative exported protein	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.027	0.000	0.013	0.67	0.97	n.d.	0.37
META1_1915	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.000	0.040	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META1_1916	putative ParA-like protein (chromosome partitioning)	0.000	0.227	0.198	0.000	0.119	0.142	0.086	0.135	0.060	0.163	0.111	0.094	0.78	0.26	1.27	0.32
META1_1923	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.040	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_1925	putative oxalate/formate antiporter	0.000	0.000	0.000	0.000	0.000	0.000	1.393	1.295	1.231	0.000	0.000	1.304	n.d.	0.00	n.d.	0.00
META1_1926	ethanolamine ammonia-lyase, heavy chain	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_1927	putative ethanolamine ammonia-lyase light chain (eutC	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1928	putative dihydroxyacid dehydratase (ilvD-like)	0.584	0.725	0.718	0.947	0.926	0.898	0.728	0.831	0.754	0.689	0.917	0.773	1.51	0.17	1.26	0.01
META1_1929	protein of unknown function	0.000	0.045	0.000	0.000	0.071	0.000	0.000	0.000	0.040	0.018	0.030	0.013	1.00	0.99	0.67	0.97
META1_1930	Exodeoxyribonuclease III (Exonuclease III) (EXO III) (AP e	0.117	0.181	0.124	0.271	0.048	0.189	0.257	0.174	0.198	0.145	0.141	0.208	1.94	0.09	2.21	0.47
META1_1932	putative Propionate-CoA ligase (Propionyl-CoA synthet	0.156	0.385	0.346	0.000	0.214	0.071	0.300	0.425	0.278	0.318	0.121	0.336	1.43	0.60	4.17	0.54
META1_1933	conserved protein of unknown function	0.117	0.136	0.223	0.000	0.000	0.047	0.171	0.000	0.119	0.163	0.020	0.094	0.78	0.38	7.00	0.59
META1_1934	conserved protein of unknown function	0.078	0.091	0.074	0.000	0.095	0.118	0.000	0.039	0.060	0.082	0.091	0.034	0.56	0.45	0.56	0.91
META1_1936	phosphoribosylaminoimidazole carboxylase = AIR carbo	0.078	0.159	0.000	0.000	0.309	0.189	0.171	0.116	0.099	0.082	0.212	0.128	2.11	0.39	0.90	0.29
META1_1937	phosphoribosylaminoimidazole carboxylase = AIR carbo	0.428	0.295	0.247	0.473	0.214	0.307	0.193	0.329	0.318	0.308	0.292	0.282	1.24	0.57	1.45	0.64
META1_1938	conserved protein of unknown function; putative expor	0.506	0.204	0.371	0.812	0.309	0.638	0.493	0.445	0.357	0.336	0.524	0.430	1.73	0.45	1.23	0.48
META1_1940	fructose 1,6-bisphosphatase II	0.701	0.340	0.495	0.338	0.380	0.543	0.300	0.290	0.357	0.481	0.443	0.316	0.89	0.11	1.07	0.16
META1_1941	Homoserine dehydrogenase	2.064	1.677	1.880	1.285	1.710	1.654	1.050	1.276	1.131	1.842	1.623	1.156	0.85	0.00	1.07	0.05
META1_1942	conserved protein of unknown function; putative expor	0.000	0.091	0.099	0.000	0.071	0.071	0.064	0.077	0.079	0.073	0.060	0.074	1.38	0.34	1.83	0.38
META1_1943	protein of unknown function; putative exported protein	0.428	0.227	0.124	0.203	0.238	0.213	0.193	0.193	0.119	0.236	0.222	0.168	0.96	0.45	1.14	0.17
META1_1948	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.095	0.165	0.000	0.077	0.079	0.000	0.111	0.054	n.d.	0.12	0.73	0.95
META1_1952	Putative cytochrome bd-quinol oxidase subunit I	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_1954	protein of unknown function	0.000	0.068	0.049	0.000	0.048	0.095	0.150	0.077	0.099	0.045	0.060	0.108	3.20	0.46	2.67	0.44
META1_1958	putative phosphotyrosine protein phosphatase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_1960	conserved protein of unknown function	0.000	0.159	0.124	0.000	0.048	0.000	0.107	0.077	0.218	0.109	0.020	0.134	1.67	0.36	10.00	0.16
META1_1961	bifunctional HisD: L-histidinal:NAD+ dehydrogenase ; L-	0.857	0.725	0.767	0.541	0.926	0.662	0.621	0.464	0.556	0.771	0.756	0.544	0.95	0.02	1.08	0.25
META1_1962	conserved protein of unknown function	0.156	0.136	0.124	0.000	0.143	0.071	0.000	0.097	0.000	0.136	0.091	0.034	0.33	0.13	0.56	0.52
META1_1963	protein of unknown function	0.273	0.091	0.173	0.000	0.119	0.142	0.064	0.174	0.159	0.163	0.111	0.134	1.11	0.55	1.82	0.37
META1_1964	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.012	1.042	0.916	0.338	1.116	1.016	0.900	1.102	0.655	0.989	0.958	0.887	1.21	0.44	1.39	0.69
META1_1968	5-aminolevulinic acid synthase (ALAS)	0.000	0.566	0.371	0.135	0.404	0.354	0.300	0.271	0.298	0.363	0.343	0.289	1.08	0.30	1.26	0.84
META1_1970	protein of unknown function; putative exported protein	0.000	0.068	0.074	0.000	0.000	0.000	0.000	0.000	0.060	0.054	0.000	0.020	0.50	0.53	n.d.	0.37
META1_1971	Alkylphosphonate uptake protein	0.156	0.159	0.049	0.000	0.000	0.000	0.150	0.116	0.099	0.118	0.000	0.121	1.38	0.79	n.d.	0.00
META1_1973	conserved protein of unknown function, putative DNA-	0.000	0.000	0.000	0.000	0.071	0.142	0.000	0.039	0.000	0.000	0.091	0.013	n.d.	0.37	0.22	0.58
META1_1974	2-dehydro-3-deoxyphosphoheptonate aldolase	1.129	1.654	1.485	0.744	1.045	1.252	1.093	1.140	1.151	1.470	1.089	1.129	1.04	0.13	1.56	0.45
META1_1977	conserved protein of unknown function	0.000	0.317	0.371	0.203	0.000	0.260	0.279	0.348	0.298	0.263	0.141	0.309	1.59	0.36	3.29	0.42
META1_1978	Guanylate kinase (GMP kinase)	0.234	0.317	0.346	0.406	0.214	0.331	0.386	0.445	0.258	0.308	0.292	0.363	1.59	0.42	1.86	0.59
META1_1979	putative ABC transporter, fused ATPase and transmemb	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_1983	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.040	0.000	0.020	0.040	n.d.	0.00	3.00	0.11
META1_1984	putative Catecholate siderophore receptor fiu precurso	2.570	0.091	0.718	1.826	0.499	0.331	0.236	0.271	0.179	0.898	0.625	0.228	0.34	0.41	0.55	0.11
META1_1985	multifunctional: 2-keto-3-deoxygluconate 6-phosphate	0.350	0.227	0.148	0.406	0.285	0.260	0.257	0.309	0.357	0.227	0.292	0.309	1.84	0.33	1.59	0.91
META1_1986	6-phosphogluconate dehydratase	0.000	0.227	0.000	0.000	0.119	0.000	0.129	0.135	0.139	0.091	0.050	0.134	2.00	0.09	4.00	0.12
META1_1987	Hsp33-like chaperonin	0.389	0.317	0.396	0.541	0.641	0.520	0.257	0.329	0.337	0.363	0.575	0.309	1.15	0.18	0.81	0.00
META1_1989	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_1990	nucleoside diphosphate kinase	1.596	1.337	1.039	1.353	2.185	1.937	1.157	1.334	1.231	1.288	1.955	1.243	1.30	0.71	0.95	0.07
META1_1992	protein of unknown function; putative exported protein	0.117	0.068	0.074	0.406	0.238	0.213	0.300	0.213	0.238	0.082	0.252	0.249	4.11	0.01	1.48	0.68
META1_1993	putative metallopeptidase	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_1994	conserved protein of unknown function; putative memb	0.000	0.159	0.124	0.000	0.095	0.000	0.150	0.000	0.000	0.109	0.040	0.047	0.58	0.51	1.75	0.97
META1_1996	carbon starvation protein A precursor	1.713	1.450	1.683	0.338	1.045	0.709	0.686	0.580	0.794	1.597	0.796	0.685	0.58	0.00	1.29	0.83
META1_1997	conserved protein of unknown function ; putative mem	0.000	0.000	0.074	0.135	0.071	0.047	0.043	0.039	0.099	0.027	0.071	0.060	3.00	0.11	1.29	0.47
META1_1998	conserved protein of unknown function; putative expor	0.156	0.113	0.173	0.000	0.048	0.000	0.086	0.097	0.079	0.145	0.020	0.087	0.81	0.02	6.50	0.14
META1_1999	conserved protein of unknown function, LemA family	1.246	1.246	1.089	0.609	0.404	0.496	0.686	0.696	0.476	1.188	0.474	0.618	0.70	0.01	1.96	0.29
META1_2001	putative Histidine protein kinase of the HWE family	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.040	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_2002	2,5-diketo-D-gluconate reductase A	1.285	1.042	0.916	0.338	0.071	0.354	0.428	0.561	0.556	1.052	0.232	0.517	0.66	0.01	3.35	0.16
META1_2003	putative Regulatory protein, Crp family	0.000	0.068	0.074	0.000	0.000	0.047	0.064	0.097	0.060	0.054	0.020	0.074	1.83	0.38	5.50	0.13
META1_2008	glycogen phosphorylase	0.935	1.201	1.410	1.826	1.710	1.796	2.335	2.068	1.627	1.216	1.764	2.003	2.22	0.03	1.70	0.36
META1_2012	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2014	diguanylate cyclase (GGDEF domain)/phosphodiesteras	0.156	0.159	0.148	0.271	0.285	0.118	0.086	0.174	0.198	0.154	0.212	0.155	1.35	0.80	1.10	0.39
META1_2016	putative UDP-glucose 4-epimerase	0.000	0.181	0.124	0.000	0.071	0.047	0.150	0.155	0.119	0.118	0.050	0.141	1.62	0.36	4.20	0.51
META1_2019	putative nucleotide sugar epimerase/dehydratase	0.117	0.136	0.272	0.000	0.238	0.142	0.257	0.309	0.258	0.181	0.161	0.276	2.05	0.12	2.56	0.44
META1_2020	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2021	protein of unknown function	0.000	0.204	0.272	0.203	0.071	0.071	0.107	0.058	0.099	0.181	0.091	0.087	0.65	0.24	1.44	0.69
META1_2024	homospermidine synthase	0.701	0.680	0.643	0.473	0.713	0.685	0.814	0.947	0.893	0.671	0.665	0.887	1.78	0.01	2.00	0.06
META1_2028	glucan biosynthesis protein, periplasmic	0.078	0.363	0.371	0.271	0.428	0.425	0.214	0.193	0.238	0.299	0.403	0.215	0.97	0.97	0.80	0.03
META1_2029	conserved protein of unknown function; putative GCN5	0.000	0.000	0.000	0.000	0.095	0.095	0.107	0.116	0.099	0.000	0.081	0.108	n.d.	0.00	2.00	0.39
META1_2030	NADH:flavin oxidoreductase/NADH oxidase; putative FM	0.000	0.000	0.000	0.000	0.048	0.047	0.107	0.097	0.060	0.000	0.040	0.087	n.d.	0.00	3.25	0.46
META1_2032	conserved protein of unknown function; putative expor	0.740	0.272	0.322	0.609	0.451	0.567	0.343	0.290	0.516	0.399	0.524	0.383	1.30	0.84	1.10	0.13
META1_2033	conserved protein of unknown function	0.000	0.136	0.049	0.000	0.048	0.118	0.043	0.116	0.099	0.073	0.071	0.087	1.63	0.37	1.86	0.38
META1_2034	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.095	0.095	0.064	0.077	0.060	0.091	0.081	0.067	1.00	0.30	1.25	0.33
META1_2035	Fatty acid/phospholipid synthesis protein	0.273	0.295	0.247	0.203	0.428	0.473	0.300	0.387	0.337	0.272	0.413	0.343	1.70	0.06	1.24	0.96
META1_2036	3-oxoacyl-[acyl-carrier-protein] synthase III; acetylCoA A	0.312	0.498	0.495	0.609	0.523	0.638	0.407	0.522	0.357	0.454	0.585	0.430	1.28	0.98	1.10	0.06
META1_2037	integration host factor (IHF), DNA-binding protein, alph	0.078	0.317	0.297	0.406	0.261	0.236	0.279	0.271	0.318	0.254	0.272	0.289	1.54	0.44	1.59	0.93
META1_2038	putative transcriptional regulator, MerR family	0.000	0.227	0.173	0.000	0.095	0.071	0.150	0.116	0.079	0.154	0.071	0.114	1.00	0.30	2.43	0.42
META1_2039	protein of unknown function	0.000	0.113	0.099	0.000	0.048	0.000	0.086	0.058	0.060	0.082	0.020	0.067	1.11	0.31	5.00	0.13
META1_2040	conserved protein of unknown function; putative expor	0.000	0.159	0.049	0.000	0.095	0.000	0.193	0.155	0.159	0.082	0.040	0.168	2.78	0.47	6.25	0.14
META1_2041	conserved protein of unknown function; putative nucle	3.543	2.266	3.068	1.623	1.591	0.898	2.378	2.397	1.846	2.858	1.300	2.204	1.04	0.15	2.54	0.08
META1_2042	conserved protein of unknown function, UPF0229 prote	0.156	0.272	0.445	0.000	0.048	0.071	0.107	0.097	0.179	0.308	0.050	0.128	0.56	0.10	3.80	0.49
META1_2043	conserved protein of unknown function	0.273	0.385	0.495	0.000	0.119	0.000	0.150	0.174	0.179	0.399	0.050	0.168	0.57	0.01	5.00	0.13
META1_2044	phosphoribosylglycinamide formyltransferase 1	0.117	0.113	0.173	0.271	0.166	0.189	0.171	0.155	0.119	0.136	0.192	0.148	1.47	0.57	1.16	0.14
META1_2045	phosphoribosylaminoimidazole synthetase (AIR synthet	0.623	0.544	0.495	0.541	0.546	0.662	0.364	0.309	0.417	0.544	0.595	0.363	0.90	0.02	0.92	0.01
META1_2048	conserved protein of unknown function	0.000	0.091	0.074	0.000	0.000	0.000	0.107	0.135	0.079	0.064	0.000	0.108	2.29	0.41	n.d.	0.00
META1_2049	polyphosphate kinase, component of RNA degradosom	0.662	0.589	0.718	0.541	0.618	0.473	0.857	0.850	0.734	0.653	0.544	0.813	1.68	0.05	2.24	0.01
META1_2050	exopolyphosphatase	0.000	0.068	0.074	0.000	0.166	0.071	0.086	0.193	0.119	0.054	0.101	0.134	3.33	0.46	2.00	0.40
META1_2053	aspartate aminotransferase A	2.142	1.133	1.410	0.947	1.235	1.323	1.178	1.044	0.794	1.470	1.230	1.001	0.92	0.13	1.22	0.38
META1_2054	putative Acyl CoA:acetate/3-ketoacid CoA transferase;	0.195	0.363	0.421	3.043	3.468	2.812	1.135	1.469	1.171	0.345	3.125	1.263	4.95	0.01	0.61	0.00
META1_2057	30S ribosomal protein S2	3.271	2.266	2.944	5.005	2.399	2.859	1.864	2.339	2.084	2.749	2.984	2.104	1.03	0.08	1.06	0.13
META1_2058	protein chain elongation factor EF-Ts	2.881	1.767	1.658	2.976	3.183	4.371	2.849	2.397	2.798	1.987	3.659	2.675	1.82	0.21	1.10	0.12
META1_2059	uridylate kinase	0.350	0.453	0.198	0.000	0.238	0.189	0.107	0.251	0.159	0.336	0.181	0.175	0.70	0.13	1.44	0.34
META1_2060	inorganic pyrophosphatase	0.506	0.385	0.322	0.203	0.523	0.543	0.107	0.213	0.476	0.390	0.484	0.269	0.93	0.26	0.83	0.36
META1_2063	conserved protein of unknown function	0.000	0.136	0.099	0.203	0.166	0.118	0.086	0.155	0.079	0.091	0.151	0.108	1.60	0.36	1.07	0.17
META1_2064	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.039	0.060	0.000	0.020	0.047	n.d.	0.00	3.50	0.12
META1_2065	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltrans	0.234	0.249	0.297	0.203	0.475	0.638	0.386	0.271	0.318	0.263	0.504	0.323	1.66	0.16	0.96	0.60
META1_2066	putative outer membrane protein assembly factor	7.126	1.563	3.291	7.101	4.062	4.158	2.442	1.894	2.005	3.493	4.556	2.104	0.81	0.36	0.69	0.01

META1_2067	membrane-associated zinc metalloprotease	0.000	0.113	0.148	0.406	0.309	0.331	0.193	0.155	0.198	0.100	0.333	0.181	2.45	0.42	0.82	0.00
META1_2068	1-deoxy-D-xylulose 5-phosphate reductoisomerase (DX	0.428	0.408	0.445	0.406	0.784	0.732	0.514	0.561	0.337	0.426	0.706	0.470	1.49	0.66	1.00	0.33
META1_2070	undecaprenyl pyrophosphate synthetase (di-trans,poly-	0.000	0.068	0.124	0.000	0.000	0.071	0.064	0.077	0.099	0.073	0.030	0.081	1.50	0.35	4.00	0.12
META1_2071	Ribosome recycling factor (Ribosome releasing factor) (	0.973	0.793	0.742	1.420	0.831	0.591	0.814	1.256	0.774	0.816	0.816	0.954	1.58	0.57	1.75	0.89
META1_2072	conserved protein of unknown function; putative mem	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.155	0.238	0.000	0.000	0.181	n.d.	0.00	n.d.	0.00
META1_2074	putative ubiquinone biosynthesis hydroxylase/monoox	0.000	0.045	0.000	0.000	0.238	0.189	0.086	0.135	0.060	0.018	0.181	0.094	7.00	0.15	0.78	0.26
META1_2077	putative 3-oxoacyl-[acyl-carrier-protein] reductase (fab	0.078	0.091	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.054	0.000	0.027	0.67	0.92	n.d.	0.12
META1_2079	putative transketolase (C-terminal domain)	0.000	0.068	0.049	0.000	0.000	0.000	0.000	0.000	0.040	0.045	0.000	0.013	0.40	0.54	n.d.	0.37
META1_2086	acyl-CoA thioesterase II	0.117	0.091	0.099	0.000	0.000	0.071	0.214	0.116	0.099	0.100	0.030	0.141	1.91	0.31	7.00	0.15
META1_2087	nitrogen assimilation regulatory protein for GlnL, GlnE,	0.000	0.113	0.000	0.271	0.214	0.402	0.193	0.174	0.119	0.045	0.302	0.161	4.80	0.13	0.80	0.07
META1_2088	ammonium transport protein (Amt family)	0.156	0.000	0.000	0.000	1.045	0.756	0.386	0.135	0.258	0.036	0.766	0.255	9.50	0.14	0.50	0.20
META1_2089	protein of unknown function; putative exported protei	0.000	0.091	0.099	0.338	0.048	0.165	0.064	0.039	0.040	0.073	0.141	0.047	0.88	0.29	0.50	0.14
META1_2090	DNA-binding membrane protein required for chromoso	0.000	0.000	0.000	0.000	0.119	0.000	0.000	0.077	0.000	0.000	0.050	0.027	n.d.	0.37	0.80	0.98
META1_2093	Formate dehydrogenase subunit B	0.000	0.091	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.036	0.040	0.000	0.00	0.37	0.00	0.12
META1_2094	Formate dehydrogenase subunit A	0.312	1.042	1.039	1.014	0.903	0.898	0.000	0.039	0.000	0.871	0.917	0.013	0.02	0.32	0.02	0.35
META1_2095	dihydro-orotate oxidase, FMN-linked	0.156	0.385	0.272	0.338	0.404	0.331	0.236	0.290	0.298	0.290	0.363	0.276	1.28	0.80	1.14	0.05
META1_2096	conserved protein of unknown function (DUF952)	0.000	0.159	0.099	0.000	0.095	0.118	0.150	0.097	0.159	0.100	0.091	0.134	1.82	0.38	2.22	0.41
META1_2097	putative LexA/Signal peptidase	0.117	0.295	0.099	0.000	0.119	0.189	0.171	0.174	0.139	0.181	0.131	0.161	1.20	0.86	1.85	0.38
META1_2100	serine acetyltransferase	0.000	0.181	0.124	0.000	0.000	0.142	0.193	0.213	0.139	0.118	0.060	0.181	2.08	0.40	4.50	0.13
META1_2101	putative shikimate kinase with helix-turn-helix domain	0.818	0.884	1.039	0.338	0.143	0.614	0.643	0.677	0.714	0.925	0.373	0.679	0.99	0.02	2.73	0.14
META1_2106	response regulator in two-component regulatory syster	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.000	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_2107	putative two-component system regulator: response re	0.000	0.181	0.173	0.000	0.000	0.000	0.107	0.077	0.000	0.136	0.000	0.060	0.60	0.92	n.d.	0.12
META1_2110	conserved protein of unknown function	0.000	0.091	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_2111	conserved protein of unknown function; putative mem	0.078	0.091	0.074	0.000	0.000	0.000	0.000	0.000	0.060	0.082	0.000	0.020	0.33	0.13	n.d.	0.37
META1_2112	TonB-dependent siderophore receptor	0.350	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2114	Oxidoreductase, molybdopterin binding	0.000	0.136	0.074	0.000	0.000	0.000	0.107	0.077	0.040	0.082	0.000	0.074	1.22	0.33	n.d.	0.00
META1_2115	putative oxidoreductase, FAD-binding domain	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2116	conserved protein of unknown function	0.000	0.159	0.198	0.473	0.119	0.142	0.086	0.058	0.119	0.136	0.181	0.087	0.87	0.28	0.72	0.15
META1_2118	3-enolpyruvylshikimate-5-phosphate synthetase	0.389	0.340	0.594	0.473	0.784	0.732	0.686	0.754	0.893	0.445	0.716	0.780	2.37	0.03	1.63	0.37
META1_2119	cytidine monophosphate (CMP) kinase	0.389	0.453	0.445	0.406	0.475	0.449	0.471	0.619	0.397	0.435	0.454	0.497	1.54	0.40	1.64	0.52
META1_2123	creatininase (creatine amidohydrolase)	0.195	0.249	0.272	0.676	0.309	0.378	0.407	0.445	0.337	0.245	0.393	0.397	2.19	0.02	1.51	0.75
META1_2124	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_2125	protein of unknown function	0.273	0.227	0.124	0.000	0.048	0.071	0.086	0.155	0.139	0.200	0.050	0.128	0.86	0.19	3.80	0.49
META1_2126	conserved protein of unknown function; putative CsbD-	0.428	0.272	0.272	0.000	0.048	0.071	0.129	0.000	0.179	0.308	0.050	0.101	0.44	0.50	3.00	0.89
META1_2127	putative oxalate/formate antiporter	0.000	0.000	0.000	0.000	0.095	0.000	0.707	0.580	0.774	0.000	0.040	0.685	n.d.	0.00	25.50	0.25
META1_2128	Fumarylacetoacetate (FAA) hydrolase family	0.000	0.000	0.000	0.203	0.214	0.236	1.307	1.353	0.913	0.000	0.222	1.190	n.d.	0.00	8.05	0.00
META1_2129	putative 2-dehydropantoate 2-reductase (ketopantoate	0.117	0.091	0.099	0.812	0.570	0.827	2.249	2.474	2.699	0.100	0.716	2.480	33.55	0.00	5.20	0.00
META1_2130	putative acyl-coenzyme A synthetase	0.000	0.113	0.148	0.609	0.618	0.496	1.628	1.604	1.707	0.100	0.564	1.647	22.27	0.89	4.38	0.00
META1_2133	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2136	4-oxalocrotonate tautomerase	0.234	0.204	0.000	0.000	0.143	0.142	0.236	0.251	0.258	0.136	0.121	0.249	2.47	0.39	3.08	0.46
META1_2137	malyl-CoA thioesterase	0.740	0.748	0.668	0.609	0.594	0.425	0.686	0.831	0.754	0.717	0.524	0.759	1.43	0.49	2.17	0.06
META1_2138	conserved protein of unknown function	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2139	putative haloacid dehalogenase family hydrolase	0.000	0.045	0.000	0.000	0.000	0.000	0.064	0.077	0.060	0.018	0.000	0.067	5.00	0.13	n.d.	0.00
META1_2141	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.060	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_2143	putative dioxygenase/glyoxalase family protein	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.000	0.040	0.000	0.020	0.034	n.d.	0.12	2.50	0.52
META1_2144	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.119	0.095	0.129	0.135	0.159	0.000	0.091	0.141	n.d.	0.00	2.33	0.42
META1_2147	protein of unknown function	0.000	0.068	0.173	0.203	0.380	0.213	0.364	0.329	0.357	0.091	0.282	0.349	5.20	0.57	1.86	0.19
META1_2148	30S ribosomal subunit protein S12	0.623	0.476	0.643	0.609	0.618	0.685	0.600	0.406	0.516	0.572	0.645	0.504	1.19	0.40	1.17	0.12
META1_2149	30S ribosomal protein S7	1.441	0.929	0.693	2.299	1.781	1.418	1.950	1.508	2.362	0.962	1.703	1.936	2.72	0.05	1.70	0.77
META1_2150	protein chain elongation factor EF-G, GTP-binding	8.294	6.548	8.165	9.063	9.121	9.167	6.898	6.997	5.617	7.548	9.132	6.499	1.16	0.19	1.07	0.01
META1_2151	protein chain elongation factor EF-Tu; GTP-binding fact	10.007	5.801	6.804	8.860	9.739	10.656	7.798	8.215	8.157	7.149	9.999	8.065	1.52	0.60	1.21	0.03
META1_2152	30S ribosomal subunit protein S10	0.779	0.498	0.445	0.744	1.259	1.040	1.243	1.295	1.449	0.544	1.089	1.331	3.30	0.01	1.83	0.14
META1_2153	50S ribosomal subunit protein L3	1.363	1.495	1.485	2.029	1.069	1.843	1.500	1.643	1.806	1.461	1.542	1.653	1.53	0.10	1.61	0.87
META1_2154	50S ribosomal subunit protein L4, regulates expression	1.752	1.020	1.188	2.164	0.879	1.725	1.200	1.527	1.627	1.252	1.431	1.458	1.57	0.58	1.53	0.92
META1_2155	50S ribosomal subunit protein L23	0.623	0.363	0.495	0.541	0.285	0.331	0.600	0.715	1.111	0.472	0.343	0.813	2.33	0.12	3.56	0.05
META1_2156	50S ribosomal subunit protein L2	2.648	1.654	1.955	2.502	1.306	2.953	1.928	2.107	2.104	1.996	2.187	2.050	1.39	1.00	1.41	0.88
META1_2157	30S ribosomal subunit protein S19	0.584	0.657	0.718	0.609	0.926	0.827	0.643	0.522	0.774	0.662	0.837	0.645	1.32	0.89	1.16	0.31
META1_2158	50S ribosomal subunit protein L22	0.779	0.748	0.718	1.285	1.235	1.394	1.178	1.044	1.429	0.744	1.310	1.216	2.21	0.01	1.39	0.48
META1_2159	30S ribosomal subunit protein S3	2.336	1.314	1.163	1.758	0.879	2.339	1.628	1.972	1.608	1.497	1.633	1.741	1.57	0.61	1.60	0.71
META1_2160	50S ribosomal subunit protein L16	0.779	0.340	0.223	0.947	0.998	0.827	0.793	0.850	1.012	0.399	0.917	0.887	3.00	0.09	1.45	0.65
META1_2161	50S ribosomal subunit protein L29	0.428	0.249	0.470	0.338	0.309	0.496	0.321	0.232	0.456	0.372	0.393	0.336	1.22	0.67	1.28	0.60
META1_2162	30S ribosomal subunit protein S17	1.207	0.838	0.767	0.271	1.188	1.040	1.350	1.024	1.647	0.898	0.988	1.337	2.01	0.14	2.03	0.26
META1_2164	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.071	0.071	0.107	0.097	0.079	0.054	0.060	0.094	2.33	0.42	2.33	0.41
META1_2165	transcriptional regulator, MarR family	0.000	0.000	0.000	0.000	0.095	0.000	0.086	0.039	0.040	0.000	0.040	0.054	n.d.	0.00	2.00	0.09
META1_2166	50S ribosomal subunit protein L17	1.168	0.838	0.916	1.961	1.829	1.937	2.249	1.778	2.203	0.943	1.895	2.070	2.96	0.00	1.64	0.37
META1_2167	DNA-directed RNA polymerase alpha chain (RNAP alpha	1.402	1.178	1.485	1.961	1.615	2.103	1.585	1.334	1.469	1.343	1.875	1.458	1.47	0.41	1.17	0.05
META1_2168	putative metallo-beta-lactamase family protein	0.662	0.476	0.569	0.609	0.000	0.331	0.471	0.387	0.397	0.553	0.232	0.417	1.02	0.06	2.70	0.36
META1_2169	30S ribosomal subunit protein S11	0.857	0.385	0.421	0.676	1.069	0.874	0.728	0.522	1.052	0.508	0.927	0.766	2.04	0.34	1.24	0.56
META1_2170	30S ribosomal subunit protein S13	0.818	0.748	0.693	1.217	1.140	1.181	1.564	1.082	1.568	0.744	1.169	1.398	2.54	0.01	1.79	0.27
META1_2171	adenylate kinase	0.545	0.702	0.693	1.420	1.188	1.181	0.900	1.256	1.072	0.662	1.220	1.082	2.21	0.02	1.33	0.22
META1_2172	preprotein translocase, membrane component, transpo	0.273	0.589	0.594	0.000	0.879	0.851	0.771	0.522	0.496	0.517	0.736	0.591	1.54	0.45	1.21	0.31
META1_2173	50S ribosomal protein L15	1.791	1.359	0.940	2.638	2.732	1.701	2.357	2.030	2.957	1.306	2.278	2.446	2.53	0.05	1.61	0.81
META1_2174	50S ribosomal subunit protein L30	0.117	0.091	0.198	0.135	0.143	0.236	0.386	0.135	0.437	0.136	0.181	0.316	3.13	0.14	2.61	0.26
META1_2175	30S ribosomal subunit protein S5	1.713	1.065	1.287	2.841	1.734	1.607	1.907	1.914	2.183	1.297	1.845	2.003	2.08	0.05	1.63	0.99
META1_2176	50S ribosomal subunit protein L18	0.662	0.476	0.643	1.285	0.713	0.803	1.285	1.024	1.548	0.581	0.837	1.284	2.98	0.01	2.30	0.19
META1_2177	50S ribosomal subunit protein L6	1.012	1.201	1.064	1.961	1.093	0.827	0.943	0.754	1.151	1.107	1.109	0.948	1.16	0.31	1.28	0.41
META1_2178	30S ribosomal subunit protein S8, and regulator	1.635	1.201	1.039	1.894	1.354	1.867	1.350	1.314	2.024	1.243	1.653	1.566	1.70	0.39	1.42	0.62
META1_2179	30S ribosomal subunit protein S14	0.350	0.204	0.223	0.541	0.356	0.284	0.728	0.464	0.635	0.245	0.353	0.605	3.33	0.02	2.57	0.12
META1_2180	50S ribosomal subunit protein L5	2.025	1.110	1.039	3.652	2.447	2.126	1.864	2.223	2.540	1.297	2.490	2.218	2.31	0.09	1.34	0.35
META1_2181	50S ribosomal subunit protein L24	0.584	0.363	0.495	0.947	0.641	0.685	0.857	0.715	1.072	0.463	0.706	0.880	2.57	0.03	1.87	0.42
META1_2182	50S ribosomal subunit protein L14	0.740	0.566	0.495	0.947	1.188	1.040	1.350	1.005	1.608	0.581	1.089	1.317	3.06	0.01	1.81	0.24
META1_2185	protein of unknown function	0.078	0.000	0.074	0.135	0.048	0.047	0.107	0.000	0.099	0.045	0.060	0.067	2.00	0.97	1.67	0.32
META1_2186	putative diguanylate cyclase (GGDEF domain)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2194	conserved exported protein of unknown function	0.000	0.136	0.124	0.000	0.095	0.000	0.000	0.039	0.040	0.100	0.040	0.027	0.36	0.87	1.00	0.47
META1_2195	putative salicylate hydroxylase, Salicylate 1-monooxyge	0.156	0.136	0.000	0.000	0.071	0.000	0.043	0.097	0.000	0.091	0.030	0.047	0.70	0.91	2.33	0.51
META1_2197	methionine aminopeptidase	0.389	0.272	0.322	0.406	0.166	0.354	0.300	0.348	0.456	0.318	0.282	0.370	1.57	0.53	1.96	0.49
META1_2199	conserved protein of unknown function	0.117	0.521	0.371	0.135	0.190	0.142	0.236	0.213	0.198	0.372	0.161	0.215	0.78	0.58	2.00	0.05
META1_2200	conserved protein of unknown function, DUF403	0.117	0.159	0.074	0.271	0.000	0.071	0.107	0.155	0.159	0.118	0.071	0.141	1.62	0.44	3.00	0.38
META1_2202	conserved protein of unknown function, putative expor	0.078	0.045	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.036	0.000	0.020	0.75	0.51	n.d.	0.37
META1_2203	protein of unknown function; putative exported protei	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.077	0.000	0.036	0.000	0.027	1.00	0.99	n.d.	0.37
META1_2207	Transglutaminase-like domain	0.195	0.295	0.247	0.135	0.095	0.000	0.236	0.135	0.278	0.254	0.060	0.215	1.14	0.56	5.33	0.47
META1_2208	conserved protein of unknown function	0.117	0.272	0.198	0.135	0.119	0.307	0.171	0.251	0.099	0.209	0.202	0.175	1.13	0.74	1.30	0.91
META1_2209	NAD-dependent protein deacetylase, regulatory protei	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.040	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_2210	putative inner membrane protein (UPF0053 family) wit	0.156	0.091	0.074	0.000	0.071	0.071	0.107	0.077	0.060	0.100	0.060	0.081	1.09	0.42	2.00	0.39
META1_2211	protein of unknown function	0.000	0.227	0.148	0.000	0.238	0.071	0.193	0.406	0.298	0.145	0.131	0.302	2.81	0.45	3.46	0.51
META1_2212	protein of unknown function	0.000	0.091	0.099	0.000	0.048	0.000	0.043	0.039	0.099	0.073	0.020	0.060	1.13	0.31	4.50	0.12
META1_2215	serine protease precursor	0.234	0.521	0.346	0.203	0.333	0.307	0.171	0.213	0.238	0.390	0.302	0.208	0.72	0.10	1.03	0.18
META1_2216	protein of unknown function	1.285	0.680	0.594	0.203	0.404	0.449	0.321	0.213	0.298	0.789	0.393	0.276	0.47	0.02	1.05	0.52
META1_2218	Granule-associated 11 kDa protein	3.037	1.495	2.276	0.812	0.784	1.087	0.707	0.580	0.734	2.141	0.917	0.672	0.42	0.01	1.10	0.09
META1_2219	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2220	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.166	0.000	0.000	0.000	0.040	0.000	0.071	0.013	n.d.	0.37	0.29	0.92
META1_2221	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.040	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_2223	methylsuccinyl-CoA dehydrogenase, putative isobutyryl	3.232	2.538	3.217	2.841	4.157	2.953	2.035	1.991	2.044	2.948	3.447	2.023	0.93	0.01	0.88	0.02
META1_2228	ATP-sulfurylase, subunit 1 (ATP:sulfate adenylyltransfer	0.584	0.793	0.792	0.338	0.760	0.780	0.514	0.561	0.536	0.744	0.706	0.538	0.98	0.05	1.14	0.77
META1_2229	Sulfate adenylyltransferase subunit 2 (Sulfate adenylate	0.312	0.295	0.322	0.271	0.380	0.567	0.450	0.367	0.357	0.308	0.443	0.390	1.71	0.04	1.32	0.99
META1_2230	Phosphoadenosine phosphosulfate reductase (PAPS red	0.000	0.091	0.099	0.000	0.166	0.142	0.129	0.135	0.238	0.073	0.131	0.168	3.13	0.45	1.92	0.38
META1_2231	putative transcriptional regulator, AsnC/Lrp family	0.000	0.000	0.049	0.000	0.190	0.095	0.214	0.193	0.238	0.018	0.121	0.215	16.00	0.19	2.67	0.45
META1_2232	sulfite reductase, alpha subunit (flavoprotein)	0.467	0.521	0.866	0.947	1.283	0.898	1.521	1.430	1.369	0.635	1.068	1.438	3.06	0.01	2.02	0.04
META1_2233	sulfite reductase, beta subunit, NADPH-dependent hem	0.273	1.269	1.336	1.488	1.853	1.040	1.778	1.643	1.667	1.061	1.451	1.694	2.15	0.21	1.75	0.36
META1_2235	Pantoate--beta-alanine ligase (Pantothenate synthetase	0.117	0.136	0.148	0.000	0.000	0.165	0.171	0.271	0.159	0.136	0.071	0.202	2.00	0.10	4.29	0.12
META1_2237	putative transcriptional regulator, XRE family	0.117	0.091	0.000	0.000	0.143	0.095	0.171	0.213	0.139	0.064	0.101	0.175	3.71	0.45	2.60	0.43
META1_2238	Single-stranded DNA-binding protein	0.896	0.612	0.421	0.744	0.618	0.567	0.814	0.793	0.695	0.608	0.615	0.766	1.70	0.38	1.87	0.13
META1_2239	putative conserved oxidoreductase, Zn-dependent and	0.467	0.385	0.272	0.000	0.119	0.189	0.300	0.213	0.318	0.363	0.131	0.276	1.03	0.22	3.15	0.47
META1_2243	conserved protein of unknown function; putative expor	0.000	0.045	0.000	0.000	0.095	0.142	0.000	0.000	0.040	0.018	0.101	0.013	1.00	0.99	0.20	0.59
META1_2244	putative NADPH-dependent flavin oxidoreductase	0.350	0.408	0.544	0.271	0.333	0.260	0.343	0.290	0.198	0.445	0.292	0.276	0.84	0.09	1.41	0.77
META1_2245	putative glutathione S-transferase	0.195	0.181	0.099	0.000	0.071	0.071	0.129	0.058	0.079	0.154	0.060	0.087	0.76	0.13	2.17	0.40
META1_2246	protein of unknown function; putative exported protei	0.350	0.204	0.000	0.271	0.048	0.095	0.086	0.155	0.139	0.163	0.101	0.128	1.06	0.27	1.90	0.81
META1_2247	thioredoxin	0.545	0.680	0.718	0.879	0.285	0.662	0.578	0.522	0.595	0.662	0.534	0.565	1.15	0.23	1.58	0.94
META1_2248	putative Lon family ATP-dependent protease	0.156	0.113	0.223	0.000	0.238	0.331	0.279	0.309	0.198	0.163	0.242	0.262	2.17	0.11	1.63	0.36
META1_2249	conserved protein of unknown function	0.000	0.204	0.124	0.203	0.214	0.165	0.107	0.135	0.179	0.127	0.192	0.141	1.50	0.35	1.11	0.11
META1_2250	conserved protein of unknown function	0.273	0.159	0.173	0.541	0.190	0.614	0.386	0.522	0.377	0.191	0.423	0.430	3.05	0.02	1.52	0.88
META1_2252	protein of unknown function	0.000	0.159	0.049	0.000	0.000	0.000	0.000	0.039	0.000	0.082	0.000	0.013	0.22	0.57	n.d.	0.37
META1_2257	putative rhomboid-like protein	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_2261	conserved protein of unknown function with 2 CBS dom	0.350	0.159	0.247	0.000	0.071	0.165	0.664	0.580	0.754	0.236	0.101	0.665	3.81	0.01	9.90	0.71

META1_2263	phosphoribosyl c-AMP cyclohydrolase	0.156	0.136	0.000	0.000	0.143	0.000	0.086	0.077	0.119	0.091	0.060	0.094	1.40	0.31	2.33	0.10
META1_2264	GTP cyclohydrolase I	0.234	0.363	0.421	0.609	0.190	0.378	0.578	0.503	0.456	0.354	0.333	0.511	1.95	0.08	2.30	0.34
META1_2266	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.039	0.119	0.000	0.020	0.074	n.d.	0.00	5.50	0.13
META1_2268	conserved protein of unknown function; putative inner	0.195	0.159	0.272	0.000	0.475	0.189	0.214	0.174	0.179	0.209	0.282	0.188	1.22	0.67	1.00	0.31
META1_2269	conserved protein of unknown function, DUF214; putat	0.156	0.159	0.247	0.000	0.143	0.071	0.150	0.193	0.179	0.191	0.091	0.175	1.24	0.76	2.89	0.46
META1_2271	Pyridoxal phosphate biosynthetic protein pdxJ (PNP syn	0.350	0.385	0.346	0.473	0.000	0.165	0.236	0.367	0.278	0.363	0.141	0.296	1.10	0.17	3.14	0.38
META1_2272	holo-[acyl-carrier-protein] synthase 1	0.000	0.000	0.000	0.000	0.095	0.142	0.000	0.058	0.000	0.000	0.101	0.020	n.d.	0.37	0.30	0.56
META1_2273	signal peptidase I (SPase I) (leader peptidase I)	0.428	0.340	0.346	0.338	0.190	0.425	0.300	0.232	0.258	0.363	0.312	0.262	0.98	0.03	1.26	0.61
META1_2274	ribonuclease III	0.000	0.113	0.148	0.203	0.000	0.047	0.129	0.174	0.099	0.100	0.050	0.134	1.82	0.38	4.00	0.42
META1_2275	GTP-binding protein	0.195	0.408	0.371	0.203	0.404	0.496	0.279	0.348	0.218	0.345	0.413	0.282	1.11	0.70	1.02	0.51
META1_2276	putative methyltransferase	0.156	0.113	0.000	0.135	0.190	0.236	0.279	0.271	0.238	0.082	0.202	0.262	4.33	0.48	1.95	0.10
META1_2277	16S rRNA pseudouridylate 516 synthase	0.000	0.000	0.000	0.135	0.095	0.071	0.086	0.155	0.179	0.000	0.091	0.141	n.d.	0.00	2.33	0.34
META1_2282	protein of unknown function; putative exported protein	0.117	0.181	0.297	0.271	0.048	0.118	0.236	0.135	0.218	0.209	0.111	0.195	1.26	0.92	2.64	0.39
META1_2284	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.077	0.060	0.000	0.030	0.047	n.d.	0.12	2.33	0.52
META1_2285	(di)nucleoside polyphosphate hydrolase (Nudix family)	0.117	0.113	0.049	0.000	0.095	0.165	0.064	0.058	0.000	0.091	0.111	0.040	0.60	0.42	0.55	0.92
META1_2288	putative periplasmic carboxyl-terminal processing prote	1.402	1.790	1.732	1.488	1.568	1.488	0.471	0.870	0.734	1.678	1.522	0.699	0.56	0.01	0.69	0.01
META1_2289	Putative membrane-bound metallopeptidase	0.000	0.000	0.000	0.000	0.119	0.071	0.000	0.039	0.040	0.000	0.081	0.027	n.d.	0.12	0.50	0.91
META1_2290	conserved protein of unknown function, UPF0247 prote	0.000	0.045	0.000	0.000	0.048	0.000	0.000	0.097	0.119	0.018	0.020	0.074	5.50	0.57	5.50	0.57
META1_2293	periplasmic oxidoreductase, DsbA family	0.195	0.159	0.198	0.135	0.095	0.071	0.236	0.135	0.079	0.181	0.091	0.148	1.10	0.41	2.44	0.40
META1_2294	argininosuccinate synthase (citrulline-aspartate ligase)	1.324	1.042	1.212	0.812	1.093	1.252	0.943	0.986	1.032	1.170	1.119	0.988	1.14	0.07	1.32	0.73
META1_2296	conserved protein of unknown function	0.273	0.408	0.099	0.406	0.095	0.402	0.171	0.213	0.318	0.263	0.272	0.235	1.21	0.97	1.30	0.86
META1_2297	putative phosphoglycolate phosphatase, putative haloa	0.078	0.000	0.000	0.271	0.214	0.260	0.236	0.193	0.079	0.018	0.242	0.168	12.50	0.15	1.04	0.24
META1_2298	protein of unknown function	0.117	0.068	0.049	0.000	0.095	0.047	0.107	0.058	0.119	0.073	0.060	0.094	1.75	0.56	2.33	0.42
META1_2299	Ribose-5-phosphate isomerase A	0.117	0.136	0.173	0.203	0.214	0.307	0.150	0.232	0.218	0.145	0.252	0.202	1.88	0.13	1.20	0.38
META1_2300	conserved protein of unknown function; putative expor	0.195	0.249	0.148	0.541	0.570	0.402	0.386	0.445	0.476	0.200	0.494	0.437	2.95	0.01	1.33	0.33
META1_2302	glutathione reductase	0.117	0.363	0.371	0.135	0.451	0.378	0.407	0.445	0.556	0.308	0.373	0.470	2.06	0.19	1.89	0.27
META1_2305	osmotically inducible protein OsmC	0.896	0.770	0.619	0.676	0.285	0.260	0.300	0.329	0.496	0.744	0.333	0.376	0.68	0.02	1.70	0.98
META1_2308	putative zink-containing alcohol dehydrogenase	0.000	0.227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2309	conserved protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2313	putative glutathione S-transferase	0.701	0.498	0.396	0.000	0.190	0.118	0.364	0.348	0.258	0.508	0.131	0.323	0.86	0.07	3.69	0.50
META1_2314	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2315	putative catalase precursor	0.623	0.634	0.792	0.676	0.546	0.662	0.428	0.599	0.456	0.689	0.615	0.497	0.97	0.06	1.21	0.12
META1_2316	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.095	0.129	0.174	0.079	0.000	0.081	0.128	n.d.	0.00	2.38	0.41
META1_2317	Nitroreductase family protein	0.312	0.159	0.223	0.338	0.309	0.307	0.279	0.309	0.159	0.218	0.312	0.249	1.54	0.81	1.19	0.25
META1_2323	threonine tRNA synthetase	0.779	0.838	1.386	0.406	1.164	0.969	0.964	0.870	0.754	1.025	0.968	0.860	1.13	0.57	1.33	0.76
META1_2324	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2325	putative kinase (mak-like) /transcriptional regulator, act	0.000	0.000	0.074	0.000	0.000	0.000	0.000	0.058	0.099	0.027	0.000	0.054	2.67	0.52	n.d.	0.12
META1_2326	sodium:dicarboxylate symporter (DAACS family)	1.168	1.065	0.990	0.000	0.475	0.520	0.643	0.541	0.615	1.061	0.423	0.598	0.76	0.00	2.12	0.41
META1_2327	isoleucine tRNA synthetase	1.207	1.337	1.336	1.623	1.473	1.110	1.671	1.682	1.369	1.306	1.341	1.573	1.63	0.06	1.76	0.40
META1_2329	conserved protein of unknown function; putative expor	0.117	0.204	0.247	0.271	0.166	0.095	0.171	0.193	0.218	0.200	0.151	0.195	1.32	0.79	1.93	0.60
META1_2330	putative protease	0.117	0.249	0.173	0.135	0.665	0.473	0.321	0.483	0.278	0.191	0.504	0.363	2.57	0.06	1.08	0.99
META1_2331	putative protease	0.662	0.634	0.619	0.473	0.618	0.921	0.557	0.464	0.476	0.635	0.726	0.497	1.06	0.01	1.03	0.27
META1_2332	putative linE	0.350	0.431	0.223	0.000	0.166	0.142	0.343	0.135	0.258	0.336	0.131	0.242	0.97	0.36	2.77	0.44
META1_2334	ferredoxin--NADP+ reductase	0.779	0.431	0.272	0.676	0.499	0.874	0.664	0.850	0.476	0.454	0.685	0.665	1.98	0.36	1.46	0.90
META1_2335	Dethiobiotin synthetase (Dethiobiotin synthase) (DTB sy	0.000	0.091	0.099	0.000	0.071	0.047	0.086	0.077	0.040	0.073	0.050	0.067	1.25	0.32	2.00	0.39
META1_2336	protein of unknown function	0.117	0.113	0.000	0.000	0.143	0.000	0.000	0.058	0.079	0.073	0.060	0.047	0.88	0.94	1.17	0.47
META1_2339	WD-40 repeat family protein	0.350	0.272	0.247	0.406	0.285	0.213	0.193	0.271	0.218	0.281	0.272	0.228	1.10	0.17	1.26	0.29
META1_2341	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.135	0.071	0.047	0.064	0.058	0.079	0.000	0.071	0.067	n.d.	0.00	1.43	0.68
META1_2342	protein of unknown function; putative membrane prote	0.000	0.136	0.000	0.000	0.143	0.000	0.043	0.000	0.000	0.054	0.060	0.013	0.33	0.94	0.33	0.93
META1_2344	putative Pyrimidine 5-nucleotidase (HAD-superfamily hy	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.039	0.000	0.000	0.030	0.013	n.d.	0.37	0.67	0.97
META1_2345	acetylglutamate kinase	1.012	0.793	0.445	0.744	0.356	1.134	0.750	0.966	0.933	0.717	0.746	0.887	1.67	0.45	1.78	0.48
META1_2347	MOSC (sulfur-carrier) domain protein	0.000	0.000	0.074	0.000	0.000	0.118	0.086	0.077	0.040	0.027	0.050	0.067	3.33	0.11	2.00	0.09
META1_2349	protein disaggregation chaperone	1.207	1.405	1.559	2.232	1.734	1.394	2.549	2.146	1.588	1.415	1.663	2.083	1.99	0.07	1.88	0.46
META1_2350	Metallophosphoesterase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2351	short-chain fatty acid transporter (scFAT family)	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_2352	conserved protein of unknown function precursor; puta	0.000	0.000	0.000	0.000	0.119	0.142	0.000	0.000	0.000	0.000	0.111	0.000	n.d.	n.d.	0.00	0.12
META1_2353	putative GTP-binding protein engB	0.234	0.204	0.173	0.473	0.309	0.449	0.450	0.561	0.278	0.200	0.393	0.430	2.91	0.03	1.64	0.93
META1_2354	transmembrane protein, OxaA-like, preprotein translocı	0.857	1.156	1.311	0.271	0.998	0.732	0.728	0.793	0.814	1.143	0.776	0.780	0.92	0.06	1.51	0.51
META1_2355	ribonuclease P protein component (RNaseP protein, RN	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.058	0.060	0.000	0.030	0.060	n.d.	0.00	3.00	0.11
META1_2356	50S ribosomal subunit protein L34	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2357	putative transcriptional regulator, AraC family	0.156	0.113	0.099	0.000	0.166	0.118	0.214	0.174	0.179	0.118	0.121	0.188	2.15	0.04	2.33	0.42
META1_2358	50S ribosomal protein L31	0.467	0.544	0.718	0.406	0.428	0.473	0.643	0.406	0.893	0.590	0.443	0.645	1.48	0.77	2.18	0.21
META1_2359	putative ABC transporter related, fused ATPase and tra	0.000	0.498	0.544	0.473	0.831	0.638	0.428	0.425	0.476	0.399	0.695	0.444	1.50	0.35	0.96	0.10
META1_2360	D-cysteine desulfhydrase, PLP-dependent enzyme	0.156	0.181	0.124	0.135	0.309	0.449	0.300	0.213	0.159	0.154	0.343	0.222	1.94	0.17	0.97	0.63
META1_2361	flagellar motor protein MotB	0.078	0.068	0.074	0.000	0.071	0.118	0.043	0.058	0.079	0.073	0.081	0.060	1.13	0.28	1.13	0.32
META1_2362	conserved protein of unknown function; putative memb	0.000	0.000	0.124	0.271	0.190	0.165	0.214	0.155	0.119	0.045	0.192	0.161	4.80	0.13	1.26	0.32
META1_2363	conserved protein of unknown function	0.350	0.181	0.124	0.271	0.000	0.165	0.257	0.271	0.298	0.200	0.111	0.276	1.86	0.35	3.73	0.42
META1_2364	putative ligase (ygfA)	0.078	0.113	0.247	0.000	0.166	0.142	0.064	0.116	0.159	0.154	0.131	0.114	1.00	0.66	1.31	0.32
META1_2365	conserved protein of unknown function	0.000	0.000	0.148	0.000	0.000	0.142	0.107	0.000	0.099	0.054	0.060	0.067	1.67	0.50	1.67	0.50
META1_2366	conserved protein of unknown function	0.000	0.091	0.074	0.203	0.095	0.213	0.064	0.116	0.060	0.064	0.161	0.081	1.71	0.37	0.75	0.09
META1_2367	Glyceraldehyde-3-phosphate dehydrogenase	4.166	2.470	2.202	2.705	2.280	3.024	2.121	2.030	1.985	2.767	2.661	2.043	1.00	0.17	1.15	0.04
META1_2368	protein of unknown function	0.779	0.476	0.445	0.744	0.475	0.425	0.493	0.715	0.496	0.535	0.494	0.571	1.44	0.93	1.73	0.82
META1_2369	phosphoglycerate kinase	1.830	1.450	1.485	1.420	1.591	1.772	0.878	1.044	0.913	1.551	1.643	0.948	0.82	0.00	0.87	0.00
META1_2370	fructose-bisphosphate aldolase	2.375	0.952	1.064	1.014	1.045	1.630	1.178	0.831	0.873	1.324	1.290	0.954	0.97	0.33	1.11	0.28
META1_2371	putative thiamine-phosphate pyrophosphorylase (TMP	0.467	0.385	0.445	0.473	0.238	0.354	0.171	0.271	0.318	0.426	0.323	0.255	0.81	0.04	1.19	0.29
META1_2372	Sel1-like repeats containing protein	0.117	0.068	0.074	0.000	0.119	0.000	0.064	0.077	0.060	0.082	0.050	0.067	1.11	0.28	2.00	0.09
META1_2375	putative carbohydrate kinase	0.000	0.000	0.049	0.135	0.214	0.165	0.150	0.193	0.258	0.018	0.181	0.202	15.00	0.19	1.67	0.51
META1_2376	regulatory protein (P-II) for nitrogen assimilation by glu	0.312	0.521	0.569	0.338	0.475	0.591	0.279	0.290	0.417	0.490	0.504	0.329	0.91	0.21	0.98	0.17
META1_2377	glutaminase	0.000	0.000	0.074	0.000	0.000	0.000	0.064	0.058	0.079	0.027	0.000	0.067	3.33	0.11	n.d.	0.00
META1_2378	glutamine synthetase II	0.000	0.000	0.000	0.338	0.736	0.827	0.386	0.367	0.476	0.000	0.716	0.410	n.d.	0.00	0.86	0.27
META1_2379	glutamine synthetase, type I	5.218	3.399	3.860	1.556	3.515	3.757	3.513	3.209	2.957	3.992	3.326	3.219	1.09	0.15	1.45	0.60
META1_2380	NADPH-dependent FMN reductase	0.078	0.181	0.198	0.203	0.143	0.213	0.214	0.232	0.179	0.163	0.181	0.208	1.72	0.28	1.72	0.46
META1_2381	protein of unknown function	0.000	0.113	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_2382	ribonuclease R	0.000	0.113	0.173	0.135	0.380	0.236	0.321	0.213	0.079	0.109	0.282	0.202	2.50	0.41	1.07	0.63
META1_2383	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.060	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_2384	putative NUDIX hydrolase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2385	methyl-accepting chemotaxis receptor/sensory transdu	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2386	putative epimerase with NAD(P)-binding Rossmann-fold	0.000	0.204	0.124	0.135	0.119	0.284	0.129	0.097	0.119	0.127	0.192	0.114	1.21	0.33	0.89	0.26
META1_2388	putative glutathione S-transferase	0.000	0.068	0.099	0.135	0.190	0.213	0.193	0.174	0.179	0.064	0.192	0.181	3.86	0.50	1.42	0.84
META1_2389	Undecaprenyl-diphosphatase (Undecaprenyl pyrophosp	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.039	0.040	0.000	0.040	0.027	n.d.	0.12	1.00	0.98
META1_2390	Methylmalonyl-CoA mutase, beta subunit	1.051	1.156	1.410	1.217	1.971	1.276	1.435	1.411	1.350	1.225	1.562	1.398	1.54	0.15	1.34	0.82
META1_2391	protein of unknown function; putative exported protein	0.156	0.204	0.247	0.203	0.119	0.095	0.064	0.077	0.079	0.209	0.121	0.074	0.48	0.00	0.92	0.07
META1_2393	conserved protein of unknown function; putative expor	0.195	0.317	0.297	0.338	0.261	0.236	0.193	0.329	0.357	0.281	0.262	0.296	1.42	0.79	1.69	0.91
META1_2394	dTDP-4-dehydrorhamnose 3,5-epimerase	0.000	0.068	0.074	0.000	0.095	0.047	0.000	0.077	0.079	0.054	0.060	0.054	1.33	0.99	1.33	0.98
META1_2395	dTDP-glucose 4,6-dehydratase	1.246	0.748	0.668	1.082	0.546	0.921	0.793	0.522	0.456	0.835	0.786	0.585	0.95	0.19	1.12	0.25
META1_2396	dTDP-4-dehydrorhamnose reductase	0.000	0.091	0.049	0.203	0.048	0.142	0.107	0.058	0.079	0.054	0.111	0.081	2.00	0.40	1.09	0.51
META1_2397	Glucose-1-phosphate thymidylyltransferase	0.117	0.136	0.148	0.000	0.000	0.000	0.064	0.058	0.060	0.136	0.000	0.060	0.60	0.00	n.d.	0.00
META1_2398	conserved protein of unknown function; putative expor	0.078	0.091	0.000	0.000	0.071	0.000	0.000	0.058	0.099	0.054	0.030	0.054	1.33	0.99	2.67	0.52
META1_2404	conserved protein of unknown function	0.000	0.204	0.272	0.135	0.071	0.118	0.129	0.058	0.079	0.181	0.101	0.087	0.65	0.24	1.30	0.51
META1_2405	putative methyltransferase/methylase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2406	conserved protein of unknown function	0.000	0.045	0.049	0.000	0.000	0.000	0.064	0.058	0.000	0.036	0.000	0.040	1.50	0.97	n.d.	0.12
META1_2407	protein of unknown function	0.000	0.136	0.198	0.000	0.000	0.000	0.171	0.116	0.099	0.127	0.000	0.128	1.36	0.34	n.d.	0.00
META1_2411	conserved protein of unknown function	0.156	0.091	0.148	0.000	0.000	0.095	0.129	0.135	0.218	0.127	0.040	0.161	1.71	0.46	6.00	0.14
META1_2412	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_2417	Putative multicopper oxidase	0.234	0.408	0.297	0.135	0.261	0.189	0.064	0.155	0.198	0.327	0.212	0.141	0.58	0.08	1.00	0.36
META1_2418	Trigger factor (TF)	3.543	4.396	4.874	4.734	4.798	3.969	3.256	3.228	4.247	4.373	4.435	3.582	1.11	0.25	1.21	0.10
META1_2419	ATP-dependent Clp protease proteolytic subunit (Endop	1.051	0.544	0.396	0.947	0.831	0.874	0.793	0.870	0.754	0.608	0.867	0.806	1.79	0.39	1.40	0.17
META1_2420	ATP-dependent Clp protease ATP-binding subunit clpX	2.258	1.722	2.078	1.691	1.781	1.772	1.457	1.430	1.350	1.978	1.764	1.411	0.96	0.01	1.20	0.00
META1_2421	ATP-dependent protease La (Lon)	2.531	3.172	3.142	4.193	3.587	3.449	4.263	4.078	3.612	3.012	3.619	3.979	1.78	0.03	1.65	0.46
META1_2428	conserved protein of unknown function	0.117	0.045	0.074	0.000	0.000	0.071	0.086	0.077	0.060	0.073	0.030	0.074	1.38	1.00	3.67	0.12
META1_2436	DNA polymerase I	0.662	0.884	0.866	0.541	0.855	0.803	0.771	0.908	1.092	0.826	0.786	0.927	1.52	0.37	1.77	0.24
META1_2437	Endonuclease V (Deoxyinosine 3'endonuclease) (Deoxy	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2438	putative GTP-binding protein with nucleoside triP hydro	0.467	0.521	0.767	0.744	0.998	0.874	0.578	0.754	0.794	0.599	0.907	0.712	1.61	0.32	1.18	0.18
META1_2439	Peptidyl-tRNA hydrolase (PTH)	0.234	0.136	0.124	0.203	0.309	0.260	0.257	0.503	0.159	0.154	0.272	0.309	2.71	0.23	1.70	0.84
META1_2440	50S ribosomal protein L25 (General stress protein CTC)	2.219	2.085	1.435	2.638	1.164	2.103	1.800	1.836	1.846	1.878	1.784	1.828	1.31	0.85	1.54	0.94
META1_2441	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2444	pilus assembly protein cpaB	0.000	0.045	0.000	0.000	0.000	0.071	0.150	0.058	0.060	0.018	0.030	0.087	6.50	0.14	4.33	0.12
META1_2445	putative pilus assembly protein; putative precursor	0.117	0.045	0.074	0.338	0.000	0.142	0.000	0.058	0.000	0.073	0.111	0.020	0.38	0.13	0.27	0.61
META1_2446	pilus assembly protein cpaD	0.078	0.000	0.000	0.338	0.119	0.165	0.129	0.077	0.079	0.018	0.171	0.094	7.00	0.12	0.82	0.11
META1_2447	pilus assembly protein cpaE	0.000	0.136	0.198	0.271	0.214	0.236	0.257	0.271	0.218	0.127	0.232	0.249	2.64	0.44	1.61	0.73
META1_2448	secretory protein kinase, cpaF	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.060	0.000	0.000	0.054	n.d.	0.00	n.d.	0.00
META1_2451	conserved protein of unknown function	0.117	0.091	0.074	0.271	0.261	0.118	0.171	0.174	0.179	0.091	0.202	0.175	2.60	0.01	1.30	0.61
META1_2453	organic hydroperoxide resistance protein	0.000	0.091	0.000	0.000	0.095	0.118	0.000	0.058	0.000	0.036	0.091	0.020	0.75	0.98	0.33	0.56
META1_2454	CoA Binding Domain protein	0.078	0.068	0.049	0.203	0.190	0.189	0.214	0.193	0.218	0.064	0.192	0.208	4.43	0.00	1.63	0.18

META1_2455	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.071	0.000	0.077	0.000	0.000	0.071	0.027	n.d.	0.37	0.57	0.52
META1_2459	conserved protein of unknown function; putative meml	1.207	0.725	0.495	0.338	0.143	0.236	0.214	0.290	0.238	0.753	0.212	0.249	0.45	0.01	1.76	0.76
META1_2460	conserved protein of unknown function	0.195	0.363	0.693	0.271	0.166	0.189	0.300	0.271	0.337	0.445	0.192	0.302	0.92	0.63	2.37	0.07
META1_2461	conserved protein of unknown function; putative expor	0.545	0.770	0.148	0.203	0.000	0.000	0.300	0.329	0.377	0.490	0.030	0.336	0.93	0.75	16.67	0.14
META1_2462	3'-5' exonuclease	0.078	0.159	0.099	0.135	0.048	0.095	0.150	0.232	0.099	0.118	0.081	0.161	1.85	0.34	3.00	0.21
META1_2464	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.048	0.095	0.086	0.058	0.079	0.000	0.060	0.074	n.d.	0.00	1.83	0.39
META1_2465	putative ABC transporter, ATPase	0.000	0.068	0.049	0.000	0.000	0.071	0.086	0.116	0.060	0.045	0.030	0.087	2.60	0.43	4.33	0.12
META1_2466	sigma N (sigma 54) factor of RNA polymerase	0.000	0.045	0.074	0.000	0.000	0.000	0.000	0.116	0.060	0.045	0.000	0.060	1.80	0.96	n.d.	0.12
META1_2467	ribosomal subunit interface protein, sigma 54 (RpoN) m	0.234	0.317	0.148	0.203	0.000	0.095	0.171	0.155	0.179	0.236	0.071	0.168	0.96	0.28	3.57	0.40
META1_2468	sugar-specific enzyme IIA component of PTS	0.195	0.227	0.198	0.000	0.261	0.284	0.643	0.348	0.536	0.209	0.232	0.504	3.26	0.01	3.26	0.48
META1_2469	protein of unknown function; putative exported protei	0.117	0.227	0.124	0.000	0.143	0.165	0.150	0.097	0.119	0.163	0.131	0.121	1.00	0.44	1.38	0.34
META1_2470	Mg chelatase subunit BchI, participate to introduce Mg	0.000	0.091	0.099	0.000	0.000	0.000	0.064	0.058	0.060	0.073	0.000	0.060	1.13	0.32	n.d.	0.00
META1_2472	phosphoglyceromutase	0.935	0.997	0.693	0.541	0.404	0.756	0.600	0.638	0.397	0.871	0.575	0.544	0.84	0.06	1.42	0.91
META1_2473	dihydrodipicolinate reductase	0.428	0.566	0.520	0.338	0.546	0.591	0.814	0.735	0.476	0.517	0.534	0.672	1.75	0.21	1.89	0.25
META1_2475	conserved protein of unknown function	0.156	0.068	0.000	0.135	0.048	0.118	0.000	0.058	0.040	0.064	0.091	0.034	0.71	0.92	0.56	0.47
META1_2476	putative hydroxyacylglutathione hydrolase (gloB-like) w	0.273	0.295	0.322	0.000	0.095	0.213	0.193	0.213	0.198	0.299	0.131	0.202	0.91	0.00	2.31	0.43
META1_2481	putative oligopeptide transporter subunit ; permease c	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2482	protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.064	0.039	0.040	0.018	0.000	0.047	3.50	0.11	n.d.	0.00
META1_2483	putative aminotransferase (putative ybdL)	0.000	0.000	0.000	0.000	0.119	0.095	0.064	0.077	0.000	0.000	0.091	0.047	n.d.	0.12	0.78	0.95
META1_2485	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2486	multidrug efflux protein, subunit A; RND efflux transpor	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.116	0.119	0.000	0.000	0.108	n.d.	0.00	n.d.	0.00
META1_2487	multidrug efflux protein, subunit B; RND efflux transpor	0.000	0.045	0.000	0.000	0.000	0.000	0.129	0.174	0.198	0.018	0.000	0.168	12.50	0.18	n.d.	0.00
META1_2488	multidrug efflux system, subunit C; RND efflux exporter	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.097	0.139	0.000	0.000	0.101	n.d.	0.00	n.d.	0.00
META1_2489	putative outer membrane lipoprotein precursor	0.000	0.000	0.000	0.000	0.166	0.142	0.000	0.039	0.000	0.000	0.131	0.013	n.d.	0.37	0.15	0.61
META1_2490	glucose-6-phosphate 1-dehydrogenase	0.000	0.249	0.272	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_2491	3-isopropylmalate dehydrogenase	1.246	1.042	1.188	1.353	1.710	2.103	1.200	1.372	1.012	1.143	1.824	1.196	1.41	0.81	0.98	0.08
META1_2492	protein of unknown function	0.000	0.091	0.099	0.000	0.000	0.071	0.000	0.000	0.000	0.073	0.030	0.000	0.00	0.12	0.00	0.37
META1_2493	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2494	Putative decarboxylase, Thiamine pyrophosphate-requi	0.156	0.521	0.594	0.271	0.143	0.118	0.107	0.193	0.258	0.463	0.151	0.188	0.55	0.22	1.87	0.89
META1_2496	geranyltranstransferase (farnesyl-diphosphate synthase	0.662	0.340	0.371	0.676	0.523	0.780	0.364	0.503	0.476	0.426	0.655	0.450	1.43	0.95	1.03	0.07
META1_2498	deoxyribodipyrimidine photolyase (DNA photolyase)	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2499	putative extracellular solute-binding protein family 7, tv	0.195	0.159	0.272	0.203	0.428	0.260	0.129	0.077	0.099	0.209	0.323	0.101	0.65	0.03	0.47	0.02
META1_2500	conserved protein of unknown function; putative phosp	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2501	putative extracellular ligand-binding receptor precurso	0.078	0.091	0.099	0.000	0.190	0.095	0.086	0.155	0.159	0.091	0.121	0.134	2.00	0.16	1.67	0.37
META1_2502	putative capsule polysaccharide export outer membran	0.312	0.000	0.148	0.338	0.119	0.095	0.064	0.000	0.000	0.127	0.141	0.020	0.21	0.60	0.21	0.16
META1_2503	putative Capsular polysaccharide biosynthesis protein	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_2504	protein of unknown function	0.000	0.068	0.173	0.000	0.143	0.000	0.150	0.232	0.119	0.091	0.060	0.168	2.50	0.44	4.17	0.12
META1_2506	Putative oxidoreductase, short-chain dehydrogenase/re	0.000	0.000	0.000	0.135	0.000	0.000	0.107	0.174	0.079	0.000	0.020	0.121	n.d.	0.00	9.00	0.11
META1_2507	putative Methionyl-tRNA formyltransferase (partial)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.060	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_2508	Trans-sulfuration enzyme (O-acetylhomoserine aminoc	1.129	0.770	1.089	0.338	0.903	0.780	0.621	0.638	0.337	0.971	0.766	0.531	0.74	0.05	1.04	0.63
META1_2509	Ubiquinol-cytochrome c reductase complex, iron-sulfur	0.428	0.431	0.297	0.473	0.594	0.543	1.028	0.812	0.695	0.381	0.554	0.840	2.98	0.01	2.27	0.03
META1_2510	Ubiquinol-cytochrome c reductase complex, cytochrom	0.389	1.065	1.064	0.879	0.950	1.181	1.114	0.773	0.973	0.907	1.038	0.948	1.41	0.58	1.37	0.71
META1_2511	Ubiquinol-cytochrome c reductase complex, cytochrom	1.090	0.702	0.643	0.947	0.641	0.780	0.814	0.599	0.695	0.771	0.746	0.699	1.22	0.54	1.41	0.48
META1_2512	putative 5'-methylthioadenosine phosphorylase (mtnP-	0.273	0.385	0.322	0.473	0.095	0.307	0.386	0.309	0.318	0.336	0.242	0.336	1.35	0.77	2.08	0.53
META1_2513	conserved protein of unknown function; putative expor	0.000	0.045	0.000	0.000	0.071	0.047	0.129	0.000	0.099	0.018	0.050	0.074	5.50	0.58	2.20	0.93
META1_2515	imidazoleglycerol-phosphate dehydratase	0.350	0.136	0.148	0.271	0.238	0.284	0.171	0.213	0.238	0.191	0.262	0.208	1.48	0.84	1.19	0.09
META1_2516	conserved protein of unknown function	0.312	0.249	0.148	0.203	0.166	0.118	0.129	0.116	0.179	0.227	0.151	0.141	0.84	0.13	1.40	0.55
META1_2517	glutamine amidotransferase, subunit with HisF	0.312	0.363	0.198	0.271	0.190	0.354	0.279	0.348	0.198	0.290	0.272	0.276	1.28	0.85	1.52	0.94
META1_2518	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'-phos	0.545	0.295	0.371	0.676	0.261	0.402	0.514	0.425	0.278	0.381	0.383	0.403	1.43	0.98	1.58	0.88
META1_2519	imidazole glycerol phosphate synthase, subunit with Hi	0.428	0.498	0.322	0.406	0.285	0.331	0.471	0.464	0.218	0.417	0.323	0.383	1.24	0.69	1.78	0.80
META1_2520	phosphoribosyl-ATP pyrophosphatase	0.350	0.544	0.718	0.338	0.285	0.284	0.150	0.329	0.357	0.562	0.292	0.282	0.68	0.12	1.45	0.63
META1_2521	pantothenate kinase	0.156	0.249	0.173	0.000	0.166	0.118	0.193	0.213	0.179	0.200	0.121	0.195	1.32	0.86	2.42	0.42
META1_2524	putative response regulator receiver (CheY-like protein	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2528	protein of unknown function; putative exported protei	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_2529	Granule-associated 20 kDa protein (phasin)	3.504	1.201	1.188	1.623	1.330	0.851	1.393	1.430	1.945	1.733	1.169	1.593	1.24	0.83	2.04	0.32
META1_2530	putative histidine kinase with HK Homodimeric domain,	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_2531	acetyl-CoA synthetase	4.595	4.554	4.800	1.623	1.710	1.418	3.406	3.595	3.076	4.654	1.572	3.360	0.97	0.00	3.21	0.00
META1_2532	conserved protein of unknown function, DUF485; putat	0.234	0.000	0.049	0.000	0.048	0.000	0.086	0.077	0.079	0.073	0.020	0.081	1.50	0.34	6.00	0.14
META1_2533	Cation/acetate symporter actP; acetate and glycolate p	0.818	1.020	0.916	0.271	0.570	0.756	0.514	0.580	0.595	0.934	0.605	0.565	0.82	0.00	1.40	0.67
META1_2534	putative MFS transporter membrane protein	0.000	0.249	0.099	0.000	0.428	0.378	0.578	0.522	0.476	0.136	0.343	0.524	5.20	0.59	2.29	0.42
META1_2535	bifunctional: IMP cyclohydrolase (N-terminal); phospho	1.051	1.292	1.410	1.150	0.903	0.732	1.050	0.715	0.774	1.279	0.867	0.840	0.89	0.05	1.45	0.64
META1_2536	conserved protein of unknown function; putative Hepa	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2537	3-mercaptopyruvate sulfurtransferase	0.545	0.272	0.346	0.406	0.000	0.260	0.471	0.445	0.417	0.363	0.171	0.444	1.65	0.44	3.88	0.43
META1_2540	RNA helicase	0.000	0.068	0.247	1.082	0.903	0.709	0.450	0.425	0.397	0.118	0.847	0.423	4.85	0.58	0.75	0.00
META1_2541	conserved protein of unknown function	0.078	0.091	0.000	0.000	0.000	0.000	0.064	0.000	0.079	0.054	0.000	0.047	1.17	0.98	n.d.	0.12
META1_2542	protein of unknown function	0.389	0.000	0.173	0.000	0.000	0.000	0.171	0.039	0.119	0.154	0.000	0.108	0.94	0.25	n.d.	0.00
META1_2544	acyl-CoA thioester hydrolase	0.000	0.091	0.000	0.000	0.000	0.000	0.129	0.077	0.159	0.036	0.000	0.121	4.50	0.13	n.d.	0.00
META1_2545	putative metal-binding hydrolase	0.117	0.272	0.173	0.203	0.261	0.260	0.236	0.309	0.198	0.200	0.252	0.249	1.68	0.31	1.48	0.92
META1_2546	DNA gyrase, subunit B (type II topoisomerase)	1.168	1.699	1.707	2.299	1.948	1.890	2.271	1.933	1.747	1.579	1.976	1.976	1.69	0.14	1.50	0.75
META1_2547	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2548	protein of unknown function	0.000	0.159	0.148	0.000	0.333	0.307	0.257	0.213	0.218	0.118	0.272	0.228	2.62	0.44	1.26	0.32
META1_2549	protein of unknown function	0.078	0.091	0.173	0.000	0.048	0.071	0.129	0.097	0.139	0.118	0.050	0.121	1.38	0.69	3.60	0.48
META1_2555	conserved protein of unknown function precursor, DUF	0.000	0.204	0.124	0.000	0.000	0.118	0.043	0.039	0.060	0.127	0.050	0.047	0.50	0.23	1.40	0.08
META1_2556	transcriptional regulator, ArsR family; putative SoxR prc	0.078	0.272	0.322	0.000	0.119	0.095	0.000	0.077	0.040	0.245	0.091	0.040	0.22	0.57	0.67	0.93
META1_2561	Thioredoxin SoxW protein	0.000	0.091	0.000	0.203	0.119	0.000	0.129	0.174	0.139	0.036	0.081	0.148	5.50	0.14	2.75	0.37
META1_2563	sulfur oxidation protein precursor (tat pathway signal)	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_2571	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.047	0.000	0.000	0.040	0.036	0.020	0.013	0.50	0.96	1.00	0.99
META1_2574	Thioredoxin-related	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2583	rhodanese domain protein, putative sulfur transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.060	0.000	0.000	0.054	n.d.	0.00	n.d.	0.00
META1_2588	transcriptional regulator, ArsR family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_2590	UvrD/REP helicase	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.060	0.000	0.020	0.020	n.d.	0.37	1.50	0.99
META1_2591	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2593	conserved protein of unknown function	0.000	0.136	0.124	0.271	0.523	0.284	0.214	0.387	0.318	0.100	0.383	0.309	4.18	0.51	1.21	0.64
META1_2596	putative deoxyguanosine triphosphate triphosphohydro	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.039	0.079	0.018	0.000	0.054	4.00	0.12	n.d.	0.00
META1_2605	cation transporting P-type ATPase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2606	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2608	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.097	0.099	0.000	0.000	0.067	n.d.	0.12	n.d.	0.12
META1_2615	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_2634	Mercuric transport protein periplasmic component pre	0.000	0.068	0.099	0.000	0.048	0.047	0.000	0.000	0.040	0.064	0.040	0.013	0.29	0.56	0.50	0.53
META1_2635	Putative mercuric reductase (MerA)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2636	molybdochelatase MogA, involved in Moco biosynthesi	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2639	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.064	0.058	0.000	0.000	0.060	0.040	n.d.	0.12	1.00	0.98
META1_2643	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_2651	protein of unknown function	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.058	0.060	0.045	0.000	0.040	1.20	0.48	n.d.	0.12
META1_2654	putative secretion protein, putative RND family efflux p	0.000	0.000	0.000	0.000	0.048	0.000	0.300	0.271	0.298	0.000	0.020	0.289	n.d.	0.00	21.50	0.22
META1_2655	Cobalt-zinc-cadmium resistance protein czcA (Cation ef	0.000	0.113	0.173	0.000	0.143	0.095	0.428	0.387	0.377	0.109	0.101	0.397	4.92	0.55	5.90	0.59
META1_2662	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2678	protein of unknown function	0.000	0.113	0.099	0.000	0.143	0.071	0.129	0.135	0.159	0.082	0.091	0.141	2.33	0.42	2.33	0.42
META1_2687	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2688	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.000	0.043	0.058	0.060	0.054	0.000	0.054	1.33	0.34	n.d.	0.00
META1_2689	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.071	0.142	0.000	0.039	0.000	0.018	0.091	0.013	1.00	0.99	0.22	0.58
META1_2690	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_2693	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_2697	protein of unknown function	0.000	0.000	0.074	0.000	0.048	0.000	0.000	0.000	0.040	0.027	0.020	0.013	0.67	0.97	1.00	0.99
META1_2698	RNA polymerase sigma factor	0.000	0.000	0.000	0.000	0.000	0.000	0.171	0.077	0.040	0.000	0.000	0.094	n.d.	0.00	n.d.	0.00
META1_2699	mechanosensitive channel	0.117	0.068	0.124	0.135	0.000	0.000	0.043	0.000	0.079	0.100	0.020	0.040	0.55	0.45	3.00	0.47
META1_2701	conserved exported protein of unknown function, DUF3	0.350	0.589	0.396	0.203	0.119	0.142	0.086	0.077	0.159	0.463	0.141	0.108	0.31	0.01	1.14	0.23
META1_2702	aspartate transaminase	0.000	0.045	0.000	0.000	0.048	0.071	0.086	0.077	0.079	0.018	0.050	0.081	6.00	0.14	2.40	0.42
META1_2705	DNA-binding response regulator in two-component reg	0.000	0.045	0.000	0.000	0.119	0.095	0.064	0.058	0.000	0.018	0.091	0.040	3.00	0.54	0.67	0.94
META1_2706	transcriptional regulator, MarR family	0.000	0.000	0.000	0.000	0.095	0.095	0.000	0.000	0.000	0.000	0.081	0.000	n.d.	n.d.	0.00	0.12
META1_2707	putative branched-chain amino acid transferase (ilvE-lik	1.012	0.385	0.223	1.082	0.428	0.685	0.557	0.503	0.576	0.472	0.635	0.544	1.56	0.67	1.29	0.45
META1_2710	protein of unknown function	0.000	0.045	0.074	0.000	0.048	0.047	0.107	0.116	0.139	0.045	0.040	0.121	3.60	0.48	4.50	0.51
META1_2713	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	0.389	0.476	0.520	0.338	0.451	0.921	0.557	0.599	0.516	0.472	0.635	0.558	1.60	0.11	1.32	0.83
META1_2714	homoserine kinase	0.195	0.249	0.223	0.203	0.143	0.307	0.578	0.406	0.417	0.227	0.222	0.464	2.76	0.01	3.14	0.03
META1_2715	putative peroxiredoxin protein, antioxidant protein, Ahp	1.519	0.861	0.569	0.812	0.855	0.780	1.071	1.063	1.131	0.907	0.816	1.089	1.62	0.56	2.00	0.00
META1_2716	conserved protein of unknown function, UPF0301 prote	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_2717	conserved protein of unknown function	0.428	0.385	0.223	0.271	0.285	0.402	0.257	0.232	0.318	0.336	0.333	0.269	1.08	0.38	1.21	0.35
META1_2718	alanyl-tRNA synthetase	1.519	1.405	1.930	2.502	2.375	2.008	1.842	1.991	1.806	1.624	2.238	1.882	1.56	0.19	1.26	0.05
META1_2720	putative glutathione S-transferase	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.077	0.040	0.000	0.050	0.040	n.d.	0.12	1.20	0.99
META1_2721	DNA strand exchange and recombination protein with p	0.623	0.680	0.520	0.879	1.045	0.992	0.493	0.677	0.754	0.608	0.998	0.645	1.43	0.78	0.97	0.04
META1_2722	sensor hybrid histidine kinase with multiple PAS and res	0.195	0.363	0.247	0.609	0.404	0.236	0.386	0.329	0.437	0.281	0.363	0.383	1.84	0.13	1.58	0.96
META1_2729	conserved protein of unknown function	0.078	0.204	0.247	0.000	0.380	0.213	0.171	0.174	0.238	0.191	0.252	0.195	1.38	0.63	1.16	0.32
META1_2732	heme exporter protein, cytochrome c-type biogenesis p	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.000	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_2734	Periplasmic protein thiol:disulfide oxidoreductase, cyto	0.078	0.136	0.124	0.135	0.166	0.189	0.171	0.193	0.139	0.118	0.171	0.168	1.92	0.10	1.47	0.86

META1_2735	putative Fe-S oxidoreductase	0.000	0.068	0.000	0.000	0.000	0.047	0.193	0.058	0.119	0.027	0.020	0.121	6.00	0.14	9.00	0.16
META1_2736	putative oxidoreductase, putative 4Fe-4S ferredoxin do	0.000	0.159	0.099	0.000	0.404	0.095	0.300	0.232	0.198	0.100	0.212	0.242	3.27	0.48	1.71	0.41
META1_2737	conserved protein of unknown function, DUF162	0.000	0.159	0.000	0.203	0.261	0.189	0.193	0.213	0.238	0.064	0.222	0.215	4.57	0.13	1.45	0.94
META1_2738	conserved protein of unknown function, transglutamina	0.156	0.113	0.099	0.000	0.000	0.047	0.000	0.000	0.060	0.118	0.020	0.020	0.23	0.15	1.50	0.99
META1_2739	50S ribosomal subunit protein L13	1.012	0.521	0.594	1.014	0.784	0.614	1.178	0.870	1.191	0.662	0.746	1.075	2.19	0.12	2.16	0.16
META1_2740	ribosomal protein S9	1.012	0.544	0.693	1.420	0.926	0.851	0.750	1.005	0.853	0.708	0.968	0.874	1.67	0.43	1.35	0.36
META1_2741	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2742	molybdenum-pterin binding protein	0.234	0.000	0.173	0.000	0.143	0.118	0.086	0.000	0.079	0.118	0.111	0.054	0.62	0.90	0.73	0.95
META1_2743	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.071	0.107	0.116	0.099	0.054	0.030	0.108	2.67	0.44	5.33	0.13
META1_2755	putative response regulator; Input and output domains	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2757	XoxF. Encodes putative PQQ-linked dehydrogenase of u	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2759	putative short chain alcohol dehydrogenase	0.000	0.000	0.000	0.000	0.143	0.189	0.064	0.135	0.000	0.000	0.141	0.067	n.d.	0.12	0.71	0.93
META1_2760	putative transcriptional regulatory protein, TetR family	0.000	0.000	0.000	0.000	0.143	0.142	0.107	0.271	0.079	0.000	0.121	0.155	n.d.	0.00	1.92	0.37
META1_2762	RND efflux transporter, HAE1 family, translocase subun	0.000	0.000	0.000	0.000	0.143	0.071	0.000	0.000	0.000	0.000	0.091	0.000	n.d.	n.d.	0.00	0.12
META1_2763	RND efflux transporter, MFP subunit	0.000	0.000	0.000	0.000	0.214	0.165	0.000	0.000	0.000	0.000	0.161	0.000	n.d.	n.d.	0.00	0.12
META1_2768	putative transcriptional regulator, XRE family	0.000	0.000	0.000	0.000	0.119	0.047	0.107	0.000	0.000	0.000	0.071	0.034	n.d.	0.37	0.71	0.50
META1_2770	Methylamine dehydrogenase large subunit precursor	0.117	0.521	0.223	0.000	0.570	0.307	0.343	0.619	0.278	0.318	0.373	0.417	1.77	0.38	1.68	0.36
META1_2772	Methylamine utilization protein mauD	0.000	0.000	0.000	0.000	0.071	0.095	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.12
META1_2773	Methylamine dehydrogenase small subunit precursor (M	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2774	Amicyanin precursor	0.117	0.181	0.173	0.000	0.119	0.000	0.107	0.213	0.179	0.163	0.050	0.168	1.39	0.90	5.00	0.13
META1_2777	Methylamine utilization protein mauL	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2780	protein of unknown function; putative exported protein	0.000	0.045	0.049	0.135	0.000	0.000	0.000	0.000	0.000	0.036	0.020	0.000	0.00	0.12	0.00	0.37
META1_2781	putative antioxidant enzyme, Tpx-related thiol peroxida	0.078	0.159	0.099	0.000	0.143	0.095	0.086	0.135	0.159	0.118	0.101	0.128	1.46	0.65	1.90	0.38
META1_2796	conserved protein of unknown function	0.000	0.091	0.074	0.000	0.000	0.095	0.150	0.000	0.079	0.064	0.040	0.074	1.57	0.97	2.75	0.53
META1_2802	protein of unknown function	0.000	0.113	0.000	0.000	0.095	0.118	0.064	0.058	0.119	0.045	0.091	0.081	2.40	0.10	1.33	0.33
META1_2817	putative septum formation protein, Maf-like protein	0.156	0.159	0.124	0.203	0.190	0.260	0.428	0.406	0.238	0.145	0.222	0.356	3.31	0.01	2.41	0.09
META1_2818	protein of unknown function	0.000	0.113	0.000	0.000	0.000	0.000	0.086	0.000	0.099	0.045	0.000	0.060	1.80	0.51	n.d.	0.12
META1_2820	putative TonB-dependent siderophore receptor	1.752	0.000	0.000	0.271	0.000	0.047	0.000	0.000	0.000	0.408	0.060	0.000	0.00	0.37	0.00	0.12
META1_2826	heme export protein, cytochrome C-type biogenesis ccr	0.000	0.000	0.000	0.000	0.095	0.095	0.086	0.116	0.119	0.000	0.081	0.108	n.d.	0.00	2.00	0.39
META1_2828	aconitate hydratase	4.711	5.823	7.868	4.464	3.230	2.835	2.699	2.184	2.024	6.314	3.246	2.292	0.49	0.00	1.06	0.06
META1_2829	Antibiotic biosynthesis monooxygenase	0.117	0.385	0.198	0.000	0.143	0.142	0.064	0.097	0.000	0.254	0.121	0.054	0.29	0.53	0.67	0.93
META1_2830	maleylacetoacetate isomerase (glutathione S-transferas	0.428	0.385	0.346	0.406	0.333	0.331	0.450	0.425	0.357	0.381	0.343	0.410	1.45	0.55	1.79	0.22
META1_2831	respiratory NADH dehydrogenase 2; cupric reductase	1.363	0.793	1.014	0.676	1.093	0.898	0.857	0.599	0.655	1.007	0.947	0.699	0.94	0.11	1.11	0.27
META1_2832	putative Ethyl tert-butyl ether degradation EthD	0.973	0.612	0.421	0.271	0.238	0.307	0.428	0.309	0.377	0.626	0.272	0.370	0.80	0.11	2.04	0.06
META1_2833	protein of unknown function	0.312	0.295	0.322	0.338	0.261	0.189	0.193	0.174	0.357	0.308	0.242	0.242	1.06	0.25	1.50	0.71
META1_2834	protein of unknown function	0.000	0.068	0.124	1.353	0.879	0.567	0.664	0.580	0.595	0.073	0.816	0.612	11.38	0.72	1.12	0.23
META1_2835	putative quinolinate synthetase A (nadA-like)	0.000	0.136	0.173	0.203	0.451	0.520	0.493	0.425	0.536	0.118	0.443	0.484	5.54	0.58	1.64	0.40
META1_2836	putative L-aspartate oxidase (nadB-like)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_2837	nicotinate-mononucleotide pyrophosphorylase	0.428	0.249	0.322	0.338	0.000	0.331	0.321	0.290	0.377	0.318	0.192	0.329	1.40	0.97	2.58	0.37
META1_2838	conserved protein of unknown function, ErfK/YbiS/YcfS,	0.195	0.113	0.173	0.406	0.618	0.520	0.450	0.232	0.337	0.154	0.544	0.336	2.94	0.04	0.93	0.13
META1_2842	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.095	0.064	0.077	0.079	0.000	0.060	0.074	n.d.	0.00	1.83	0.39
META1_2843	molybdenum biosynthetic protein A	0.000	0.000	0.074	0.000	0.071	0.236	0.150	0.116	0.060	0.027	0.131	0.108	5.33	0.13	1.23	0.34
META1_2844	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.071	0.000	0.058	0.040	0.036	0.030	0.034	1.25	0.48	1.67	0.50
META1_2845	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.116	0.079	0.000	0.060	0.067	n.d.	0.12	1.67	0.97
META1_2846	putative 2-hydroxy-3-oxopropionate reductase	0.545	0.589	0.817	0.338	0.095	0.425	0.750	0.754	1.151	0.662	0.272	0.887	1.81	0.18	4.89	0.06
META1_2847	delta(2)-isopentenylpyrophosphate tRNA-adenosine tra	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2848	putative phosphoserine phosphatase (serB-like)	0.312	0.136	0.223	0.000	0.238	0.260	0.386	0.251	0.258	0.209	0.212	0.296	1.91	0.31	2.10	0.40
META1_2849	putative serine protease precursor	0.896	0.974	0.965	0.676	0.499	1.016	0.728	0.735	0.814	0.953	0.746	0.759	1.08	0.01	1.53	0.72
META1_2850	HflC protein precursor, modulator for HflB protease spe	1.480	0.906	1.064	1.082	0.713	1.110	0.750	0.773	1.012	1.098	0.937	0.847	1.04	0.16	1.35	0.51
META1_2851	protease subunit hflK	1.674	0.861	0.891	0.541	0.713	1.040	0.557	0.425	0.516	1.061	0.827	0.497	0.63	0.03	0.90	0.13
META1_2852	dihydrofolate reductase	0.000	0.068	0.074	0.000	0.048	0.000	0.107	0.097	0.079	0.054	0.020	0.094	2.33	0.41	7.00	0.15
META1_2853	thymidylate synthetase	0.000	0.113	0.124	0.000	0.048	0.095	0.086	0.058	0.060	0.091	0.060	0.067	1.00	0.30	1.67	0.37
META1_2855	conserved protein of unknown function	0.273	0.453	0.371	0.271	0.166	0.402	0.214	0.271	0.198	0.381	0.282	0.228	0.81	0.06	1.21	0.61
META1_2857	fumarase C	4.088	2.900	2.821	0.744	1.164	0.969	1.671	1.546	1.369	3.148	1.018	1.526	0.65	0.00	2.25	0.03
META1_2858	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2860	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2863	pyridoxal kinase 2/pyridoxine kinase	0.078	0.113	0.049	0.000	0.166	0.071	0.129	0.135	0.079	0.082	0.101	0.114	1.89	0.26	1.70	0.38
META1_2864	Phenazine biosynthesis PhzC/PhzF-like protein	0.234	0.340	0.173	0.338	0.143	0.165	0.150	0.232	0.397	0.254	0.181	0.262	1.39	1.00	2.17	0.66
META1_2865	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.047	0.064	0.000	0.040	0.054	0.020	0.034	0.83	0.97	2.50	0.52
META1_2866	conserved protein of unknown function	0.350	0.136	0.247	0.203	0.071	0.118	0.279	0.116	0.159	0.227	0.111	0.181	1.08	0.50	2.45	0.41
META1_2867	2-isopropylmalate synthase	0.740	0.431	0.643	0.947	1.069	1.063	1.028	1.102	1.092	0.581	1.048	1.075	2.50	0.02	1.54	0.36
META1_2868	dihydroxyacid dehydratase	0.312	0.317	0.346	0.338	2.090	1.323	1.414	1.063	1.290	0.327	1.502	1.250	5.17	0.00	1.25	0.68
META1_2869	conserved protein of unknown function	0.078	0.295	0.272	0.203	0.238	0.307	0.193	0.290	0.179	0.236	0.262	0.222	1.27	0.75	1.27	0.53
META1_2870	L-Ala-D/L-Glu epimerase	0.000	0.045	0.074	0.000	0.119	0.071	0.064	0.039	0.000	0.045	0.081	0.034	1.00	0.98	0.63	0.93
META1_2872	inositol-3-phosphate synthase	0.935	0.702	1.039	0.203	0.356	0.402	0.750	0.599	0.655	0.880	0.353	0.665	1.02	0.10	2.83	0.02
META1_2873	protein of unknown function	0.078	0.000	0.000	0.000	0.000	0.000	0.064	0.058	0.040	0.018	0.000	0.054	4.00	0.10	n.d.	0.00
META1_2874	protein of unknown function	0.000	0.136	0.124	0.000	0.095	0.071	0.064	0.077	0.060	0.100	0.071	0.067	0.91	0.29	1.43	0.35
META1_2875	putative oxidoreductase	0.078	0.045	0.000	0.000	0.048	0.000	0.043	0.058	0.040	0.036	0.020	0.047	1.75	0.34	3.50	0.12
META1_2876	conserved protein of unknown function	0.117	0.249	0.495	0.203	0.285	0.284	0.386	0.406	0.397	0.308	0.272	0.397	1.74	0.31	2.19	0.02
META1_2877	Putaive isomerase	0.117	0.045	0.148	0.000	0.000	0.000	0.086	0.077	0.079	0.100	0.000	0.081	1.09	0.73	n.d.	0.00
META1_2878	putative glycosyl transferase	0.117	0.249	0.124	0.000	0.143	0.118	0.171	0.193	0.159	0.172	0.111	0.175	1.37	0.64	2.36	0.42
META1_2879	conserved protein of unknown function; GlcNAc-PI de-N	0.117	0.204	0.000	0.000	0.000	0.071	0.043	0.077	0.000	0.109	0.030	0.040	0.50	0.89	2.00	0.51
META1_2882	PhoR-like sensor histidine kinase	0.000	0.045	0.000	0.000	0.000	0.047	0.064	0.077	0.000	0.018	0.020	0.047	3.50	0.55	3.50	0.54
META1_2883	copper-transporting P-type ATPase	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_2888	tRNA pseudouridine synthase B (tRNA pseudouridine 55	0.000	0.068	0.099	0.000	0.570	0.662	0.171	0.329	0.218	0.064	0.524	0.242	5.14	0.54	0.69	0.24
META1_2889	ribosome-binding factor A	0.195	0.181	0.247	0.473	0.499	0.543	0.364	0.387	0.536	0.209	0.514	0.430	2.78	0.01	1.25	0.23
META1_2890	Translation initiation factor IF-2	2.804	2.243	2.895	3.787	4.679	3.402	3.749	3.537	3.434	2.613	4.002	3.569	1.84	0.02	1.34	0.39
META1_2891	conserved protein of unknown function	0.117	0.068	0.074	0.000	0.048	0.000	0.064	0.058	0.060	0.082	0.020	0.060	1.00	0.13	4.50	0.13
META1_2892	transcription termination/antitermination L factor	1.519	1.631	1.955	2.435	1.876	1.748	1.821	1.798	1.766	1.724	1.905	1.794	1.41	0.48	1.41	0.35
META1_2893	conserved protein of unknown function, UPF0090 prote	0.156	0.181	0.000	0.135	0.333	0.354	0.257	0.251	0.298	0.109	0.312	0.269	3.33	0.45	1.29	0.85
META1_2896	aspartate-semialdehyde dehydrogenase	2.103	1.903	2.029	1.353	2.447	3.331	1.714	1.604	2.064	1.996	2.661	1.794	1.21	0.21	1.01	0.47
META1_2898	protein of unknown function; putative exported protein	0.467	0.113	0.074	0.135	0.095	0.118	0.086	0.000	0.000	0.181	0.111	0.027	0.20	0.15	0.36	0.13
META1_2902	putative transcriptional regulator, TetR family	0.000	0.068	0.124	0.000	0.095	0.095	0.107	0.097	0.040	0.073	0.081	0.081	1.50	0.35	1.50	0.34
META1_2903	conserved transmembrane protein of unknown functio	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.116	0.000	0.000	0.000	0.067	n.d.	0.12	n.d.	0.12
META1_2904	putative malto-oligosyltrehalose trehalohydrolase	0.779	0.702	0.495	0.000	0.119	0.118	0.257	0.290	0.099	0.644	0.101	0.215	0.45	0.03	3.20	0.45
META1_2905	putative malto-oligosyltrehalose synthase	2.687	3.149	3.415	2.638	1.449	1.252	1.735	1.972	2.282	3.139	1.542	2.003	0.86	0.01	1.95	0.54
META1_2906	putative glycosyl hydrolase, catalytic domain	2.609	2.515	2.153	1.217	0.736	0.473	1.264	1.198	1.369	2.404	0.695	1.277	0.72	0.00	2.75	0.13
META1_2908	putative maltose alpha-D-glucosyltransferase	0.350	0.272	0.223	0.000	0.309	0.118	0.150	0.232	0.357	0.272	0.181	0.249	1.23	0.56	2.06	0.41
META1_2909	putative trehalose synthase	1.129	1.201	1.212	1.014	0.784	0.567	1.093	1.198	1.012	1.188	0.726	1.102	1.25	0.25	2.28	0.11
META1_2910	1,4-alpha-glucan branching enzyme	0.740	0.861	0.693	0.473	0.285	0.260	0.493	0.387	0.357	0.771	0.302	0.410	0.72	0.01	2.03	0.35
META1_2916	conserved protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.000	0.064	0.077	0.040	0.054	0.000	0.060	1.50	0.36	n.d.	0.00
META1_2917	Diaminopimelate epimerase (DAP epimerase)	0.000	0.113	0.148	0.000	0.238	0.142	0.193	0.155	0.159	0.100	0.161	0.168	2.27	0.41	1.56	0.36
META1_2919	pseudouridine synthase	0.000	0.045	0.000	0.000	0.000	0.047	0.043	0.077	0.000	0.018	0.020	0.040	3.00	0.53	3.00	0.53
META1_2920	fused Signal Recognition Particle (SRP) receptor: memb	0.078	0.068	0.148	0.203	0.190	0.142	0.214	0.271	0.298	0.100	0.171	0.262	3.55	0.02	2.29	0.06
META1_2922	Putative hydroxyneurosporene dehydrogenase (Hydrox	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2923	putative methoxyneurosporene dehydrogenase	0.273	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2925	hydroxyneurosporene methyltransferase CrtF	0.156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2927	bacteriochlorophyllide reductase iron protein subunit B	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2933	photosynthetic reaction center L subunit	0.117	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2934	photosynthetic reaction center M protein	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2935	photosynthetic reaction center cytochrome c subunit-re	1.402	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.327	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_2936	putative type I secretion system ATPase	0.117	0.317	0.173	0.000	0.048	0.047	0.043	0.039	0.040	0.218	0.040	0.040	0.25	0.01	1.50	0.35
META1_2937	putative type I secretion membrane fusion protein, Hlyl	0.000	0.317	0.124	0.000	0.000	0.000	0.000	0.039	0.000	0.172	0.000	0.013	0.11	0.63	n.d.	0.37
META1_2938	50S ribosomal protein L36	0.000	0.000	0.000	0.000	0.000	0.000	0.129	0.097	0.079	0.000	0.000	0.101	n.d.	0.00	n.d.	0.00
META1_2939	putative tetratrico peptide repeat (TPR) protein precurs	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.027	0.000	0.013	0.67	0.97	n.d.	0.37
META1_2941	Pyruvate kinase	0.545	0.453	0.841	1.556	2.518	1.961	0.643	0.735	0.814	0.617	2.137	0.733	1.60	0.35	0.51	0.00
META1_2942	putative outer membrane protein	0.935	0.725	0.891	1.623	0.214	0.543	0.643	0.541	0.536	0.835	0.564	0.571	0.92	0.02	1.52	1.00
META1_2943	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_2944	glycerate kinase	0.545	0.657	0.643	2.367	2.352	2.032	1.071	1.160	1.250	0.626	2.217	1.163	2.51	0.00	0.79	0.00
META1_2945	conserved protein of unknown function	0.000	0.000	0.074	0.000	0.000	0.000	0.064	0.077	0.000	0.027	0.000	0.047	2.33	0.52	n.d.	0.12
META1_2946	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.143	0.165	0.064	0.058	0.099	0.018	0.131	0.074	5.50	0.13	0.85	0.28
META1_2947	conserved protein of unknown function, UPF0335 prote	0.195	0.272	0.346	0.338	0.143	0.165	0.129	0.097	0.198	0.281	0.181	0.141	0.68	0.07	1.17	0.31
META1_2949	conserved protein of unknown function	0.000	0.113	0.148	0.135	0.166	0.047	0.193	0.039	0.060	0.100	0.111	0.094	1.27	0.31	1.27	0.66
META1_2950	two-component sigma-54 specific transcriptional regula	0.000	0.000	0.000	0.000	0.071	0.095	0.064	0.077	0.060	0.000	0.071	0.067	n.d.	0.00	1.43	0.35
META1_2951	putative oligoendopeptidase F	1.363	1.427	1.831	1.014	1.164	0.780	1.028	0.831	1.072	1.560	0.978	0.974	0.84	0.02	1.49	0.99
META1_2952	conserved protein of unknown function	0.000	0.091	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.073	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_2953	Death-on-curing family protein	0.000	0.159	0.148	0.000	0.095	0.142	0.000	0.058	0.040	0.118	0.101	0.034	0.38	0.87	0.50	0.90
META1_2954	conserved protein of unknown function	0.000	0.544	0.421	0.135	0.428	0.260	0.279	0.425	0.238	0.372	0.312	0.316	1.15	0.31	1.52	0.61
META1_2955	protein of unknown function, putative membrane prote	0.273	0.227	0.371	0.000	0.451	0.331	0.364	0.213	0.298	0.290	0.333	0.289	1.34	0.99	1.30	0.33
META1_2956	NAD(P)+ transhydrogenase, subunit alpha part 1.	16.899	7.681	8.908	1.082	0.831	0.756	8.441	6.901	8.772	10.278	0.837	8.018	1.05	0.34	14.37	0.00
META1_2957	NAD(P) transhydrogenase, subunit alpha part 2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.615	0.000	0.000	0.208	n.d.	0.37	n.d.	0.37
META1_2958	NAD(P) transhydrogenase, subunit beta	3.427	2.492	3.439	0.000	0.451	0.307	2.999	2.378	2.580	3.057	0.323	2.641	1.17	0.29	12.28	0.81
META1_2960	putative transcriptional regulator, Crp/Fnr family	0.078	0.204	0.148	0.271	0.048	0.142	0.236	0.406	0.198	0.154	0.121	0.282	2.47	0.12	3.50	0.23
META1_2961	putative signal transduction histidine kinase of the HWE	0.234	0.317	0.173	0.203	0.166	0.378	0.236	0.213	0.139	0.245	0.262	0.195	1.07	0.44	1.12	0.53

META1_2962	conserved protein of unknown function; putative outer	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_2963	conserved protein of unknown function	0.428	0.249	0.371	0.203	0.594	0.591	0.193	0.174	0.298	0.336	0.534	0.222	0.89	0.12	0.62	0.17
META1_2966	Cyanate lyase	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_2969	putative di-haem cytochrome c peroxidase	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.039	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_2975	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.060	0.000	0.020	0.020	n.d.	0.37	1.50	0.99
META1_2977	Putative spermidine synthase	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.077	0.060	0.000	0.050	0.047	n.d.	0.12	1.40	0.98
META1_2980	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.048	0.071	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_2981	3-deoxy-8-phosphooctulonate synthase	0.389	0.408	0.297	0.473	0.143	0.331	0.428	0.329	0.397	0.363	0.272	0.383	1.43	0.68	2.11	0.45
META1_2982	protein of unknown function; putative exported protein	0.000	0.136	0.173	0.203	0.000	0.260	0.000	0.058	0.060	0.118	0.141	0.040	0.46	0.89	0.43	0.84
META1_2983	GTP cyclohydrolase family protein	0.350	0.249	0.124	0.000	0.143	0.118	0.129	0.155	0.159	0.227	0.111	0.148	0.88	0.26	2.00	0.39
META1_2984	enolase	3.193	2.878	2.598	2.097	1.971	1.914	1.821	2.146	2.024	2.849	1.966	2.003	0.95	0.01	1.53	1.00
META1_2985	Septum formation initiator	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_2986	pyruvate dehydrogenase E1 alpha subunit	3.271	1.359	1.930	0.271	0.475	0.449	0.728	0.599	0.695	2.014	0.433	0.672	0.45	0.01	2.33	0.04
META1_2987	pyruvate dehydrogenase E1 beta subunit	5.880	3.489	3.365	0.879	1.188	0.732	1.778	1.585	1.508	4.001	0.947	1.620	0.55	0.01	2.56	0.02
META1_2988	conserved protein of unknown function	0.000	0.249	0.148	0.000	0.000	0.000	0.107	0.097	0.099	0.154	0.000	0.101	0.88	0.29	n.d.	0.00
META1_2989	dihydrolipoamide acetyltransferase	7.632	4.600	4.973	0.812	0.855	0.425	1.478	1.372	1.548	5.443	0.665	1.465	0.36	0.00	3.30	0.03
META1_2990	dihydrolipoamide dehydrogenase, E3 Component of Py	4.711	3.625	3.909	0.338	0.380	0.378	1.135	1.314	1.270	3.983	0.373	1.243	0.42	0.00	5.00	0.00
META1_2992	conserved protein of unknown function	0.273	0.227	0.198	0.000	0.000	0.000	0.000	0.058	0.139	0.227	0.000	0.067	0.40	0.53	n.d.	0.12
META1_2995	conserved protein of unknown function; putative expor	0.078	0.204	0.124	0.000	0.000	0.047	0.086	0.000	0.079	0.145	0.020	0.054	0.50	0.44	4.00	0.55
META1_3000	Lipoate synthase	0.078	0.159	0.148	0.000	0.095	0.118	0.107	0.116	0.198	0.136	0.091	0.141	1.40	0.76	2.33	0.41
META1_3001	cyclase/dehydrase	0.195	0.181	0.223	0.000	0.166	0.142	0.171	0.116	0.198	0.200	0.131	0.161	1.09	0.25	1.85	0.38
META1_3004	putative 3-oxoacyl-(Acyl-carrier-protein) synthase III	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3005	putative acyl carrier protein	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3007	putative short chain alcohol dehydrogenase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_3009	Putative acetyltransferase	0.000	0.091	0.000	0.135	0.000	0.000	0.064	0.155	0.079	0.036	0.020	0.101	3.75	0.12	7.50	0.10
META1_3010	Conserved protein, TPR repeat containing	0.000	0.000	0.000	0.000	0.071	0.000	0.086	0.097	0.099	0.000	0.030	0.094	n.d.	0.00	4.67	0.13
META1_3012	putative ABC transporter, fused ATPase and permease	0.000	0.000	0.000	0.000	0.071	0.047	0.086	0.058	0.079	0.000	0.050	0.074	n.d.	0.00	2.20	0.41
META1_3014	oxidoreductase, 2Fe-2S subunit	0.000	0.159	0.049	0.000	0.071	0.000	0.064	0.116	0.099	0.082	0.030	0.094	1.56	0.38	4.67	0.13
META1_3015	oxidoreductase, FAD-binding subunit; putative molybdo	0.000	0.385	0.223	0.135	0.285	0.189	0.343	0.174	0.278	0.236	0.222	0.262	1.50	0.35	1.77	0.40
META1_3016	oxidoreductase, molybdopterin-binding subunit	0.000	0.612	0.421	0.271	0.190	0.331	0.471	0.232	0.179	0.399	0.262	0.289	0.98	0.28	1.65	0.90
META1_3017	CinA (competence-damaged protein) family protein	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_3018	IspD/IspF bifunctional enzyme (2-C-methyl-D-erythritol	0.467	0.408	0.247	0.406	0.451	0.473	0.450	0.677	0.734	0.363	0.454	0.625	2.33	0.10	2.07	0.12
META1_3019	tRNA-dihydrouridine synthase B	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.060	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_3020	sensory histdine kinase (soluble) in two-component reg	0.000	0.113	0.099	0.000	0.166	0.165	0.129	0.155	0.060	0.082	0.141	0.114	1.89	0.38	1.21	0.31
META1_3021	two-component sigma-54 specific nitrogen transcriptio	0.000	0.204	0.198	0.000	0.261	0.189	0.236	0.271	0.278	0.154	0.192	0.262	2.29	0.42	2.05	0.40
META1_3023	nitrogen regulatory signal transduction histidine kinase	0.000	0.091	0.148	0.000	0.095	0.095	0.150	0.077	0.000	0.091	0.081	0.074	1.10	0.99	1.38	0.99
META1_3024	two-component sigma-54 specific nitrogen transcriptio	0.428	0.748	0.594	0.473	0.475	0.543	0.600	0.715	0.675	0.617	0.504	0.665	1.46	0.46	1.98	0.01
META1_3025	Protein hfq, RNA-binding host factor	0.312	0.498	0.445	0.000	0.309	0.425	0.450	0.213	0.357	0.435	0.312	0.336	1.04	0.42	1.61	0.36
META1_3026	putative GTPase (HflX)	0.117	0.612	0.470	0.271	0.594	0.402	0.600	0.541	0.536	0.445	0.464	0.558	1.69	0.35	1.80	0.22
META1_3031	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.095	0.071	0.000	0.058	0.060	0.000	0.071	0.040	n.d.	0.12	0.86	0.96
META1_3032	conserved protein of unknown function; putative expor	0.000	0.113	0.148	0.000	0.095	0.118	0.150	0.077	0.119	0.100	0.091	0.114	1.55	0.35	1.89	0.38
META1_3033	Heavy metal efflux pump CzcA (precursor)	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.079	0.000	0.000	0.081	n.d.	0.00	n.d.	0.00
META1_3036	putative transcriptional regulator, MucR family	1.168	0.566	0.718	1.556	1.164	1.087	1.157	1.198	1.469	0.762	1.189	1.277	2.26	0.10	1.61	0.94
META1_3037	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.064	0.077	0.040	0.000	0.060	0.060	n.d.	0.00	1.50	0.35
META1_3039	cheW-like protein	0.000	0.113	0.099	0.000	0.119	0.000	0.086	0.077	0.159	0.082	0.050	0.108	1.78	0.37	3.20	0.11
META1_3040	methyl-accepting chemotaxis sensory transducer	0.506	0.702	0.668	0.000	0.998	0.496	0.600	0.831	0.794	0.644	0.635	0.746	1.56	0.30	1.76	0.38
META1_3041	signal transduction histidine kinase with N-terminal pho	0.078	0.181	0.272	0.338	0.238	0.165	0.386	0.348	0.139	0.191	0.222	0.289	2.05	0.34	1.95	0.78
META1_3042	Chemotaxis response regulator protein-glutamate meth	0.000	0.000	0.000	0.000	0.000	0.071	0.043	0.039	0.060	0.000	0.030	0.047	n.d.	0.00	2.33	0.10
META1_3043	putative Sensor protein, CheY-like domain	0.000	0.091	0.049	0.000	0.000	0.000	0.064	0.116	0.000	0.054	0.000	0.060	1.50	0.97	n.d.	0.12
META1_3044	putative sensor hybrid histidine kinase with two PAS an	0.117	0.159	0.322	0.135	0.333	0.354	0.386	0.561	0.357	0.209	0.312	0.437	2.83	0.06	2.10	0.20
META1_3045	Putative metallothionein	0.000	0.068	0.124	0.135	0.000	0.047	0.129	0.039	0.099	0.073	0.040	0.087	1.63	0.36	3.25	0.38
META1_3047	putative molybdopterin biosynthesis-related protein	0.000	0.000	0.000	0.000	0.190	0.165	0.107	0.097	0.040	0.000	0.151	0.081	n.d.	0.00	0.80	0.27
META1_3048	putative molybdopterin biosynthesis-related protein	0.000	0.227	0.272	0.000	0.166	0.095	0.214	0.290	0.179	0.191	0.111	0.228	1.62	0.36	3.09	0.47
META1_3049	molybdopterin-guanine dinucleotide biosynthesis prote	0.000	0.113	0.049	0.000	0.071	0.095	0.064	0.135	0.060	0.064	0.071	0.087	1.86	0.39	1.86	0.37
META1_3050	Putative molybdopterin biosynthesis-related protein	0.078	0.136	0.099	0.000	0.166	0.189	0.107	0.174	0.099	0.109	0.151	0.128	1.58	0.47	1.27	0.32
META1_3051	putative Regulatory protein, LysR	0.000	0.000	0.074	0.000	0.048	0.000	0.064	0.039	0.000	0.027	0.020	0.034	1.67	0.49	2.50	0.52
META1_3052	putative Sulfate/tungstate uptake transporter, membra	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_3053	ABC transporter related ATP-binding protein, putative r	0.000	0.000	0.000	0.000	0.000	0.071	0.043	0.077	0.079	0.000	0.030	0.067	n.d.	0.00	3.33	0.11
META1_3054	Molybdate or tungstate transport precursor	0.740	0.748	0.742	0.812	0.523	0.732	0.514	0.541	0.437	0.744	0.655	0.497	0.90	0.00	1.14	0.10
META1_3056	conserved protein of unknown function; putative expor	0.195	0.113	0.198	0.000	0.000	0.047	0.043	0.058	0.040	0.163	0.020	0.047	0.39	0.00	3.50	0.12
META1_3057	putative periplasmic glucan biosynthesis protein	0.000	0.000	0.099	0.000	0.000	0.047	0.000	0.000	0.000	0.036	0.020	0.000	0.00	0.37	0.00	0.37
META1_3059	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3060	putative cystathionine gamma-synthase, PLP-dependen	0.857	0.544	0.643	0.000	0.380	0.449	0.257	0.290	0.119	0.653	0.353	0.222	0.46	0.02	0.94	0.28
META1_3062	putative response regulator (CheY-like protein)	0.000	0.204	0.148	0.000	0.095	0.071	0.000	0.000	0.060	0.136	0.071	0.020	0.20	0.59	0.43	0.54
META1_3063	Hypoxanthine phosphoribosyl transferase	0.623	0.793	0.841	0.609	0.546	0.449	0.643	0.657	0.714	0.771	0.514	0.672	1.18	0.33	1.96	0.07
META1_3064	Predicted transcriptional regulator containing the CopG	0.000	0.068	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META1_3067	transporter subunit: ATP-binding component of ABC su	0.156	0.181	0.074	0.000	0.095	0.095	0.236	0.213	0.179	0.136	0.081	0.208	2.07	0.17	3.88	0.50
META1_3068	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.043	0.097	0.099	0.018	0.000	0.081	6.00	0.13	n.d.	0.00
META1_3069	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_3070	putative response regulator receiver	0.078	0.113	0.074	0.000	0.000	0.047	0.000	0.039	0.040	0.091	0.020	0.027	0.40	0.49	2.00	0.51
META1_3071	Glutamate 5-kinase (Gamma-glutamyl kinase) (GK)	0.273	0.431	0.346	0.000	0.380	0.520	0.321	0.329	0.278	0.363	0.383	0.309	1.15	0.49	1.21	0.32
META1_3072	Gamma-glutamyl phosphate reductase (GPR) (Glutamat	0.273	0.612	0.396	0.338	0.594	0.520	0.321	0.425	0.337	0.454	0.524	0.363	1.08	0.66	1.04	0.23
META1_3073	nicotinate-nucleotide adenylyltransferase (Deamido-NA	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3075	conserved protein of unknown function, lojap family pr	0.273	0.159	0.124	0.338	0.119	0.142	0.214	0.232	0.179	0.172	0.161	0.208	1.63	0.53	1.94	0.68
META1_3077	Putative transcriptional regulator	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3079	putative ABC transporter, fused ATPase and transmemb	0.000	0.091	0.124	0.000	0.166	0.071	0.086	0.116	0.139	0.082	0.101	0.114	1.89	0.38	1.70	0.38
META1_3080	putative ABC transporter, periplasmic protein	0.000	0.091	0.049	0.000	0.000	0.071	0.043	0.000	0.079	0.054	0.030	0.040	1.00	0.98	2.00	0.51
META1_3081	molybdopterin converting factor, subunit 1	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.099	0.018	0.000	0.034	2.50	0.96	n.d.	0.37
META1_3083	DNA exisiton repair enzyme together with UvrAB	0.000	0.000	0.000	0.000	0.095	0.142	0.107	0.077	0.040	0.000	0.101	0.074	n.d.	0.00	1.10	0.31
META1_3084	conserved protein of unknown function, putative cheZ	0.000	0.068	0.074	0.000	0.071	0.165	0.107	0.135	0.258	0.054	0.101	0.168	4.17	0.49	2.50	0.43
META1_3087	conserved protein of unknown function	0.779	0.725	0.693	0.609	0.784	0.496	0.921	0.928	0.754	0.726	0.635	0.867	1.61	0.09	2.05	0.09
META1_3088	putative 31 kDa outer-membrane immunogenic protein	1.635	1.110	1.138	1.758	0.974	1.748	0.836	0.638	0.714	1.243	1.421	0.726	0.79	0.02	0.77	0.03
META1_3089	conserved protein of unknown function, putative doma	0.078	0.113	0.148	0.000	0.166	0.213	0.343	0.271	0.238	0.118	0.161	0.282	3.23	0.01	2.63	0.44
META1_3090	conserved protein of unknown function	0.000	0.068	0.049	0.000	0.119	0.118	0.107	0.135	0.119	0.045	0.101	0.121	3.60	0.48	1.80	0.38
META1_3091	Prolipoprotein diacylglyceryl transferase	0.000	0.113	0.049	0.000	0.119	0.142	0.129	0.155	0.079	0.064	0.111	0.121	2.57	0.44	1.64	0.36
META1_3093	phosphoglucomutase	0.779	1.156	1.163	0.473	0.974	0.520	0.728	0.561	0.595	1.070	0.706	0.625	0.79	0.03	1.33	0.99
META1_3097	Pyruvate phosphate dikinase (Pyruvate, orthophosphat	6.697	4.872	6.507	3.720	3.729	2.812	3.728	3.634	3.453	5.897	3.336	3.602	0.82	0.01	1.62	0.56
META1_3099	conserved protein of unknown function, ErfK/YbiS/YcfS	0.156	0.000	0.049	0.271	0.238	0.260	0.193	0.135	0.159	0.054	0.252	0.161	4.00	0.47	0.96	0.01
META1_3100	lactoylglutathione lyase family protein	0.000	0.068	0.074	0.000	0.000	0.000	0.064	0.077	0.000	0.054	0.000	0.047	1.17	1.00	n.d.	0.12
META1_3102	conserved protein of unknown function, putative cAMP	0.000	0.113	0.049	0.000	0.214	0.165	0.086	0.116	0.139	0.064	0.161	0.114	2.43	0.43	1.06	0.30
META1_3104	putative transcriptional regulator, MarR family	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3105	conserved protein of unknown function; putative memb	0.000	0.113	0.000	0.000	0.071	0.000	0.064	0.000	0.060	0.045	0.030	0.040	1.20	0.48	2.00	0.51
META1_3106	conserved protein of unknown function, putative doma	0.000	0.113	0.173	0.203	0.285	0.284	0.257	0.232	0.119	0.109	0.272	0.202	2.50	0.42	1.11	0.35
META1_3112	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.099	0.000	0.000	0.034	n.d.	0.37	n.d.	0.37
META1_3113	putative aminotransferase	0.428	0.657	0.421	0.000	0.190	0.307	0.150	0.406	0.298	0.517	0.212	0.289	0.75	0.13	2.05	0.39
META1_3114	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.119	0.047	0.064	0.000	0.040	0.018	0.071	0.034	2.50	0.52	0.71	0.96
META1_3116	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3120	Ribonuclease D (RNase D)	0.078	0.091	0.148	0.203	0.356	0.354	0.279	0.290	0.119	0.109	0.333	0.228	2.83	0.10	1.03	0.40
META1_3122	putative penicillin binding protein, beta-lactamase/tran	0.195	0.408	0.495	0.135	0.356	0.425	0.279	0.329	0.278	0.390	0.353	0.296	1.02	0.64	1.26	0.85
META1_3124	acetyl-CoA:acetoacetyl-CoA transferase, alpha subunit	0.896	0.770	0.792	0.676	0.190	0.473	0.621	0.561	0.655	0.807	0.383	0.612	1.02	0.01	2.39	0.31
META1_3125	acetyl-CoA:acetoacetyl-CoA transferase, beta subunit	0.740	0.272	0.148	0.338	0.356	0.354	0.471	0.580	0.615	0.336	0.353	0.558	2.24	0.29	2.37	0.01
META1_3135	GMP synthetase (glutamine aminotransferase)	0.584	0.498	0.891	0.541	1.116	1.063	0.707	0.638	0.754	0.662	1.008	0.699	1.42	0.64	1.04	0.43
META1_3139	putative SUN-family protein, RNA methyltransferase	0.117	0.340	0.421	0.406	0.594	0.496	0.536	0.580	0.437	0.318	0.524	0.517	2.20	0.16	1.48	0.78
META1_3141	conserved protein of unknown function, putative doma	0.545	0.566	0.569	0.812	0.119	0.449	0.364	0.387	0.496	0.562	0.363	0.417	1.00	0.03	1.72	0.80
META1_3142	protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.129	0.116	0.119	0.000	0.040	0.121	n.d.	0.00	4.50	0.13
META1_3143	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.118	0.064	0.058	0.099	0.000	0.050	0.074	n.d.	0.00	2.20	0.10
META1_3145	IMP dehydrogenase	3.621	2.651	3.340	1.623	2.280	1.772	2.228	1.759	1.826	3.130	1.966	1.929	0.83	0.01	1.47	0.83
META1_3147	Undecaprenyldiphospho-muramoylpentapeptide beta-l	0.117	0.227	0.198	0.541	0.214	0.284	0.236	0.290	0.417	0.191	0.292	0.316	2.24	0.10	1.62	0.89
META1_3148	UDP-N-acetylmuramate--L-alanine ligase	0.779	0.793	0.792	0.135	0.546	0.732	0.600	0.657	0.635	0.789	0.564	0.632	1.08	0.00	1.68	0.38
META1_3150	UDP-N-acetylenolpyruvoylglucosamine reductase	0.195	0.340	0.297	0.406	0.000	0.165	0.300	0.367	0.298	0.290	0.131	0.323	1.50	0.40	3.69	0.41
META1_3151	D-alanine--D-alanine ligase	0.117	0.317	0.223	0.203	0.000	0.071	0.193	0.097	0.119	0.236	0.060	0.134	0.77	0.29	3.33	0.39
META1_3153	cell division protein FtsA	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.058	0.000	0.000	0.050	0.020	n.d.	0.37	0.60	0.52
META1_3154	Cell division GTPase	0.000	0.136	0.198	0.338	0.404	0.118	0.321	0.329	0.357	0.127	0.272	0.336	3.57	0.49	1.85	0.50
META1_3155	UDP-3-O-acyl N-acetylglucosamine deacetylase	0.000	0.045	0.000	0.000	0.071	0.071	0.000	0.000	0.000	0.018	0.060	0.000	0.00	0.37	0.00	0.12
META1_3156	putative lipoprotein UPF0169; putative exported protei	0.935	0.793	0.643	1.014	0.831	1.134	1.135	1.063	1.111	0.771	0.988	1.102	1.93	0.03	1.67	0.29
META1_3158	DNA repair protein RecN	0.000	0.227	0.198	0.000	0.380	0.142	0.386	0.329	0.456	0.163	0.222	0.390	3.22	0.48	2.64	0.46
META1_3162	putative molybdopterin oxidoreductase	0.000	0.181	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.073	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3163	protein of unknown function	0.000	0.091	0.000	0.135	0.095	0.071	0.214	0.135	0.179	0.036	0.091	0.175	6.50	0.15	2.89	0.07
META1_3164	Chaperone protein DnaK	4.011	4.350	4.602	4.464	5.534	4.867	3.363	3.499	2.898	4.364	5.090	3.253	1.01	0.02	0.96	0.01
META1_3165	heat shock protein (Hsp40), co-chaperone with DnaK	0.389	0.363	0.272	0.609	0.618	0.662	0.343	0.271	0.318	0.336	0.635	0.309	1.24	0.53	0.73	0.00
META1_3166	Phospholipid N-methyltransferase	0.000	0.000	0.000	0.000	0.071	0.142	0.086	0.000	0.040	0.000	0.091	0.040	n.d.	0.12	0.67	0.94
META1_3168	thymidine phosphorylase	0.156	0.181	0.198	0.000	0.190	0.095	0.107	0.155	0.099	0.181	0.121	0.121	0.90	0.06	1.50	0.36
META1_3169	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked	0.156	0.249	0.297	0.271	0.190	0.236	0.236	0.213	0.159	0.245	0.222	0.202	1.11	0.61	1.36	0.42
META1_3170	xanthosine phosphorylase (purine nucleoside phosphor	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.097	0.060	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00

META1_3171	cytidine deaminase (cytidine aminohydrolase)	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.155	0.079	0.000	0.060	0.081	n.d.	0.12	2.00	0.95
META1_3172	conserved protein of unknown function	0.000	0.159	0.124	0.000	0.143	0.071	0.214	0.077	0.179	0.109	0.091	0.155	1.92	0.38	2.56	0.43
META1_3173	Tetraacyldisaccharide 4'-kinase	0.000	0.068	0.000	0.000	0.000	0.047	0.086	0.000	0.060	0.027	0.020	0.047	2.33	0.52	3.50	0.54
META1_3174	3-deoxy-D-manno-octulosonic acid transferase	0.000	0.000	0.000	0.000	0.048	0.095	0.043	0.135	0.060	0.000	0.060	0.081	n.d.	0.00	2.00	0.38
META1_3175	conserved protein of unknown function, DUF374	0.312	0.227	0.148	0.000	0.095	0.165	0.150	0.290	0.099	0.218	0.111	0.181	1.13	0.48	2.45	0.42
META1_3176	putative metallophosphatase/metallophosphoesterase	0.000	0.045	0.049	0.000	0.071	0.000	0.107	0.000	0.079	0.036	0.030	0.060	2.25	0.93	3.00	0.54
META1_3178	putative transcriptional regulator, cold shock protein	5.023	3.082	3.167	6.019	1.449	3.237	3.342	3.731	4.307	3.565	2.893	3.804	1.44	0.87	1.97	0.64
META1_3180	leucine aminopeptidase	0.117	0.363	0.223	0.271	0.285	0.189	0.321	0.290	0.278	0.254	0.242	0.296	1.57	0.37	1.83	0.23
META1_3181	conserved protein of unknown function, tetratricopept	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3182	50S ribosomal protein L28	0.973	0.702	0.718	0.473	0.784	1.016	0.814	0.793	0.992	0.771	0.837	0.867	1.52	0.52	1.55	0.49
META1_3184	lysyl tRNA synthetase	0.389	0.657	0.792	0.271	1.093	0.520	0.578	0.503	0.675	0.644	0.726	0.585	1.23	0.96	1.21	0.85
META1_3187	peptide chain release factor RF-2	0.000	0.272	0.272	0.135	0.214	0.260	0.236	0.251	0.258	0.209	0.222	0.249	1.61	0.36	1.68	0.29
META1_3189	putative thiol peroxidase, putative peroxiredoxin	0.117	0.204	0.124	0.203	0.261	0.189	0.193	0.155	0.198	0.154	0.222	0.181	1.59	0.30	1.23	0.24
META1_3190	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.119	0.047	0.064	0.077	0.099	0.000	0.071	0.081	n.d.	0.00	1.71	0.38
META1_3192	tyrosine tRNA synthetase	0.545	0.340	0.371	0.406	0.665	0.591	0.364	0.425	0.377	0.399	0.595	0.390	1.32	0.74	0.98	0.10
META1_3193	putative homologue anmK	0.000	0.091	0.074	0.000	0.000	0.095	0.064	0.058	0.099	0.064	0.040	0.074	1.57	0.36	2.75	0.11
META1_3197	chorismate synthase	0.078	0.272	0.297	0.000	0.523	0.402	0.364	0.387	0.377	0.236	0.393	0.376	2.15	0.18	1.44	0.34
META1_3198	3,4-dihydroxy-2-butanone-4-phoshate synthase/GTP cy	0.662	0.544	0.495	1.150	0.808	1.181	0.621	0.619	0.655	0.553	1.018	0.632	1.54	0.26	0.93	0.02
META1_3199	Histone deacetylase family protein	0.156	0.249	0.223	0.338	0.309	0.118	0.257	0.251	0.298	0.218	0.232	0.269	1.67	0.15	1.74	0.69
META1_3203	propionyl-CoA carboxylase alpha subunit	3.037	2.130	3.019	3.314	4.941	4.796	2.871	2.455	2.719	2.667	4.637	2.675	1.35	0.96	0.87	0.03
META1_3204	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.047	0.000	0.000	0.000	0.000	0.050	0.000	n.d.	n.d.	0.00	0.12
META1_3206	Acylphosphatase (Acylphosphate phosphohydrolase)	0.000	0.091	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3207	conserved protein of unknown function, DUF599; putat	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3208	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.018	0.000	0.034	2.50	0.53	n.d.	0.12
META1_3209	conserved protein of unknown function, DUF218; putat	0.000	0.181	0.000	0.000	0.000	0.118	0.064	0.039	0.040	0.073	0.050	0.047	0.88	0.07	1.40	0.08
META1_3210	putative glutathione S-transferase	0.312	0.295	0.272	0.406	0.119	0.118	0.279	0.251	0.238	0.290	0.161	0.255	1.19	0.09	2.38	0.43
META1_3212	putative lysyl-tRNA synthetase (poxA-like)	0.078	0.091	0.000	0.000	0.000	0.047	0.150	0.058	0.099	0.054	0.020	0.101	2.50	0.39	7.50	0.15
META1_3213	elongation factor P (EF-P)	0.350	0.272	0.247	0.676	0.380	0.591	0.321	0.367	0.198	0.281	0.514	0.296	1.42	0.99	0.86	0.07
META1_3215	putative tandem cold-shock DNA-binding domain prote	0.195	0.227	0.124	0.000	0.190	0.213	0.214	0.213	0.198	0.181	0.171	0.208	1.55	0.41	1.82	0.38
META1_3216	conserved protein of unknown function; putative expor	0.156	0.091	0.099	0.203	0.190	0.118	0.129	0.135	0.139	0.109	0.161	0.134	1.67	0.34	1.25	0.29
META1_3218	putative alpha/beta hydrolase, putative magnesium che	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_3219	phytoene dehydrogenase (phytoene desaturase)	0.117	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3221	urease accessory protein UreG	0.000	0.000	0.049	0.000	0.166	0.118	0.000	0.077	0.099	0.018	0.121	0.060	4.50	0.55	0.75	0.95
META1_3224	urease alpha subunit	0.000	0.091	0.173	0.203	0.166	0.000	0.193	0.309	0.179	0.100	0.101	0.228	3.09	0.46	3.40	0.40
META1_3227	urease gamma (N-terminal) and beta (C-terminal) subu	0.000	0.091	0.074	0.000	0.143	0.095	0.214	0.193	0.139	0.064	0.101	0.181	3.86	0.49	2.70	0.44
META1_3229	flavin:NADH oxidoreductase, putative alternative pyrim	0.000	0.000	0.000	0.000	0.048	0.047	0.086	0.039	0.000	0.000	0.040	0.040	n.d.	0.12	1.50	0.98
META1_3230	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3233	protein of unknown function	0.078	0.181	0.173	0.135	0.119	0.189	0.064	0.116	0.060	0.154	0.151	0.081	0.71	0.18	0.80	0.06
META1_3234	UDP-glucuronate 5'-epimerase (UDP-glucuronic acid ep	0.000	0.204	0.173	0.135	0.214	0.189	0.257	0.213	0.238	0.145	0.192	0.235	2.19	0.41	1.84	0.12
META1_3240	protein of unknown function	0.000	0.045	0.074	0.135	0.071	0.095	0.171	0.039	0.119	0.045	0.091	0.108	3.20	0.44	1.78	0.93
META1_3241	threonine deaminase	0.273	0.249	0.396	0.000	0.214	0.378	0.364	0.483	0.417	0.308	0.252	0.423	1.85	0.11	2.52	0.44
META1_3244	conserved protein of unknown function, SlyX family	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3246	DnaK suppressor protein	0.428	0.340	0.148	0.338	0.333	0.189	0.428	0.464	0.437	0.290	0.272	0.444	2.06	0.22	2.44	0.07
META1_3257	Flagellar L-ring protein precursor (Basal body L-ring pro	0.000	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_3261	Flagellar fliL protein	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.039	0.099	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00
META1_3265	putative Glutathione peroxidase	0.000	0.091	0.049	0.000	0.095	0.000	0.086	0.116	0.060	0.054	0.040	0.087	2.17	0.41	3.25	0.11
META1_3266	protein of unknown function	0.312	0.340	0.396	0.609	0.356	0.260	0.343	0.483	0.318	0.354	0.353	0.383	1.46	0.63	1.63	0.94
META1_3267	putative membrane bound lytic murein transglycosylase	0.000	0.113	0.049	0.000	0.119	0.189	0.000	0.000	0.000	0.064	0.131	0.000	0.00	0.12	0.00	0.12
META1_3268	putative NAD(P)H quinone oxidoreductasease	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3270	conserved protein of unknown function; putative doma	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.018	0.000	0.020	1.50	0.99	n.d.	0.37
META1_3273	two-component DctB-like sigma-54 specific transcriptio	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.058	0.079	0.000	0.030	0.067	n.d.	0.00	3.33	0.11
META1_3277	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase sub	0.623	1.201	1.608	0.812	1.093	0.638	0.943	0.793	0.814	1.216	0.857	0.847	0.94	0.47	1.48	0.89
META1_3283	S-adenosylmethionine:tRNA ribosyltransferase-isomera	0.000	0.000	0.000	0.000	0.095	0.118	0.043	0.077	0.060	0.000	0.091	0.060	n.d.	0.00	1.00	0.30
META1_3284	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.058	0.099	0.000	0.020	0.067	n.d.	0.00	5.00	0.13
META1_3285	Queuine tRNA-ribosyltransferase (tRNA-guanine transg	0.000	0.000	0.074	0.000	0.071	0.118	0.064	0.116	0.040	0.027	0.081	0.074	3.67	0.11	1.38	0.33
META1_3288	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.047	0.043	0.058	0.000	0.000	0.060	0.034	n.d.	0.12	0.83	0.97
META1_3289	conserved protein of unknown function	0.545	1.156	0.668	0.203	0.285	0.354	0.514	0.425	0.417	0.835	0.302	0.450	0.73	0.09	2.23	0.05
META1_3290	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_3298	protein of unknown function; putative exported protein	0.000	0.091	0.000	0.000	0.000	0.071	0.000	0.058	0.000	0.036	0.030	0.020	0.75	0.98	1.00	0.99
META1_3299	H+ translocating pyrophosphate synthase	0.584	0.657	0.594	0.000	0.000	0.000	0.450	0.387	0.456	0.617	0.000	0.430	0.94	0.01	n.d.	0.00
META1_3300	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.166	0.047	0.000	0.000	0.040	0.018	0.091	0.013	1.00	0.99	0.22	0.57
META1_3301	protein of unknown function; putative exported protein	0.000	0.045	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.018	0.030	0.000	0.00	0.37	0.00	0.37
META1_3302	putative PLP-dependent aminotransferase (yfdZ)	0.818	0.725	0.742	0.473	0.950	0.780	0.600	0.870	0.496	0.753	0.806	0.659	1.18	0.35	1.23	0.72
META1_3303	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.095	0.118	0.129	0.000	0.119	0.000	0.091	0.081	n.d.	0.12	1.33	0.98
META1_3304	Poly(3-hydroxyalkanoate) polymerase (PHA polymerase	0.779	2.085	1.831	0.000	0.380	0.189	1.007	0.986	0.834	1.687	0.242	0.941	0.75	0.25	5.83	0.62
META1_3307	glycine tRNA synthetase, beta subunit	1.012	1.722	1.633	1.758	1.591	1.630	1.393	1.411	1.211	1.524	1.633	1.337	1.18	0.75	1.23	0.02
META1_3310	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_3311	glycine tRNA synthetase, alpha subunit	0.312	0.113	0.173	0.541	0.380	0.307	0.236	0.193	0.198	0.181	0.373	0.208	1.55	0.69	0.84	0.02
META1_3315	conserved protein of unknown function	0.078	0.181	0.074	0.135	0.166	0.118	0.236	0.193	0.238	0.118	0.141	0.222	2.54	0.06	2.36	0.02
META1_3316	protease SohB, belong to MEROPS peptidase family S49	0.000	0.295	0.148	0.203	0.000	0.118	0.171	0.135	0.198	0.172	0.081	0.168	1.32	0.34	3.13	0.39
META1_3317	putative methyltransferase small	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.058	0.000	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_3319	octaprenyl diphosphate synthase	0.156	0.204	0.198	0.338	0.641	0.780	0.450	0.406	0.397	0.191	0.655	0.417	2.95	0.00	0.95	0.33
META1_3320	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMI	0.078	0.159	0.297	0.271	0.143	0.142	0.150	0.367	0.238	0.191	0.161	0.255	1.81	0.41	2.38	0.43
META1_3322	conserved protein of unknown function, TPR repeat pre	1.207	1.405	1.856	0.879	1.045	0.638	0.900	1.179	0.734	1.524	0.847	0.941	0.83	0.07	1.67	0.66
META1_3323	protein of unknown function	0.000	0.136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3326	protein of unknown function	0.117	0.181	0.000	0.000	0.048	0.000	0.043	0.000	0.000	0.100	0.020	0.013	0.18	0.60	1.00	0.99
META1_3327	Putative oxidoreductase	0.156	0.204	0.148	0.000	0.048	0.071	0.000	0.116	0.119	0.172	0.050	0.081	0.63	0.43	2.40	0.92
META1_3328	Putative integral membrane protein, putative Band 7 pr	0.000	0.000	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3330	putative ABC transporter, fused permease and ATPase s	0.078	0.453	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.263	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_3331	DNA topoisomerase IV, subunit B	0.000	0.136	0.223	0.135	0.380	0.425	0.407	0.406	0.139	0.136	0.363	0.316	3.13	0.46	1.31	0.98
META1_3334	Low-specificity L-threonine aldolase (Low-specificity L-T	0.312	0.385	0.322	0.000	0.143	0.260	0.214	0.116	0.139	0.345	0.171	0.155	0.61	0.01	1.35	0.34
META1_3335	putative ABC transporter, fused ATPase and permease d	0.117	0.521	0.297	0.271	0.451	0.354	0.279	0.367	0.337	0.345	0.383	0.329	1.29	0.65	1.29	0.68
META1_3337	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.000	0.000	0.043	0.000	0.040	0.091	0.000	0.027	0.40	0.89	n.d.	0.12
META1_3338	protein of unknown function precursor	0.312	0.453	0.421	0.203	0.404	0.331	0.193	0.193	0.337	0.408	0.343	0.242	0.80	0.08	1.06	0.41
META1_3339	conserved protein of unknown function, putative Photo	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3340	conserved protein of unknown function	0.662	0.589	0.544	0.879	0.855	0.921	0.771	0.889	1.052	0.590	0.887	0.907	2.08	0.02	1.53	0.89
META1_3341	Short-chain dehydrogenase/reductase SDR	0.078	0.181	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_3343	putative alpha/beta hydrolase precursor	0.350	0.748	0.520	0.541	0.166	0.213	0.343	0.309	0.516	0.572	0.242	0.390	0.92	0.32	2.42	0.42
META1_3344	putative NAD-binding dehydrogenase, putative 2-hydro	0.662	0.521	0.297	0.000	0.048	0.189	0.343	0.425	0.417	0.472	0.101	0.397	1.13	0.52	5.90	0.62
META1_3345	putative glutathione S-transferase	0.195	0.136	0.074	0.135	0.119	0.165	0.193	0.116	0.139	0.127	0.141	0.148	1.57	0.66	1.57	0.78
META1_3347	putative NADH dehydrogenase (ubiquinone) Fe-S prote	0.195	0.453	0.421	0.203	0.261	0.165	0.257	0.213	0.337	0.381	0.212	0.269	0.95	0.48	1.90	0.26
META1_3348	Guanine deaminase (Guanase) (Guanine aminase) (Gua	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_3350	conserved protein of unknown function	0.350	0.385	0.223	0.000	0.000	0.189	0.236	0.174	0.159	0.318	0.081	0.188	0.80	0.07	3.50	0.12
META1_3351	glycogen debranching enzyme	1.558	1.609	1.608	0.541	0.546	0.496	0.836	0.793	0.556	1.597	0.524	0.726	0.61	0.00	2.08	0.08
META1_3352	putative hybrid histidine kinase with PAS/PAC and resp	0.000	0.113	0.074	0.000	0.048	0.000	0.000	0.058	0.060	0.073	0.020	0.040	0.75	0.95	3.00	0.53
META1_3354	NADP-dependent isocitrate dehydrogenase	6.308	3.807	4.008	1.488	2.185	2.150	1.757	1.334	1.250	4.463	2.066	1.438	0.43	0.00	1.04	0.15
META1_3356	formaldehyde activating enzyme homolog	0.623	0.748	0.520	0.338	0.499	0.307	0.343	0.290	0.377	0.635	0.393	0.336	0.71	0.01	1.28	0.55
META1_3357	tRNA/rRNA methyltransferase	0.078	0.091	0.148	0.000	0.071	0.071	0.107	0.174	0.159	0.109	0.060	0.148	1.83	0.23	3.67	0.48
META1_3358	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3359	putative alcohol dehydrogenase	0.623	0.657	0.668	0.541	0.309	0.284	0.407	0.367	0.318	0.653	0.333	0.363	0.75	0.00	1.64	1.00
META1_3360	methyl-accepting chemotaxis receptor transducer precu	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.039	0.000	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_3362	trans-sulfuration enzyme (O-acetylhomoserine aminoca	1.129	0.906	1.163	0.406	0.665	0.732	0.364	0.561	0.437	1.052	0.655	0.457	0.59	0.00	1.05	0.30
META1_3364	glycolate oxidase iron-sulfur subunit	0.000	0.000	0.000	0.000	0.309	0.236	0.236	0.213	0.179	0.000	0.232	0.208	n.d.	0.00	1.35	0.33
META1_3365	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.060	0.000	0.020	0.047	n.d.	0.00	3.50	0.12
META1_3366	putative lipase/esterase	0.312	0.295	0.247	0.473	0.309	0.378	0.578	0.348	0.397	0.281	0.363	0.437	2.10	0.07	1.81	0.56
META1_3367	ATP-dependent DNA helicase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_3368	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.048	0.095	0.043	0.058	0.000	0.018	0.060	0.034	2.50	0.52	0.83	0.97
META1_3372	putative short-chain dehydrogenase/reductase SDR	0.117	0.091	0.148	0.000	0.000	0.000	0.000	0.000	0.040	0.118	0.000	0.013	0.15	0.17	n.d.	0.37
META1_3373	thiamin-monophosphate kinase	0.000	0.045	0.000	0.000	0.071	0.000	0.043	0.058	0.000	0.018	0.030	0.034	2.50	0.52	1.67	0.50
META1_3374	transcription antitermination factor	0.195	0.113	0.099	0.135	0.095	0.118	0.129	0.135	0.198	0.127	0.111	0.155	1.64	0.57	2.09	0.19
META1_3375	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthas	0.389	0.431	0.223	0.338	0.546	0.307	0.471	0.445	0.476	0.345	0.413	0.464	1.82	0.19	1.68	0.35
META1_3379	protein of unknown function; putative exported protein	0.000	0.068	0.000	0.000	0.000	0.000	0.086	0.077	0.040	0.027	0.000	0.067	3.33	0.11	n.d.	0.00
META1_3380	riboflavin synthase, alpha subunit	0.428	0.272	0.198	0.135	0.238	0.189	0.193	0.193	0.278	0.281	0.202	0.222	1.06	0.35	1.65	0.43
META1_3381	fused diaminohydroxyphosphoribosylaminopyrimidine	0.000	0.000	0.049	0.000	0.000	0.000	0.043	0.039	0.060	0.018	0.000	0.047	3.50	0.11	n.d.	0.00
META1_3382	transcriptional regulator NrdR	0.000	0.000	0.049	0.000	0.071	0.047	0.043	0.000	0.139	0.018	0.050	0.060	4.50	0.55	1.80	0.97
META1_3383	putative transcriptional regulator, Rrf2 family	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3384	serine hydroxymethyltransferase	4.906	3.467	4.528	5.952	5.724	6.379	4.799	4.426	4.485	4.191	6.038	4.563	1.47	0.55	1.13	0.00
META1_3385	putative F0F1 ATP synthase, subunit b (atpF)	1.207	0.816	0.916	1.082	1.116	0.803	0.921	0.735	1.052	0.943	0.978	0.901	1.29	0.64	1.38	0.52
META1_3386	putative F0F1 ATP synthase, subunit b (atpF)	1.947	0.929	0.916	1.420	0.879	1.016	1.221	1.121	1.191	1.161	1.018	1.176	1.37	0.98	1.73	0.59
META1_3387	F0 sector of membrane-bound ATP synthase, subunit c	0.000	0.634	0.421	0.000	0.428	0.567	0.129	0.097	0.179	0.408	0.423	0.134	0.44	0.20	0.48	0.20
META1_3388	Fo ATP synthase subunit A	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3389	putative FoF1 ATP synthase, subunit I (atpI)	0.000	0.000	0.000	0.000	0.095	0.071	0.000	0.000	0.079	0.000	0.071	0.027	n.d.	0.37	0.57	0.52
META1_3390	putative protein disulfide isomerase, putative protein p	0.506	0.680	0.495	1.217	0.713	0.709	0.664	0.793	0.834	0.572	0.786	0.766	1.81	0.06	1.46	0.59
META1_3395	conserved protein of unknown function	0.117	0.113	0.000	0.000	0.000	0.189	0.193	0.077	0.139	0.073	0.081	0.134	2.50	0.39	2.50	0.10

META1_3397	putative ATP-binding protein with two ATPase domains	0.000	0.091	0.272	0.000	0.190	0.000	0.171	0.213	0.218	0.136	0.081	0.202	2.00	0.41	3.75	0.12
META1_3398	putative porin precursor ; putative exported protein	2.297	1.292	1.782	3.382	1.116	2.504	1.628	0.908	1.429	1.706	2.046	1.311	1.04	0.28	0.96	0.25
META1_3400	Putative adenylate cyclase protein	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.039	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_3403	dihydrodipicolinate synthase	0.467	0.340	0.247	0.609	0.760	0.732	0.578	0.483	0.615	0.336	0.726	0.558	2.24	0.07	1.15	0.09
META1_3404	trans-translation protein, binds tmRNA and tRNA	0.000	0.000	0.000	0.135	0.095	0.000	0.129	0.077	0.218	0.000	0.060	0.141	n.d.	0.00	3.50	0.40
META1_3405	Conserved protein of unknown function (DUF88)	0.000	0.408	0.445	0.744	0.261	0.449	0.364	0.329	0.278	0.327	0.413	0.323	1.33	0.33	1.17	0.36
META1_3406	orotate phosphoribosyltransferase (OPRT) (OPRTase)	0.545	0.408	0.297	0.541	0.380	0.473	0.343	0.483	0.258	0.399	0.443	0.363	1.23	0.60	1.23	0.26
META1_3408	GTP pyrophosphokinase	0.078	0.385	0.322	0.203	0.261	0.307	0.321	0.271	0.238	0.290	0.272	0.276	1.28	0.65	1.52	0.62
META1_3409	DNA-directed RNA polymerase omega chain (RNAP ome	0.312	0.272	0.148	0.541	0.641	0.473	0.257	0.367	0.298	0.236	0.554	0.309	1.77	0.34	0.84	0.01
META1_3410	NifU-like	0.273	0.317	0.346	0.473	0.238	0.236	0.193	0.271	0.238	0.318	0.272	0.235	1.00	0.07	1.30	0.37
META1_3411	Peptidase M22, glycoprotease	0.117	0.385	0.371	0.135	0.143	0.236	0.171	0.193	0.198	0.318	0.181	0.188	0.80	0.47	1.56	0.54
META1_3412	Ribosomal-protein-alanine N-acetyltransferase	0.312	0.159	0.124	0.000	0.119	0.118	0.257	0.406	0.595	0.181	0.101	0.423	3.15	0.10	6.30	0.58
META1_3413	Putative 1-acylglycerol-3-phosphate O-acyltransferase (	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.079	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00
META1_3415	tRNA modification enzyme MiaB, putative isopentenyl-a	0.000	0.000	0.000	0.000	0.119	0.142	0.107	0.097	0.139	0.000	0.111	0.114	n.d.	0.00	1.55	0.35
META1_3416	putative enzyme with nucleoside triphosphate hydrolas	0.350	0.249	0.198	0.271	0.309	0.354	0.300	0.251	0.179	0.254	0.323	0.242	1.29	0.73	1.13	0.20
META1_3417	putative metalloprotease	0.000	0.045	0.049	0.000	0.166	0.000	0.000	0.097	0.060	0.036	0.071	0.054	2.00	0.95	1.14	0.47
META1_3418	Putative HlyC/CorC family of transporters with CBS dom	0.000	0.068	0.049	0.000	0.143	0.000	0.193	0.155	0.218	0.045	0.060	0.188	5.60	0.56	4.67	0.13
META1_3419	apolipoprotein N-acyltransferase, copper homeostasis p	0.078	0.159	0.223	0.000	0.000	0.000	0.086	0.116	0.099	0.163	0.000	0.101	0.83	0.35	n.d.	0.00
META1_3420	conserved protein of unknown function, putative expor	0.273	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.064	0.020	0.000	0.00	0.37	0.00	0.37
META1_3421	catalase (hydroperoxidase II)	1.791	3.082	3.637	3.720	2.494	1.725	2.271	2.204	2.481	2.985	2.349	2.319	1.05	0.50	1.48	0.73
META1_3422	oxidative stress transcriptional regulator, LysR family	0.000	0.000	0.000	0.000	0.071	0.000	0.043	0.000	0.000	0.000	0.030	0.013	n.d.	0.37	0.67	0.97
META1_3428	glutamate racemase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.000	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_3429	conserved protein of unknown function	0.234	0.136	0.074	0.000	0.071	0.095	0.043	0.077	0.060	0.136	0.071	0.060	0.60	0.09	1.29	0.33
META1_3430	conserved protein of unknown function	0.000	0.113	0.074	0.000	0.119	0.118	0.086	0.097	0.218	0.073	0.101	0.134	2.50	0.42	2.00	0.38
META1_3432	conserved protein of unknown function	0.117	0.136	0.198	0.000	0.095	0.095	0.150	0.135	0.079	0.154	0.081	0.121	1.06	0.43	2.25	0.41
META1_3434	Siroheme synthase	0.000	0.113	0.124	0.000	0.333	0.284	0.193	0.193	0.238	0.091	0.262	0.208	3.10	0.46	1.19	0.32
META1_3435	Electron transport protein SenC-related	0.156	0.159	0.148	0.135	0.143	0.189	0.150	0.174	0.179	0.154	0.161	0.168	1.47	0.24	1.56	0.52
META1_3437	extracellular solute-binding protein family 3	0.000	0.045	0.000	0.000	0.000	0.071	0.000	0.058	0.000	0.018	0.030	0.020	1.50	0.99	1.00	0.99
META1_3440	Cobaltochelatase (cobT protein)	0.467	0.589	0.841	0.676	0.665	0.827	0.621	0.503	0.397	0.653	0.736	0.504	1.04	0.39	1.03	0.07
META1_3441	Cobaltochelatase (cobS protein)	1.363	1.042	0.792	1.217	1.021	1.370	0.664	0.599	0.853	1.025	1.199	0.706	0.93	0.10	0.88	0.02
META1_3443	BolA-like protein	0.078	0.113	0.000	0.000	0.190	0.142	0.129	0.039	0.079	0.064	0.141	0.081	1.71	0.34	0.86	0.27
META1_3445	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3446	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.000	0.099	0.000	0.020	0.054	n.d.	0.12	4.00	0.55
META1_3449	conserved protein of unknown function	0.000	0.113	0.000	0.000	0.000	0.000	0.107	0.000	0.060	0.045	0.000	0.054	1.60	0.50	n.d.	0.12
META1_3452	putative fatty acid oxidation complex subunit alpha (en	2.103	1.699	2.177	1.353	2.138	1.772	1.950	2.281	1.667	1.969	1.865	1.969	1.35	0.90	1.58	0.49
META1_3454	protein of unknown function; putative exported protein	0.350	0.227	0.173	0.609	0.570	0.473	0.536	0.677	0.655	0.236	0.534	0.625	3.58	0.01	1.75	0.31
META1_3455	putative 3-ketoacyl-CoA thiolase (Fatty oxidation compl	0.973	0.589	0.693	0.473	0.475	0.591	0.343	0.619	0.476	0.717	0.524	0.484	0.91	0.11	1.38	0.65
META1_3456	acyl-CoA dehydrogenase	0.117	0.612	0.569	0.000	0.428	0.284	0.557	0.580	0.576	0.481	0.302	0.571	1.60	0.40	2.83	0.46
META1_3457	conserved protein of unknown function	0.000	0.091	0.124	0.338	0.831	0.449	0.536	0.522	0.576	0.082	0.595	0.544	9.00	0.67	1.37	0.78
META1_3460	conserved protein of unknown function	0.156	0.136	0.148	0.135	0.095	0.071	0.171	0.174	0.159	0.145	0.091	0.168	1.56	0.05	2.78	0.04
META1_3461	conserved membrane protein of unknown function; put	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.077	0.000	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_3462	putative oxidoreductase precursor (tat pathway signal)	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3464	putative protease	0.234	0.612	0.520	0.000	0.475	0.378	0.428	0.387	0.397	0.490	0.363	0.403	1.11	0.90	1.67	0.37
META1_3465	threonine synthase	1.051	0.929	0.742	0.947	1.378	1.229	0.836	0.928	0.913	0.889	1.250	0.894	1.36	0.94	1.07	0.08
META1_3467	putative surfeit locus 1 family protein (surf1-like)	0.000	0.068	0.000	0.000	0.119	0.095	0.107	0.116	0.060	0.027	0.091	0.094	4.67	0.13	1.56	0.35
META1_3468	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_3469	cytochrome c oxidase subunit III	0.000	0.136	0.124	0.000	0.190	0.284	0.107	0.000	0.000	0.100	0.202	0.034	0.45	0.53	0.25	0.57
META1_3470	putative cytochrome-c oxidase assembly protein (coxG)	0.000	0.000	0.000	0.000	0.071	0.047	0.129	0.077	0.099	0.000	0.050	0.101	n.d.	0.00	3.00	0.45
META1_3471	putative CoxF	0.000	0.000	0.000	0.000	0.119	0.071	0.064	0.000	0.000	0.000	0.081	0.020	n.d.	0.37	0.38	0.54
META1_3473	cytochrome c oxidase subunit I	0.195	0.521	0.445	0.338	0.594	0.614	0.364	0.309	0.258	0.417	0.564	0.309	1.00	0.67	0.82	0.09
META1_3474	cytochrome c oxidase subunit II	1.986	1.110	0.792	1.353	0.475	0.969	0.857	0.889	0.714	1.197	0.816	0.820	0.92	0.23	1.51	0.89
META1_3475	putative formate dehydrogenase accesory protein	0.117	0.136	0.198	0.135	0.214	0.071	0.214	0.193	0.238	0.154	0.141	0.215	1.88	0.09	2.29	0.18
META1_3477	glutamate synthase, large subunit	3.037	5.189	5.444	8.116	5.867	6.025	5.827	5.625	6.589	4.781	6.269	6.015	1.70	0.19	1.44	0.46
META1_3478	glutamate synthase, small subunit, nucleotide-binding,	0.545	0.929	1.039	0.744	1.330	1.465	1.200	1.295	1.171	0.880	1.300	1.223	1.88	0.11	1.41	0.74
META1_3483	protein of unknown function; putative exported protein	0.000	0.045	0.124	0.000	0.095	0.095	0.000	0.000	0.060	0.064	0.081	0.020	0.43	0.53	0.38	0.55
META1_3484	putative membrane bound lytic murein transglycosylase	0.000	0.045	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.018	0.020	0.000	0.00	0.37	0.00	0.37
META1_3485	UDP-galactose 4-epimerase	0.935	0.544	0.445	0.473	0.404	0.780	0.578	0.619	0.397	0.599	0.575	0.531	1.20	0.58	1.39	0.95
META1_3486	glucose-1-phosphate uridylyltransferase	1.558	1.224	1.188	1.420	0.214	0.803	1.028	0.947	1.052	1.288	0.645	1.008	1.06	0.04	2.34	0.44
META1_3487	N-formylglutamate amidohydrolase (Beta-citryl-L-glutar	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3488	putative response regulator receiver; CheY-like protein	0.000	0.181	0.272	0.203	0.143	0.260	0.150	0.097	0.218	0.172	0.202	0.155	1.21	0.32	1.15	0.38
META1_3489	glutaredoxin 3	0.000	0.113	0.074	0.000	0.071	0.071	0.150	0.135	0.139	0.073	0.060	0.141	2.63	0.44	3.50	0.48
META1_3490	Nitrilase/cyanide hydratase and apolipoprotein N-acylt	0.000	0.227	0.223	0.000	0.000	0.118	0.086	0.155	0.238	0.172	0.050	0.161	1.26	0.32	4.80	0.13
META1_3491	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.043	0.000	0.060	0.000	0.060	0.034	n.d.	0.12	0.83	0.96
META1_3492	Putative histidine kinase; putative HK, ATPase and sens	0.000	0.227	0.247	0.000	0.071	0.118	0.150	0.097	0.119	0.181	0.081	0.121	0.90	0.28	2.25	0.41
META1_3493	Peptide methionine sulfoxide reductase msrA (Protein-	0.156	0.000	0.099	0.203	0.095	0.095	0.086	0.097	0.099	0.073	0.111	0.094	1.75	0.34	1.27	0.36
META1_3494	putative membrane protein	0.000	0.000	0.000	0.000	0.166	0.000	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.37
META1_3495	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.071	0.000	0.064	0.039	0.060	0.018	0.030	0.054	4.00	0.12	2.67	0.10
META1_3497	murein DD-endopeptidase, penicillin-insensitive	0.000	0.068	0.074	0.000	0.000	0.000	0.043	0.077	0.000	0.054	0.000	0.040	1.00	0.98	n.d.	0.12
META1_3499	conserved protein of unknown function; putative expor	0.078	0.113	0.099	0.135	0.071	0.142	0.043	0.058	0.099	0.100	0.111	0.067	0.91	0.19	0.91	0.16
META1_3502	Redoxin domain protein	0.000	0.000	0.000	0.000	0.071	0.118	0.129	0.097	0.079	0.000	0.081	0.101	n.d.	0.00	1.88	0.39
META1_3503	argininosuccinate lyase	0.779	0.431	0.569	0.406	1.069	0.992	0.578	0.696	0.516	0.562	0.937	0.598	1.44	0.89	0.96	0.49
META1_3505	protein of unknown function; putative exported protein	0.273	0.249	0.322	0.406	0.190	0.118	0.171	0.174	0.258	0.281	0.192	0.202	0.97	0.09	1.58	0.89
META1_3507	putative haloacid dehalogenase family hydrolase	0.000	0.045	0.074	0.000	0.095	0.047	0.086	0.097	0.000	0.045	0.060	0.060	1.80	0.95	1.50	0.97
META1_3508	putative carbamoyl transferase	0.000	0.113	0.000	0.000	0.000	0.000	0.193	0.097	0.000	0.045	0.000	0.094	2.80	0.53	n.d.	0.12
META1_3509	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.142	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.37
META1_3510	haloacid dehalogenase, type II	0.000	0.000	0.000	0.000	0.048	0.000	0.107	0.077	0.040	0.000	0.020	0.074	n.d.	0.00	5.50	0.13
META1_3512	superoxide dismutase	1.635	1.088	1.212	1.082	0.760	0.780	0.836	0.966	0.675	1.261	0.816	0.827	0.88	0.05	1.52	0.74
META1_3513	protein of unknown function; putative exported protein	0.000	0.159	0.148	0.000	0.285	0.189	0.193	0.271	0.218	0.118	0.202	0.228	2.62	0.43	1.70	0.37
META1_3514	putative histidine kinase of the HWE family	0.000	0.317	0.223	0.000	0.356	0.000	0.279	0.232	0.337	0.209	0.151	0.282	1.83	0.38	2.80	0.10
META1_3516	putative Glycosyl transferase, family 2	0.000	0.045	0.000	0.135	0.166	0.095	0.129	0.077	0.060	0.018	0.131	0.087	6.50	0.14	1.00	0.20
META1_3517	Peptidase	0.195	0.000	0.000	0.000	0.238	0.213	0.107	0.000	0.119	0.045	0.192	0.074	2.20	0.48	0.58	0.92
META1_3519	putative transcriptional regulator	0.273	0.521	0.421	0.000	0.428	0.331	0.514	0.561	0.754	0.426	0.323	0.612	1.94	0.13	2.84	0.46
META1_3521	methionine adenosyltransferase 1 (AdoMet synthetase)	1.908	1.495	1.559	2.841	3.373	3.851	1.264	1.662	0.913	1.615	3.498	1.284	1.07	0.21	0.55	0.01
META1_3522	tRNA (guanine-N(7)-)-methyltransferase (tRNA(m7G46)	0.000	0.113	0.074	0.000	0.000	0.142	0.129	0.174	0.139	0.073	0.060	0.148	2.75	0.44	3.67	0.12
META1_3523	DNA topoisomerase I	0.818	1.110	1.336	1.623	1.663	1.347	1.285	1.450	1.627	1.125	1.522	1.458	1.75	0.13	1.44	0.56
META1_3524	Sulfite oxidase, oxidoreductase molybdopterin binding	0.117	0.068	0.000	0.000	0.071	0.071	0.000	0.039	0.000	0.054	0.060	0.013	0.33	0.57	0.33	0.56
META1_3527	aspartate carbamoyltransferase	0.350	0.498	0.396	0.338	0.166	0.449	0.450	0.561	0.456	0.426	0.312	0.491	1.55	0.25	2.35	0.17
META1_3528	putative dihydroorotase-like protein	0.234	0.612	0.470	0.271	0.713	0.614	0.600	0.657	0.417	0.472	0.605	0.558	1.60	0.40	1.38	0.76
META1_3529	Putative 1-acyl glycerol-3-phosphate synthetase (PlsY)	0.000	0.091	0.074	0.135	0.071	0.047	0.000	0.077	0.079	0.064	0.071	0.054	1.14	0.99	1.14	0.37
META1_3533	isonitrile hydratase, ThiJ/Pfpl family protein	0.000	0.000	0.000	0.203	0.095	0.095	0.129	0.155	0.099	0.000	0.111	0.128	n.d.	0.00	1.73	0.93
META1_3534	putative Holliday junction resolvase	0.000	0.091	0.000	0.000	0.000	0.000	0.086	0.000	0.000	0.036	0.000	0.027	1.00	1.00	n.d.	0.37
META1_3535	protein of unknown function	0.273	0.181	0.198	0.000	0.166	0.118	0.171	0.213	0.099	0.209	0.121	0.161	1.04	0.27	2.00	0.39
META1_3537	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase sub	0.156	0.091	0.074	0.000	0.095	0.071	0.064	0.135	0.139	0.100	0.071	0.114	1.55	0.89	2.43	0.41
META1_3538	Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-A	1.168	1.246	1.410	0.744	0.998	1.040	0.943	0.986	0.873	1.288	0.978	0.934	0.98	0.01	1.43	0.89
META1_3541	protein of unknown function	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.045	0.000	0.020	0.60	0.96	n.d.	0.37
META1_3542	multidrug efflux system protein (acrB ou acrF)	0.000	0.113	0.247	0.203	0.689	0.402	0.214	0.155	0.258	0.136	0.494	0.208	2.07	0.41	0.63	0.18
META1_3543	putative RND efflux transporter, membrane fusion prot	0.078	0.159	0.099	0.203	0.451	0.449	0.171	0.174	0.139	0.118	0.413	0.161	1.85	0.14	0.59	0.05
META1_3546	conserved protein of unknown function, ErfK/YbiS/YcfS	0.156	0.091	0.124	0.203	0.404	0.142	0.300	0.232	0.298	0.118	0.262	0.276	3.15	0.01	1.58	0.58
META1_3552	60 kDa chaperonin (protein Cpn60, groEL protein)	0.000	0.181	0.124	0.135	0.095	0.047	0.257	0.232	0.218	0.118	0.081	0.235	2.69	0.45	4.38	0.03
META1_3557	putative extracellular solute-binding protein precursor,	0.000	0.091	0.000	0.000	0.000	0.118	0.257	0.174	0.298	0.036	0.050	0.242	9.00	0.17	7.20	0.15
META1_3560	alkanesulfonate transport protein, periplasmic-binding	0.000	0.000	0.049	0.000	0.000	0.000	0.043	0.077	0.000	0.018	0.000	0.040	3.00	0.53	n.d.	0.12
META1_3561	Alkanesulfonate monooxygenase	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_3563	2-hydroxychromene-2-carboxylate isomerase (HCCA isc	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3568	conserved protein of unknown function; putative HEAT	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3577	putative membrane protein, diguanylate cyclase (GGDE	0.000	0.045	0.074	0.000	0.048	0.095	0.150	0.174	0.179	0.045	0.060	0.168	5.00	0.54	4.17	0.52
META1_3580	protein of unknown function	0.312	0.408	0.346	0.541	0.356	0.449	0.257	0.445	0.337	0.363	0.423	0.349	1.30	0.82	1.24	0.25
META1_3582	Putative transcription elongation factor (GreA/GreB dor	0.000	0.000	0.000	0.000	0.071	0.095	0.000	0.000	0.040	0.000	0.071	0.013	n.d.	0.37	0.29	0.56
META1_3586	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_3601	formamidase	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3609	putative response regulator; input and output domains	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.027	0.000	0.013	0.67	0.97	n.d.	0.37
META1_3611	conserved protein of unknown function; putative expor	1.402	0.997	1.138	2.570	1.188	1.985	1.671	1.759	1.806	1.143	1.734	1.747	2.06	0.02	1.51	0.86
META1_3613	Precorrin-6A synthase [deacetylating]	0.000	0.000	0.049	0.000	0.071	0.071	0.086	0.000	0.000	0.018	0.060	0.027	2.00	0.97	0.67	0.51
META1_3616	putative ATPase, putative partition protein (ParA)	0.000	0.000	0.074	0.000	0.000	0.000	0.000	0.116	0.079	0.027	0.000	0.067	3.33	0.54	n.d.	0.12
META1_3617	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.150	0.000	0.159	0.000	0.030	0.101	n.d.	0.12	5.00	0.57
META1_3619	protein of unknown function, Anthranilate phosphoribo	0.000	0.340	0.445	0.203	0.713	0.165	0.557	0.677	0.675	0.299	0.403	0.638	2.88	0.46	2.38	0.16
META1_3620	iron-sulfur cluster assembly accessory protein	0.000	0.045	0.000	0.000	0.095	0.142	0.107	0.058	0.060	0.018	0.101	0.074	5.50	0.14	1.10	0.31
META1_3621	Deoxyguanosinetriphosphate triphosphohydrolase-like	0.000	0.113	0.099	0.000	0.048	0.047	0.043	0.077	0.060	0.082	0.040	0.060	1.00	0.30	2.25	0.40
META1_3623	thioesterase superfamily protein	0.000	0.045	0.049	0.000	0.071	0.000	0.043	0.000	0.000	0.036	0.030	0.013	0.50	0.52	0.67	0.97
META1_3624	arginyl-tRNA synthetase	0.467	1.042	0.940	0.744	1.520	0.945	1.050	1.044	0.893	0.871	1.159	0.995	1.54	0.38	1.29	0.90
META1_3625	conserved protein of unknown function	0.000	0.204	0.124	0.609	0.261	0.118	0.279	0.309	0.337	0.127	0.252	0.309	3.29	0.48	1.84	0.78
META1_3626	putative beta N-acetyl-glucosaminidase (nagZ-like)	0.078	0.204	0.173	0.271	0.380	0.425	0.279	0.251	0.218	0.163	0.383	0.249	2.06	0.13	0.97	0.08
META1_3627	Sec-independent protein translocase protein	0.195	0.091	0.124	0.135	0.119	0.118	0.257	0.193	0.139	0.127	0.121	0.195	2.07	0.25	2.42	0.08
META1_3628	Sec-independent protein translocase protein	0.000	0.136	0.099	0.000	0.143	0.142	0.107	0.077	0.119	0.091	0.121	0.101	1.50	0.35	1.25	0.33
META1_3629	Sec-independent protein translocase protein	0.000	0.045	0.049	0.000	0.000	0.000	0.000	0.077	0.060	0.036	0.000	0.047	1.75	0.96	n.d.	0.12

META1_3630	conserved protein of unknown function; putative expor	0.000	0.068	0.000	0.000	0.048	0.000	0.043	0.155	0.060	0.027	0.020	0.087	4.33	0.12	6.50	0.14
META1_3632	NAD(P)H-dependent FMN reductase	0.000	0.068	0.074	0.000	0.285	0.189	0.300	0.483	0.437	0.054	0.202	0.410	10.17	0.67	3.05	0.47
META1_3633	alkanesulfonate transport protein, periplasmic-binding	0.000	0.000	0.000	0.000	0.000	0.000	0.236	0.155	0.179	0.000	0.000	0.188	n.d.	0.00	n.d.	0.00
META1_3636	alkanesulfonate transport protein, ATP-binding protein	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_3637	alkanesulfonate monooxygenase	0.000	0.091	0.000	0.000	0.143	0.189	0.343	0.232	0.298	0.036	0.141	0.289	10.75	0.18	3.07	0.47
META1_3638	alkanesulfonate transport protein, periplasmic-binding	0.000	0.068	0.000	0.000	0.000	0.071	0.171	0.135	0.119	0.027	0.030	0.141	7.00	0.15	7.00	0.15
META1_3639	alkanesulfonate transport protein, periplasmic-binding	0.000	0.181	0.074	0.000	0.000	0.118	0.321	0.232	0.258	0.100	0.050	0.269	3.64	0.51	8.00	0.16
META1_3641	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.071	0.047	0.064	0.000	0.119	0.036	0.050	0.060	2.25	0.52	1.80	0.95
META1_3642	conserved protein of unknown function; putative expor	0.857	0.816	0.742	0.541	0.499	0.425	0.343	0.483	0.397	0.798	0.474	0.410	0.69	0.00	1.30	0.20
META1_3644	conserved protein of unknown function; putative Trans	0.000	0.045	0.049	0.000	0.238	0.095	0.107	0.213	0.159	0.036	0.141	0.161	6.00	0.55	1.71	0.38
META1_3645	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.048	0.000	0.129	0.097	0.040	0.091	0.020	0.087	1.30	0.33	6.50	0.14
META1_3646	Transglutaminase-like domain	0.000	0.113	0.049	0.000	0.095	0.047	0.086	0.077	0.060	0.064	0.060	0.074	1.57	0.37	1.83	0.39
META1_3648	putative short-chain dehydrogenase/reductase SDR	0.389	0.385	0.445	0.338	0.261	0.402	0.471	0.367	0.258	0.408	0.333	0.363	1.20	0.50	1.64	0.74
META1_3652	aldehyde dehydrogenase; chloroacetaldehyde dehydro	5.919	2.470	3.439	2.908	1.758	1.630	2.507	2.435	1.846	3.629	1.875	2.258	0.84	0.14	1.81	0.65
META1_3654	putative ornithine/diaminopimelate PLP-dependent de	0.000	0.295	0.272	0.000	0.214	0.213	0.257	0.193	0.159	0.218	0.181	0.202	1.25	0.32	1.67	0.36
META1_3655	putative AMP-dependent synthetase and ligase	0.000	0.227	0.223	0.000	0.356	0.284	0.364	0.251	0.298	0.172	0.272	0.302	2.37	0.42	1.67	0.37
META1_3659	conserved protein of unknown function; putative expor	0.896	0.136	0.247	0.676	0.309	0.543	0.214	0.174	0.159	0.354	0.464	0.181	0.69	0.39	0.59	0.02
META1_3660	Adenine deaminase (Adenase) (Adenine aminase)	0.117	0.159	0.223	0.000	0.048	0.000	0.129	0.039	0.040	0.172	0.020	0.067	0.53	0.08	5.00	0.13
META1_3661	Ribosomal RNA large subunit methyltransferase J (rRNA	0.078	0.136	0.124	0.000	0.095	0.142	0.107	0.174	0.060	0.118	0.101	0.114	1.31	0.88	1.70	0.36
META1_3662	exopolyphosphatase	0.000	0.045	0.000	0.000	0.000	0.047	0.000	0.039	0.000	0.018	0.020	0.013	1.00	0.99	1.00	0.99
META1_3663	putative glycosyl transferase precursor, putative memb	0.000	0.000	0.000	0.000	0.048	0.047	0.064	0.039	0.060	0.000	0.040	0.054	n.d.	0.00	2.00	0.39
META1_3665	phytoene desaturase (phytoene dehydrogenase)	0.273	0.136	0.371	0.135	0.404	0.165	0.364	0.425	0.496	0.254	0.262	0.430	2.29	0.14	2.46	0.11
META1_3667	putative membrane component of an ABC transporter	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.077	0.000	0.018	0.000	0.027	2.00	0.98	n.d.	0.37
META1_3670	putative phytoene dehydrogenase	0.000	0.295	0.297	0.203	0.356	0.165	0.257	0.232	0.357	0.227	0.252	0.282	1.68	0.36	1.68	0.51
META1_3671	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.119	0.071	0.107	0.077	0.139	0.000	0.081	0.108	n.d.	0.00	2.00	0.39
META1_3672	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.086	0.097	0.079	0.018	0.000	0.087	6.50	0.15	n.d.	0.00
META1_3673	conserved protein of unknown function	0.000	0.068	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3675	crotonase	0.701	0.521	0.198	0.473	0.594	0.331	0.343	0.290	0.437	0.445	0.464	0.356	1.08	0.69	1.15	0.29
META1_3677	putative metallophosphoesterase	0.000	0.000	0.000	0.000	0.000	0.142	0.086	0.097	0.060	0.000	0.060	0.081	n.d.	0.00	2.00	0.09
META1_3678	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3679	conserved protein of unknown function; putative expor	0.623	0.566	0.371	0.135	0.309	0.496	0.300	0.251	0.179	0.508	0.363	0.242	0.64	0.03	1.00	0.74
META1_3680	putative glutathione S-transferase	0.896	0.589	0.668	0.879	0.713	0.614	0.836	0.793	0.595	0.689	0.695	0.739	1.45	0.83	1.59	0.96
META1_3682	Glycine amidinotransferase (L-arginine:glycine amidinot	1.012	1.065	1.113	1.217	1.995	1.843	1.028	1.411	1.290	1.070	1.814	1.250	1.58	0.21	1.03	0.18
META1_3683	conserved protein of unknown function; putative meml	0.000	0.000	0.000	0.000	0.095	0.142	0.000	0.000	0.000	0.000	0.101	0.000	n.d.	n.d.	0.00	0.12
META1_3684	protein of unknown function; putative exported protein	0.506	0.566	0.594	0.676	0.428	0.449	0.471	0.464	0.675	0.562	0.474	0.538	1.29	0.73	1.70	0.83
META1_3685	putative glycosyl transferase, putative membrane-assoc	0.000	0.000	0.000	0.000	0.048	0.118	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.12
META1_3686	Radical SAM superfamily protein	0.662	0.770	0.742	0.744	0.879	1.110	0.814	1.082	0.973	0.735	0.958	0.961	1.77	0.05	1.51	0.72
META1_3687	conserved protein of unknown function; putative YdjC-l	0.000	0.091	0.074	0.000	0.000	0.000	0.171	0.174	0.159	0.064	0.000	0.168	3.57	0.48	n.d.	0.00
META1_3689	putative membrane protein with sterol sensing domain	1.207	1.156	1.311	2.299	2.162	1.748	2.057	1.933	2.104	1.225	2.006	2.030	2.24	0.00	1.52	0.89
META1_3690	Radical SAM superfamily protein	0.273	0.249	0.247	0.406	1.093	1.276	0.493	0.483	0.218	0.254	1.068	0.397	2.11	0.24	0.56	0.15
META1_3691	putative nucleoside phosphorylase	0.078	0.159	0.124	0.000	0.190	0.213	0.150	0.193	0.198	0.127	0.171	0.181	1.93	0.12	1.59	0.36
META1_3692	putative capsule polysaccharide export outer membran	1.480	0.227	0.520	1.014	0.784	1.040	0.343	0.329	0.437	0.626	0.927	0.370	0.80	0.49	0.60	0.00
META1_3693	Putative hydrolase, Cof-subfamily	0.000	0.091	0.049	0.000	0.000	0.000	0.043	0.039	0.060	0.054	0.000	0.047	1.17	0.33	n.d.	0.00
META1_3694	gluconokinase; gluconate transport, GNT I system	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3696	50S ribosomal subunit protein L32	0.234	0.363	0.346	0.338	0.309	0.378	0.150	0.135	0.258	0.327	0.343	0.181	0.75	0.08	0.79	0.03
META1_3699	putative regulator for granule-associated proteins, PHB	0.623	0.385	0.396	0.473	0.736	0.662	0.750	0.715	0.794	0.445	0.665	0.753	2.29	0.03	1.70	0.21
META1_3700	beta-ketothiolase	9.073	5.461	5.468	4.734	3.682	4.158	3.385	3.151	3.434	6.305	4.042	3.320	0.71	0.02	1.23	0.04
META1_3701	acetoacetyl-CoA reductase	2.609	1.790	1.757	3.787	1.021	1.488	1.028	1.411	1.012	1.969	1.633	1.156	0.79	0.03	1.06	0.32
META1_3702	lipid A biosynthesis lauroyl acyltransferase	0.156	0.249	0.074	0.000	0.143	0.260	0.171	0.251	0.119	0.163	0.171	0.181	1.50	0.67	1.59	0.36
META1_3703	aminopeptidase	1.051	0.997	0.841	0.203	0.499	0.473	0.300	0.522	0.437	0.953	0.443	0.423	0.60	0.01	1.43	0.74
META1_3704	conserved protein of unknown function	0.000	0.113	0.198	0.000	0.095	0.095	0.000	0.000	0.000	0.118	0.081	0.000	0.00	0.12	0.00	0.12
META1_3705	putative D-lactate dehydrogenase (cytochrome)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_3706	putative Fumarylacetoacetate (FAA) hydrolase	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_3707	NUDIX superfamily hydrolase	0.000	0.000	0.000	0.000	0.095	0.000	0.064	0.097	0.079	0.000	0.040	0.081	n.d.	0.00	3.00	0.11
META1_3712	putative transcriptional regulator, Crp/Fnr family	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_3713	protein of unknown function; putative exported protein	0.078	0.000	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3716	putative acyl-CoA dehydrogenase	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.000	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_3717	conserved protein of unknown function; putative OsmC	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.058	0.099	0.000	0.000	0.087	n.d.	0.00	n.d.	0.00
META1_3719	putative ABC transporter, periplasmic protein	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_3726	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_3730	putative molecular chaperone, heat shock Hsp20 family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.040	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_3732	UspA (universal stress protein) domain protein	0.000	0.113	0.099	0.000	0.000	0.000	0.107	0.097	0.179	0.082	0.000	0.128	2.11	0.40	n.d.	0.00
META1_3733	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.036	0.000	0.013	0.50	0.96	n.d.	0.37
META1_3735	protein of unknown function	0.234	0.204	0.198	0.000	0.000	0.000	0.086	0.058	0.079	0.209	0.000	0.074	0.48	0.00	n.d.	0.00
META1_3737	conserved protein of unknown function	0.000	0.159	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.064	0.000	0.013	0.29	0.92	n.d.	0.37
META1_3742	conserved protein of unknown function, putative unive	0.000	0.227	0.099	0.000	0.048	0.047	0.064	0.039	0.060	0.127	0.040	0.054	0.57	0.25	2.00	0.39
META1_3748	Alcohol dehydrogenase, zinc-binding. Isopropanol dehy	0.000	0.159	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3768	bifunctional: nitric oxide dioxygenase (N-terminal); dihy	0.000	0.091	0.099	0.609	0.499	0.473	0.279	0.445	0.218	0.073	0.504	0.316	5.88	0.57	0.94	0.07
META1_3782	putative molecular chaperone, heat shock Hsp20 family	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.077	0.000	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_3791	putative biotin/lipoyl attachment domain	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3793	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3801	putative cytochrome c, class I	0.000	0.091	0.074	0.000	0.000	0.000	0.000	0.000	0.060	0.064	0.000	0.020	0.43	0.54	n.d.	0.37
META1_3802	Putative universal stress protein, UspA-like	0.078	0.272	0.173	0.000	0.000	0.000	0.107	0.077	0.040	0.191	0.000	0.074	0.52	0.16	n.d.	0.00
META1_3805	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3806	D-xylulose 5-phosphate/D-fructose 6-phosphate phosph	0.000	0.159	0.000	0.000	0.000	0.000	0.000	0.077	0.060	0.064	0.000	0.047	1.00	0.47	n.d.	0.12
META1_3808	protein of unknown function	0.234	0.204	0.074	0.000	0.119	0.000	0.064	0.116	0.060	0.163	0.050	0.081	0.67	0.17	2.40	0.10
META1_3810	conserved protein of unknown function	0.000	0.159	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3819	conserved protein of unknown function; putative unive	0.195	0.566	0.223	0.000	0.000	0.047	0.150	0.116	0.139	0.354	0.020	0.134	0.51	0.09	10.00	0.17
META1_3820	putative transcriptional regulator, Crp/Fnr family [	0.000	0.113	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3822	protein of unknown function	0.117	0.091	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_3825	two component transcriptional regulator, LuxR family; p	0.000	0.181	0.148	0.000	0.048	0.000	0.107	0.155	0.119	0.127	0.020	0.128	1.36	0.34	9.50	0.16
META1_3826	two component low oxygen sensor histidine kinase with	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.135	0.139	0.018	0.000	0.108	8.00	0.15	n.d.	0.00
META1_3830	putative cytochrome c, class I	0.000	0.068	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META1_3837	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.071	0.064	0.039	0.000	0.000	0.050	0.034	n.d.	0.12	1.00	0.98
META1_3842	conserved protein of unknown function; putative meml	0.000	0.000	0.000	0.000	0.071	0.165	0.043	0.039	0.000	0.000	0.101	0.027	n.d.	0.12	0.40	0.89
META1_3843	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3844	conserved protein of unknown function, ErfK/YbiS/YcfS/	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_3851	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.097	0.159	0.000	0.000	0.114	n.d.	0.00	n.d.	0.00
META1_3853	protein of unknown function	0.195	0.340	0.297	0.135	0.285	0.307	0.107	0.174	0.218	0.290	0.272	0.168	0.78	0.12	0.93	0.35
META1_3854	DNA-binding transcriptional regulator of mntH	0.000	0.091	0.049	0.203	0.095	0.071	0.150	0.116	0.139	0.054	0.101	0.134	3.33	0.48	2.00	0.59
META1_3860	Succinate dehydrogenase delta subunit	0.078	0.068	0.000	0.000	0.071	0.000	0.000	0.039	0.060	0.045	0.030	0.034	1.00	0.95	1.67	0.50
META1_3861	succinate dehydrogenase, flavoprotein subunit	1.713	2.062	2.326	0.406	0.879	0.425	0.750	0.793	0.516	2.077	0.615	0.685	0.45	0.00	1.67	0.46
META1_3862	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META1_3863	succinate dehydrogenase, iron-sulfur subunit	0.234	0.498	0.346	0.000	0.000	0.260	0.086	0.135	0.099	0.381	0.111	0.108	0.38	0.01	1.45	0.08
META1_3864	protein of unknown function	0.234	0.136	0.099	0.271	0.143	0.118	0.086	0.039	0.139	0.145	0.151	0.087	0.81	0.23	0.87	0.16
META1_3866	Arabinose-5-phosphate isomerase	0.000	0.000	0.000	0.135	0.071	0.165	0.086	0.058	0.079	0.000	0.121	0.074	n.d.	0.00	0.92	0.17
META1_3870	Enoyl-CoA hydratase/isomerase family protein	0.078	0.000	0.000	0.000	0.071	0.095	0.150	0.232	0.119	0.018	0.071	0.168	12.50	0.15	3.57	0.48
META1_3871	putative short-chain dehydrogenase/reductase SDR	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_3872	Short-chain dehydrogenase/reductase SDR	0.234	0.272	0.148	0.000	0.000	0.118	0.300	0.251	0.278	0.218	0.050	0.276	1.71	0.23	8.20	0.16
META1_3873	putative magnesium/cobalt transport protein	0.000	0.045	0.049	0.000	0.095	0.071	0.107	0.077	0.099	0.036	0.071	0.094	3.50	0.47	2.00	0.39
META1_3874	conserved protein of unknown function, DUF892	0.312	0.589	0.322	0.000	0.071	0.071	0.000	0.213	0.139	0.426	0.060	0.121	0.38	0.51	3.00	0.90
META1_3877	protein of unknown function	0.117	0.068	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_3882	Short-chain dehydrogenase/reductase SDR	0.234	0.453	0.421	0.541	0.000	0.236	0.407	0.348	0.238	0.390	0.181	0.329	1.14	0.74	2.72	0.36
META1_3883	conserved protein of unknown function	0.078	0.227	0.148	0.135	0.143	0.118	0.321	0.329	0.218	0.163	0.131	0.289	2.39	0.10	3.31	0.01
META1_3884	non-heme haloperoxidase	0.623	0.748	0.520	0.271	0.048	0.165	0.300	0.290	0.318	0.635	0.131	0.302	0.64	0.00	3.46	0.17
META1_3887	protein of unknown function	0.000	0.045	0.000	0.000	0.119	0.071	0.000	0.039	0.119	0.018	0.081	0.054	4.00	0.54	1.00	0.97
META1_3888	conserved protein of unknown function	0.000	0.159	0.272	0.000	0.048	0.000	0.064	0.000	0.159	0.163	0.020	0.074	0.61	0.91	5.50	0.57
META1_3889	conserved protein of unknown function	0.078	0.159	0.099	0.000	0.071	0.095	0.150	0.058	0.040	0.118	0.071	0.081	0.92	0.40	1.71	0.36
META1_3894	4-hydroxythreonine-4-phosphate dehydrogenase (4-(ph	0.078	0.159	0.099	0.000	0.166	0.307	0.171	0.232	0.218	0.118	0.202	0.208	2.38	0.05	1.55	0.36
META1_3895	dimethyladenosine transferase	0.000	0.000	0.099	0.000	0.000	0.071	0.171	0.174	0.179	0.036	0.030	0.175	6.50	0.14	8.67	0.16
META1_3903	conserved protein of unknown function; putative expor	0.078	0.045	0.000	0.000	0.143	0.118	0.000	0.077	0.079	0.036	0.111	0.054	2.00	0.97	0.73	0.94
META1_3904	protein of unknown function	0.000	0.068	0.049	0.000	0.000	0.000	0.064	0.058	0.000	0.045	0.000	0.040	1.20	0.99	n.d.	0.12
META1_3905	Putative organic solvent tolerance protein	0.584	0.000	0.148	0.879	0.523	0.402	0.129	0.116	0.079	0.191	0.524	0.108	0.76	0.25	0.31	0.00
META1_3908	cytosol aminopeptidase (putative leucine aminopeptida	1.986	1.631	1.559	0.406	1.306	1.299	1.221	1.140	1.191	1.687	1.169	1.183	0.95	0.01	1.52	0.49
META1_3909	protein of unknown function; putative membrane prote	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3910	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)	0.195	0.408	0.495	0.203	0.238	0.165	0.407	0.309	0.357	0.390	0.202	0.356	1.23	0.89	2.65	0.01
META1_3912	putative thioredoxin domain protein precursor	0.273	0.521	0.520	0.271	0.261	0.473	0.428	0.522	0.278	0.463	0.353	0.410	1.20	0.85	1.74	0.48
META1_3913	putative metal-dependent phosphohydrolase (HD doma	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.099	0.000	0.000	0.054	n.d.	0.12	n.d.	0.12
META1_3915	aspartate aminotransferase	0.195	0.136	0.124	0.000	0.214	0.189	0.171	0.155	0.159	0.145	0.171	0.161	1.50	0.59	1.41	0.34
META1_3916	putative ribonuclease E or G	2.414	2.515	2.870	3.855	2.328	3.119	3.021	2.300	2.838	2.622	2.893	2.708	1.39	0.69	1.40	0.53
META1_3918	putative N-acetylmuramoyl-L-alanine amidase amiC pre	0.000	0.000	0.000	0.000	0.166	0.000	0.000	0.058	0.060	0.000	0.071	0.040	n.d.	0.12	0.86	0.46
META1_3919	putative bifunctional N-terminal transglycosylase/C-ter	0.234	0.544	0.346	0.541	0.713	0.473	0.214	0.251	0.099	0.399	0.585	0.188	0.64	0.14	0.48	0.02
META1_3920	Alkanesulfonate monooxygenase	0.000	0.000	0.000	0.000	0.071	0.071	0.129	0.039	0.099	0.000	0.060	0.087	n.d.	0.00	2.17	0.39
META1_3921	acyl-CoA dehydrogenase	0.000	0.000	0.000	0.000	0.095	0.095	0.064	0.000	0.040	0.000	0.081	0.034	n.d.	0.12	0.63	0.93

META1_3923	putative oxidoreductase, xanthine dehydrogenase, FAD	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_3924	oxidoreductase, molybdopterin-binding subunit	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.039	0.000	0.054	0.000	0.013	0.33	0.55	n.d.	0.37
META1_3928	putative monooxygenase with ATPase activity, luciferas	0.000	0.113	0.074	0.135	0.261	0.165	0.236	0.232	0.198	0.073	0.202	0.222	4.13	0.51	1.65	0.37
META1_3930	Putative riboflavin biosynthesis protein RibD	0.000	0.068	0.000	0.000	0.095	0.000	0.000	0.077	0.079	0.027	0.040	0.054	2.67	0.53	2.00	0.51
META1_3931	protein of unknown function	0.273	0.317	0.371	0.338	0.356	0.402	0.257	0.213	0.198	0.327	0.373	0.222	0.92	0.04	0.89	0.01
META1_3932	putative periplasmic glucan biosynthesis protein precur	0.000	0.159	0.148	0.000	0.143	0.189	0.043	0.039	0.000	0.118	0.141	0.027	0.31	0.85	0.29	0.84
META1_3933	putative membrane-associated glycosyl transferase	0.000	0.068	0.124	0.000	0.190	0.047	0.214	0.271	0.218	0.073	0.101	0.235	4.38	0.52	3.50	0.52
META1_3934	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.058	0.000	0.000	0.040	0.020	n.d.	0.37	0.75	0.97
META1_3937	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.039	0.000	0.000	0.060	0.013	n.d.	0.37	0.33	0.56
META1_3938	conserved protein of unknown function	0.000	0.045	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_3958	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_3962	protein of unknown function	0.000	0.249	0.124	0.000	0.000	0.118	0.193	0.077	0.119	0.145	0.050	0.128	1.19	0.32	3.80	0.12
META1_3993	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.238	0.189	0.000	0.058	0.000	0.000	0.181	0.020	n.d.	0.37	0.17	0.61
META1_3994	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4019	Phage-related protein	0.078	0.113	0.049	0.000	0.238	0.284	0.129	0.155	0.099	0.082	0.222	0.128	2.11	0.14	0.86	0.28
META1_4039	Glucose-1-phosphate thymidylyltransferase	0.350	0.385	0.148	0.271	0.048	0.142	0.364	0.367	0.238	0.290	0.121	0.323	1.50	0.67	4.00	0.14
META1_4040	dTDP-4-dehydrorhamnose reductase	0.273	0.453	0.346	0.203	0.190	0.236	0.343	0.367	0.298	0.372	0.212	0.336	1.22	0.80	2.38	0.01
META1_4041	dTDP-glucose 4,6-dehydratase	0.701	0.295	0.272	0.203	0.214	0.213	0.300	0.174	0.179	0.381	0.212	0.215	0.76	0.16	1.52	0.99
META1_4042	dTDP-4-dehydrorhamnose 3,5-epimerase	0.818	0.793	0.792	0.744	0.760	0.638	0.814	0.619	0.595	0.798	0.706	0.672	1.14	0.14	1.43	0.61
META1_4070	conserved protein of unknown function	0.467	0.589	0.445	0.000	0.166	0.071	0.193	0.135	0.238	0.508	0.101	0.188	0.50	0.01	2.80	0.46
META1_4072	conserved protein of unknown function	0.234	0.340	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.254	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_4087	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4089	protein of unknown function	0.000	0.045	0.099	0.000	0.095	0.189	0.043	0.058	0.079	0.054	0.121	0.060	1.50	0.36	0.75	0.27
META1_4094	ATP-dependent urea carboxylase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.060	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_4098	putative glutamine synthetase III (glnT)	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4105	glycine/betaine/proline transporter, Substrate-binding	0.078	0.295	0.074	0.000	0.000	0.000	0.000	0.000	0.040	0.163	0.000	0.013	0.11	0.17	n.d.	0.37
META1_4114	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_4118	putative NADH:flavin oxidoreductase/NADH oxidase, m	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.058	0.000	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_4129	tonB-dependent siderophore receptor protein	0.428	0.000	0.000	0.338	0.000	0.000	0.000	0.000	0.000	0.100	0.050	0.000	0.00	0.37	0.00	0.37
META1_4132	Siderophore synthetase component	0.117	0.045	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_4133	putative non-ribosomal peptide synthetase, putative ac	0.896	0.068	0.297	0.271	0.000	0.000	0.000	0.000	0.000	0.345	0.040	0.000	0.00	0.00	0.00	0.37
META1_4134	conserved protein of unknown function	0.973	0.159	0.520	0.000	0.000	0.000	0.000	0.000	0.000	0.481	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_4136	conserved protein of unknown function	0.000	0.045	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_4137	GCN5-related N-acetyltransferase	0.818	0.340	0.247	0.338	0.000	0.000	0.000	0.058	0.000	0.417	0.050	0.020	0.07	0.24	0.60	0.90
META1_4138	protein of unknown function; putative exported protein	0.273	0.181	0.198	0.000	0.000	0.000	0.000	0.058	0.079	0.209	0.000	0.047	0.30	0.56	n.d.	0.12
META1_4139	putative transcriptional regulator, TetR family	0.273	0.249	0.346	0.135	0.451	0.520	0.621	0.406	0.417	0.290	0.433	0.477	2.22	0.04	1.65	0.42
META1_4140	pyrroline-5-carboxylate reductase	0.000	0.000	0.074	0.271	0.095	0.095	0.150	0.116	0.040	0.027	0.121	0.101	5.00	0.13	1.25	0.48
META1_4142	conserved protein of unknown function	0.000	0.136	0.173	0.203	0.214	0.189	0.171	0.174	0.238	0.118	0.202	0.195	2.23	0.41	1.45	0.69
META1_4143	response regulator in two-component regulatory syster	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.271	0.198	0.000	0.000	0.208	n.d.	0.00	n.d.	0.00
META1_4144	putative signal transduction histidine kinase precursor	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.155	0.099	0.000	0.000	0.114	n.d.	0.00	n.d.	0.00
META1_4147	putative glutathione S-transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.116	0.000	0.000	0.000	0.060	n.d.	0.12	n.d.	0.12
META1_4148	intracellular PHB depolymerase, polyhydroxyalkanoate	0.000	0.113	0.223	0.000	0.143	0.213	0.171	0.135	0.079	0.127	0.151	0.128	1.36	0.34	1.27	0.33
META1_4149	Ribosomal protein S21	0.935	0.159	0.148	0.947	0.475	0.449	0.964	0.754	1.032	0.336	0.534	0.914	3.68	0.13	2.57	0.17
META1_4150	Putative response regulator; (CheY-like protein)	0.078	0.181	0.099	0.000	0.048	0.071	0.000	0.097	0.060	0.127	0.050	0.054	0.57	0.43	1.60	0.97
META1_4153	Mesaconyl-CoA hydratase. Part of the ethylmalonyl-CoA	0.584	0.770	0.421	2.029	1.211	1.630	0.643	0.503	0.536	0.599	1.512	0.558	1.26	0.88	0.55	0.00
META1_4154	conserved protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4167	putative sensory box/GGDEF family protein	0.000	0.000	0.049	0.000	0.071	0.071	0.064	0.039	0.079	0.018	0.060	0.060	4.50	0.12	1.50	0.35
META1_4169	protein of unknown function	0.000	0.091	0.000	0.135	0.071	0.071	0.129	0.000	0.079	0.036	0.081	0.067	2.50	0.53	1.25	0.36
META1_4178	conserved protein of unknown function	0.000	0.045	0.049	0.000	0.048	0.000	0.000	0.000	0.040	0.036	0.020	0.013	0.50	0.53	1.00	0.99
META1_4179	protein of unknown function	0.273	0.317	0.247	0.203	0.309	0.260	0.214	0.271	0.258	0.281	0.272	0.249	1.19	0.31	1.37	0.85
META1_4187	conserved protein of unknown function	0.000	0.136	0.074	0.000	0.000	0.000	0.000	0.039	0.040	0.082	0.000	0.027	0.44	0.90	n.d.	0.12
META1_4188	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4210	putative peroxidase, putative peroxiredoxin	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4213	putative alpha/beta hydrolase, putative epoxide hydrol	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.039	0.040	0.027	0.000	0.027	1.33	0.49	n.d.	0.12
META1_4214	putative ABC transporter, periplasmic protein; putative	0.000	0.113	0.148	0.000	0.071	0.071	0.064	0.077	0.000	0.100	0.060	0.047	0.64	0.93	1.17	1.00
META1_4222	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4223	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4225	putative oxidoreductase, aldo/keto reductase family	0.389	0.317	0.198	0.135	0.000	0.071	0.086	0.135	0.079	0.290	0.050	0.101	0.47	0.01	3.00	0.37
META1_4227	putative Isochorismatase hydrolase	0.740	0.544	0.520	0.406	0.380	0.307	0.428	0.522	0.417	0.581	0.353	0.457	1.06	0.11	1.94	0.11
META1_4231	conserved protein of unknown function, putative doma	0.857	0.657	0.445	0.812	0.475	0.260	0.450	0.425	0.437	0.626	0.433	0.437	0.94	0.13	1.51	0.86
META1_4232	putative oxidoreductase precursor, putative aldo/keto	0.273	0.544	0.371	0.000	0.000	0.071	0.171	0.213	0.238	0.417	0.030	0.208	0.67	0.05	10.33	0.17
META1_4233	putative methyltransferase with SAM-dependent meth	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4234	conserved protein of unknown function; putative pseud	0.000	0.498	0.421	0.406	0.618	0.732	0.557	0.638	0.357	0.354	0.635	0.517	1.97	0.39	1.22	0.65
META1_4242	putative short-chain dehydrogenase/reductase SDR	0.000	0.136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4243	tRNA-specific adenosine deaminase	0.000	0.045	0.000	0.000	0.048	0.047	0.043	0.000	0.079	0.018	0.040	0.040	3.00	0.53	1.50	0.98
META1_4244	phosphoribosylglycinamide synthetase (GAR synthetase	0.273	0.317	0.322	0.338	0.641	0.496	0.450	0.503	0.437	0.308	0.534	0.464	2.03	0.00	1.30	0.89
META1_4247	putative exonuclease VII, large subunit OB-fold nucleic	0.000	0.091	0.173	0.000	0.333	0.071	0.236	0.174	0.238	0.100	0.171	0.215	2.91	0.46	1.88	0.43
META1_4248	conserved protein of unknown function	0.389	0.498	0.594	0.000	0.143	0.165	0.107	0.058	0.139	0.508	0.131	0.101	0.27	0.00	1.15	0.31
META1_4249	phosphoribosylpyrophosphate synthetase	0.545	0.521	0.742	1.082	0.760	0.709	0.664	0.599	0.774	0.608	0.786	0.679	1.51	0.40	1.29	0.23
META1_4250	putative GreA/GreB family transcription elongation fact	0.000	0.181	0.124	0.000	0.095	0.095	0.107	0.097	0.099	0.118	0.081	0.101	1.15	0.32	1.88	0.38
META1_4251	putative Zn-dependent oxidoreductase, NAD(P)-binding	0.584	0.612	0.445	0.271	0.214	0.213	0.450	0.309	0.357	0.544	0.222	0.370	0.92	0.06	2.50	0.03
META1_4252	conserved protein of unknown function; putative expor	0.312	0.000	0.049	0.473	0.071	0.118	0.000	0.000	0.000	0.091	0.151	0.000	0.00	0.12	0.00	0.00
META1_4253	4Fe-4S ferredoxin, iron-sulfur binding domain protein	0.000	0.340	0.272	0.203	0.000	0.071	0.086	0.097	0.119	0.236	0.060	0.101	0.58	0.23	2.50	0.35
META1_4254	transcriptional regulator, CarD family	0.389	0.453	0.421	0.879	0.641	0.827	0.836	0.908	0.615	0.426	0.756	0.786	2.49	0.01	1.56	1.00
META1_4255	RNA polymerase sigma-32 (sigma H) factor	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.040	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_4261	tRNA uridine 5-carboxymethylaminomethyl modificatio	0.000	0.317	0.272	0.271	0.451	0.425	0.407	0.522	0.456	0.227	0.413	0.464	2.76	0.45	1.68	0.30
META1_4263	putative serine protease, htrA-like	0.117	0.272	0.148	0.000	0.143	0.095	0.193	0.193	0.258	0.191	0.101	0.215	1.52	0.43	3.20	0.47
META1_4264	RNA polymerase sigma factor	0.000	0.068	0.049	0.000	0.048	0.047	0.000	0.000	0.000	0.045	0.040	0.000	0.00	0.12	0.00	0.12
META1_4265	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.039	0.000	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_4266	putative CoxB-related	0.857	0.476	0.767	1.758	0.594	1.772	0.900	0.657	0.933	0.671	1.270	0.827	1.66	0.42	0.98	0.35
META1_4267	DNA excision repair enzyme subunit, with UvrBC	0.312	0.408	0.544	0.744	0.903	0.520	0.728	0.928	0.714	0.435	0.716	0.793	2.46	0.02	1.66	0.58
META1_4268	conserved protein of unknown function; putative Meth	0.000	0.000	0.000	0.000	0.048	0.047	0.043	0.000	0.000	0.000	0.040	0.013	n.d.	0.37	0.50	0.52
META1_4269	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4273	Putative histidine kinase of the HWE family	0.117	0.295	0.371	0.000	0.048	0.000	0.000	0.000	0.000	0.281	0.020	0.000	0.00	0.00	0.00	0.37
META1_4274	putative transcriptional regulator, Crp/Fnr family	0.273	0.295	0.272	0.000	0.000	0.047	0.064	0.058	0.060	0.281	0.020	0.060	0.29	0.00	4.50	0.13
META1_4276	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.048	0.047	0.064	0.058	0.040	0.018	0.040	0.054	4.00	0.12	2.00	0.39
META1_4277	2-octaprenyl-6-methoxyphenol hydroxylase (FAD-depe	0.000	0.113	0.148	0.000	0.095	0.095	0.043	0.000	0.060	0.100	0.081	0.034	0.45	0.89	0.63	0.93
META1_4280	quinone oxidoreductase, NADPH-dependent	1.051	1.201	0.990	0.947	0.903	0.992	1.007	0.715	0.714	1.089	0.947	0.806	1.00	0.08	1.28	0.23
META1_4281	nicotinamidase	0.000	0.045	0.000	0.000	0.071	0.071	0.043	0.058	0.040	0.018	0.060	0.047	3.50	0.12	1.17	0.32
META1_4282	Putative branched-chain amino acid aminotransferase	0.117	0.159	0.124	0.000	0.000	0.095	0.086	0.077	0.079	0.136	0.040	0.081	0.80	0.01	3.00	0.11
META1_4283	aminodeoxychorismate synthase subunit II, component	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.040	0.000	0.000	0.067	n.d.	0.00	n.d.	0.00
META1_4284	para-aminobenzoate synthase component I (ADC synth	0.000	0.204	0.198	0.000	0.214	0.213	0.150	0.251	0.099	0.154	0.181	0.168	1.47	0.34	1.39	0.33
META1_4285	Addiction module antitoxin, RelB/DinJ family (plasmid s	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.058	0.099	0.045	0.000	0.054	1.60	0.49	n.d.	0.12
META1_4287	putative AdoMet-dependent methyltransferase, UPF00	0.000	0.000	0.049	0.000	0.238	0.142	0.150	0.155	0.179	0.018	0.161	0.161	12.00	0.18	1.50	0.36
META1_4290	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_4292	Plasmid replication protein RepA	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_4295	malyl-CoA lyase	1.558	0.884	0.965	1.488	1.354	1.914	1.371	1.411	1.092	1.070	1.613	1.290	1.63	0.47	1.20	0.20
META1_4296	putative DNA-binding protein, hemimethylated (yccV-li	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.039	0.040	0.018	0.000	0.040	3.00	0.11	n.d.	0.00
META1_4299	putative efflux transporter, membrane fusion protein s	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_4300	efflux transporter, AcrB/AcrD/AcrF family protein	0.000	0.068	0.000	0.135	0.143	0.095	0.000	0.097	0.099	0.027	0.121	0.067	3.33	0.54	0.83	0.41
META1_4303	agmatinase (ureohydrolase)	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4307	Coenzyme A biosynthesis bifunctional protein coaBC (D	0.078	0.340	0.223	0.203	0.404	0.331	0.279	0.387	0.218	0.236	0.343	0.296	1.69	0.38	1.29	0.87
META1_4308	putative stabilisation protein	0.000	0.091	0.049	0.000	0.000	0.000	0.064	0.077	0.000	0.054	0.000	0.047	1.17	0.99	n.d.	0.12
META1_4309	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4310	ubiquinone biosynthesis protein, putative 2-polyprenyl	0.000	0.181	0.198	0.000	0.190	0.189	0.236	0.290	0.258	0.145	0.161	0.262	2.44	0.42	2.44	0.42
META1_4311	Ubiquinone/menaquinone biosynthesis methyltransfera	0.156	0.272	0.247	0.473	0.119	0.331	0.386	0.406	0.318	0.236	0.262	0.370	2.12	0.05	2.12	0.48
META1_4312	Dihydromethanopterin reductase	0.000	0.159	0.124	0.203	0.190	0.142	0.150	0.155	0.198	0.109	0.171	0.168	2.08	0.40	1.47	0.71
META1_4313	Short-chain dehydrogenase/reductase SDR	0.312	0.498	0.346	0.000	0.190	0.378	0.407	0.329	0.238	0.399	0.242	0.323	1.09	0.45	2.00	0.40
META1_4314	amidophosphoribosyltransferase (PRPP amidotransfera	0.467	0.952	0.668	0.406	0.546	0.591	0.364	0.445	0.714	0.735	0.544	0.511	0.94	0.33	1.41	0.87
META1_4315	Colicin V-related production protein (membrane protei	0.195	0.431	0.371	0.203	0.166	0.307	0.214	0.193	0.337	0.354	0.232	0.249	0.95	0.42	1.61	0.71
META1_4316	putative metallo-hydrolase/oxidoreductase precursor, p	0.000	0.000	0.000	0.000	0.071	0.095	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.12
META1_4318	DNA repair protein RadA	0.000	0.000	0.000	0.000	0.071	0.000	0.086	0.077	0.000	0.000	0.030	0.054	n.d.	0.12	2.67	0.53
META1_4320	replicative DNA helicase (dnaB)	0.000	0.091	0.099	0.000	0.238	0.213	0.171	0.213	0.258	0.073	0.192	0.215	4.00	0.50	1.68	0.36
META1_4321	50S ribosomal protein L9	2.375	1.654	1.707	2.570	1.900	1.867	1.842	1.817	1.925	1.842	1.986	1.862	1.36	0.91	1.41	0.33
META1_4323	30S ribosomal protein S18	0.389	0.385	0.668	0.473	0.808	0.851	0.707	0.619	0.635	0.490	0.776	0.652	1.80	0.14	1.26	0.80
META1_4324	30S ribosomal protein S6	1.869	0.952	0.742	1.758	2.352	2.197	2.121	1.836	1.945	1.089	2.197	1.962	2.43	0.11	1.34	0.57
META1_4327	conserved protein of unknown function	0.000	0.249	0.198	0.000	0.190	0.118	0.129	0.174	0.218	0.172	0.131	0.175	1.37	0.34	2.00	0.39
META1_4328	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.047	0.086	0.000	0.000	0.000	0.020	0.027	n.d.	0.37	2.00	0.97
META1_4329	conserved protein of unknown function	0.234	0.091	0.148	0.473	0.356	0.165	0.428	0.232	0.516	0.145	0.292	0.390	3.63	0.06	2.00	0.64
META1_4330	cold shock protein A	0.000	0.045	0.000	0.000	0.048	0.047	0.064	0.000	0.040	0.018	0.040	0.034	2.50	0.53	1.25	0.99
META1_4332	Peptide deformylase (PDF) (Polypeptide deformylase)	0.000	0.068	0.049	0.000	0.071	0.000	0.000	0.058	0.079	0.045	0.030	0.047	1.40	0.98	2.33	0.52
META1_4333	protein of unknown function; putative exported protein	0.000	0.045	0.000	0.000	0.000	0.047	0.043	0.039	0.000	0.018	0.020	0.027	2.00	0.51	2.00	0.51
META1_4337	GCN5-related N-acetyltransferase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4340	putative oxidoreductase	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.045	0.000	0.013	0.40	0.94	n.d.	0.37

META1_4341	Aspartate ammonia-lyase (Aspartase)	0.273	0.612	0.445	0.000	0.166	0.047	0.279	0.309	0.218	0.472	0.091	0.269	0.77	0.15	4.44	0.56
META1_4345	putative porin	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4346	glutamate and aspartate transporter subunit ; periplasm	0.818	0.453	0.619	0.541	0.000	0.189	0.321	0.367	0.198	0.599	0.161	0.296	0.67	0.04	2.75	0.36
META1_4347	glutamate and aspartate transporter subunit ; membra	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.058	0.060	0.000	0.030	0.040	n.d.	0.12	2.00	0.51
META1_4349	glutamate and aspartate transporter subunit ; ATP-bind	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.077	0.000	0.054	0.000	0.027	0.67	0.51	n.d.	0.37
META1_4353	conserved protein of unknown function; putative expor	2.414	1.541	1.732	1.285	0.546	0.496	0.557	0.850	0.675	1.814	0.635	0.699	0.52	0.01	1.65	0.93
META1_4354	conserved protein of unknown function; putative MutT	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4357	putative non-ribosomal peptide synthetase	0.156	0.498	0.520	0.406	0.451	0.378	0.386	0.367	0.516	0.426	0.413	0.423	1.34	0.65	1.54	0.89
META1_4359	conserved protein of unknown function; putative alpha	0.156	0.159	0.124	0.338	0.238	0.354	0.279	0.232	0.218	0.145	0.302	0.242	2.25	0.01	1.20	0.18
META1_4360	cysteine desulfurase (tRNA sulfurtransferase), PLP-depe	0.000	0.091	0.074	0.271	0.428	0.496	0.279	0.290	0.278	0.064	0.433	0.282	6.00	0.58	0.98	0.16
META1_4361	FeS assembly protein SufB	0.779	1.065	1.212	1.082	1.544	1.536	0.964	0.986	1.052	1.052	1.472	1.001	1.28	0.99	1.02	0.06
META1_4363	FeS assembly ATPase SufC	1.129	0.906	1.014	1.420	0.523	1.181	1.028	1.005	1.012	0.998	0.937	1.015	1.37	0.97	1.62	0.86
META1_4364	FeS assembly protein SufD	1.090	1.518	2.004	1.488	1.164	1.040	0.921	1.102	0.992	1.597	1.159	1.008	0.85	0.10	1.30	0.18
META1_4365	cysteine desulfurase	0.312	0.453	0.346	0.406	0.451	0.591	0.557	0.309	0.278	0.381	0.504	0.376	1.33	0.98	1.12	0.33
META1_4366	conserved protein of unknown function; putative DUF5	0.000	0.000	0.000	0.000	0.095	0.095	0.000	0.097	0.000	0.000	0.081	0.034	n.d.	0.37	0.63	0.52
META1_4368	iron-sulfur cluster assembly accessory protein	0.000	0.000	0.000	0.135	0.095	0.071	0.107	0.077	0.060	0.000	0.091	0.081	n.d.	0.00	1.33	0.46
META1_4369	putative diguanylate cyclase (2 GGDEF motifs)	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.000	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META1_4370	RNA helicase	0.662	0.997	1.163	0.879	1.259	0.827	0.943	0.850	1.032	0.980	1.018	0.941	1.30	0.89	1.39	0.82
META1_4374	protein of unknown function	0.234	0.272	0.148	0.203	0.380	0.307	0.236	0.232	0.377	0.218	0.323	0.282	1.75	0.34	1.31	0.86
META1_4376	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.039	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_4377	protein of unknown function	0.078	0.000	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_4378	putative haloacid dehalogenase family hydrolase	0.000	0.227	0.099	0.000	0.000	0.000	0.086	0.058	0.060	0.127	0.000	0.067	0.71	0.27	n.d.	0.00
META1_4379	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.058	0.060	0.000	0.030	0.040	n.d.	0.12	2.00	0.51
META1_4380	putative ABC transporter, ATPase	0.078	0.136	0.074	0.000	0.119	0.095	0.193	0.213	0.119	0.100	0.091	0.175	2.36	0.08	2.89	0.45
META1_4381	putative acyl-CoA thioesterase precursor (tesA-like)	0.273	0.498	0.470	0.473	0.428	0.425	0.407	0.483	0.496	0.435	0.433	0.464	1.44	0.52	1.60	0.59
META1_4382	putative 2'-5' RNA ligase	0.467	0.431	0.223	0.000	0.166	0.189	0.279	0.193	0.198	0.363	0.151	0.222	0.83	0.14	2.20	0.41
META1_4383	Preprotein translocase subunit SecE-like protein	0.117	0.000	0.049	0.000	0.071	0.142	0.086	0.097	0.099	0.045	0.091	0.094	2.80	0.40	1.56	0.37
META1_4384	transcription termination factor	1.363	0.929	0.940	1.894	1.354	1.158	0.857	1.160	1.072	1.034	1.351	1.035	1.35	0.82	1.15	0.12
META1_4385	50S ribosomal protein L11	0.584	0.181	0.148	1.082	1.069	0.921	1.178	1.218	1.171	0.263	1.008	1.190	6.10	0.02	1.77	0.05
META1_4386	50S ribosomal subunit protein L1	1.713	1.337	1.856	3.923	1.116	1.937	2.035	2.609	2.143	1.615	1.885	2.272	1.90	0.06	1.81	0.80
META1_4388	putative cytochrome P450 reductase	0.000	0.000	0.000	0.000	0.071	0.000	0.043	0.058	0.000	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META1_4390	putative Ferredoxin; putative 4Fe-4S ferredoxins domai	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4392	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.000	0.047	0.107	0.077	0.099	0.000	0.020	0.094	n.d.	0.00	7.00	0.15
META1_4393	aspartate tRNA synthetase	1.363	1.110	1.509	1.488	1.924	1.252	1.564	1.353	1.052	1.315	1.572	1.317	1.35	0.96	1.26	0.40
META1_4394	biotin synthetase	0.000	0.000	0.000	0.135	0.143	0.213	0.257	0.174	0.099	0.000	0.171	0.175	n.d.	0.00	1.53	0.94
META1_4395	protein of unknown function; putative exported protein	0.117	0.227	0.198	0.000	0.000	0.000	0.000	0.000	0.000	0.191	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_4396	2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase/5-carb	0.584	0.498	0.297	0.406	0.000	0.213	0.236	0.348	0.357	0.445	0.151	0.316	0.96	0.21	3.13	0.38
META1_4397	putative long-chain fatty acid outer membrane transpo	0.701	0.408	0.544	0.947	0.190	0.402	0.514	0.329	0.417	0.526	0.393	0.417	1.07	0.26	1.59	0.99
META1_4398	conserved protein of unknown function; putative preph	0.000	0.000	0.000	0.000	0.214	0.142	0.000	0.058	0.000	0.000	0.151	0.020	n.d.	0.37	0.20	0.59
META1_4400	conserved protein of unknown function, putative Fe-S c	0.000	0.136	0.272	0.000	0.261	0.118	0.171	0.213	0.159	0.154	0.161	0.181	1.59	0.36	1.69	0.38
META1_4403	50S ribosomal subunit protein L10	1.830	1.654	1.386	2.705	2.874	2.457	2.228	2.242	3.116	1.597	2.671	2.534	2.14	0.03	1.42	0.60
META1_4404	50S ribosomal subunit protein L7/L12	1.480	1.767	2.450	3.855	2.304	3.048	0.964	1.856	2.044	1.950	2.853	1.640	1.13	0.54	0.86	0.08
META1_4405	RNA polymerase, beta subunit	7.865	8.021	9.427	17.787	13.302	12.168	10.519	10.592	11.591	8.500	13.486	10.907	1.73	0.02	1.21	0.09
META1_4406	RNA polymerase, beta prime subunit	6.697	8.361	9.452	16.773	11.425	11.199	10.155	9.549	10.182	8.373	12.126	9.953	1.60	0.11	1.23	0.12
META1_4408	putrescine transporter subunit: periplasmic-binding cor	0.117	0.181	0.124	0.135	0.166	0.165	0.129	0.077	0.060	0.145	0.161	0.087	0.81	0.13	0.81	0.06
META1_4409	conserved protein of unknown function	0.000	0.136	0.124	0.000	0.048	0.000	0.000	0.058	0.099	0.100	0.020	0.054	0.73	0.94	4.00	0.55
META1_4411	conserved protein of unknown function	0.000	0.068	0.074	0.000	0.000	0.000	0.086	0.116	0.060	0.054	0.000	0.087	2.17	0.40	n.d.	0.00
META1_4413	conserved protein of unknown function	0.000	0.045	0.099	0.000	0.000	0.000	0.000	0.000	0.040	0.054	0.000	0.013	0.33	0.55	n.d.	0.37
META1_4414	putative glutathione S-transferase	0.156	0.091	0.074	0.135	0.190	0.118	0.171	0.213	0.099	0.100	0.151	0.161	2.18	0.26	1.60	0.84
META1_4416	polynucleotide phosphorylase/polyadenylase	5.529	4.917	5.196	7.169	6.057	6.734	5.442	4.639	4.942	5.162	6.511	4.993	1.31	0.51	1.15	0.01
META1_4417	30S ribosomal subunit protein S15	0.312	0.272	0.544	0.473	0.570	0.543	0.471	0.406	0.536	0.381	0.544	0.470	1.67	0.31	1.30	0.29
META1_4420	Exodeoxyribonuclease III (Exonuclease III) (EXO III) (AP e	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.040	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_4421	putative activator of photopigment and puc with BLUF	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.040	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META1_4423	conserved protein of unknown function; putative expor	0.000	0.091	0.099	0.135	0.428	0.307	0.193	0.174	0.218	0.073	0.333	0.195	3.63	0.49	0.88	0.44
META1_4424	Cell division protein	0.000	0.204	0.223	0.000	0.641	0.473	0.386	0.425	0.456	0.163	0.474	0.423	3.50	0.49	1.34	0.33
META1_4425	NAD(+) synthase (glutamine-hydrolyzing) with a nitrilas	0.389	0.363	0.594	0.338	0.261	0.189	0.407	0.503	0.456	0.454	0.242	0.457	1.36	0.84	2.83	0.03
META1_4428	putative transport transmembrane protein, AmpG	0.000	0.091	0.099	0.000	0.071	0.000	0.043	0.039	0.040	0.073	0.030	0.040	0.75	0.27	2.00	0.09
META1_4429	conserved protein of unknown function	0.156	0.045	0.099	0.000	0.095	0.047	0.214	0.155	0.119	0.091	0.060	0.161	2.40	0.22	4.00	0.51
META1_4432	protein of unknown function	0.273	0.249	0.124	0.473	0.356	0.425	0.493	0.290	0.258	0.209	0.403	0.343	2.22	0.20	1.28	0.36
META1_4433	GTP-binding protein EngA, GTPase	0.000	0.249	0.198	0.135	0.404	0.354	0.279	0.135	0.198	0.172	0.343	0.202	1.58	0.36	0.88	0.48
META1_4435	conserved protein of unknown function, putative carbo	0.000	0.068	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_4436	Formamidopyrimidine-DNA glycosylase (Fapy-DNA glyc	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4441	putative hybrid histidine kinase with multiple PAS and a	0.078	0.227	0.247	0.812	0.309	0.354	0.471	0.387	0.238	0.200	0.403	0.363	2.45	0.14	1.35	0.55
META1_4442	putative glutathione S-transferase	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4443	conserved protein of unknown function	0.000	0.204	0.124	0.000	0.000	0.000	0.064	0.039	0.079	0.127	0.000	0.060	0.64	0.25	n.d.	0.00
META1_4445	UvrABC system protein B (UvrB protein) (Excinuclease A	0.000	0.136	0.148	0.000	0.404	0.142	0.279	0.387	0.357	0.109	0.232	0.343	4.25	0.52	2.22	0.43
META1_4453	conserved protein of unknown function, ankyrin repeat	0.000	0.136	0.049	0.000	0.261	0.118	0.257	0.135	0.218	0.073	0.161	0.202	3.75	0.51	1.88	0.39
META1_4455	glycerol kinase	0.000	0.113	0.099	0.000	0.000	0.047	0.107	0.174	0.079	0.082	0.020	0.121	2.00	0.39	9.00	0.16
META1_4456	putative hydrolase	0.156	0.408	0.470	0.744	0.523	0.638	0.129	0.251	0.238	0.372	0.605	0.208	0.76	0.33	0.52	0.01
META1_4457	putative methyl-accepting chemotaxis sensory transduc	0.000	0.000	0.000	0.135	0.000	0.000	0.171	0.058	0.179	0.000	0.020	0.134	n.d.	0.00	10.00	0.11
META1_4458	putative glycerophosphoryl diester phosphodiesterase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.077	0.099	0.000	0.000	0.074	n.d.	0.00	n.d.	0.00
META1_4459	Endoribonuclease L-PSP	0.273	0.272	0.148	0.203	0.166	0.095	0.214	0.213	0.198	0.227	0.141	0.208	1.24	0.76	2.21	0.21
META1_4460	putative bacteriocin/pheromone secretion/processing A	0.000	0.000	0.099	0.000	0.261	0.284	0.129	0.387	0.198	0.036	0.232	0.242	9.00	0.16	1.57	0.34
META1_4461	putative secretion protein	0.000	0.000	0.000	0.000	0.119	0.142	0.000	0.000	0.000	0.000	0.111	0.000	n.d.	n.d.	0.00	0.12
META1_4464	succinylornithine transaminase, also has acetylornitine	0.973	0.884	0.742	0.744	0.760	1.016	0.686	0.715	0.556	0.853	0.867	0.652	1.03	0.06	1.13	0.12
META1_4465	ornithine carbamoyltransferase	0.584	0.431	0.520	0.947	0.736	0.969	0.707	0.619	0.655	0.499	0.867	0.659	1.78	0.05	1.14	0.04
META1_4467	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4468	conserved protein of unknown function (putative Glyox	0.000	0.045	0.000	0.000	0.071	0.071	0.000	0.039	0.060	0.018	0.060	0.034	2.50	0.52	0.83	0.96
META1_4469	putative 3-ketoacyl-acyl carrier protein reductase (fabG	0.078	0.000	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_4471	putative Bacteriophytochrome (light-regulated signal tr	0.506	0.816	1.163	0.609	0.713	0.449	0.557	0.445	0.536	0.871	0.585	0.511	0.79	0.16	1.31	0.45
META1_4472	putative Heme oxygenase (BphO-like)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.099	0.000	0.000	0.034	n.d.	0.37	n.d.	0.37
META1_4475	Putative capsule polysaccharide export inner-membran	0.000	0.000	0.000	0.000	0.143	0.071	0.000	0.000	0.000	0.000	0.091	0.000	n.d.	n.d.	0.00	0.12
META1_4476	protein of unknown function	0.000	0.091	0.049	0.000	0.071	0.000	0.000	0.077	0.079	0.054	0.030	0.054	1.33	0.98	2.67	0.52
META1_4478	two-component flagellar sigma-54 dependent transcrip	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.039	0.040	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META1_4481	Flagellar motor switch protein	0.000	0.000	0.000	0.000	0.119	0.095	0.086	0.058	0.079	0.000	0.091	0.074	n.d.	0.00	1.22	0.33
META1_4483	conserved protein of unknown function	0.000	0.113	0.124	0.271	0.143	0.165	0.086	0.155	0.198	0.091	0.171	0.148	2.20	0.40	1.29	0.40
META1_4486	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltra	0.000	0.000	0.000	0.000	0.166	0.165	0.000	0.116	0.060	0.000	0.141	0.060	n.d.	0.12	0.64	0.92
META1_4487	putative phosphatidylethanolamine-N-methyltransfera	0.389	0.249	0.297	0.676	0.475	0.307	0.621	0.503	0.437	0.299	0.433	0.517	2.33	0.04	1.79	0.69
META1_4489	putative integral membrane sensor signal transduction	0.000	0.000	0.000	0.000	0.071	0.000	0.064	0.000	0.040	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META1_4490	Carbonic anhydrase	0.000	0.045	0.124	0.203	0.095	0.095	0.193	0.213	0.159	0.064	0.111	0.188	4.00	0.52	2.55	0.19
META1_4493	transcriptional regulator, TetR family	0.078	0.091	0.000	0.000	0.119	0.118	0.086	0.116	0.099	0.054	0.101	0.101	2.50	0.40	1.50	0.35
META1_4494	acyl-CoA dehydrogenase	0.117	0.249	0.272	0.271	0.380	0.260	0.300	0.271	0.278	0.227	0.312	0.282	1.68	0.27	1.35	0.67
META1_4495	conserved protein of unknown function, Sua5/YciO/Yrd	0.000	0.045	0.000	0.135	0.190	0.071	0.150	0.116	0.139	0.018	0.131	0.134	10.00	0.17	1.54	0.77
META1_4496	putative hybrid histidine kinase; HK, ATPase, PAS and a	0.000	0.091	0.148	0.135	0.190	0.047	0.193	0.213	0.179	0.091	0.121	0.195	2.90	0.45	2.42	0.23
META1_4497	thiol disulfide isomerase	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_4498	thiol disulfide isomerase	0.000	0.136	0.000	0.000	0.166	0.142	0.086	0.097	0.119	0.054	0.131	0.101	2.50	0.10	1.15	0.32
META1_4499	RecA-superfamily ATPase implicated in signal transduct	0.078	0.249	0.297	0.135	0.309	0.095	0.236	0.271	0.298	0.227	0.192	0.269	1.60	0.40	2.11	0.22
META1_4502	putative phoP: DNA-binding response regulator in two-	0.000	0.000	0.000	0.000	0.071	0.118	0.193	0.116	0.119	0.000	0.081	0.141	n.d.	0.00	2.63	0.44
META1_4503	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.071	0.000	0.000	0.000	0.040	0.036	0.030	0.013	0.50	0.96	0.67	0.97
META1_4505	protein of unknown function	0.000	0.000	0.074	0.000	0.000	0.000	0.064	0.039	0.060	0.027	0.000	0.054	2.67	0.10	n.d.	0.00
META1_4507	conserved protein of unknown function, putative memb	0.078	0.068	0.124	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_4509	putative TonB-dependent siderophore receptor	1.791	0.000	0.148	1.691	0.214	0.331	0.064	0.000	0.040	0.472	0.484	0.034	0.10	0.73	0.10	0.78
META1_4513	putative Phosphomannomutase/phosphoglucomutase	0.156	0.227	0.247	0.000	0.119	0.118	0.171	0.193	0.119	0.218	0.101	0.161	1.00	0.26	2.40	0.42
META1_4525	MxaB	0.234	0.340	0.346	0.541	0.285	0.449	0.321	0.677	0.476	0.318	0.393	0.497	2.11	0.15	1.90	0.66
META1_4526	MxaH	0.195	0.159	0.124	0.135	0.119	0.142	0.193	0.329	0.179	0.154	0.131	0.235	2.06	0.19	2.69	0.05
META1_4527	MxaE	0.273	0.204	0.223	0.406	0.000	0.118	0.214	0.309	0.179	0.227	0.111	0.235	1.40	0.94	3.18	0.38
META1_4528	MxaD protein precursor	0.779	0.521	0.396	0.609	0.499	0.260	0.514	0.696	0.794	0.535	0.413	0.672	1.69	0.46	2.44	0.21
META1_4529	MxaL protein precursor	0.156	0.136	0.124	0.338	0.071	0.071	0.000	0.077	0.000	0.136	0.111	0.027	0.27	0.14	0.36	0.14
META1_4530	MxaK protein	0.350	0.340	0.272	0.609	0.261	0.260	0.343	0.503	0.238	0.318	0.312	0.363	1.54	0.75	1.74	0.99
META1_4531	MxaC protein	0.156	0.091	0.074	0.271	0.333	0.260	0.214	0.193	0.278	0.100	0.292	0.228	3.09	0.03	1.17	0.15
META1_4532	MxaA protein	0.350	0.272	0.247	0.203	0.000	0.260	0.300	0.271	0.198	0.281	0.141	0.255	1.23	0.48	2.71	0.39
META1_4533	MxaS protein, involved in methanol oxidation	0.000	0.045	0.074	0.271	0.261	0.213	0.257	0.232	0.139	0.045	0.242	0.208	6.20	0.57	1.29	0.39
META1_4534	Protein MxaR (Protein MoxR)	0.740	0.453	0.470	1.556	0.831	1.063	0.964	0.889	0.734	0.526	1.038	0.860	2.21	0.06	1.24	0.26
META1_4535	Methanol dehydrogenase subunit 2 precursor (MDH sm	0.156	0.227	0.396	1.488	0.261	0.354	0.943	0.638	1.171	0.272	0.484	0.914	4.53	0.02	2.83	0.39
META1_4536	Cytochrome c-L precursor.	0.818	0.770	0.718	1.961	0.808	0.543	0.621	0.638	0.834	0.762	0.867	0.699	1.24	0.36	1.21	0.46
META1_4537	MxaJ	3.621	2.243	2.202	6.831	0.974	2.481	2.635	2.919	2.997	2.549	2.490	2.856	1.51	0.64	1.72	0.85
META1_4538	Methanol dehydrogenase subunit 1 precursor (MDH lar	10.124	8.293	8.611	20.222	13.349	11.931	13.690	14.632	13.734	8.836	13.769	14.032	2.14	0.00	1.53	0.76
META1_4539	conserved exported protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4540	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4544	putative glmU-like gene; bifunctional: N-acetyl glucosar	0.428	0.521	0.445	0.406	0.594	0.473	0.686	0.735	0.635	0.472	0.514	0.685	1.96	0.01	2.00	0.04
META1_4546	L-glutamine:D-fructose-6-phosphate aminotransferase	1.441	1.473	1.880	0.812	1.211	0.543	1.114	1.044	1.052	1.615	0.867	1.069	0.89	0.01	1.85	0.30
META1_4547	conserved protein of unknown function, DUF336	0.779	0.317	0.223	0.879	0.404	0.260	0.557	0.503	0.476	0.390	0.413	0.511	1.77	0.48	1.85	0.75
META1_4548	conserved protein of unknown function; putative memb	0.000	0.136	0.124	0.000	0.071	0.071	0.129	0.077	0.060	0.100	0.060	0.087	1.18	0.32	2.17	0.40
META1_4550	DNA helicase, ATP-dependent resolution of Holliday jun	0.000	0.113	0.148	0.000	0.166	0.142	0.171	0.193	0.119	0.100	0.131	0.161	2.18	0.40	1.85	0.38

META1_4551	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.000	0.079	0.000	0.020	0.047	n.d.	0.12	3.50	0.54
META1_4552	transcription repair coupling protein, ATP-dependent he	0.273	0.589	0.841	1.014	1.544	1.016	1.157	1.218	1.270	0.608	1.240	1.216	2.70	0.06	1.47	0.80
META1_4553	DNA-binding transcriptional repressor	0.000	0.000	0.000	0.271	0.000	0.000	0.000	0.000	0.040	0.000	0.040	0.013	n.d.	0.37	0.50	0.89
META1_4554	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.079	0.000	0.000	0.054	n.d.	0.00	n.d.	0.00
META1_4557	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.043	0.077	0.040	0.000	0.060	0.054	n.d.	0.00	1.33	0.33
META1_4560	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4561	putative AMP-dependent synthetase/acyl-CoA ligase	0.000	0.091	0.000	0.000	0.000	0.000	0.086	0.174	0.179	0.036	0.000	0.148	5.50	0.14	n.d.	0.00
META1_4562	protein of unknown function	0.156	0.159	0.247	0.000	0.095	0.118	0.086	0.097	0.159	0.191	0.091	0.114	0.81	0.10	1.89	0.38
META1_4564	glycosyl transferase	0.000	0.045	0.049	0.000	0.000	0.047	0.000	0.039	0.060	0.036	0.020	0.034	1.25	1.00	2.50	0.52
META1_4565	conserved protein of unknown function; putative Lipid	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4567	putative flavin-binding monooxygenase	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.039	0.079	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_4568	putative Acetyl-hydrolase	0.000	0.068	0.049	0.000	0.048	0.047	0.107	0.193	0.099	0.045	0.040	0.134	4.00	0.49	5.00	0.52
META1_4569	Short-chain dehydrogenase/reductase SDR ; putative ex	0.000	0.091	0.074	0.000	0.095	0.047	0.086	0.193	0.139	0.064	0.060	0.141	3.00	0.45	3.50	0.48
META1_4570	conserved protein of unknown function	0.000	0.045	0.148	0.000	0.071	0.095	0.171	0.174	0.179	0.073	0.071	0.175	3.25	0.49	3.71	0.49
META1_4576	putative metal-dependent hydrolase	0.117	0.181	0.099	0.135	0.000	0.047	0.193	0.251	0.139	0.136	0.040	0.195	1.93	0.19	7.25	0.51
META1_4577	putative metallo-dependent hydrolase, putative deoxyr	0.117	0.227	0.148	0.676	0.238	0.331	0.193	0.135	0.179	0.172	0.343	0.168	1.32	0.81	0.74	0.07
META1_4578	methionyl-tRNA synthetase	0.545	0.838	0.990	0.406	0.689	0.591	0.728	0.870	0.754	0.826	0.605	0.786	1.29	0.93	1.95	0.10
META1_4579	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.116	0.179	0.000	0.000	0.148	n.d.	0.00	n.d.	0.00
META1_4581	DNA polymerase III, delta prime subunit	0.000	0.068	0.099	0.000	0.071	0.071	0.043	0.000	0.000	0.064	0.060	0.013	0.29	0.56	0.33	0.55
META1_4582	thymidylate kinase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.077	0.079	0.000	0.000	0.067	n.d.	0.00	n.d.	0.00
META1_4585	putrescine transporter, ATP-binding component of ABC	0.000	0.068	0.074	0.000	0.119	0.165	0.043	0.058	0.060	0.054	0.121	0.054	1.33	0.34	0.67	0.25
META1_4590	protein of unknown function	0.000	0.091	0.074	0.000	0.190	0.213	0.150	0.155	0.119	0.064	0.171	0.141	3.00	0.45	1.24	0.32
META1_4593	putative transcriptional regulator, GntR family	0.000	0.091	0.000	0.000	0.000	0.071	0.107	0.097	0.159	0.036	0.030	0.121	4.50	0.13	6.00	0.14
META1_4594	hydroxypyruvate isomerase	0.000	0.068	0.000	0.000	0.000	0.000	0.043	0.000	0.099	0.027	0.000	0.047	2.33	0.52	n.d.	0.12
META1_4595	putative glucose dehydrogenase, NAD(P)-binding doma	0.506	0.612	0.421	0.000	0.000	0.165	0.214	0.135	0.218	0.517	0.071	0.188	0.49	0.01	4.00	0.12
META1_4596	putative D-lactate dehydrogenase (cytochrome)	0.000	0.068	0.074	0.000	0.000	0.000	0.386	0.387	0.258	0.054	0.000	0.343	8.50	0.64	n.d.	0.00
META1_4598	succinate-semialdehyde dehydrogenase I, NADP-depen	1.246	1.563	1.287	0.609	0.784	0.945	0.771	0.793	1.012	1.388	0.827	0.860	0.84	0.01	1.56	0.53
META1_4599	protein of unknown function	0.000	0.000	0.000	0.541	0.000	0.118	0.000	0.193	0.000	0.000	0.131	0.067	n.d.	0.37	0.77	0.54
META1_4603	putative flagellar motor switch protein FliN	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_4604	Lipoyltransferase (Lipoyl-[acyl-carrier protein]-protein-	0.000	0.000	0.049	0.000	0.095	0.142	0.150	0.116	0.179	0.018	0.101	0.148	11.00	0.17	2.20	0.41
META1_4605	putative glycosyl transferase	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.039	0.099	0.000	0.000	0.094	n.d.	0.00	n.d.	0.00
META1_4608	putative response regulator receiver	0.000	0.091	0.000	0.000	0.000	0.000	0.043	0.000	0.099	0.036	0.000	0.047	1.75	0.50	n.d.	0.12
META1_4610	putative hybrid histidine kinase; Domains: two PAS, two	0.000	0.204	0.173	0.000	0.166	0.142	0.257	0.174	0.060	0.145	0.131	0.161	1.50	0.34	1.85	0.36
META1_4613	two-component response regulator	0.078	0.113	0.223	0.000	0.000	0.118	0.193	0.155	0.099	0.145	0.050	0.148	1.38	0.73	4.40	0.13
META1_4614	putative GCN5-related N-acetyltransferase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_4615	conserved protein of unknown function; putative memb	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.060	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_4616	glycolate permease (LctP family)	0.000	0.159	0.074	0.000	0.048	0.095	0.150	0.193	0.218	0.091	0.060	0.188	2.80	0.46	4.67	0.53
META1_4617	Manganese catalase	0.000	0.272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4618	terpenoid synthase, putative phytoene synthase	0.195	0.091	0.099	0.203	0.000	0.142	0.407	0.483	0.318	0.118	0.091	0.403	4.62	0.01	6.67	0.52
META1_4619	conserved protein of unknown function	0.000	0.068	0.124	0.000	0.095	0.071	0.150	0.193	0.278	0.073	0.071	0.208	3.88	0.50	4.43	0.51
META1_4620	putative protein-export membrane protein, SecD/SecF	0.195	0.181	0.173	0.338	0.190	0.165	0.343	0.271	0.258	0.181	0.202	0.289	2.15	0.01	2.15	0.32
META1_4621	putative protein-export membrane protein, SecD/SecF	0.896	1.088	0.990	0.271	1.211	1.087	1.500	1.121	1.151	1.007	1.018	1.250	1.68	0.10	1.84	0.31
META1_4622	preprotein translocase, auxillary membrane component	0.234	0.227	0.346	0.473	0.356	0.213	0.236	0.232	0.496	0.272	0.312	0.323	1.60	0.67	1.55	0.80
META1_4623	conserved protein of unknown function, ATPase family	0.234	0.272	0.272	0.609	0.641	0.614	0.471	0.464	0.357	0.263	0.625	0.430	2.21	0.01	1.03	0.01
META1_4624	putative protein precursor, N-terminal membrane lipop	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.058	0.000	0.000	0.020	0.040	n.d.	0.12	3.00	0.53
META1_4626	5'-nucleotidase surE (Nucleoside 5'-monophosphate ph	0.467	0.408	0.297	0.406	0.238	0.354	0.214	0.348	0.238	0.381	0.312	0.269	0.95	0.12	1.29	0.37
META1_4627	serine tRNA synthetase; also charges selenocystein tRN	0.701	0.612	0.569	0.609	1.140	0.662	0.557	0.619	0.635	0.617	0.857	0.605	1.32	0.64	1.06	0.29
META1_4630	putative transcriptional regulator, MarR family	0.000	0.181	0.124	0.338	0.261	0.165	0.364	0.348	0.318	0.118	0.232	0.343	3.92	0.51	2.22	0.19
META1_4632	putative enoyl-CoA hydratase/isomerase family protein	0.234	0.136	0.148	0.000	0.380	0.402	0.171	0.193	0.099	0.163	0.333	0.155	1.28	0.67	0.70	0.24
META1_4633	porphobilinogen synthase	0.428	0.521	0.322	0.203	0.475	0.520	0.386	0.387	0.337	0.426	0.454	0.370	1.17	0.47	1.22	1.00
META1_4635	protein of unknown function; putative membrane prote	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.119	0.000	0.020	0.040	n.d.	0.37	3.00	0.95
META1_4638	conserved protein of unknown function, putative transc	0.000	0.159	0.148	0.000	0.071	0.142	0.000	0.000	0.139	0.118	0.091	0.047	0.54	0.53	0.78	0.50
META1_4639	maltose o-acetyltransferase	0.078	0.068	0.074	0.000	0.048	0.000	0.064	0.077	0.060	0.073	0.020	0.067	1.25	0.34	5.00	0.13
META1_4640	conserved protein of unknown function	0.467	0.249	0.223	0.000	0.000	0.142	0.064	0.174	0.139	0.290	0.060	0.128	0.59	0.07	3.17	0.11
META1_4641	putative phage DNA polymerase	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4642	electron transfer flavoprotein ubiquinone oxidoreducta	0.623	0.884	0.792	0.676	1.259	0.709	0.707	0.599	0.794	0.789	0.937	0.699	1.20	0.55	1.12	0.42
META1_4646	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4647	cystathionine beta-lyase, PLP-dependent (beta-cystathi	0.000	0.000	0.099	0.135	0.214	0.165	0.150	0.155	0.198	0.036	0.181	0.168	6.25	0.14	1.39	0.94
META1_4648	putative zink-containing alcohol dehydrogenase	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4653	putative sensor hybrid histidine kinase with multiple PA	0.000	0.159	0.148	0.000	0.166	0.047	0.107	0.155	0.198	0.118	0.091	0.155	1.77	0.37	2.56	0.45
META1_4654	putative glycosyl transferase, family 2	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.040	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_4658	small heat shock protein	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4660	DNA mismatch repair protein mutL	0.000	0.000	0.000	0.000	0.095	0.095	0.064	0.077	0.000	0.000	0.081	0.047	n.d.	0.12	0.88	0.97
META1_4661	putative Short-chain specific acyl-CoA dehydrogenase	0.312	0.272	0.247	0.000	0.000	0.071	0.064	0.039	0.119	0.272	0.030	0.074	0.37	0.01	3.67	0.11
META1_4662	putative ATP-binding protein with two ATPase domains	0.000	0.091	0.173	0.203	0.285	0.095	0.236	0.329	0.159	0.100	0.192	0.242	3.27	0.47	1.89	0.52
META1_4664	Alpha/beta hydrolase related	0.078	0.227	0.099	0.000	0.119	0.047	0.150	0.135	0.159	0.145	0.071	0.148	1.38	0.57	3.14	0.48
META1_4665	putative deaminase reductase domain-containing prote	0.156	0.181	0.223	0.000	0.000	0.000	0.107	0.097	0.139	0.191	0.000	0.114	0.81	0.03	n.d.	0.00
META1_4667	conserved protein of unknown function, DUF336	0.117	0.249	0.223	0.676	0.428	0.284	0.300	0.329	0.417	0.209	0.403	0.349	2.26	0.07	1.30	0.44
META1_4672	Major facilitator superfamily MFS-1, putative sugar tran	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4674	conserved protein of unknown function	0.857	0.612	0.346	0.812	0.380	0.662	0.600	0.638	0.675	0.572	0.564	0.638	1.51	0.68	1.70	0.75
META1_4676	WrbA protein, flavodoxin-like domain, trp repressor-bin	0.467	0.272	0.247	0.135	0.095	0.118	0.171	0.193	0.040	0.308	0.111	0.134	0.59	0.12	1.82	0.93
META1_4677	putative thiol:disulfide interchange protein precursor	0.195	0.340	0.371	0.203	0.095	0.095	0.150	0.271	0.218	0.318	0.111	0.215	0.91	0.27	2.91	0.16
META1_4678	DNA mismatch repair protein mutS	0.000	0.045	0.124	0.000	0.641	0.378	0.364	0.445	0.357	0.064	0.433	0.390	8.29	0.66	1.35	0.34
META1_4679	protein of unknown function; putative membrane prote	0.428	0.702	0.297	0.000	0.095	0.118	0.150	0.058	0.099	0.490	0.091	0.101	0.28	0.01	1.67	0.36
META1_4680	helicase, ATP-dependent	0.000	0.045	0.000	0.135	0.190	0.118	0.150	0.077	0.079	0.018	0.151	0.101	7.50	0.15	1.00	0.20
META1_4682	protein of unknown function; putative exported protein	0.000	0.000	0.074	0.000	0.048	0.047	0.000	0.000	0.040	0.027	0.040	0.013	0.67	0.97	0.50	0.53
META1_4683	putative lactoylglutathione lyase	0.000	0.136	0.074	0.000	0.071	0.000	0.000	0.058	0.060	0.082	0.030	0.040	0.67	0.94	2.00	0.51
META1_4686	putative phosphoglycerate mutase	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_4687	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4688	MOSC domain protein, YiiM-like protein	0.000	0.045	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.018	0.000	0.020	1.50	0.98	n.d.	0.37
META1_4689	Enoyl-[acyl-carrier-protein] reductase (NADH)	1.051	0.634	0.619	1.217	0.594	0.969	0.857	0.657	0.774	0.726	0.847	0.759	1.41	0.93	1.35	0.52
META1_4690	Chaperone DnaJ domain protein, putative heat shock p	0.195	0.227	0.198	0.406	0.333	0.307	0.257	0.483	0.476	0.209	0.333	0.410	2.65	0.04	1.85	0.62
META1_4692	pyridoxine 5'-phosphate oxidase	0.000	0.091	0.074	0.000	0.095	0.095	0.193	0.097	0.099	0.064	0.081	0.128	2.71	0.43	2.38	0.41
META1_4694	Short-chain dehydrogenase/reductase SDR	0.545	0.521	0.371	0.812	0.214	0.284	0.536	0.425	0.318	0.472	0.333	0.423	1.21	0.55	1.91	0.78
META1_4695	conserved protein of unknown function; putative expor	0.117	0.363	0.223	0.000	0.071	0.118	0.129	0.097	0.099	0.254	0.081	0.108	0.57	0.12	2.00	0.40
META1_4696	putative GDP-mannose mannosyl hydrolase (nudD)	0.000	0.136	0.049	0.000	0.000	0.000	0.043	0.039	0.040	0.073	0.000	0.040	0.75	0.29	n.d.	0.00
META1_4697	conserved protein of unknown function	0.078	0.113	0.049	0.000	0.095	0.000	0.000	0.077	0.079	0.082	0.040	0.054	0.89	0.37	2.00	0.51
META1_4700	putative dihydroorotase-like protein	0.506	0.453	0.297	0.203	0.475	0.709	0.300	0.406	0.298	0.408	0.534	0.336	1.11	0.33	0.94	0.61
META1_4701	Glycine cleavage T protein (aminomethyl transferase)	0.428	0.408	0.371	0.271	0.071	0.189	0.364	0.387	0.397	0.399	0.151	0.383	1.30	0.37	3.80	0.08
META1_4702	3-methyl-adenine DNA glycosylase I	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4703	Metal-dependent phosphohydrolase	0.000	0.045	0.099	0.000	0.119	0.095	0.043	0.039	0.119	0.054	0.091	0.067	1.67	0.36	1.11	0.30
META1_4704	conserved protein of unknown function; putative phosp	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.097	0.060	0.000	0.000	0.087	n.d.	0.00	n.d.	0.00
META1_4705	exodeoxyribonuclease VII small subunit (exonuclease V	0.000	0.068	0.074	0.000	0.166	0.142	0.129	0.097	0.179	0.054	0.131	0.134	3.33	0.46	1.54	0.35
META1_4706	1-deoxy-D-xylulose-5-phosphate synthase	1.519	1.699	1.683	1.488	1.710	1.134	1.778	1.604	1.528	1.651	1.431	1.633	1.34	0.98	1.71	0.35
META1_4707	Superoxide dismutase [Cu-Zn] precursor	0.350	0.159	0.099	0.203	0.000	0.165	0.086	0.058	0.060	0.181	0.101	0.067	0.50	0.07	1.00	0.25
META1_4708	hemolysin	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4709	23S rRNA (Uracil-5-)-methyltransferase	0.000	0.000	0.000	0.000	0.333	0.260	0.107	0.155	0.099	0.000	0.252	0.121	n.d.	0.00	0.72	0.25
META1_4710	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.071	0.043	0.039	0.000	0.000	0.060	0.027	n.d.	0.12	0.67	0.94
META1_4711	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META1_4712	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.039	0.000	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_4713	conserved protein of unknown function	0.078	0.181	0.124	0.000	0.071	0.047	0.064	0.058	0.060	0.136	0.050	0.060	0.60	0.05	1.80	0.38
META1_4714	Amidohydrolase	0.740	0.589	0.544	0.203	0.309	0.425	0.279	0.348	0.258	0.608	0.343	0.296	0.66	0.00	1.29	0.93
META1_4715	fused DNA-binding transcriptional dual regulator ; O6-m	0.000	0.000	0.000	0.203	0.119	0.331	0.043	0.058	0.000	0.000	0.222	0.034	n.d.	0.12	0.23	0.59
META1_4716	putative cation transport protein	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4717	putative histidine triad family protein, putative nucleos	0.195	0.204	0.000	0.271	0.214	0.284	0.257	0.193	0.318	0.127	0.252	0.255	2.71	0.41	1.52	0.94
META1_4718	conserved protein of unknown function	0.000	0.113	0.000	0.000	0.119	0.000	0.150	0.174	0.119	0.045	0.050	0.148	4.40	0.13	4.40	0.13
META1_4722	putative N-acetylglucosamine-6-phosphate deacetylase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4723	putative Glucosamine-fructose-6-phosphate aminotran	0.000	0.136	0.049	0.000	0.048	0.000	0.043	0.000	0.040	0.073	0.020	0.027	0.50	0.93	2.00	0.51
META1_4724	putative sugar phosphate isomerase (SIS); putative regu	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4726	putative periplasmic L-asparaginase (ansB)	0.312	0.363	0.297	0.338	0.285	0.284	0.064	0.058	0.079	0.327	0.292	0.067	0.28	0.00	0.34	0.00
META1_4730	putative surfeit locus 1 family protein (surf1-like)	0.000	0.159	0.074	0.000	0.000	0.047	0.043	0.000	0.000	0.091	0.020	0.013	0.20	0.58	1.00	0.99
META1_4732	cytochrome o ubiquinol oxidase, subunit III	0.234	0.000	0.000	0.000	0.119	0.047	0.000	0.000	0.000	0.054	0.071	0.000	0.00	0.37	0.00	0.12
META1_4733	cytochrome o ubiquinol oxidase, subunit I	0.312	0.566	0.668	0.000	0.309	0.213	0.064	0.232	0.000	0.544	0.222	0.101	0.25	0.62	0.68	0.91
META1_4734	cytochrome o ubiquinol oxidase subunit II	1.402	0.770	0.742	0.271	0.546	0.496	0.300	0.174	0.139	0.907	0.484	0.202	0.30	0.01	0.63	0.07
META1_4735	MFS transporter membrane protein	0.428	0.770	0.841	0.203	0.356	0.354	0.129	0.058	0.139	0.717	0.333	0.108	0.20	0.01	0.48	0.03
META1_4736	RND efflux transporter, AcrB/AcrD/AcrF family	0.506	0.634	0.643	0.271	0.784	0.425	0.257	1.024	0.456	0.608	0.554	0.591	1.31	0.68	1.60	0.86
META1_4737	RND efflux transporter, membrane fusion protein subu	0.234	0.091	0.074	0.338	0.309	0.236	0.107	0.271	0.079	0.118	0.282	0.155	1.77	0.82	0.82	0.11
META1_4738	RND efflux transporter, membrane fusion protein subu	0.234	0.091	0.148	0.406	0.404	0.307	0.000	0.329	0.060	0.145	0.363	0.134	1.25	0.39	0.56	0.54
META1_4739	putative transcriptional regulator, TetR family	0.000	0.091	0.000	0.000	0.143	0.142	0.107	0.174	0.159	0.036	0.121	0.148	5.50	0.14	1.83	0.38
META1_4765	putative phage repressor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4778	protein of unknown function; putative membrane prote	0.350	0.249	0.297	0.000	0.119	0.095	0.171	0.116	0.099	0.290	0.091	0.128	0.59	0.01	2.11	0.40
META1_4788	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4792	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4798	protein of unknown function	0.000	0.000	0.000	0.000	0.143	0.095	0.086	0.135	0.099	0.000	0.101	0.108	n.d.	0.00	1.60	0.36

META1_4799	putative glycerate dehydrogenase (gyaR-like)	0.000	0.068	0.074	0.000	0.166	0.118	0.150	0.135	0.119	0.054	0.121	0.134	3.33	0.47	1.67	0.37
META1_4800	3-isopropylmalate isomerase, subunit with LeuD	0.000	0.181	0.223	0.203	1.021	0.685	0.493	0.425	0.456	0.154	0.756	0.457	4.00	0.52	0.91	0.80
META1_4805	putative transcriptional regulator, TetR family	0.000	0.000	0.000	0.000	0.071	0.047	0.086	0.097	0.079	0.000	0.050	0.087	n.d.	0.00	2.60	0.43
META1_4808	transcriptional regulator, TetR family	0.000	0.000	0.000	0.000	0.000	0.047	0.107	0.135	0.079	0.000	0.020	0.108	n.d.	0.00	8.00	0.15
META1_4809	conserved protein of unknown function; putative prote	0.000	0.091	0.000	0.000	0.119	0.142	0.129	0.116	0.119	0.036	0.111	0.121	4.50	0.13	1.64	0.36
META1_4811	Putative Zn-dependent protease	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_4813	Putative cyclic nucleotide-regulated FAD-dependent py	0.000	0.113	0.074	0.000	0.119	0.000	0.064	0.039	0.079	0.073	0.050	0.060	1.13	0.32	1.80	0.09
META1_4819	conserved protein of unknown function	0.467	0.181	0.074	0.406	0.095	0.118	0.043	0.058	0.119	0.209	0.151	0.074	0.48	0.17	0.73	0.17
META1_4820	putative ABC transporter, periplasmic protein; putative	0.312	0.317	0.272	0.812	0.071	0.331	0.364	0.464	0.456	0.299	0.292	0.430	1.94	0.02	2.21	0.55
META1_4821	Putative aliphatic sulfonates transport permease protei	0.000	0.000	0.000	0.135	0.190	0.118	0.086	0.077	0.099	0.000	0.151	0.087	n.d.	0.00	0.87	0.03
META1_4822	alkanesulfonate transporter subunit ; ATP-binding comp	0.000	0.068	0.000	0.203	0.000	0.260	0.171	0.116	0.139	0.027	0.141	0.141	7.00	0.15	1.50	0.31
META1_4823	conserved protein of unknown function	0.000	0.113	0.173	0.203	0.095	0.095	0.107	0.097	0.079	0.109	0.111	0.094	1.17	0.32	1.27	0.38
META1_4825	peptide chain release factor RF-3; GTP-binding factor	0.000	0.227	0.148	0.000	0.428	0.165	0.193	0.251	0.278	0.145	0.252	0.242	2.25	0.42	1.44	0.36
META1_4828	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4834	conserved protein of unknown function; putative ATP-c	1.635	2.062	2.351	1.623	1.900	1.843	2.121	1.817	1.806	2.068	1.834	1.909	1.25	0.73	1.56	0.40
META1_4837	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.079	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_4838	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_4840	putative Glucokinase (Glucose kinase)	0.428	0.363	0.173	0.135	0.285	0.213	0.364	0.290	0.258	0.308	0.232	0.302	1.32	0.99	1.96	0.17
META1_4841	putative trehalose-6-phosphate phosphatase (otsB)	0.078	0.113	0.099	0.271	0.000	0.071	0.129	0.039	0.139	0.100	0.071	0.101	1.36	0.86	2.14	0.32
META1_4842	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.086	0.058	0.000	0.000	0.020	0.047	n.d.	0.12	3.50	0.54
META1_4843	Beta-lactamase	0.117	0.159	0.297	0.271	0.261	0.354	0.193	0.135	0.298	0.200	0.302	0.208	1.41	0.76	1.03	0.19
META1_4846	NAD-dependent formate dehydrogenase, Molybdenum	0.000	0.000	0.000	0.000	0.119	0.000	0.386	0.329	0.357	0.000	0.050	0.356	n.d.	0.00	10.60	0.18
META1_4847	NAD-dependent formate dehydrogenase, Molybdenum	0.000	0.000	0.000	0.338	0.950	1.087	3.278	2.803	2.719	0.000	0.917	2.923	n.d.	0.00	4.78	0.02
META1_4848	NAD-dependent formate dehydrogenase, molybdenum	0.000	0.000	0.000	1.014	1.876	1.229	4.285	4.813	4.366	0.000	1.472	4.496	n.d.	0.00	4.58	0.00
META1_4849	NAD-linked formate dehydrogenase, Molybdenum cont	0.000	0.000	0.000	0.000	0.238	0.354	0.471	0.290	0.516	0.000	0.252	0.423	n.d.	0.00	2.52	0.43
META1_4850	transcriptional regulator, LysR family	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.077	0.060	0.000	0.000	0.081	n.d.	0.00	n.d.	0.00
META1_4851	protein of unknown function; putative exported protein	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4852	small GTP-binding protein, putative GTPase	0.195	0.204	0.124	0.135	0.641	0.662	0.300	0.367	0.218	0.172	0.575	0.296	2.32	0.07	0.77	0.62
META1_4853	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.039	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_4854	putative acetyltransferase, putative N-acetylase of ribos	0.117	0.113	0.148	0.000	0.119	0.236	0.171	0.193	0.159	0.127	0.151	0.175	1.86	0.03	1.73	0.38
META1_4855	50S ribosomal protein L27	0.584	0.476	0.569	0.541	0.689	1.016	0.814	0.580	0.834	0.535	0.806	0.739	1.86	0.09	1.38	0.96
META1_4856	50S ribosomal protein L21	0.623	0.385	0.322	0.406	0.428	0.331	0.793	0.483	0.853	0.417	0.383	0.706	2.28	0.14	2.76	0.04
META1_4857	putative enzyme with nucleoside triphosphate hydrolas	0.000	0.317	0.371	0.000	0.238	0.284	0.321	0.174	0.238	0.263	0.222	0.242	1.24	0.32	1.64	0.36
META1_4858	conserved protein of unknown function; putative doma	0.467	0.295	0.396	0.676	0.641	0.449	0.107	0.348	0.397	0.372	0.564	0.289	1.05	0.38	0.77	0.12
META1_4861	conserved protein of unknown function	0.117	0.000	0.000	0.000	0.000	0.000	0.107	0.000	0.060	0.027	0.000	0.054	2.67	0.49	n.d.	0.12
META1_4862	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_4863	Putative patatin-like phospholipase	0.662	0.000	0.173	0.271	0.143	0.307	0.129	0.116	0.079	0.218	0.232	0.108	0.67	0.23	0.70	0.05
META1_4865	protein of unknown function	0.078	0.249	0.247	0.135	0.166	0.142	0.107	0.097	0.139	0.209	0.151	0.114	0.74	0.37	1.13	0.10
META1_4866	conserved protein of unknown function; putative expor	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4868	putative metallophosphatase/metallophosphoesterase	0.000	0.091	0.000	0.000	0.000	0.000	0.064	0.039	0.040	0.036	0.000	0.047	1.75	0.09	n.d.	0.00
META1_4871	putative PAS sensor hybrid histidine kinase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.079	0.000	0.000	0.054	n.d.	0.00	n.d.	0.00
META1_4872	conserved protein of unknown function; putative Tellur	0.000	0.068	0.099	0.135	0.048	0.165	0.129	0.213	0.198	0.064	0.111	0.181	3.86	0.49	2.45	0.26
META1_4873	putative Nucleotidyl transferase	0.234	0.159	0.148	0.271	0.048	0.189	0.107	0.174	0.099	0.172	0.141	0.128	1.00	0.18	1.36	0.88
META1_4874	conserved protein of unknown function	0.350	0.498	0.445	0.203	0.546	0.165	0.407	0.387	0.456	0.445	0.333	0.417	1.27	0.83	1.88	0.29
META1_4875	putative histidine kinase, Putative HK, ATPase and Sens	0.078	0.295	0.223	0.271	0.428	0.236	0.300	0.271	0.337	0.218	0.323	0.302	1.88	0.24	1.41	1.00
META1_4876	S-adenosyl L-homocysteine hydrolase	2.258	0.906	1.534	1.961	1.995	2.245	1.264	1.237	1.052	1.451	2.097	1.183	1.10	0.47	0.85	0.00
META1_4877	putative acetyl-coenzyme A synthetase (acsA-like)	0.000	0.091	0.000	0.000	0.000	0.000	0.064	0.077	0.040	0.036	0.000	0.060	2.25	0.10	n.d.	0.00
META1_4878	putative OXIDOREDUCTASE PROTEIN	0.779	0.340	0.445	0.676	0.238	0.142	0.386	0.406	0.456	0.481	0.262	0.417	1.17	0.54	2.38	0.46
META1_4879	enoyl-CoA hydratase	0.078	0.113	0.148	0.000	0.048	0.047	0.150	0.193	0.099	0.118	0.040	0.148	1.69	0.39	5.50	0.54
META1_4881	Cardiolipin synthase (cls-like)	0.000	0.000	0.000	0.000	0.048	0.071	0.086	0.077	0.079	0.000	0.050	0.081	n.d.	0.00	2.40	0.42
META1_4882	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.37
META1_4883	putative helicase-exonuclease type V protein family	0.000	0.000	0.000	0.000	0.071	0.000	0.043	0.039	0.079	0.000	0.030	0.054	n.d.	0.00	2.67	0.10
META1_4884	PQQ-dependent aldose sugar dehydrogenase precursor	2.142	1.246	1.089	0.947	0.570	0.473	0.279	0.387	0.635	1.397	0.585	0.437	0.42	0.02	1.12	0.24
META1_4886	thioredoxin	0.623	0.453	0.594	0.541	0.333	0.520	0.493	0.503	0.456	0.544	0.443	0.484	1.20	0.27	1.64	0.71
META1_4887	putative 31 kDa outer-membrane immunogenic protein	0.389	0.453	0.520	0.473	0.285	0.638	0.321	0.213	0.258	0.463	0.464	0.262	0.76	0.02	0.85	0.12
META1_4888	bifunctional folylpolyglutamate synthase and dihydrofo	0.467	0.657	0.594	0.271	0.641	0.567	0.279	0.406	0.298	0.590	0.554	0.329	0.75	0.02	0.89	0.29
META1_4889	acetyl-CoA carboxylase, carboxyltransferase subunit be	0.234	0.159	0.124	0.271	0.285	0.307	0.300	0.367	0.397	0.163	0.292	0.356	2.94	0.02	1.83	0.09
META1_4890	tryptophan synthase alpha subunit	0.701	0.566	0.742	1.082	0.380	0.638	0.450	0.657	0.635	0.662	0.595	0.585	1.19	0.36	1.47	0.75
META1_4891	Putative nucleotide pyrophosphatase	0.000	0.045	0.000	0.000	0.048	0.000	0.086	0.077	0.040	0.018	0.020	0.067	5.00	0.13	5.00	0.13
META1_4892	Putative histidine triad (HIT) protein	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.000	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_4893	putative metal dependent phosphohydrolase with a res	0.000	0.068	0.000	0.000	0.000	0.071	0.000	0.077	0.079	0.027	0.030	0.054	2.67	0.53	2.67	0.52
META1_4894	putative ATP-independent RNA helicase, DEAD/DEAH-b	0.350	1.133	0.841	0.406	1.188	0.402	0.450	0.348	0.377	0.844	0.736	0.390	0.62	0.18	0.79	0.34
META1_4896	integral membrane sensor signal transduction histidine	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.039	0.040	0.000	0.020	0.047	n.d.	0.00	3.50	0.12
META1_4897	two component transcriptional regulator	0.662	0.884	0.569	0.676	0.546	0.756	0.643	1.063	0.635	0.717	0.655	0.786	1.48	0.70	1.80	0.49
META1_4898	putative transcriptional activator (TenA family)	0.078	0.181	0.000	0.135	0.119	0.118	0.129	0.116	0.099	0.091	0.121	0.114	1.70	0.37	1.42	0.40
META1_4899	putative amino acid transporter	0.156	0.159	0.173	0.000	0.071	0.095	0.129	0.116	0.159	0.163	0.071	0.134	1.11	0.11	2.86	0.45
META1_4905	glutamine amidotransferase class II	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META1_4906	RNA polymerase sigma factor	0.506	1.042	0.990	0.541	0.285	0.425	0.707	0.483	0.576	0.898	0.383	0.585	0.88	0.27	2.29	0.17
META1_4907	transcriptional regulator (Ros/MucR family)	1.363	1.065	1.014	1.285	0.546	0.591	0.814	0.850	0.695	1.116	0.675	0.786	0.95	0.03	1.75	0.87
META1_4909	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.118	0.043	0.039	0.000	0.000	0.081	0.027	n.d.	0.12	0.50	0.91
META1_4911	ferredoxin	0.117	0.272	0.247	0.135	0.428	0.425	0.300	0.251	0.357	0.227	0.383	0.302	1.80	0.22	1.18	0.94
META1_4913	protein of unknown function	0.701	4.690	4.627	3.314	4.133	4.158	5.013	4.214	5.299	3.738	4.022	4.832	1.75	0.35	1.80	0.09
META1_4914	putative transcriptional regulator, XRE family	0.000	0.136	0.173	0.000	0.143	0.095	0.107	0.155	0.079	0.118	0.101	0.114	1.31	0.33	1.70	0.37
META1_4915	bifunctional: hydroxy-methylpyrimidine kinase (HMP ki	0.000	0.317	0.198	0.000	0.143	0.189	0.386	0.522	0.377	0.200	0.141	0.430	2.91	0.46	4.57	0.54
META1_4916	thiamine-phosphate pyrophosphorylase (TMP pyrophos	0.156	0.159	0.000	0.203	0.119	0.260	0.214	0.329	0.238	0.100	0.192	0.262	3.55	0.45	2.05	0.28
META1_4917	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_4919	transcriptional regulator (Ros/MucR family)	1.363	0.861	0.916	1.420	0.523	0.638	0.707	0.947	0.714	0.998	0.706	0.793	1.07	0.19	1.69	0.99
META1_4920	N-acetylglutamate semialdehyde dehydrogenase (NAGS	0.195	0.227	0.148	0.338	0.143	0.236	0.257	0.271	0.337	0.191	0.212	0.289	2.05	0.05	2.05	0.41
META1_4922	molybdate ABC transporter, periplasmic molybdate-bin	0.195	0.295	0.272	0.000	0.095	0.165	0.129	0.116	0.119	0.263	0.111	0.121	0.62	0.01	1.64	0.37
META1_4925	Ribosomal protein L11 methyltransferase (L11 Mtase)	0.234	0.295	0.223	0.338	0.143	0.284	0.257	0.251	0.159	0.254	0.232	0.222	1.18	0.50	1.43	0.77
META1_4926	aminopeptidase	0.078	0.249	0.297	0.203	0.261	0.000	0.150	0.213	0.139	0.227	0.141	0.168	1.00	0.85	1.79	0.33
META1_4928	conserved protein of unknown function	0.000	0.045	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_4929	phosphotyrosine protein phosphatase	0.000	0.000	0.000	0.000	0.071	0.000	0.086	0.058	0.099	0.000	0.030	0.081	n.d.	0.00	4.00	0.12
META1_4933	putative ABC transporter, fused permease and ATPase c	0.000	0.272	0.322	0.000	0.143	0.000	0.214	0.155	0.198	0.227	0.060	0.188	1.12	0.31	4.67	0.13
META1_4934	conserved protein of unknown function precursor ; put	0.000	0.068	0.099	0.135	0.000	0.047	0.000	0.039	0.000	0.064	0.040	0.013	0.29	0.57	0.50	0.56
META1_4940	putative ferredoxin--nitrite reductase (nirA-like)	0.000	0.000	0.000	0.000	0.143	0.000	0.064	0.039	0.000	0.000	0.060	0.034	n.d.	0.12	0.83	0.46
META1_4944	nitrate transporter component	0.000	0.000	0.000	0.000	0.048	0.095	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META1_4945	putative nitrate transporter component, nrtA	0.078	0.000	0.049	0.000	0.166	0.165	0.150	0.135	0.119	0.036	0.141	0.134	5.00	0.49	1.43	0.34
META1_4946	Two-component response regulator	0.000	0.181	0.124	0.000	0.214	0.213	0.150	0.193	0.179	0.118	0.181	0.175	2.00	0.40	1.44	0.34
META1_4948	putative glycoside hydrolase	0.273	0.385	0.569	0.203	0.166	0.000	0.364	0.348	0.258	0.426	0.101	0.323	1.02	0.45	4.80	0.47
META1_4949	transketolase	1.674	1.677	1.757	0.879	1.876	1.418	1.607	1.662	1.528	1.706	1.532	1.599	1.27	0.10	1.57	0.45
META1_4950	putative Transaldolase Phosphoglucose isomerase	2.959	3.421	3.613	2.502	2.185	1.630	1.907	1.972	2.124	3.384	1.996	2.003	0.80	0.00	1.51	0.79
META1_4953	putative methyl-accepting chemotaxis receptor/sensor	0.000	0.204	0.148	0.135	0.119	0.047	0.150	0.116	0.179	0.136	0.091	0.148	1.47	0.35	2.44	0.26
META1_4954	conserved protein of unknown function	0.078	0.000	0.000	0.000	0.000	0.071	0.086	0.058	0.040	0.018	0.030	0.060	4.50	0.11	3.00	0.11
META1_4955	Short-chain dehydrogenase/reductase SDR	0.000	0.068	0.099	0.000	0.000	0.000	0.000	0.039	0.000	0.064	0.000	0.013	0.29	0.57	n.d.	0.37
META1_4956	multidrug transport protein, acriflavin resistance protei	0.389	0.408	0.495	0.000	0.428	0.213	0.214	0.445	0.437	0.435	0.272	0.370	1.15	0.45	2.04	0.40
META1_4957	RND efflux transporter, membrane fusion protein subu	0.428	0.295	0.322	0.135	0.309	0.260	0.257	0.290	0.198	0.336	0.262	0.249	1.00	0.10	1.42	0.73
META1_4958	rhodanese domain protein, putative sulfur transferase	0.000	0.295	0.173	0.203	0.119	0.118	0.086	0.077	0.079	0.181	0.131	0.081	0.60	0.24	0.92	0.04
META1_4959	putative Glycosyl transferase, group 1	0.000	0.000	0.000	0.000	0.048	0.071	0.043	0.058	0.079	0.000	0.050	0.060	n.d.	0.00	1.80	0.38
META1_4971	protein of unknown function	0.156	0.181	0.124	0.135	0.166	0.142	0.214	0.174	0.159	0.154	0.151	0.181	1.59	0.28	1.80	0.13
META1_4972	protein of unknown function	0.312	0.589	0.396	0.676	0.404	0.378	0.300	0.503	0.635	0.454	0.433	0.484	1.44	0.77	1.67	0.93
META1_4973	putative Quinoprotein alcohol dehydrogenase	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4975	signal transduction histidine kinase; GAF domain	0.000	0.068	0.000	0.000	0.000	0.000	0.064	0.039	0.040	0.027	0.000	0.047	2.33	0.10	n.d.	0.00
META1_4976	conserved protein of unknown function; putative expor	0.000	0.113	0.124	0.000	0.000	0.000	0.000	0.058	0.079	0.091	0.000	0.047	0.70	0.94	n.d.	0.12
META1_4977	putative aldehyde dehydrogenase precursor (tat pathw	0.156	0.453	0.470	0.271	0.618	0.662	0.214	0.348	0.159	0.390	0.585	0.242	0.84	0.47	0.62	0.11
META1_4978	oxidoreductase, 2Fe-2S subunit	0.000	0.068	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META1_4981	protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.043	0.000	0.040	0.018	0.000	0.027	2.00	0.51	n.d.	0.12
META1_4982	putative phosphoenolpyruvate carboxylase	0.467	0.725	0.693	0.203	0.760	0.354	0.471	0.696	0.794	0.653	0.504	0.659	1.36	0.88	1.96	0.28
META1_4983	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.058	0.000	0.000	0.020	0.034	n.d.	0.12	2.50	0.52
META1_4984	protein of unknown function; putative exported protein	0.000	0.091	0.074	0.135	0.048	0.071	0.086	0.116	0.040	0.064	0.071	0.081	1.71	0.36	1.71	0.92
META1_4987	putative oxidoreductase precursor (tat pathway signal)	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_4990	alcohol dehydrogenase	0.117	0.000	0.124	0.000	0.214	0.260	0.150	0.155	0.218	0.073	0.202	0.175	3.25	0.43	1.30	0.33
META1_4991	putative hybrid histidine kinase; Domains: two PAS, two	0.000	0.068	0.049	0.000	0.000	0.000	0.000	0.000	0.079	0.045	0.000	0.027	0.80	0.50	n.d.	0.37
META1_4993	putative 3-oxoacyl-[acyl-carrier-protein] reductase (fab	0.234	0.159	0.124	0.135	0.143	0.236	0.171	0.329	0.159	0.163	0.181	0.222	1.83	0.49	1.83	0.48
META1_4994	putative 3-oxoacyl-[acyl-carrier-protein] synthase (fabF	0.195	0.227	0.272	0.203	0.451	0.354	0.621	0.696	0.476	0.236	0.373	0.598	3.42	0.00	2.41	0.08
META1_4995	putative beta-ketoacyl-acyl-carrier-protein synthase (fa	0.156	0.295	0.297	0.271	0.238	0.496	0.321	0.251	0.159	0.263	0.353	0.242	1.24	0.95	1.03	0.38
META1_4996	Putative beta-hydroxyacyl-(acyl-carrier-protein) dehydr	0.078	0.000	0.000	0.000	0.095	0.189	0.107	0.077	0.040	0.018	0.121	0.074	5.50	0.11	0.92	0.29
META1_4997	Specialized acyl carrier protein (ACP)	0.234	0.340	0.495	0.541	0.333	0.425	0.321	0.251	0.397	0.372	0.403	0.323	1.17	0.80	1.20	0.21
META1_5001	conserved protein of unknown function	0.506	0.544	0.643	0.609	0.071	0.260	0.643	0.619	0.595	0.572	0.232	0.618	1.46	0.26	4.00	0.18
META1_5005	heat shock chaperone	0.000	0.045	0.000	0.000	0.000	0.000	0.279	0.135	0.179	0.018	0.000	0.195	14.50	0.19	n.d.	0.00
META1_5006	putative lysophospholipase L2 (pldB-like)	0.078	0.091	0.000	0.000	0.119	0.118	0.171	0.116	0.119	0.054	0.101	0.134	3.33	0.44	2.00	0.39
META1_5008	putative inositol mono-phosphatase (suhB-like)	0.000	0.091	0.074	0.000	0.071	0.118	0.107	0.135	0.099	0.064	0.081	0.114	2.43	0.42	2.13	0.40
META1_5010	Hypothetical UPF0271 protein	0.000	0.113	0.074	0.000	0.048	0.047	0.064	0.058	0.079	0.073	0.040	0.067	1.25	0.33	2.50	0.42
META1_5011	Nicotinate phosphoribosyltransferase (NAPRTase)	0.117	0.249	0.173	0.000	0.048	0.000	0.043	0.097	0.060	0.191	0.020	0.067	0.48	0.04	5.00	0.13

META1_5012	putative General stress protein 26; putative FMN-bindi	0.467	0.476	0.247	0.000	0.000	0.000	0.129	0.116	0.179	0.390	0.000	0.141	0.49	0.02	n.d.	0.00
META1_5014	antiporter inner membrane protein	0.584	0.612	0.520	0.879	0.594	0.591	0.364	0.348	0.516	0.572	0.635	0.410	0.97	0.06	0.97	0.05
META1_5016	DNA gyrase, subunit A (type II topoisomerase)	1.012	1.156	1.361	1.691	1.639	0.874	1.414	1.508	1.508	1.197	1.320	1.479	1.67	0.06	1.68	0.68
META1_5017	putative 31 kDa outer-membrane immunogenic protein	0.000	0.068	0.124	0.135	0.000	0.047	0.064	0.000	0.040	0.073	0.040	0.034	0.63	0.93	1.25	0.95
META1_5018	Pantetheine-phosphate adenylyltransferase	0.000	0.045	0.000	0.000	0.119	0.071	0.171	0.116	0.139	0.018	0.081	0.141	10.50	0.17	2.63	0.44
META1_5019	peptidyl-prolyl cis-trans isomerase (rotamase) precurso	0.428	0.476	0.247	0.473	0.309	0.189	0.300	0.271	0.278	0.381	0.282	0.282	1.00	0.26	1.50	0.81
META1_5020	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_5021	peptidyl-prolyl cis-trans isomerase B (rotamase B)(PPIas	1.090	0.702	0.495	0.879	0.618	0.473	0.707	0.599	1.012	0.717	0.595	0.773	1.46	0.89	1.95	0.51
META1_5022	putative response regulator receiver (CheY-like protein)	0.195	0.295	0.124	0.000	0.095	0.095	0.086	0.155	0.139	0.209	0.081	0.128	0.83	0.22	2.38	0.41
META1_5026	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.000	0.040	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_5030	protein of unknown function	0.467	0.363	0.396	0.135	0.214	0.236	0.214	0.213	0.337	0.399	0.212	0.255	0.86	0.04	1.81	0.30
META1_5031	Tungsten-containing formate dehydrogenase beta subu	0.467	0.838	0.866	0.271	0.285	0.189	1.114	1.063	1.290	0.762	0.242	1.156	2.05	0.07	7.17	0.00
META1_5032	Tungsten-containing formate dehydrogenase alpha sub	0.818	1.359	1.856	0.744	1.093	0.520	3.106	3.325	3.354	1.415	0.796	3.266	3.12	0.02	6.15	0.00
META1_5040	putative succinoglycan biosynthesis transport protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5043	putative 3-oxoacyl-acyl carrier protein reductase (fabG-	0.000	0.068	0.049	0.000	0.000	0.000	0.000	0.077	0.000	0.045	0.000	0.027	0.80	0.50	n.d.	0.37
META1_5045	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.036	0.000	0.013	0.50	0.95	n.d.	0.37
META1_5047	putative seryl-tRNA synthetase (Serine--tRNA ligase)	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.058	0.079	0.027	0.000	0.047	2.33	0.52	n.d.	0.12
META1_5051	putative acetolactate synthase large subunit (ilvG)	0.117	0.498	0.470	0.203	0.238	0.213	0.236	0.251	0.377	0.399	0.222	0.289	0.98	0.90	1.95	0.17
META1_5052	protein of unknown function	0.000	0.136	0.173	0.135	0.119	0.095	0.064	0.058	0.079	0.118	0.111	0.067	0.77	0.27	0.91	0.02
META1_5053	putative branched-chain amino acid aminotransferase	0.078	0.136	0.049	0.000	0.000	0.000	0.107	0.039	0.079	0.091	0.000	0.074	1.10	0.73	n.d.	0.00
META1_5054	conserved protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.064	0.039	0.060	0.027	0.000	0.054	2.67	0.11	n.d.	0.00
META1_5061	conserved protein of unknown function, UPF0313 prote	0.000	0.136	0.124	0.000	0.119	0.118	0.171	0.097	0.179	0.100	0.101	0.148	2.00	0.39	2.20	0.40
META1_5068	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.027	0.000	0.013	0.67	0.98	n.d.	0.37
META1_5069	putative UDP-N-acetyl-D-mannosaminuronic acid dehyd	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.077	0.079	0.000	0.000	0.081	n.d.	0.00	n.d.	0.00
META1_5070	Putative UDP-glucose 4-epimerase	0.000	0.045	0.000	0.541	0.000	0.000	0.300	0.155	0.119	0.018	0.081	0.188	14.00	0.19	3.50	0.07
META1_5071	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-r	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.058	0.040	0.000	0.020	0.054	n.d.	0.00	4.00	0.12
META1_5078	Phosphoglycerate/bisphosphoglycerate mutase	0.273	0.159	0.099	0.203	0.190	0.213	0.321	0.271	0.337	0.163	0.202	0.309	2.56	0.10	2.30	0.00
META1_5079	NAD(P)-dependent aldo/keto reductase	0.234	0.227	0.322	0.135	0.143	0.118	0.236	0.193	0.179	0.263	0.131	0.202	1.03	0.15	2.31	0.01
META1_5080	AAA ATPase	0.117	0.113	0.198	0.203	0.071	0.213	0.343	0.290	0.298	0.145	0.151	0.309	2.88	0.01	3.07	0.10
META1_5081	protein of unknown function	0.000	0.113	0.049	0.000	0.143	0.213	0.214	0.155	0.099	0.064	0.151	0.155	3.29	0.48	1.53	0.35
META1_5082	protein of unknown function; putative membrane prote	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_5084	UDP-N-acetylmuramoylalanine--D-glutamate ligase	0.467	0.498	0.223	0.406	0.523	0.378	0.193	0.348	0.318	0.390	0.443	0.289	1.00	0.40	0.98	0.10
META1_5086	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine l	0.389	0.702	0.569	0.271	0.428	0.402	0.257	0.406	0.377	0.581	0.393	0.349	0.81	0.11	1.33	0.80
META1_5087	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diamino	0.350	0.249	0.247	0.203	0.356	0.354	0.386	0.251	0.238	0.272	0.333	0.289	1.43	0.91	1.30	0.89
META1_5090	S-adenosyl-dependent methyltransferase	0.117	0.000	0.049	0.000	0.095	0.071	0.107	0.097	0.060	0.045	0.071	0.087	2.60	0.39	1.86	0.38
META1_5091	DNA ligase, NAD(+)-dependent	0.234	0.544	0.594	0.609	0.546	0.378	0.600	0.580	0.437	0.490	0.484	0.538	1.48	0.50	1.67	0.74
META1_5094	Carbohydrate kinase, PfkB	1.090	0.748	0.742	1.217	1.021	1.418	1.221	1.063	1.171	0.826	1.220	1.149	1.88	0.08	1.41	0.66
META1_5095	peptidyl-prolyl cis-trans isomerase (Rotamase)	1.324	1.201	0.668	0.744	0.641	0.614	1.028	1.237	1.012	1.034	0.645	1.095	1.43	0.79	2.55	0.00
META1_5096	protein of unknown function	0.156	0.113	0.173	0.000	0.000	0.071	0.000	0.000	0.000	0.145	0.030	0.000	0.00	0.00	0.00	0.37
META1_5098	3-hydroxybutyryl-CoA dehydratase	0.389	0.544	0.322	0.271	0.000	0.213	0.279	0.309	0.258	0.426	0.131	0.282	0.89	0.08	3.23	0.40
META1_5099	putative transcriptional regulator, GntR family	0.000	0.204	0.049	0.203	0.048	0.236	0.343	0.387	0.377	0.100	0.151	0.370	5.00	0.60	3.67	0.11
META1_5100	putative L-allo-threonine aldolase (ltaE-like)	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.097	0.079	0.000	0.000	0.094	n.d.	0.00	n.d.	0.00
META1_5101	conserved protein of unknown function; putative expor	0.234	0.295	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.172	0.000	0.027	0.21	0.60	n.d.	0.37
META1_5103	conserved protein of unknown function, putative expor	0.000	0.000	0.000	0.000	0.071	0.118	0.107	0.000	0.040	0.000	0.081	0.047	n.d.	0.12	0.88	0.96
META1_5104	conserved protein of unknown function, putative serine	0.078	0.227	0.272	0.000	0.071	0.142	0.086	0.077	0.060	0.209	0.091	0.074	0.48	0.11	1.22	0.33
META1_5105	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5110	CTP synthetase	1.207	1.427	1.410	0.406	1.259	0.756	1.371	1.102	1.012	1.370	0.917	1.156	1.14	0.22	1.89	0.25
META1_5111	putative secG: preprotein translocase	0.234	0.181	0.099	0.135	0.285	0.331	0.321	0.251	0.198	0.163	0.282	0.255	2.11	0.20	1.36	0.82
META1_5112	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.095	0.000	0.000	0.060	0.036	0.040	0.020	0.75	0.98	0.75	0.97
META1_5115	triosephosphate isomerase	0.779	0.521	0.445	0.609	0.285	0.543	0.557	0.464	0.357	0.553	0.443	0.457	1.11	0.35	1.55	0.98
META1_5116	putative peptidyl-prolyl cis-trans isomerse D	0.896	1.314	1.361	1.691	2.423	1.630	1.200	1.392	1.111	1.234	1.976	1.237	1.35	0.76	0.94	0.04
META1_5117	anthranilate synthase component I	0.195	0.453	0.619	0.271	0.594	0.803	0.600	0.619	0.476	0.454	0.635	0.565	1.68	0.33	1.33	0.77
META1_5119	aminodeoxychorismate synthase component II, Glutam	0.078	0.068	0.000	0.203	0.143	0.047	0.214	0.174	0.119	0.045	0.111	0.168	5.00	0.50	2.27	0.45
META1_5120	anthranilate phosphoribosyltransferase	0.000	0.159	0.198	0.135	0.143	0.095	0.150	0.135	0.139	0.136	0.121	0.141	1.40	0.34	1.75	0.33
META1_5121	indole-3-glycerol phosphate synthase	0.078	0.204	0.148	0.135	0.190	0.118	0.236	0.135	0.139	0.154	0.151	0.168	1.47	0.57	1.67	0.61
META1_5122	molybdenum cofactor biosynthesis protein C	0.000	0.091	0.049	0.000	0.190	0.095	0.214	0.155	0.119	0.054	0.121	0.161	4.00	0.51	2.00	0.40
META1_5123	putative molybdopterin biosynthesis-related protein	0.000	0.045	0.000	0.000	0.071	0.000	0.086	0.058	0.000	0.018	0.030	0.047	3.50	0.55	2.33	0.52
META1_5124	Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase	0.389	0.159	0.124	0.271	0.665	0.213	0.386	0.329	0.437	0.200	0.413	0.383	2.59	0.14	1.39	0.75
META1_5125	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O	0.312	0.249	0.198	0.406	0.333	0.307	0.386	0.541	0.318	0.245	0.333	0.417	2.30	0.07	1.88	0.43
META1_5126	conserved protein of unknown function	0.000	0.204	0.124	0.000	0.000	0.118	0.171	0.116	0.099	0.127	0.050	0.128	1.36	0.34	3.80	0.12
META1_5127	Lipid-A-disaccharide synthase	0.000	0.091	0.000	0.000	0.119	0.118	0.086	0.116	0.079	0.036	0.101	0.094	3.50	0.12	1.40	0.34
META1_5128	conserved protein of unknown function, UPF0178 prote	0.000	0.091	0.049	0.000	0.048	0.000	0.107	0.097	0.079	0.054	0.020	0.094	2.33	0.42	7.00	0.15
META1_5129	citrate synthase	7.087	3.875	4.701	1.691	1.568	1.748	1.757	2.107	2.322	4.926	1.663	2.070	0.57	0.01	1.87	0.08
META1_5130	glutamate tRNA synthetase, catalytic subunit	0.467	1.065	0.965	0.406	0.713	0.591	0.814	0.908	0.635	0.889	0.615	0.786	1.19	0.98	1.92	0.16
META1_5132	SOS response transcriptional repressor, lexA	0.156	0.295	0.421	0.473	0.143	0.236	0.386	0.232	0.377	0.308	0.232	0.329	1.44	0.61	2.13	0.55
META1_5133	conserved protein of unknown function	0.000	0.227	0.148	0.000	0.048	0.000	0.064	0.097	0.060	0.145	0.020	0.074	0.69	0.26	5.50	0.13
META1_5134	alpha-ketoglutarate permease (MFS transporter membr	0.000	0.045	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.018	0.020	0.000	0.00	0.37	0.00	0.37
META1_5135	conserved protein of unknown function	0.000	0.091	0.074	0.000	0.000	0.000	0.000	0.039	0.000	0.064	0.000	0.013	0.29	0.57	n.d.	0.37
META1_5136	Tartrate dehydrogenase/decarboxylase (TDH) (D-malate	0.350	0.544	0.322	0.000	0.143	0.142	0.129	0.155	0.119	0.417	0.121	0.134	0.43	0.00	1.67	0.36
META1_5138	putative oxidoreductase, aldo/keto reductase family	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5140	conserved protein of unknown function; putative Meth	0.000	0.000	0.000	0.000	0.119	0.071	0.086	0.000	0.060	0.000	0.081	0.047	n.d.	0.12	0.88	0.97
META1_5141	periplasmic serine protease (DegP)	0.000	0.000	0.049	0.000	0.000	0.071	3.299	3.073	3.076	0.018	0.030	3.145	234.00	0.50	156.00	0.46
META1_5143	valine tRNA synthetase	1.246	1.178	1.237	1.623	1.876	1.559	1.264	1.508	1.270	1.216	1.703	1.351	1.50	0.19	1.19	0.05
META1_5144	conserved protein of unknown function	0.000	0.068	0.000	0.000	0.095	0.095	0.064	0.058	0.079	0.027	0.081	0.067	3.33	0.12	1.25	0.33
META1_5145	putative type I secretion outer membrane protein, TolC	1.869	0.295	0.569	1.014	1.093	1.110	0.364	0.387	0.298	0.762	1.089	0.349	0.62	0.29	0.48	0.00
META1_5146	putative protein-L-isoaspartate O-methyltransferase	1.090	1.201	0.767	1.691	0.879	0.827	0.771	0.928	0.893	1.016	0.978	0.867	1.15	0.36	1.33	0.41
META1_5154	conserved protein of unknown function	0.117	0.091	0.049	0.000	0.000	0.000	0.043	0.058	0.000	0.082	0.000	0.034	0.56	0.44	n.d.	0.12
META1_5155	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.043	0.000	0.000	0.000	0.020	0.013	n.d.	0.37	1.00	0.99
META1_5158	protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_5164	phosphate ABC transporter, periplasmic phosphate bin	0.779	1.224	1.089	0.947	0.380	0.567	0.664	0.773	0.695	1.070	0.544	0.712	0.90	0.07	1.96	0.53
META1_5165	phosphate ABC transporter, permease	0.000	0.068	0.099	0.000	0.119	0.118	0.064	0.077	0.119	0.064	0.101	0.087	1.86	0.38	1.30	0.33
META1_5166	phosphate ABC transporter, permease	0.000	0.000	0.000	0.000	0.095	0.095	0.000	0.000	0.000	0.000	0.081	0.000	n.d.	n.d.	0.00	0.12
META1_5167	phosphate ABC transporter, ATPase	0.350	0.272	0.272	0.203	0.048	0.331	0.257	0.290	0.278	0.290	0.192	0.276	1.28	0.46	2.16	0.35
META1_5168	negative regulator of PhoR/PhoB two-component regul	0.273	0.340	0.371	0.406	0.380	0.378	0.600	0.387	0.318	0.336	0.383	0.430	1.73	0.29	1.68	0.70
META1_5169	phosphate regulon transcriptional regulatory protein PI	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5170	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.095	0.118	0.086	0.116	0.079	0.018	0.091	0.094	7.00	0.15	1.56	0.36
META1_5171	conserved protein of unknown function; putative expor	0.078	0.227	0.247	0.000	0.000	0.213	0.214	0.213	0.159	0.200	0.091	0.195	1.32	0.68	3.22	0.11
META1_5173	Precorrin-6A reductase (Precorrin-6X reductase)	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.099	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_5175	Cobalamin biosynthesis protein cobD	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_5176	Threonine-phosphate decarboxylase (L-threonine-O-3-	0.000	0.045	0.000	0.000	0.095	0.000	0.064	0.077	0.079	0.018	0.040	0.074	5.50	0.14	2.75	0.11
META1_5179	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5180	malonyl-CoA decarboxylase	0.389	0.521	0.544	0.135	0.380	0.307	0.279	0.329	0.218	0.499	0.312	0.276	0.75	0.02	1.32	0.83
META1_5181	conserved protein of unknown function; putative CsbD-	0.312	0.431	0.346	0.000	0.071	0.095	0.107	0.135	0.179	0.372	0.071	0.141	0.51	0.01	3.00	0.45
META1_5182	D-beta-hydroxybutyrate dehydrogenase	0.623	0.680	0.817	0.609	0.190	0.189	0.386	0.445	0.278	0.717	0.252	0.370	0.70	0.01	2.20	0.56
META1_5183	acetyl-CoA carboxylase, carboxytransferase subunit alp	0.389	0.702	0.718	0.676	0.143	0.449	0.364	0.464	0.456	0.635	0.353	0.430	0.91	0.22	1.83	0.70
META1_5185	conserved protein of unknown function; putative expor	0.000	0.000	0.000	0.000	0.000	0.047	0.086	0.000	0.060	0.000	0.020	0.047	n.d.	0.12	3.50	0.54
META1_5186	50S ribosomal subunit protein L19	0.973	0.408	0.297	1.353	1.520	1.394	1.307	1.411	1.568	0.499	1.441	1.431	3.87	0.04	1.49	0.97
META1_5189	putative membrane-bound lytic murein transglycosylas	0.000	0.204	0.148	0.000	0.285	0.213	0.000	0.000	0.040	0.136	0.212	0.013	0.13	0.62	0.10	0.65
META1_5190	30S ribosomal protein S4	2.181	1.903	1.732	2.638	1.401	2.457	1.864	2.262	2.203	1.905	2.036	2.117	1.50	0.40	1.56	0.97
META1_5191	2-nitropropane dioxygenase, (nitroalkane oxidase) (2-N	0.156	0.181	0.223	0.135	0.166	0.142	0.300	0.290	0.179	0.191	0.151	0.255	1.81	0.20	2.53	0.04
META1_5193	phosphatidylserine decarboxylase (psd-like)	0.506	0.498	0.223	0.338	0.546	0.543	0.643	0.425	0.437	0.399	0.514	0.497	1.68	0.45	1.45	0.80
META1_5196	putative ABC transporter, fused ATPase and permease	0.117	0.317	0.297	0.135	0.404	0.260	0.193	0.271	0.377	0.263	0.302	0.282	1.45	0.63	1.40	0.78
META1_5198	conserved protein of unknown function	0.078	0.113	0.000	0.338	0.214	0.047	0.236	0.232	0.198	0.064	0.161	0.222	4.71	0.51	2.06	0.55
META1_5199	protein of unknown function	0.156	0.113	0.049	0.000	0.095	0.189	0.129	0.155	0.060	0.100	0.121	0.114	1.55	0.83	1.42	0.34
META1_5200	cysteine tRNA synthetase	0.156	0.136	0.322	0.000	0.119	0.189	0.214	0.232	0.159	0.209	0.131	0.202	1.30	0.87	2.31	0.42
META1_5202	conserved protein of unknown function CreA family; pu	0.195	0.204	0.099	0.000	0.143	0.047	0.086	0.058	0.099	0.163	0.081	0.081	0.67	0.07	1.50	0.37
META1_5203	protein of unknown function; putative exported protein	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META1_5204	conserved protein of unknown function; putative OmpA	0.857	0.521	0.594	0.541	0.166	0.213	0.279	0.329	0.238	0.626	0.242	0.282	0.61	0.01	1.75	0.91
META1_5206	putative 3-demethylubiquinone-9 3-methyltransferase	0.117	0.181	0.074	0.000	0.071	0.047	0.129	0.077	0.040	0.127	0.050	0.081	0.86	0.34	2.40	0.41
META1_5207	putative S-adenosyl-L-methionine-dependent methyltra	0.000	0.227	0.173	0.203	0.000	0.000	0.150	0.097	0.139	0.154	0.030	0.128	1.12	0.31	6.33	0.10
META1_5208	Glutamyl-tRNA synthetase	0.000	0.204	0.198	0.135	0.333	0.307	0.214	0.232	0.258	0.154	0.292	0.235	2.06	0.40	1.21	0.94
META1_5213	protein of unknown function; putative exported protein	0.000	0.091	0.049	0.000	0.095	0.047	0.086	0.077	0.099	0.054	0.060	0.087	2.17	0.41	2.17	0.41
META1_5215	putative glutathione S-transferase	0.195	0.227	0.322	0.000	0.119	0.142	0.129	0.290	0.278	0.254	0.111	0.235	1.25	0.75	3.18	0.46
META1_5216	protein tolB precursor	0.195	0.431	0.272	0.135	0.618	0.402	0.107	0.348	0.139	0.318	0.454	0.202	0.86	0.31	0.67	0.34
META1_5218	uptake of enterobactin; tonB-dependent uptake of B co	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.060	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META1_5219	membrane spanning protein in TolA-TolQ-TolR complex	0.000	0.136	0.099	0.473	0.214	0.165	0.343	0.309	0.238	0.091	0.232	0.296	4.40	0.53	1.91	0.70
META1_5220	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META1_5222	conserved protein of unknown function; putative expor	0.312	0.181	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.209	0.000	0.000	0.00	0.00	n.d.	n.d.
META1_5225	Holliday junction ATP-dependent DNA helicase	0.000	0.136	0.099	0.135	0.143	0.213	0.171	0.077	0.040	0.091	0.171	0.094	1.40	0.33	0.82	0.20
META1_5227	Dps protein family starvation-inducible DNA-binding pr	1.012	0.566	0.569	0.000	0.238	0.260	0.214	0.193	0.258	0.671	0.212	0.222	0.45	0.01	1.57	0.36
META1_5228	conserved protein of unknown function; putative acyl-C	0.195	0.498	0.520	0.135	0.404	0.284	0.557	0.677	0.695	0.435	0.312	0.645	2.00	0.17	3.10	0.05
META1_5229	L-fuculose-1-phosphate aldolase	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5230	Putative transcriptional regulator MucR	0.818	0.657	0.371	0.000	0.214	0.142	0.236	0.155	0.218	0.590	0.151	0.202	0.46	0.02	2.00	0.40
META1_5232	conserved protein of unknown function; putative mem	0.000	0.045	0.000	0.000	0.190	0.213	0.064	0.077	0.060	0.018	0.171	0.067	5.00	0.13	0.59	0.24

META1_5234	putative transmembrane adenylate/guanylate cyclase	0.000	0.068	0.049	0.135	0.095	0.071	0.086	0.039	0.040	0.045	0.091	0.054	1.60	0.36	0.89	0.11
META1_5236	Putative cobyrinic acid a,c-diamide synthase	0.000	0.136	0.099	0.000	0.000	0.000	0.129	0.077	0.060	0.091	0.000	0.087	1.30	0.33	n.d.	0.00
META1_5237	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META1_5239	60 kDa chaperonin (protein Cpn60, groEL protein)	15.653	12.122	14.376	23.874	19.952	20.413	17.096	16.314	20.065	13.771	20.734	17.830	1.75	0.07	1.29	0.09
META1_5240	10 kDa chaperonin (protein Cpn10, groES protein)	1.285	1.178	1.188	1.623	1.639	1.299	1.307	1.624	1.846	1.207	1.492	1.599	1.79	0.07	1.61	0.76
META1_5241	putative magnesium/cobalt transport protein	0.000	0.000	0.099	0.000	0.095	0.118	0.107	0.058	0.159	0.036	0.091	0.108	4.00	0.12	1.78	0.37
META1_5244	putative glycolate oxidase subunit GlcE	0.195	0.521	0.371	0.406	0.309	0.331	0.386	0.367	0.377	0.390	0.333	0.376	1.30	0.71	1.70	0.37
META1_5250	Mannose-1-phosphate guanylyltransferase/mannose-6-	0.000	0.045	0.173	0.000	0.285	0.284	0.257	0.309	0.218	0.082	0.242	0.262	4.33	0.55	1.63	0.36
META1_5251	methylmalonyl-CoA mutase, alpha subunit	0.935	0.861	1.089	1.623	2.138	2.008	1.757	1.604	1.389	0.962	2.006	1.579	2.22	0.01	1.18	0.15
META1_5255	serine protease	0.000	0.045	0.000	0.000	0.095	0.071	0.000	0.039	0.060	0.018	0.071	0.034	2.50	0.52	0.71	0.94
META1_5256	conserved protein of unknown function, containing N-t	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META1_5258	ATP-dependent Clp protease adaptor protein clpS	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.077	0.040	0.018	0.000	0.054	4.00	0.12	n.d.	0.00
META1_5259	ATPase and specificity subunit of ClpA-ClpP ATP-depend	1.246	1.835	1.757	1.488	1.449	1.252	1.735	1.392	1.052	1.669	1.371	1.384	1.12	0.47	1.51	0.90
META1_5260	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.058	0.060	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META1_5261	5-aminolevulinic acid synthase (ALAS)	0.156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5263	aerobic magnesium-protoporphyrin IX monomethyl est	0.857	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5267	photosynthetic reaction center subunit H	1.129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.263	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5269	Mg-protoporphyrin IX methyl transferase	0.117	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5272	protochlorophyllide reductase BchB subunit	0.156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5273	protochlorophyllide reductase subunit BchN	0.545	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.127	0.000	0.000	0.00	0.37	n.d.	n.d.
META1_5276	transcriptional regulator PpsR-CrtJ; Fis family	0.000	0.227	0.198	0.000	0.333	0.331	0.150	0.232	0.258	0.163	0.282	0.215	1.78	0.37	1.14	0.31
META1_5282	putative Gluconate 2-dehydrogenase cytochrome c sub	0.545	0.136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.181	0.000	0.000	0.00	0.12	n.d.	n.d.
META1_5283	6-phosphogluconate dehydrogenase	0.156	0.317	0.198	0.203	0.166	0.189	0.086	0.213	0.159	0.236	0.181	0.155	0.88	0.30	1.28	0.39
META1_5284	6-phosphogluconolactonase	0.117	0.091	0.049	0.000	0.000	0.047	0.064	0.077	0.040	0.082	0.020	0.060	1.00	0.37	4.50	0.13
META1_5286	putative beta-1,2-glucan ABC transporter, ATPase and p	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.060	0.000	0.000	0.067	n.d.	0.00	n.d.	0.00
META1_5289	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.000	0.000	0.000	0.020	0.020	n.d.	0.37	1.50	0.98
META1_5290	conserved protein of unknown function; putative memb	0.701	0.793	0.866	0.812	0.404	0.331	0.793	0.541	0.595	0.798	0.433	0.638	1.08	0.18	2.21	0.39
META1_5291	putative endonuclease	0.000	0.045	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.018	0.000	0.013	1.00	1.00	n.d.	0.37
META1_5293	putative outer-membrane immunogenic protein precur	0.000	0.000	0.000	0.000	0.166	0.118	0.000	0.000	0.000	0.000	0.121	0.000	n.d.	n.d.	0.00	0.12
META1_5294	conserved protein of unknown function; omp like	0.195	0.113	0.198	0.541	0.000	0.331	0.150	0.058	0.139	0.163	0.222	0.114	0.94	0.29	0.77	0.20
META1_5295	conserved protein of unknown function; omp like	0.000	0.045	0.049	0.000	0.048	0.213	0.000	0.000	0.000	0.036	0.111	0.000	0.00	0.12	0.00	0.12
META1_5297	phosphoglucosamine mutase	0.156	0.249	0.421	0.406	0.523	0.307	0.300	0.329	0.337	0.290	0.413	0.323	1.50	0.46	1.17	0.23
META1_5299	cell division protease; ATP-dependent metalloprotease	0.779	0.680	1.089	0.676	1.473	0.756	1.007	1.160	0.814	0.853	1.048	0.995	1.57	0.39	1.42	0.78
META1_5300	tRNA(Ile)-lysidine synthase (tRNA(Ile)-lysidine synthetas	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META1_5301	conserved protein of unknown function; putative expor	0.078	0.159	0.198	0.135	0.285	0.260	0.386	0.271	0.377	0.154	0.252	0.343	3.00	0.04	2.04	0.16
META1_5302	Outer membrane lipoprotein omp16 precursor	0.701	0.249	0.173	0.473	0.451	0.331	0.236	0.155	0.357	0.327	0.403	0.249	1.03	0.59	0.93	0.10
META1_5305	protein of unknown function	0.000	0.091	0.049	0.000	0.000	0.071	0.064	0.058	0.079	0.054	0.030	0.067	1.67	0.37	3.33	0.11
META1_5306	conserved protein of unknown function	0.000	0.000	0.074	0.000	0.000	0.047	0.000	0.039	0.000	0.027	0.020	0.013	0.67	0.96	1.00	0.99
META1_5307	Porphobilinogen deaminase (PBG) (Hydroxymethylbilan	0.273	0.295	0.322	0.203	0.499	0.402	0.321	0.348	0.516	0.299	0.413	0.397	1.79	0.16	1.44	0.72
META1_5319	conserved protein of unknown function, DUF892	0.156	0.566	0.124	0.000	0.000	0.000	0.043	0.039	0.079	0.308	0.000	0.054	0.24	0.05	n.d.	0.00
META1_5320	conserved protein of unknown function, UPF0061 prote	0.000	0.000	0.000	0.000	0.048	0.000	0.064	0.077	0.119	0.000	0.020	0.087	n.d.	0.00	6.50	0.14
META1_5321	acetolactate synthase III, large subunit	1.830	1.926	2.326	1.150	2.399	1.772	1.692	1.624	1.985	2.050	1.945	1.767	1.16	0.23	1.36	0.88
META1_5322	conserved protein of unknown function; putative SAM-	0.000	0.068	0.099	0.000	0.071	0.000	0.043	0.116	0.040	0.064	0.030	0.067	1.43	0.33	3.33	0.11
META1_5323	acetolactate synthase III, small subunit	0.935	1.110	0.792	0.947	1.235	1.016	0.964	1.198	1.052	0.953	1.099	1.075	1.52	0.32	1.47	0.94
META1_5324	putative glutathione S-transferase	0.195	0.159	0.173	0.000	0.071	0.000	0.150	0.135	0.159	0.172	0.030	0.148	1.16	0.09	7.33	0.15
META1_5325	putative asparagine synthase, glutamine-hydrolyzing	0.117	0.295	0.124	0.000	0.000	0.047	0.086	0.077	0.079	0.191	0.020	0.081	0.57	0.08	6.00	0.14
META1_5326	putative aminohydrolase/amidotransferase	0.156	0.068	0.124	0.000	0.000	0.047	0.171	0.174	0.159	0.109	0.020	0.168	2.08	0.16	12.50	0.18
META1_5327	RNA polymerase sigma factor	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.060	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META1_5330	putative hybrid histidine kinase	0.000	0.091	0.000	0.000	0.119	0.165	0.086	0.116	0.099	0.036	0.121	0.101	3.75	0.12	1.25	0.33
META1_5345	30S ribosomal protein S20	0.156	0.249	0.322	0.812	0.285	0.449	0.536	0.251	0.437	0.254	0.433	0.403	2.14	0.17	1.40	0.64
META1_CDS1132842D	protein of unknown function; RMQ09746	0.000	0.113	0.148	0.000	0.071	0.047	0.000	0.077	0.099	0.100	0.050	0.060	0.82	0.95	1.80	0.95
META1_CDS1135482D	protein of unknown function; RMQ09748	0.000	0.045	0.000	0.000	0.119	0.000	0.000	0.039	0.060	0.018	0.050	0.034	2.50	0.52	1.00	0.46
META1_CDS2273736R	protein of unknown function, RMQ08659	0.000	0.113	0.074	0.000	0.000	0.000	0.086	0.077	0.060	0.073	0.000	0.074	1.38	0.34	n.d.	0.00
META1_CDS3243855D	protein of unknown function; RMQ08162	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
META2_0003	protein of unknown function	0.000	0.068	0.049	0.203	0.190	0.047	0.064	0.097	0.139	0.045	0.131	0.101	3.00	0.45	1.15	0.66
META2_0004	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0006	protein of unknown function	0.117	0.249	0.223	0.744	0.618	0.449	0.343	0.232	0.298	0.209	0.564	0.289	1.87	0.18	0.77	0.02
META2_0008	putative beta-ketoacyl synthase	8.255	6.730	7.052	5.478	1.995	2.174	1.393	1.392	1.350	7.203	2.590	1.378	0.26	0.00	0.80	0.09
META2_0009	Putative flavin-containing monooxygenase	2.920	1.835	1.955	0.473	0.404	0.284	0.000	0.097	0.000	2.132	0.363	0.034	0.02	0.38	0.14	0.19
META2_0010	protein of unknown function	5.957	7.205	8.141	4.531	1.734	1.252	0.578	1.160	1.052	7.257	1.945	0.941	0.18	0.00	0.73	0.12
META2_0011	protein of unknown function	3.037	3.036	3.415	1.014	0.594	0.331	0.236	0.309	0.198	3.175	0.544	0.249	0.11	0.00	0.69	0.07
META2_0012	Putative malonyl-CoA-acyl-carrier-protein	0.156	0.227	0.421	0.000	0.000	0.000	0.000	0.000	0.000	0.281	0.000	0.000	0.00	0.00	n.d.	n.d.
META2_0013	protein of unknown function	0.273	0.385	0.396	0.135	0.071	0.000	0.064	0.058	0.060	0.363	0.050	0.060	0.23	0.00	1.80	0.31
META2_0014	putative fatty-acid--CoA ligase (Acyl-CoA synthetase)	5.957	5.007	5.023	0.947	0.641	0.142	0.386	0.715	0.337	5.234	0.474	0.484	0.12	0.00	1.53	0.97
META2_0015	Putative thioesterase	0.312	0.680	0.470	0.000	0.000	0.047	0.000	0.077	0.000	0.517	0.020	0.027	0.07	0.23	2.00	0.97
META2_0016	protein of unknown function, plant induced	3.310	2.560	2.177	0.541	0.333	0.236	0.171	0.251	0.139	2.595	0.323	0.188	0.10	0.00	0.88	0.09
META2_0017	Putative cytochrome P450	3.855	5.415	5.023	0.541	0.380	0.047	0.279	0.387	0.258	4.908	0.262	0.309	0.09	0.00	1.77	0.67
META2_0026	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0031	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0032	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_0044	putative ParM-like ATPase	0.000	0.068	0.000	0.000	0.048	0.000	0.107	0.077	0.060	0.027	0.020	0.081	4.00	0.12	6.00	0.14
META2_0059	protein of unknown function	0.000	0.181	0.074	0.000	0.048	0.213	0.150	0.135	0.119	0.100	0.111	0.134	1.82	0.40	1.82	0.42
META2_0070	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.018	0.020	0.000	0.00	0.37	0.00	0.37
META2_0071	protein of unknown function	0.195	0.272	0.272	0.271	0.190	0.189	0.214	0.232	0.179	0.254	0.202	0.208	1.11	0.30	1.55	0.84
META2_0083	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_0084	Heavy metal efflux pump, CzcA family	0.000	0.000	0.000	0.000	0.000	0.000	0.343	0.309	0.258	0.000	0.000	0.302	n.d.	0.00	n.d.	0.00
META2_0085	conserved protein of unknown function	0.156	0.181	0.173	0.000	0.190	0.142	0.300	0.290	0.278	0.172	0.141	0.289	2.26	0.00	3.07	0.47
META2_0086	protein of unknown function	0.078	0.091	0.000	0.000	0.048	0.000	0.450	0.387	0.278	0.054	0.020	0.370	9.17	0.62	27.50	0.24
META2_0087	conserved protein of unknown function	0.000	0.272	0.074	0.000	0.000	0.165	0.428	0.232	0.278	0.136	0.071	0.309	3.07	0.50	6.57	0.15
META2_0088	protein of unknown function	0.000	0.249	0.173	0.000	0.000	0.000	0.064	0.000	0.000	0.163	0.000	0.020	0.17	0.60	n.d.	0.37
META2_0089	putative cation transporting P-type ATPase	0.078	0.363	0.148	0.135	0.071	0.071	0.728	0.425	0.397	0.218	0.081	0.511	3.17	0.08	9.50	0.00
META2_0090	Conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.058	0.000	0.000	0.000	0.047	n.d.	0.12	n.d.	0.12
META2_0099	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_0100	conserved protein of unknown function	0.000	0.091	0.099	0.000	0.048	0.000	0.150	0.000	0.060	0.073	0.020	0.067	1.25	1.00	5.00	0.56
META2_0101	conserved protein of unknown function, putative Type	0.000	0.091	0.124	0.000	0.095	0.000	0.107	0.174	0.099	0.082	0.040	0.128	2.11	0.40	4.75	0.13
META2_0113	heavy metal efflux pump, CzcA family	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0121	RNA polymerase ECF-type sigma factor	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0128	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0129	Putative outer membrane efflux protein	0.000	0.000	0.000	0.000	0.095	0.071	0.407	0.309	0.377	0.000	0.071	0.363	n.d.	0.00	7.71	0.63
META2_0130	Putative multicopper oxidase	0.000	0.181	0.173	0.000	0.000	0.095	0.236	0.290	0.099	0.136	0.040	0.208	2.07	0.39	7.75	0.15
META2_0131	conserved protein of unknown function	0.273	0.680	0.470	0.135	0.190	0.071	0.450	0.387	0.814	0.508	0.131	0.551	1.46	0.67	6.31	0.02
META2_0132	conserved protein of unknown function	0.234	0.227	0.297	0.203	0.143	0.095	0.428	0.387	0.357	0.254	0.131	0.390	2.07	0.01	4.46	0.01
META2_0133	conserved protein of unknown function	0.000	0.113	0.124	0.000	0.071	0.142	0.171	0.213	0.258	0.091	0.091	0.215	3.20	0.46	3.56	0.49
META2_0135	conserved protein of unknown function	0.000	0.227	0.272	0.000	0.071	0.095	0.000	0.058	0.079	0.191	0.071	0.047	0.33	0.85	1.00	0.98
META2_0137	protein of unknown function	0.078	0.091	0.000	0.000	0.000	0.000	0.129	0.097	0.079	0.054	0.000	0.101	2.50	0.40	n.d.	0.00
META2_0140	pyruvate kinase	0.234	0.340	0.198	0.000	0.071	0.095	0.171	0.135	0.099	0.263	0.071	0.134	0.69	0.05	2.86	0.44
META2_0173	putative homolog czrB; cation efflux system protein	0.000	0.453	0.322	0.000	0.119	0.213	0.557	0.445	0.714	0.299	0.141	0.571	2.58	0.44	6.07	0.60
META2_0174	Heavy metal efflux pump CzcA	0.000	0.408	0.544	0.135	0.499	0.307	1.178	1.102	1.012	0.363	0.363	1.095	4.08	0.54	4.53	0.02
META2_0175	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0176	Cation efflux system protein czcD	0.000	0.113	0.148	0.000	0.000	0.000	0.043	0.000	0.040	0.100	0.000	0.027	0.36	0.87	n.d.	0.12
META2_0203	zinc, cobalt and lead efflux system	0.000	0.000	0.000	0.135	0.095	0.000	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
META2_0209	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_0210	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.071	0.047	0.043	0.039	0.060	0.018	0.050	0.047	3.50	0.12	1.40	0.35
META2_0243	protein of unknown function	0.000	0.000	0.000	0.135	0.143	0.047	0.064	0.097	0.040	0.000	0.101	0.067	n.d.	0.00	1.00	0.38
META2_0245	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_0246	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0253	Putative transcriptional regulator	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0254	Conserved HipA-like protein	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.058	0.040	0.000	0.030	0.034	n.d.	0.12	1.67	0.50
META2_0266	protein of unknown function	0.234	0.431	0.322	0.271	0.166	0.165	0.214	0.058	0.179	0.345	0.181	0.148	0.58	0.12	1.22	0.41
META2_0286	General secretion pathway protein E (Type II traffic war	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.060	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META2_0289	General secretion pathway protein G	0.078	0.068	0.099	0.000	0.048	0.000	0.064	0.058	0.079	0.082	0.020	0.067	1.11	0.26	5.00	0.13
META2_0301	putative transcriptional regulator, MucR family	0.234	0.340	0.421	1.014	0.618	0.591	0.557	0.696	0.675	0.345	0.665	0.645	2.53	0.02	1.45	0.57
META2_0313	protein of unknown function	0.000	0.068	0.049	0.000	0.000	0.000	0.043	0.000	0.060	0.045	0.000	0.034	1.00	0.99	n.d.	0.12
META2_0319	protein of unknown function	0.000	0.068	0.099	0.000	0.048	0.095	0.064	0.077	0.099	0.064	0.060	0.081	1.71	0.37	2.00	0.40
META2_0344	protein of unknown function	0.117	0.113	0.322	0.000	0.071	0.071	0.107	0.058	0.139	0.191	0.060	0.101	0.71	0.28	2.50	0.42
META2_0345	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_0346	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.095	0.043	0.039	0.060	0.000	0.060	0.047	n.d.	0.00	1.17	0.33
META2_0358	putative phosphonate transport system substrate-bindi	0.000	0.091	0.074	0.000	0.071	0.071	0.000	0.077	0.000	0.064	0.060	0.027	0.57	0.52	0.67	0.51
META2_0360	Phosphonate dehydrogenase (NAD-dependent phosphi	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0362	Transcriptional regulator	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.000	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META2_0363	NADPH-dependent FMN reductase	0.117	0.068	0.074	0.271	0.166	0.189	0.257	0.232	0.159	0.082	0.192	0.215	3.56	0.01	1.68	0.87
META2_0365	Putative protein tyrosine phosphatase (arsenate reduct	0.000	0.136	0.173	0.338	0.214	0.213	0.171	0.135	0.238	0.118	0.232	0.181	2.08	0.40	1.17	0.20
META2_0396	putative DNA methylase N-4/N-6	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_0418	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37

META2_0419	protein of unknown function, putative Response regula	0.000	0.113	0.049	0.000	0.261	0.307	0.279	0.271	0.298	0.064	0.242	0.282	6.00	0.59	1.75	0.37
META2_0421	putative multi-sensor Histidine kinase	0.000	0.068	0.000	0.000	0.000	0.000	0.043	0.077	0.000	0.027	0.000	0.040	2.00	0.51	n.d.	0.12
META2_0421	putative multi-sensor Histidine kinase	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0444	protein of unknown function	1.324	0.884	0.990	0.879	1.330	1.134	0.857	0.793	0.754	1.025	1.179	0.800	1.05	0.10	1.02	0.07
META2_0446	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.039	0.040	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META2_0468	Putative transcriptional regulator	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_0469	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_0475	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0494	protein of unknown function	0.000	0.068	0.074	0.000	0.000	0.047	0.064	0.000	0.000	0.054	0.020	0.020	0.50	0.52	1.50	0.98
META2_0497	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META2_0497	protein of unknown function	0.078	0.136	0.148	0.000	0.000	0.165	0.086	0.097	0.099	0.127	0.071	0.094	1.00	0.36	2.00	0.09
META2_0504	protein of unknown function	1.246	1.065	1.435	2.029	1.948	1.559	1.542	1.585	1.548	1.243	1.794	1.559	1.69	0.06	1.30	0.12
META2_0520	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0526	putative replication protein B	0.000	0.000	0.000	0.000	0.048	0.071	0.107	0.000	0.060	0.000	0.050	0.054	n.d.	0.12	1.60	0.96
META2_0526	putative replication protein B	0.000	0.045	0.099	0.000	0.214	0.213	0.129	0.135	0.159	0.054	0.181	0.141	3.50	0.49	1.17	0.31
META2_0527	putative replication protein A	0.000	0.113	0.124	0.000	0.166	0.165	0.086	0.116	0.099	0.091	0.141	0.101	1.50	0.35	1.07	0.31
META2_0529	protein of unknown function	0.156	0.181	0.148	0.000	0.071	0.071	0.129	0.097	0.079	0.163	0.060	0.101	0.83	0.03	2.50	0.42
META2_0534	protein of unknown function	1.090	1.178	1.113	1.488	1.093	1.536	0.836	0.580	0.734	1.134	1.341	0.712	0.85	0.01	0.80	0.01
META2_0554	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.058	0.099	0.000	0.000	0.067	n.d.	0.00	n.d.	0.00
META2_0562	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META2_0570	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_0573	conserved protein of unknown function	0.195	0.431	0.297	0.000	0.000	0.000	0.279	0.174	0.278	0.327	0.000	0.242	1.00	0.50	n.d.	0.00
META2_0577	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.107	0.155	0.139	0.000	0.020	0.134	n.d.	0.00	10.00	0.17
META2_0636	putative metal dependent phosphohydrolase (HD doma	0.078	0.159	0.148	0.000	0.119	0.142	0.086	0.058	0.079	0.136	0.111	0.074	0.73	0.12	1.00	0.30
META2_0638	protein of unknown function	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.045	0.000	0.013	0.40	0.94	n.d.	0.37
META2_0642	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META2_0652	protein of unknown function	0.000	0.091	0.124	0.338	0.285	0.236	0.129	0.271	0.139	0.082	0.272	0.181	3.00	0.45	1.00	0.12
META2_0678	putative multi-sensor hybrid Histidine kinase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_0684	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.043	0.039	0.040	0.000	0.020	0.040	n.d.	0.00	3.00	0.11
META2_0691	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0692	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.058	0.060	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META2_0693	N-acyl-L-homoserine lactone synthetase MsaI	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_0697	two component transcriptional regulator, winged helix	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.000	0.000	0.000	0.027	n.d.	0.12	n.d.	0.12
META2_0698	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.107	0.097	0.099	0.000	0.030	0.101	n.d.	0.00	5.00	0.13
META2_0699	protein of unknown function	0.234	0.317	0.124	0.000	0.000	0.000	0.236	0.271	0.337	0.227	0.000	0.282	1.68	0.39	n.d.	0.00
META2_0707	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.095	0.043	0.000	0.079	0.000	0.040	0.040	n.d.	0.12	1.50	0.49
META2_0719	protein of unknown function	0.000	0.091	0.074	0.000	0.000	0.047	0.000	0.000	0.119	0.064	0.020	0.040	0.86	0.50	3.00	0.95
META2_0738	DNA topoisomerase III	0.350	0.544	0.470	0.338	0.000	0.095	0.193	0.193	0.278	0.472	0.091	0.222	0.63	0.02	3.67	0.41
META2_0771	putative site-specific DNA-methyltransferase	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_0780	protein of unknown function	0.078	0.000	0.000	0.000	0.143	0.071	0.000	0.000	0.000	0.018	0.091	0.000	0.00	0.37	0.00	0.12
META2_0816	Superfamily I DNA and RNA helicase, helicase subunits-l	0.312	0.476	0.396	0.473	0.499	0.591	0.450	0.464	0.337	0.408	0.534	0.417	1.38	0.72	1.17	0.13
META2_0823	protein of unknown function	0.117	0.068	0.000	0.203	0.119	0.000	0.107	0.097	0.179	0.054	0.081	0.128	3.17	0.42	2.38	0.34
META2_0844	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0863	AAA superfamily ATPase	0.000	0.000	0.000	0.000	0.048	0.000	0.107	0.077	0.079	0.000	0.020	0.087	n.d.	0.00	6.50	0.14
META2_0870	2,5-diketo-D-gluconate reductase	0.000	0.068	0.074	0.000	0.000	0.047	0.064	0.116	0.099	0.054	0.020	0.094	2.33	0.41	7.00	0.15
META2_0871	flavin-dependent oxidoreductase, putative chromate re	0.000	0.136	0.124	0.135	0.095	0.047	0.129	0.058	0.099	0.100	0.081	0.094	1.27	0.33	1.75	0.87
META2_0883	putative alcohol dehydrogenase cytochrome c subunit	0.000	0.136	0.000	0.000	0.119	0.095	0.000	0.000	0.000	0.054	0.091	0.000	0.00	0.37	0.00	0.12
META2_0885	Putative membrane-bound aldehyde dehydrogenase [p	0.000	0.159	0.000	0.000	0.048	0.071	0.043	0.000	0.000	0.064	0.050	0.013	0.29	0.93	0.40	0.54
META2_0887	Putative bacteriocin protein	0.779	0.816	0.520	0.203	0.071	0.189	0.407	0.445	0.437	0.699	0.141	0.430	0.83	0.03	4.57	0.03
META2_0888	putative peroxidase family protein	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_0891	Putative ATP-dependent protease ATP-binding subunit	1.519	3.014	2.623	1.082	1.449	1.394	1.907	1.488	1.310	2.522	1.371	1.559	0.83	0.17	1.71	0.28
META2_0893	putative homolog cbpA; a curved DNA-binding protein;	0.000	0.068	0.074	0.000	0.000	0.000	0.000	0.077	0.040	0.054	0.000	0.040	1.00	0.97	n.d.	0.12
META2_0894	chaperone Hsp70 in DNA biosynthesis/cell division	1.012	2.674	1.782	0.676	0.713	0.425	0.728	0.619	0.496	1.960	0.585	0.612	0.42	0.03	1.57	0.89
META2_0905	conserved protein of unknown function	0.000	0.136	0.099	0.000	0.071	0.047	0.043	0.077	0.000	0.091	0.050	0.040	0.60	0.92	1.20	1.00
META2_0906	Putative heat shock protein Hsp20	0.935	0.770	0.693	0.609	0.499	0.543	0.857	0.831	0.595	0.780	0.534	0.759	1.31	0.73	2.13	0.07
META2_0907	putative molecular chaperone small heat shock protein	1.090	0.770	0.495	0.338	0.570	0.425	0.321	0.445	0.516	0.744	0.474	0.430	0.78	0.10	1.36	0.87
META2_0908	Heat shock protein Hsp20	0.740	0.521	0.371	0.541	0.404	0.331	0.750	0.754	0.496	0.517	0.393	0.665	1.74	0.41	2.54	0.09
META2_0909	putative Transcriptional regulator	0.234	0.295	0.272	0.135	0.166	0.213	0.257	0.213	0.218	0.272	0.181	0.228	1.13	0.17	1.89	0.10
META2_0910	protease, ATP-dependent zinc-metallo	0.000	0.091	0.049	0.203	0.119	0.000	0.193	0.193	0.079	0.054	0.081	0.155	3.83	0.49	2.88	0.37
META2_0911	protein disaggregation chaperone	10.669	8.973	9.699	10.551	6.627	5.411	6.941	6.688	6.232	9.634	6.693	6.613	0.93	0.00	1.48	0.68
META2_0912	protein of unknown function	2.258	2.153	2.549	0.947	0.926	1.158	1.007	1.450	1.369	2.322	1.028	1.284	0.75	0.01	1.87	0.17
META2_0913	conserved protein of unknown function	0.389	0.272	0.272	0.473	0.285	0.213	0.171	0.097	0.139	0.299	0.282	0.134	0.61	0.01	0.71	0.04
META2_0915	conserved protein of unknown function	0.195	0.272	0.272	0.271	0.095	0.118	0.129	0.097	0.139	0.254	0.131	0.121	0.64	0.01	1.38	0.61
META2_0916	conserved protein of unknown function	0.701	0.725	0.594	0.338	0.404	0.284	0.343	0.329	0.318	0.671	0.343	0.329	0.66	0.00	1.44	0.81
META2_0918	conserved protein of unknown function	5.763	6.888	6.285	7.507	1.591	3.237	3.835	4.117	4.307	6.405	3.175	4.093	0.86	0.00	1.93	0.70
META2_0919	conserved protein of unknown function	6.697	6.072	6.062	5.140	3.634	4.442	4.285	4.156	4.029	6.214	4.203	4.153	0.90	0.00	1.48	0.66
META2_0924	conserved protein of unknown function	0.000	0.068	0.074	0.135	0.048	0.071	0.086	0.058	0.119	0.054	0.071	0.087	2.17	0.40	1.86	0.82
META2_0925	putative ATPase, ParA type	0.156	0.249	0.173	0.000	0.333	0.236	0.279	0.309	0.198	0.200	0.242	0.262	1.77	0.19	1.63	0.36
META2_0927	conserved protein of unknown function	0.000	0.113	0.074	0.000	0.071	0.095	0.043	0.058	0.060	0.073	0.071	0.054	1.00	0.30	1.14	0.32
META2_0928	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.118	0.000	0.000	0.000	0.000	0.071	0.000	n.d.	n.d.	0.00	0.12
META2_0932	transposase of ISMex10, ISL3 family	0.000	0.159	0.124	0.000	0.190	0.000	0.171	0.000	0.119	0.109	0.081	0.094	1.17	1.00	1.75	0.50
META2_0946	conserved protein of unknown function	0.935	0.657	0.619	0.676	0.808	0.567	0.728	0.696	0.913	0.708	0.685	0.780	1.49	0.69	1.71	0.37
META2_0952	protein of unknown function	0.506	0.317	0.371	0.609	0.475	0.945	0.728	0.503	0.595	0.381	0.695	0.605	2.14	0.07	1.30	0.76
META2_0952	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.039	0.040	0.000	0.020	0.027	n.d.	0.12	2.00	0.51
META2_0955	protein of unknown function	0.000	0.000	0.000	0.203	0.095	0.071	0.171	0.097	0.060	0.000	0.101	0.108	n.d.	0.00	1.60	0.82
META2_0956	protein of unknown function	0.117	0.000	0.000	0.000	0.000	0.095	0.086	0.077	0.000	0.027	0.040	0.054	2.67	0.50	2.00	0.51
META2_0956	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META2_0963	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0970	protein of unknown function	0.000	0.000	0.000	0.135	0.119	0.095	0.064	0.116	0.099	0.000	0.111	0.094	n.d.	0.00	1.27	0.31
META2_0971	DNA polymerase I	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.040	0.000	0.000	0.034	n.d.	0.12	n.d.	0.12
META2_0971	DNA polymerase I	0.000	0.045	0.074	0.135	0.048	0.047	0.086	0.097	0.198	0.045	0.060	0.128	3.80	0.48	3.17	0.27
META2_0982	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_0992	DNA ligase, NAD(+)-dependent	0.000	0.113	0.099	0.203	0.190	0.165	0.171	0.271	0.139	0.082	0.181	0.195	3.22	0.46	1.61	0.99
META2_0993	protein of unknown function	0.000	0.159	0.074	0.135	0.190	0.165	0.236	0.251	0.198	0.091	0.171	0.228	3.40	0.49	2.00	0.05
META2_1007	beta-lactamase domain protein	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.077	0.040	0.000	0.000	0.060	n.d.	0.00	n.d.	0.00
META2_1015	DNA-binding response regulator in two-component reg	0.000	0.000	0.000	0.000	0.000	0.095	0.064	0.039	0.000	0.000	0.040	0.034	n.d.	0.12	1.25	0.48
META2_1017	putative DNA-binding transcriptional regulator	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
META2_1018	putative nodulin-related protein	0.000	0.000	0.124	0.000	0.000	0.000	0.000	0.039	0.000	0.045	0.000	0.013	0.40	0.94	n.d.	0.37
META2_1020	putative DNA-binding ferritin-like protein	0.000	0.113	0.124	0.000	0.048	0.047	0.000	0.000	0.000	0.091	0.040	0.000	0.00	0.12	0.00	0.12
META2_1024	DNA-binding response regulator in two-component reg	0.000	0.159	0.124	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000	0.000	0.00	0.12	n.d.	n.d.
META2_1042	protein of unknown function	0.000	0.091	0.049	0.000	0.095	0.118	0.150	0.232	0.159	0.054	0.091	0.181	4.50	0.53	3.00	0.45
META2_1051	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
META2_1082	protein of unknown function	0.000	0.091	0.124	0.000	0.095	0.095	0.107	0.135	0.139	0.082	0.081	0.128	2.11	0.40	2.38	0.42
META2_1087	conserved protein of unknown function	0.000	0.227	0.124	0.203	0.095	0.165	0.214	0.251	0.119	0.136	0.141	0.195	1.93	0.39	2.07	0.51
META2_1088	conserved protein of unknown function	0.000	0.000	0.049	0.000	0.095	0.118	0.107	0.097	0.079	0.018	0.091	0.094	7.00	0.15	1.56	0.36
META2_1095	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_1097	conserved protein of unknown function	0.000	0.113	0.346	0.000	0.143	0.000	0.214	0.155	0.258	0.172	0.060	0.208	1.63	0.38	5.17	0.13
META2_1102	putative helicase (ATP-dependent exodeoxyribonucleas	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_1102	putative helicase (ATP-dependent exodeoxyribonucleas	0.000	0.000	0.049	0.271	0.214	0.260	0.064	0.116	0.119	0.018	0.242	0.101	7.50	0.15	0.63	0.01
META2_1119	Putative HTH-type transcriptional regulator	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
META2_1126	Putative HTH-type transcriptional regulator	0.000	0.000	0.000	0.000	0.000	0.047	0.064	0.058	0.099	0.000	0.020	0.074	n.d.	0.00	5.50	0.13
META2_1135	sodium-proton antiporter	0.000	0.091	0.049	0.000	0.238	0.284	0.043	0.116	0.060	0.054	0.222	0.074	1.83	0.38	0.50	0.21
META2_1142	protein of unknown function	0.000	0.068	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.027	0.020	0.000	0.00	0.37	0.00	0.37
META2_1142	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_1145	conserved protein of unknown function; putative expor	0.000	0.159	0.148	0.541	0.451	0.331	0.279	0.271	0.258	0.118	0.413	0.269	3.08	0.46	0.98	0.03
META2_1152	conserved protein of unknown function	0.117	0.045	0.074	0.203	0.143	0.142	0.107	0.058	0.000	0.073	0.151	0.054	1.00	0.37	0.53	0.48
META2_1160	protein of unknown function	0.117	0.159	0.198	0.000	0.119	0.142	0.129	0.097	0.139	0.163	0.111	0.121	1.00	0.25	1.64	0.36
META2_1185	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.077	0.040	0.000	0.000	0.040	n.d.	0.12	n.d.	0.12
META2_1189	putative Phage integrase	0.000	0.000	0.000	0.203	0.000	0.000	0.043	0.039	0.060	0.000	0.030	0.047	n.d.	0.00	2.33	0.07
META2_1190	DEAD/DEAH box helicase domain protein	0.156	0.748	0.693	0.812	0.689	0.425	0.450	0.483	0.675	0.590	0.595	0.538	1.23	0.72	1.36	0.52
META2_1191	Helicase domain protein	0.000	0.068	0.000	0.000	0.048	0.000	0.000	0.155	0.060	0.027	0.020	0.074	3.67	0.54	5.50	0.56
META2_1192	putative type II DNA modification enzyme	0.000	0.045	0.000	0.000	0.071	0.000	0.043	0.058	0.119	0.018	0.030	0.074	5.50	0.13	3.67	0.11
META2_1211	NADPH quinone oxidoreductase, Zinc-containing alcoho	0.000	0.136	0.000	0.000	0.095	0.047	0.043	0.097	0.060	0.054	0.060	0.067	1.67	0.09	1.67	0.37
META2_1213	Transcriptional regulator, LysR family	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.039	0.060	0.000	0.000	0.047	n.d.	0.00	n.d.	0.00
META2_1214	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.020	0.000	n.d.	n.d.	0.00	0.37
META2_1219	putative alcohol dehydrogenase	0.000	0.136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.054	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_1221	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_1221	conserved protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
META2_1223	conserved protein of unknown function	0.078	0.317	0.297	0.000	0.000	0.047	0.000	0.000	0.000	0.254	0.020	0.000	0.00	0.00	0.00	0.37
META2_1231	putative phosphonate transport system substrate-bindi	0.000	0.000	0.000	0.000	0.048	0.047	0.000	0.000	0.000	0.000	0.040	0.000	n.d.	n.d.	0.00	0.12
META2_1233	Phosphonate dehydrogenase (NAD-dependent phosphi	0.000	0.136	0.049	0.000	0.071	0.071	0.086	0.058	0.040	0.073	0.060	0.060	1.13	0.33	1.50	0.35
META2_1235	Putative homolog short-chain dehydrogenase, involved	0.000	0.113	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.00	0.12	n.d.	n.d.
META2_1258	protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.000	0.086	0.097	0.060	0.000	0.040	0.081	n.d.	0.00	3.00	0.11
META2_1298	protein of unknown function	0.000	0.045	0.000	0.000	0.119	0.071	0.107	0.097	0.119	0.018	0.081	0.108	8.00	0.16	2.00	0.40

META2_1333	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
META2_1356	protein of unknown function	0.078	0.045	0.074	0.135	0.095	0.095	0.086	0.077	0.060	0.064	0.101	0.074	1.57	0.54	1.10	0.08
META2_CDS509485D	protein of unknown function; RMQ09476	0.000	0.204	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.37	n.d.	n.d.
p1META_0006	putative ATPase, ParA type	0.000	0.159	0.173	0.000	0.071	0.118	0.086	0.193	0.000	0.127	0.081	0.094	1.00	0.97	1.75	0.96
p1META_0009	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
p1META_0010	protein of unknown function	0.000	0.113	0.099	0.000	0.143	0.095	0.000	0.058	0.119	0.082	0.101	0.060	1.00	0.97	0.90	0.96
p1META_0012	DNA invertase gene rlgA	0.000	0.181	0.049	0.203	0.143	0.095	0.236	0.116	0.179	0.091	0.131	0.175	2.60	0.47	2.00	0.56
p1META_0014	protein of unknown function	0.234	0.159	0.297	0.135	0.095	0.095	0.107	0.000	0.040	0.227	0.101	0.047	0.28	0.57	0.70	0.45
p1META_0018	protein of unknown function of	0.234	0.249	0.198	0.203	0.190	0.118	0.107	0.097	0.179	0.227	0.161	0.128	0.76	0.04	1.19	0.30
p1META_0020	RND divalent metal cation efflux transporter CzcA	0.000	0.159	0.099	0.000	0.261	0.095	0.000	0.000	0.000	0.100	0.151	0.000	0.00	0.12	0.00	0.12
p1META_0021	efflux transporter, RND family, MFP subunit	0.000	0.045	0.000	0.000	0.190	0.165	0.000	0.000	0.000	0.018	0.151	0.000	0.00	0.37	0.00	0.12
p1META_0029	conserved protein of unknown function	0.000	0.068	0.074	0.203	0.166	0.142	0.064	0.077	0.099	0.054	0.161	0.081	2.00	0.39	0.75	0.01
p1META_0034	conserved protein of unknown function	0.000	0.068	0.099	0.000	0.048	0.118	0.129	0.000	0.079	0.064	0.071	0.067	1.43	0.98	1.43	0.97
p1META_0047	putative mobilization protein C	0.000	0.317	0.124	0.271	0.333	0.213	0.343	0.425	0.417	0.172	0.272	0.397	3.11	0.49	2.19	0.06
p2META_0004	protein of unknown function	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.058	0.000	0.000	0.020	0.020	n.d.	0.37	1.50	0.99
p2META_0005	protein of unknown function	0.000	0.000	0.049	0.000	0.048	0.000	0.000	0.000	0.060	0.018	0.020	0.020	1.50	0.99	1.50	0.99
p2META_0006	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.095	0.118	0.129	0.116	0.159	0.000	0.091	0.134	n.d.	0.00	2.22	0.41
p2META_0009	conserved protein of unknown function	0.000	0.045	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.018	0.030	0.000	0.00	0.37	0.00	0.37
p2META_0010	conserved protein of unknown function	0.623	0.770	0.619	0.406	0.546	0.165	0.514	0.522	0.437	0.680	0.363	0.491	0.97	0.03	2.03	0.35
p2META_0012	site-specific DNA recombinase	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.030	0.000	n.d.	n.d.	0.00	0.37
p2META_0019	transposase of ISMex38, Tn3 family	0.000	0.000	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
p2META_0020	putative Plasmid stabilization protain	0.000	0.091	0.000	0.000	0.000	0.000	0.043	0.077	0.040	0.036	0.000	0.054	2.00	0.09	n.d.	0.00
p2META_0022	DNA invertase gene rlgA	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
p2META_0029	Copper resistance copB protein	0.584	0.000	0.124	0.338	0.333	0.284	0.043	0.000	0.079	0.181	0.312	0.040	0.30	0.82	0.19	0.66
p2META_0030	Copper resistance protein copA	0.000	0.000	0.074	0.000	0.190	0.000	0.086	0.000	0.000	0.027	0.081	0.027	1.33	0.99	0.50	0.95
p2META_0033	integration host factor (IHF) like DNA-binding protein	0.000	0.000	0.000	0.000	0.000	0.071	0.086	0.000	0.040	0.000	0.030	0.040	n.d.	0.12	2.00	0.51
p2META_0035	conserved protein of unknown function	0.117	0.181	0.099	0.000	0.071	0.095	0.064	0.039	0.000	0.136	0.071	0.034	0.33	0.52	0.71	0.95
p2META_0041	conserved protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.020	n.d.	0.37	n.d.	0.37
p2META_0042	Conjugal transfer protein TraD	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
p3META_0006	putative partitioning protein/Cobyrinic acid a,c-diamide	0.000	0.113	0.000	0.271	0.166	0.165	0.171	0.097	0.159	0.045	0.181	0.141	4.20	0.13	1.17	0.23
p3META_0007	protein of unknown function	0.000	0.000	0.000	0.000	0.071	0.000	0.000	0.039	0.079	0.000	0.030	0.040	n.d.	0.12	2.00	0.50
p3META_0008	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.013	n.d.	0.37	n.d.	0.37
p3META_0010	conserved protein of unknown function	0.000	0.113	0.124	0.000	0.071	0.047	0.000	0.058	0.079	0.091	0.050	0.047	0.70	0.94	1.40	0.98
p3META_0012	protein of unknown function	0.000	0.068	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.027	0.000	0.013	0.67	0.98	n.d.	0.37
p3META_0013	protein of unknown function	0.117	0.091	0.000	0.271	0.095	0.189	0.129	0.135	0.119	0.064	0.161	0.128	2.71	0.41	1.19	0.41
p3META_0015	protein of unknown function	0.000	0.091	0.000	0.000	0.000	0.000	0.043	0.058	0.000	0.036	0.000	0.034	1.25	0.48	n.d.	0.12
p3META_0024	conserved protein of unknown function	0.000	0.091	0.000	0.000	0.071	0.000	0.000	0.039	0.040	0.036	0.030	0.027	1.00	0.47	1.33	0.48
p3META_0028	protein of unknown function	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.000	0.013	1.00	0.99	n.d.	0.37
p3META_0030	DNA invertase gene rlgA	0.000	0.000	0.000	0.000	0.071	0.095	0.086	0.039	0.060	0.000	0.071	0.060	n.d.	0.00	1.29	0.33
p3META_CDS5359D	protein of unknown function	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
#N/A	#N/A	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.000	0.000	0.000	0.060	0.000	n.d.	n.d.	0.00	0.12
#N/A	#N/A	0.000	0.000	0.074	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.00	0.37	n.d.	n.d.
#N/A	#N/A	0.000	0.000	0.000	0.000	0.000	0.000	0.086	0.000	0.000	0.000	0.000	0.027	n.d.	0.37	n.d.	0.37
#N/A	#N/A	0.156	0.000	0.000	0.135	0.071	0.000	0.064	0.058	0.099	0.036	0.050	0.074	2.75	0.09	2.20	0.33
#N/A	#N/A	0.584	1.178	1.237	1.014	0.404	0.756	0.728	1.005	1.092	1.061	0.645	0.948	1.21	0.94	2.20	0.35
#N/A	#N/A	0.234	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.082	0.000	0.013	0.22	0.60	n.d.	0.37
#N/A	#N/A	3.076	3.353	2.771	3.111	6.841	6.285	2.357	1.856	2.560	3.075	6.048	2.251	0.99	0.05	0.56	0.04
#N/A	#N/A	0.117	0.113	0.074	0.000	0.000	0.142	0.064	0.000	0.000	0.100	0.060	0.020	0.27	0.14	0.50	0.95
#N/A	#N/A	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.00	0.37	n.d.	n.d.
#N/A	#N/A	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.119	0.000	0.000	0.040	n.d.	0.37	n.d.	0.37
#N/A	#N/A	1.441	1.314	1.237	1.691	4.703	3.780	1.071	0.696	1.369	1.315	3.860	1.042	1.07	0.24	0.40	0.04
#N/A	#N/A	0.156	0.340	0.074	0.000	0.000	0.118	0.107	0.000	0.079	0.200	0.050	0.060	0.41	0.46	1.80	0.50
#N/A	#N/A	0.000	0.181	0.000	0.000	0.000	0.000	0.000	0.000	0.079	0.073	0.000	0.027	0.50	0.95	n.d.	0.37
#N/A	#N/A	0.000	0.068	0.000	0.000	0.048	0.071	0.000	0.000	0.000	0.027	0.050	0.000	0.00	0.37	0.00	0.12
#N/A	#N/A	1.519	2.288	1.782	1.082	4.371	3.497	1.071	0.831	1.409	1.923	3.508	1.102	0.77	0.05	0.47	0.13
#N/A	#N/A	0.545	1.881	1.386	0.879	2.162	1.961	0.686	0.309	0.556	1.388	1.885	0.511	0.50	0.13	0.41	0.04
#N/A	#N/A	0.000	0.113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.00	0.37	n.d.	n.d.
#N/A	#N/A	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	0.00	0.37	n.d.	n.d.
#N/A	#N/A	1.869	2.062	1.806	2.705	1.686	1.630	1.864	1.430	1.786	1.923	1.814	1.687	1.18	0.24	1.39	0.46
#N/A	#N/A	0.117	0.363	0.297	0.135	0.190	0.142	0.043	0.000	0.079	0.281	0.161	0.040	0.19	0.60	0.38	0.52
#N/A	#N/A	0.000	0.159	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000	0.000	0.00	0.12	n.d.	n.d.
#N/A	#N/A	0.078	0.000	0.000	0.000	0.000	0.095	0.000	0.000	0.060	0.018	0.040	0.020	1.50	0.99	0.75	0.97
#N/A	#N/A	0.078	0.521	0.322	0.000	0.166	0.165	0.064	0.000	0.040	0.345	0.141	0.034	0.13	0.63	0.36	0.87

Suplemental Table 2: List of proteins of the central metabolism

Gene Number	Gene	Description (gene name)	oxalate vs acetate		oxalate vs methanol		Normalized sprectra (‰)		
			fold- change	p-value	fold-change	p-value	Acetate	Methanol	oxalate
Oxalate metabolism									
META1_0988	*frc1*	formyl-CoA transferase, NAD(P)-binding	only on oxalate	0.00	n.d.	0.00	0.00	0.00	11.53
META1_0990	*oxc*	oxalyl-CoA decarboxylase (oxc, yfdU)	n.d.	0.00	n.d.	0.00	0.00	0.00	11.61
META1_0992	*oxlT*	oxalate/formate antiporter	n.d.	0.00	n.d.	0.00	0.00	0.00	0.67
META1_0993	*oxlT*	oxalate/formate antiporter	n.d.	0.00	n.d.	0.00	0.00	0.00	1.08
META1_0999	*frc2*	formyl-CoA transferase, NAD(P)-binding	n.d.	0.00	n.d.	0.00	0.00	0.00	1.47
META1_1925	*oxlT*	putative oxalate/formate antiporter	n.d.	0.00	n.d.	0.00	0.00	0.00	1.30
META1_2127	*oxlT*	putative oxalate/formate antiporter	n.d.	0.00	17.00	0.25	0.00	0.04	0.69
META1_2129	*panE2*	oxalyl-CoA reductase	24.85	0.00	3.46	0.00	0.10	0.72	2.48
META1_2130	*oxs*	oxalyl-CoA synthetase	16.50	0.89	2.92	0.00	0.10	0.56	1.65
C1 oxidation									
META1_5031	*fdh1B*	tungsten-containing formate dehydrogenase beta subunit	1.52	0.07	4.78	0.00	0.76	0.24	1.16
META1_5032	*fdh1A*	tungsten-containing formate dehydrogenase alpha subunit	2.31	0.02	4.10	0.00	1.42	0.80	3.27
META1_4846	*fdh2C*	NAD-dependent formate dehydrogenase, Molybdenum containing, gamma subunit	n.d.	0.00	7.07	0.18	0.00	0.05	0.36
META1_4847	*fdh2B*	NAD-dependent formate dehydrogenase, Molybdenum containing, beta subunit	n.d.	0.00	n.d.	0.02	0.00	0.00	0.00
META1_4848	*fdh2A*	NAD-dependent formate dehydrogenase, molybdenum containing, alpha subunit	n.d.	0.00	3.05	0.00	0.00	1.47	4.50
META1_4849	*fdh2D*	NAD-linked formate dehydrogenase, Molybdenum containing, delta subunit	n.d.	0.00	1.68	0.44	0.00	0.25	0.42
META1_0303	*fdh3A*	formate dehydrogenase alpha subunit precursor (tat pathway signal)	2.06	0.46	0.68	0.83	33.57	101.82	69.22
META1_0304	*fdh3B*	formate dehydrogenase iron-sulfur (beta) subunit	n.d.	0.00	0.95	0.35	0.00	14.11	13.44
META1_0305	*fdh3C*	formate dehydrogenase gamma (cytochrome) subunit	0.56	0.95	0.67	0.98	7.26	6.05	4.03
META1_2093	*fdh4B*	formate dehydrogenase subunit B	0.00	0.37	n.d.	0.12	0.04	0.00	0.00
META1_2094	*fdh4A*	formate dehydrogenase subunit A	0.02	0.32	0.01	0.35	0.87	0.92	0.01
Energy metabolism									
META1_2956	*pntAA*	NAD(P)+ transhydrogenase, subunit alpha part 1.	0.78	0.34	9.58	0.00	10.28	0.84	8.02
META1_2957	*pntAB*	NAD(P) transhydrogenase, subunit alpha part 2	0.86	0.37	8.19	0.37	3.06	0.32	2.64
META1_3299	*hppa*	H+ translocating pyrophosphate synthase	0.70	0.01	n.d.	0.00	0.62	0.00	0.43
TCA cycle									
META1_2531	*acs*	acetyl-CoA synthetase	0.72	0.00	2.14	0.00	4.65	1.57	3.36
META1_5129	*gltA (icdB)*	citrate synthase	0.42	0.01	1.24	0.08	4.93	1.66	2.07
META1_2828	*acnA*	aconitate hydratase	0.36	0.01	0.71	0.06	6.32	3.25	2.29
META1_3354	*icd*	NADP-dependent isocitrate dehydrogenase	0.32	0.00	0.70	0.15	4.46	2.07	1.44
META1_1540	*sucA*	2-oxoglutarate dehydrogenase complex, E1 component	0.45	0.00	1.21	0.06	5.44	2.01	2.43
META1_1541	*sucB*	2-oxoglutarate dehydrogenase complex, dihydrolipoamide succinyltransferase	0.34	0.00	1.07	0.43	3.43	1.11	1.18
META1_1542	*lpd*	2-oxoglutarate dehydrogenase, dihydrolipoamide dehydrogenase	0.29	0.00	0.97	0.63	2.70	0.81	0.78
META1_1538	*sucC*	succinyl-CoA synthetase, beta subunit	0.36	0.00	0.67	0.07	3.77	2.00	1.34
META1_1539	*sucD*	succinyl-CoA synthetase, alpha subunit	0.48	0.02	0.76	0.09	2.33	1.47	1.12
META1_3860	*sdhD*	succinate dehydrogenase delta subunit	0.74	0.95	1.11	0.50	0.05	0.03	0.03
META1_3861	*sdhA/B*	succinate dehydrogenase, flavoprotein subunit	0.33	0.00	1.11	0.46	2.08	0.61	0.69
META1_3863	*sdhB*	succinate dehydrogenase, iron-sulfur subunit	0.28	0.01	0.97	0.08	0.38	0.11	0.11
META1_2857	*fumC*	fumarase C	0.48	0.01	1.50	0.03	3.15	1.02	1.53
META1_1537	*mdh*	malate dehydrogenase	0.47	0.01	0.79	0.13	3.69	2.19	1.73
EMC pathway									
META1_3700	*phaA*	beta-ketothiolase	0.53	0.02	0.82	0.04	6.31	4.04	3.32
META1_3701	*phaB*	acetoacetyl-CoA reductase	0.59	0.03	0.71	0.32	1.97	1.63	1.16
META1_3675	*croR*	crotonase	0.80	0.69	0.77	0.29	0.44	0.46	0.36
META1_0178	*ccr*	crotonyl-CoA carboxylase/reductase	0.54	0.01	0.48	0.00	2.78	3.14	1.51
META1_0839	*epm*	ethylmalonyl-CoA/methylmalonyl-CoA epimerase	0.74	0.27	0.85	0.27	0.34	0.29	0.25
META1_0180	*ecm*	ethylmalonyl-CoA mutase	1.01	0.73	0.70	0.02	2.00	2.85	2.01
META1_2223	*msd*	methylsuccinyl-CoA dehydrogenase, putative isobutyryl-CoA dehydrogenase	0.69	0.01	0.59	0.02	2.95	3.45	2.02
META1_4153	*mcd*	mesaconyl-CoA hydratase	0.93	0.88	0.37	0.00	0.60	1.51	0.56
META1_0172	*pccB*	propionyl-CoA carboxylase beta chain	0.66	0.04	0.67	0.03	3.08	3.04	2.04
META1_3203	*pccA*	propionyl-CoA carboxylase alpha subunit	1.00	0.96	0.58	0.03	2.67	4.64	2.67
META1_2390	*mcmB*	methylmalonyl-CoA mutase, beta subunit	1.14	0.15	0.89	0.82	1.22	1.56	1.40
META1_5251	*mcmA*	methylmalonyl-CoA mutase, alpha subunit	1.64	0.01	0.79	0.15	0.96	2.01	1.58
META1_2137	*mcl2*	malyl-CoA thioesterase	1.06	0.49	1.45	0.06	0.72	0.52	0.76
PHB metabolism									
META1_3304	*phaC*	poly(3-hydroxyalkanoate) polymerase	0.56	0.25	3.89	0.62	1.69	0.24	0.94
META1_0419	*depA*	intracellular PHB depolymerase	1.35	0.56	1.40	0.41	0.20	0.19	0.27
Serine cycle									
META1_3384	*glyA*	serine hydroxymethyltransferase	1.09	0.55	0.76	0.00	4.19	6.04	4.56
META1_1726	*sga*	serine glyoxylate aminotransferase	3.74	0.00	0.48	0.00	1.42	11.02	5.32
META1_1727	*hprA*	hydroxypyruvate reductase, NAD(P)H-dependent.	3.20	0.01	0.63	0.02	0.48	2.44	1.54
META1_2944	*gck*	glycerate kinase	1.86	0.00	0.52	0.00	0.63	2.22	1.16
META1_2984	*eno*	enolase	0.70	0.01	1.02	1.00	2.85	1.97	2.00
META1_1732	*ppc*	phosphoenolpyruvate carboxylase	9.48	0.00	0.58	0.00	0.23	3.70	2.15
META1_1731	*mtkB*	malate thiokinase, small subunit	3.78	0.00	0.46	0.00	0.64	5.21	2.40
META1_1730	*mtkA*	malate thiokinase, large subunit	5.81	0.00	0.43	0.00	0.23	3.04	1.32
META1_1733	*mclA1*	malyl-CoA lyase/beta-methylmalyl-CoA lyase	2.18	0.00	0.40	0.00	1.76	9.51	3.84
C1 pathways									
META1_1729	*fch*	methenyl tetrahydrofolate cyclohydrolase	3.27	0.03	0.59	0.05	0.37	2.07	1.22
META1_1728	*mtdA*	NADP-dependent methylene-tetrahydromethanopterin/methylene-tetrahydrofolate dehydrogenase	4.86	0.00	0.84	0.64	0.81	4.67	3.92
META1_0329	*ftfL*	formate-tetrahydrofolate ligase (formyltetrahydrofolate synthetase)	2.74	0.00	0.91	0.21	1.36	4.10	3.73
META1_1766	*fae*	formaldehyde-activating enzyme (translation)	0.73	0.16	0.45	0.01	3.77	6.09	2.76
META1_1761	*mtdB*	NAD(P)-dependent methylene tetrahydromethanopterin dehydrogenase	1.18	0.21	0.99	0.06	1.40	1.84	1.22
META1_1763	*mch*	N(5),N(10)-methenyltetrahydromethanopterin cyclohydrolase (methenyl-H4MPT cyclohydrolase)	0.87	0.21	0.66	0.07	1.40	1.84	1.22
META1_1755	*fhcC*	formyltransferase/hydrolase complex Fhc subunit C	0.57	0.23	1.01	0.93	0.57	0.72	0.73
META1_1756	*fhcD*	formyltransferase/hydrolase complex Fhc subunit D	0.47	0.95	0.62	0.03	0.47	0.79	0.49
META1_1757	*fhcA*	formyltransferase/hydrolase complex Fhc subunit A	0.87	0.73	0.89	0.43	0.87	0.98	0.87
META1_1758	*fhcB*	formyltransferase/hydrolase complex Fhc subunit B	0.82	1.00	0.66	0.01	0.82	1.16	0.77
Serine / glycine metabolism									
META1_0620	*gcvP*	glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	1.10	0.55	29.09	0.92	3.75	0.14	4.11
META1_0622	*gcvT*	glycine cleavage complex protein T, aminomethyltransferase, tetrahydrofolate-dependent	2.08	0.08	72.22	0.31	1.05	0.03	2.18
META1_0485	*serC*	phosphoserine aminotransferase	1.22	0.39	0.52	0.02	0.21	0.49	0.26
META1_2848	-	putative phosphoserine phosphatase (serB-like)	1.42	0.31	1.40	0.40	0.21	0.21	0.30
META1_0105	*serA*	D-3-phosphoglycerate dehydrogenase	0.45	0.00	1.13	0.37	2.88	1.14	1.29
META1_0486	*serA*	phosphoglycerate dehydrogenase	1.35	0.38	0.90	0.95	0.21	0.31	0.28
C3 metabolism									
META1_1533	*pck*	phosphoenolpyruvate carboxykinase	0.03	0.99	n.d.	0.12	1.37	0.00	0.04
META1_3097	*ppdK*	pyruvate phosphate dikinase (Pyruvate, orthophosphate dikinase)	0.61	0.01	1.08	0.56	5.90	3.34	3.60
META1_2941	*pyk*	pyruvate kinase	1.19	0.35	0.34	0.00	0.62	2.14	0.73
META1_0594	*dme*	NAD-dependent malic enzyme	0.44	0.00	1.55	0.01	5.38	1.51	2.35
META1_2987	*pdhB*	pyruvate dehydrogenase E1 beta subunit	0.40	0.01	1.71	0.02	4.00	0.95	1.62
META1_2986	*pdhA*	pyruvate dehydrogenase E1 alpha subunit	0.33	0.01	1.55	0.04	2.01	0.43	0.67
META1_2989	*pdhC*	dihydrolipoamide acetyltransferase	0.27	0.00	2.20	0.03	5.44	0.67	1.47
META1_2990	*lpd*	dihydrolipoamide dehydrogenase, E3 Component of Pyruvate dehydrogenase multienzyme complex	0.31	0.00	3.33	0.00	3.98	0.37	1.24

Scenario 1: flux distribution calculated from constrained oxalate uptake rate to experimentally determined value
Secnatio 2: flux distribution calculated from constrained oxalate uptake rate and growth rate to experimentally determined values

Scenario 1				Scenario 2						
Reaction number	Constrains	Reaction number	Results	Reaction number	Constrains	Reaction number	Results	Reaction number	Enzyme name	Reaction
EX-0007	0	EX-0001	0	EX-0007	0	EX-0001	0	EX-0001	exchange flux : methanol	= methanol[e]
EX-0009	0	EX-0002	9.2224	EX-0009	0	EX-0002	12.3621	EX-0002	exchange flux : oxygen	= O2[e]
EX-0010	0	EX-0003	1.7869	EX-0010	0	EX-0003	1.0561	EX-0003	exchange flux : nitrogen	= NH3[e]
EX-0011	0	EX-0004	-60.1211	EX-0011	0	EX-0004	-63.1796	EX-0004	exchange flux : CO2	= CO2[e]
EX-0012	0	EX-0007	0	EX-0012	0	EX-0007	0	EX-0007	exchange flux : formaldehyde	= formaldehyde[e]
EX-0013	0	EX-0008	0.2256	EX-0013	0	EX-0008	0.1333	EX-0008	exchange flux : phosphate	= phosphate[e]
EX-0014	33.8	EX-0009	0	EX-0014	33.8	EX-0009	0	EX-0009	exchange flux : succinate	= succinate[e]
EX-0015	0	EX-0010	0	EX-0015	0	EX-0010	0	EX-0010	exchange flux : fumarate	= fumarate[e]
EX-0016	0	EX-0011	0	EX-0016	0	EX-0011	0	EX-0011	exchange flux : citrate	= citrate[e]
EX-0017	0	EX-0012	0	EX-0017	0	EX-0012	0	EX-0012	exchange flux : glycolate	= glycolate[e]
EX-0019	0	EX-0013	0	EX-0019	0	EX-0013	0	EX-0013	exchange flux : formate	= formate[e]
EX-0022	0	EX-0014	33.8	EX-0022	0	EX-0014	33.8	EX-0014	exchange flux : oxalate	= oxalate[e]
EX-0024	0	EX-0015	0	EX-0024	0	EX-0015	0	EX-0015	exchange flux : acetate	= acetate[e]
EX-0025	0	EX-0016	0	EX-0025	0	EX-0016	0	EX-0016	exchange flux : D-gluconate	= D-gluconate[e]
EX-0027	0	EX-0017	0	EX-0027	0	EX-0017	0	EX-0017	exchange flux : putrescine	= putrescine[e]
EX-0028	0	EX-0019	0	EX-0028	0	EX-0019	0	EX-0019	exchange flux : 2-oxoglutarate	= 2-oxoglutarate[e]
EX-0029	0	EX-0020	0.0143	EX-0029	0	EX-0020	0.0084	EX-0020	exchange flux : SO42-	= SO42-[e]
EX-0030	0	EX-0021	0.0008	EX-0030	0	EX-0021	0.0004	EX-0021	exchange flux : Na+	= Na+[e]
EX-0031	0	EX-0022	0	EX-0031	0	EX-0022	0	EX-0022	exchange flux : thiosulfate	= thiosulfate[e]
EX-0032	0	EX-0023	0	EX-0032	0	EX-0023	0	EX-0023	exchange flux : nitrate	= NO3-[e]
R-0001	0	EX-0024	0	R-0001	0	EX-0024	0	EX-0024	exchange flux : L-glutamate	= L-glutamate[e]
R-0002	0	EX-0025	0	R-0002	0	EX-0025	0	EX-0025	exchange flux : L-aspartate	= L-aspartate[e]
R-0026	0	EX-0026	-30.5264	R-0026	0	EX-0026	-31.8651	EX-0026	exchange flux : H2O	= H2O[e]
R-0028	0	EX-0027	0	R-0028	0	EX-0027	0	EX-0027	exchange flux : ethanolamine	= ethanolamine[e]
R-0029	0	EX-0028	0	R-0029	0	EX-0028	0	EX-0028	exchange flux : (S)-malate	= (S)-malate[e]
R-0031	0	EX-0029	0	R-0031	0	EX-0029	0	EX-0029	exchange flux : pyruvate	= pyruvate[e]
R-0033	0	EX-0030	0	R-0033	0	EX-0030	0	EX-0030	exchange flux : D-glucose	= D-glucose[e]
R-0106	0	EX-0031	0	R-0106	0	EX-0031	0	EX-0031	exchange flux : D-ribose	= D-ribose[e]
R-0230	0	EX-0032	0	R-0230	0	EX-0032	0	EX-0032	exchange flux : 5-dehydro-D-gluconate	= 5-dehydro-D-gluconate[e]
R-0234	0	EX-0033	0	R-0234	0	EX-0033	0	EX-0033	exchange flux : Co2+	= Co2+[e]
R-0269	0	EX-0034	0.1136	R-0269	0	EX-0034	0.0671	EX-0034	Biomass flux : L-rhamnose	dTDP-a-L-rhamnose + H2O = L-rhamnose + dTDP
R-0402	0	EX-0035	0.0062	R-0402	0	EX-0035	0.0037	EX-0035	Biomass flux : N-acetyl-D-glucosamine	UDP-N-acetyl-D-glucosamine + H2O = N-acetyl-D-glucosamine + UDP
R-0425	0	EX-0036	0.0252	R-0425	0	EX-0036	0.0149	EX-0036	exchange flux : proton	= H+[e]
R-0487	0	EX-0037	0	R-0487	0	EX-0037	0	EX-0037	exchange flux : H2O2	= H2O2[e]
R-0621	0	EX-0038	0.0014	R-0621	0	EX-0038	0.0008	EX-0038	exchange flux : Fe2+	= Fe2+[e]
R-0703	0	EX-0039	0.0006	R-0703	0	EX-0039	0.0004	EX-0039	exchange flux : molybdate	= molybdate[e]
R-0890	0	EX-0040	0.0343	R-0890	0	EX-0040	0.0203	EX-0040	exchange flux : potassium	= K+[e]
EX-0037	0	EX-0041	0.0015	EX-0037	0	EX-0041	0.0009	EX-0041	exchange flux : magnesium	= Mg2+[e]
NGAM	9.5	EX-0042	0.0009	NGAM	9.5	EX-0042	0.0005	EX-0042	exchange flux : calcium	= Ca2+[e]
EX-0047	0	EX-0043	0.0006	EX-0047	0	EX-0043	0.0004	EX-0043	exchange flux : copper	= Cu2+[e]
EX-0048	0	EX-0044	0.0006	EX-0048	0	EX-0044	0.0004	EX-0044	exchange flux : manganese	= Mn2+[e]
EX-0049	0	EX-0045	0.0006	EX-0049	0	EX-0045	0.0004	EX-0045	exchange flux : zinc	= Zn2+[e]
EX-0050	0	EX-0046	0.0009	EX-0050	0	EX-0046	0.0005	EX-0046	exchange flux : chloride	= Cl-[e]
EX-0051	0	EX-0047	0	EX-0051	0	EX-0047	0	EX-0047	exchange flux : light	= photon
EX-0052	0	EX-0048	0	EX-0052	0	EX-0048	0	EX-0048	exchange flux : D-arabinose	= D-arabinose[e]
EX-0053	0	EX-0049	0	EX-0053	0	EX-0049	0	EX-0049	exchange flux : L-arabinose	= L-arabinose[e]
EX-0054	0	EX-0050	0	EX-0054	0	EX-0050	0	EX-0050	exchange flux : D-arabinonate	= D-arabinonate[e]
EX-0055	0	EX-0051	0	EX-0055	0	EX-0051	0	EX-0051	exchange flux : L-arabinonate	= L-arabinonate[e]
EX-0056	0	EX-0052	0	EX-0056	0	EX-0052	0	EX-0052	exchange flux : L-lyxose	= L-lyxose[e]
EX-0057	0	EX-0053	0	EX-0057	0	EX-0053	0	EX-0053	exchange flux : D-xylose	= D-xylose[e]
EX-0058	0	EX-0054	0	EX-0058	0	EX-0054	0	EX-0054	exchange flux : D-xylonate	= D-xylonate[e]
EX-0059	0	EX-0055	0	EX-0059	0	EX-0055	0	EX-0055	exchange flux : L-lyxonate	= L-lyxonate[e]
EX-0060	0	EX-0056	0	EX-0060	0	EX-0056	0	EX-0056	exchange flux : D-ribonate	= D-ribonate[e]
EX-0061	0	EX-0057	0	EX-0061	0	EX-0057	0	EX-0057	exchange flux : 2-deoxy-D-ribonate	= 2-deoxy-D-ribonate[e]
EX-0062	0	EX-0058	0	EX-0062	0	EX-0058	0	EX-0058	exchange flux : acetoacetate	= acetoacetate[e]
EX-0063	0	EX-0059	0	EX-0063	0	EX-0059	0	EX-0059	exchange flux : propanoate	= propanoate[e]
EX-0064	0	EX-0060	0	EX-0064	0	EX-0060	0	EX-0060	exchange flux : 3-O-b-D-galactopyranosyl-D-arabinose	= 3-O-b-D-galactopyranosyl-D-arabinose[e]
EX-0065	0	EX-0061	0	EX-0065	0	EX-0061	0	EX-0061	exchange flux : 3-O-b-D-galactopyranosyl-D-arabinonate	= 3-O-b-D-galactopyranosyl-D-arabinonate[e]
R-1026	0	EX-0062	0	R-1026	0	EX-0062	0	EX-0062	exchange flux : decanoate	= decanoate[e]
EX-0066	0	EX-0063	0	EX-0066	0	EX-0063	0	EX-0063	exchange flux : 2-deoxy-D-ribose	= 2-deoxy-D-ribose[e]
EX-0067	0	EX-0064	0	EX-0067	0	EX-0064	0	EX-0064	exchange flux : methylamine	= methylamine[e]
EX-0068	0	EX-0065	0	EX-0068	0	EX-0065	0	EX-0065	exchange flux : ethylamine	= ethylamine[e]
EX-0069	0	EX-0066	0	EX-0069	0	EX-0066	0	EX-0066	exchange flux : ethanol	= ethanol[e]
EX-0070	0	EX-0067	0	EX-0070	0	EX-0067	0	EX-0067	exchange flux : L-tartrate	= L-tartrate[e]
		EX-0068	0	mue	0.11	EX-0068	0	EX-0068	exchange flux : glycerone	= glycerone[e]
		EX-0069	0			EX-0069	0	EX-0069	exchange flux : (S)-lactate	= (S)-lactate[e]
		EX-0070	0			EX-0070	0	EX-0070	exchange flux : 1,2-propanediol	= 1,2-propanediol[e]
COFAC	0.0005	R-0001	0	COFAC	0.0005	R-0001	0	R-0001	methanol dehydrogenase	methanol[p] + 2 oxidized-cytochrome-c = formaldehyde[p] + 2 H+[p] + 2
SECMET	0.00023	R-0002	0	SECMET	0.00023	R-0002	0	R-0002	H4F-dependent formaldehyde activating	formaldehyde + tetrahydrofolate = 5,10-methylenetetrahydrofolate + H2O
POLYN	0.004	R-0003	0	POLYN	0.004	R-0003	0	R-0003	H4MPT-dependent formaldehyde activating	formaldehyde + tetrahydromethanopterin = 5,10-methylenetetrahydrome
PROTEIN	0.5913	R-0004	0	PROTEIN	0.5913	R-0004	0	R-0004	methylenetetrahydromethanopterin dehydrogenase 1	5,10-methylenetetrahydromethanopterin + NADP+ = 5,10-methenyltetra
RNA	0.082	R-0005	0	RNA	0.082	R-0005	0	R-0005	methylenetetrahydromethanopterin dehydrogenase 2	5,10-methylenetetrahydromethanopterin + NAD+ = 5,10-methenyltetrah
DNA	0.03	R-0006	0	DNA	0.03	R-0006	0	R-0006	methenyltetrahydrometanopterin cyclohydrolase	5,10-methenyltetrahydromethanopterin + H2O = 5-formyltetrahydrometh
Fatty	0.0362	R-0007	0	Fatty	0.0362	R-0007	0	R-0007	formylmethanofuran:H4MPT formyltransferase	methanofuran + 5-formyltetrahydromethanopterin = tetrahydromethanop
Carbohydrate	0.1643	R-0008	0	Carbohydrate	0.1643	R-0008	0	R-0008	formyl-MFS hydrolysis	formylmethanofuran + H2O = formate + methanofuran
PHB	0.0236	R-0011	29.07	PHB	0.0236	R-0011	7.779	R-0011	formate dehydrogenase	formate + NAD+ = CO2 + NADH + H+
intra-metabolite	0.0264	R-0012	2.6035	Intra-metabolite	0.0264	R-0012	1.5388	R-0012	formate-tetrahydrofolate ligase	formate + ATP + tetrahydrofolate = 10-formyltetrahydrofolate + ADP + p
GAM	0.01	R-0013	2.5136	GAM	0.01	R-0013	1.4857	R-0013	methenyltetrahydrofolate cyclohydrolase	10-formyltetrahydrofolate + H+ = 5,10-methenyltetrahydrofolate + H2O
NOQUANTY	0.001	R-0014	2.5136	NOQUANTY	0.001	R-0014	1.4857	R-0014	methylenetetrahydrofolate dehydrogenase	5,10-methenyltetrahydrofolate + NADPH = 5,10-methylenetetrahydrofola
Inorganic	0.011	R-0015	2.4972	Inorganic	0.011	R-0015	1.476	R-0015	serine hydroxymethyltransferase	5,10-methylenetetrahydrofolate + glycine + H2O = tetrahydrofolate + L-s
		R-0016	2.7569			R-0016	1.6295	R-0016	L-serine-glyoxylate aminotransferase	L-serine + glyoxylate = hydroxypyruvate + glycine
		R-0017	2.7569			R-0017	1.6295	R-0017	hydroxypyruvate reductase	hydroxypyruvate + NADH + H+ = D-glycerate + NAD+
		R-0018	2.7569			R-0018	1.6295	R-0018	glycerate kinase	D-glycerate + ATP = 2-phospho-D-glycerate + ADP
		R-0019	1.8285			R-0019	1.0807	R-0019	enolase	2-phospho-D-glycerate = phosphoenolpyruvate + H2O
		R-0020	1.1451			R-0020	0.6768	R-0020	phosphoenolpyruvate carboxylase	phosphoenolpyruvate + CO2 + H2O = oxaloacetate + phosphate
		R-0021	-0.5663			R-0021	-0.3347	R-0021	malate dehydrogenase	(S)-malate + NAD+ = oxaloacetate + NADH + H+
		R-0022	0.6323			R-0022	0.3737	R-0022	malyl-CoA synthetase	(S)-malate + CoA + ATP = (S)-malyl-CoA + ADP + phosphate
		R-0023	0.6323			R-0023	0.3737	R-0023	malyl-CoA lyase	(S)-malyl-CoA = acetyl-CoA + glyoxylate
		R-0024	0.0541			R-0024	0.032	R-0024	acetyl-CoA C-acetyltransferase	2 acetyl-CoA = CoA + acetoacetyl-CoA
		R-0025	0.0541			R-0025	0.032	R-0025	acetoacetyl-CoA reductase 1	acetoacetyl-CoA + NADPH + H+ = (R)-3-hydroxybutanoyl-CoA + NADP+
		R-0026	0			R-0026	0	R-0026	poly(3-hydroxyalkanoate) depolymerase	poly-beta-hydroxybutyrate(n) + H2O = poly-beta-hydroxybutyrate(n-1) +
		R-0027	0.0516			R-0027	0.0305	R-0027	poly(3-hydroxyalkanoate) polymerase	(R)-3-hydroxybutanoyl-CoA + poly-beta-hydroxybutyrate(n-1) = poly-beta
		R-0028	0			R-0028	0	R-0028	D-beta-hydroxybutyrate dehydrogenase	(R)-3-hydroxybutanoate + NAD+ = acetoacetate + NADH + H+
		R-0029	0			R-0029	0	R-0029	succinyl-CoA:3-oxo-acid CoA-transferase	succinyl-CoA + acetoacetate = succinate + acetoacetyl-CoA
		R-0031	0			R-0031	0	R-0031	3-hydroxybutyryl-CoA dehydratase	(S)-3-hydroxybutanoyl-CoA = crotonyl-CoA + H2O
		R-0032	0			R-0032	0	R-0032	crotonyl-CoA reductase/carboxylase	crotonyl-CoA + NADPH + H+ + CO2 = (2S)-ethylmalonyl-CoA + NADP+
		R-0033	0			R-0033	0	R-0033	crotonyl-CoA reductase	crotonyl-CoA + NADPH + H+ = butyryl-CoA + NADP+
		R-0034	0			R-0034	0	R-0034	butyryl-CoA carboxylase	ATP + butyryl-CoA + HCO3- + H+ = ADP + phosphate + (2S)-ethylmalo
		R-0035	0			R-0035	0	R-0035	ethylmalonyl-CoA mutase	(2R)-ethylmalonyl-CoA = (2S)-methylsuccinyl-CoA
		R-0036	0			R-0036	0	R-0036	mesaconyl-CoA hydratase	mesaconyl-CoA + H2O = erythro-b-methylmalyl-CoA
		R-0037	0			R-0037	0	R-0037	methylsuccinyl-CoA dehydrogenase	(2S)-methylsuccinyl-CoA + oxidized-ETF = mesaconyl-CoA + reduced-E
		R-0038	0			R-0038	0	R-0038	b-methylmalyl-CoA lyase	erythro-b-methylmalyl-CoA = propionyl-CoA + glyoxylate
		R-0044	0			R-0044	0	R-0044	propionyl-CoA carboxylase 1	ATP + propionyl-CoA + HCO3- + H+ = ADP + phosphate + (S)-methylm
		R-0045	0			R-0045	0	R-0045	methylmalonyl-CoA epimerase	(S)-methylmalonyl-CoA = (R)-methylmalonyl-CoA
		R-0046	0			R-0046	0	R-0046	methylmalonyl-CoA mutase	(R)-methylmalonyl-CoA = succinyl-CoA
		R-0047	0.2268			R-0047	0.134	R-0047	citrate synthase	acetyl-CoA + H2O + oxaloacetate = citrate + CoA
		R-0048	0.2265			R-0048	0.1339	R-0048	aconitate hydratase	citrate = threo-D-isocitrate
		R-0049	0.2265			R-0049	0.1339	R-0049	isocitrate dehydrogenase	threo-D-isocitrate + NADP+ = 2-oxoglutarate + CO2 + NADPH + H+
		R-0050	0			R-0050	0	R-0050	2-oxoglutarate dehydrogenase	2-oxoglutarate + CoA + NAD+ = succinyl-CoA + CO2 + NADH + H+
		R-0051	0			R-0051	0	R-0051	succinyl-CoA hydrolase	succinyl-CoA + H2O = CoA + succinate
		R-0052	-0.0007			R-0052	-0.0004	R-0052	succinate dehydrogenase	succinate + UQ = fumarate + UQH2
		R-0053	0.0664			R-0053	0.0392	R-0053	fumarate hydratase	fumarate + H2O = (S)-malate
		R-0054	0			R-0054	0	R-0054	malate dehydrogenase (decarboxylating)	(S)-malate + NAD+ = pyruvate + CO2 + NADH + H+
		R-0055	0			R-0055	0	R-0055	pyruvate dehydrogenase	pyruvate + CoA + NAD+ = acetyl-CoA + CO2 + NADH + H+
		R-0056	0			R-0056	0	R-0056	oxaloacetate decarboxylase	oxaloacetate = pyruvate + CO2
		R-0057	0			R-0057	0	R-0057	phosphoenolpyruvate carboxykinase	ATP + oxaloacetate = ADP + phosphoenolpyruvate + CO2
		R-0058	0.9282			R-0058	0.5486	R-0058	phosphoglyceromutase	2-phospho-D-glycerate = 3-phospho-D-glycerate
		R-0059	0.5994			R-0059	0.3543	R-0059	phosphoglycerate kinase	ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroylphosphate

	R-0060	-0.5994	R-0060	-0.3543	R-0060	glyceraldehyde-3-phosphate dehydrogenase	D-glyceraldehyde-3-phosphate + phosphate + NAD+ = 3-phospho-D-gly
	R-0061	0.2756	R-0061	0.1629	R-0061	triosephosphate isomerase	D-glyceraldehyde-3-phosphate = glycerone-phosphate
	R-0062	0.2593	R-0062	0.1533	R-0062	fructose-bisphosphate aldolase	glycerone-phosphate + D-glyceraldehyde-3-phosphate = D-fructose-1,6-
	R-0063	0.2593	R-0063	0.1533	R-0063	fructose-1,6-bisphosphatase	D-fructose-1,6-bisphosphate + H2O = D-fructose-6-phosphate + phosph
	R-0064	0.192	R-0064	0.1135	R-0064	phosphoglucose isomerase	D-fructose-6-phosphate = D-glucose-6-phosphate
	R-0065	0	R-0065	0	R-0065	glucokinase	ATP + D-glucose = ADP + D-glucose-6-phosphate
	R-0066	0.0001	R-0066	0.0001	R-0066	glucose-6-phosphate 1-dehydrogenase	D-glucose-6-phosphate + NADP+ = D-glucono-1,5-lactone-6-phosphate
	R-0067	0.0001	R-0067	0.0001	R-0067	6-phosphogluconolactonase	D-glucono-1,5-lactone-6-phosphate + H2O = 6-phospho-D-gluconate
	R-0068	0	R-0068	0	R-0068	6-phosphogluconate dehydrogenase	6-phospho-D-gluconate + NADP+ = D-ribulose-5-phosphate + CO2 + N
	R-0069	-0.0746	R-0069	-0.0441	R-0069	D-ribulose-5-phosphate 3-epimerase	D-ribulose-5-phosphate = D-xylulose-5-phosphate
	R-0070	-0.0745	R-0070	-0.0441	R-0070	ribose-5-phosphate isomerase	D-ribose-5-phosphate = D-ribulose-5-phosphate
	R-0071	-0.0638	R-0071	-0.0377	R-0071	D-xylulose 5-phosphate phosphoketolase	D-xylulose-5-phosphate + phosphate = acetylphosphate + D-glyceraldeh
	R-0072	0.0503	R-0072	0.0297	R-0072	D-fructose 6-phosphate phosphoketolase	D-fructose-6-phosphate + phosphate = acetylphosphate + D-erythrose-4
	R-0073	-0.0108	R-0073	-0.0064	R-0073	transaldolase	sedoheptulose-7-phosphate + D-glyceraldehyde-3-phosphate = D-erythr
	R-0074	0.0108	R-0074	0.0064	R-0074	transketolase	sedoheptulose-7-phosphate + D-glyceraldehyde-3-phosphate = D-ribose
	R-0075	0.0853	R-0075	0.0637	R-0075	phosphoribosylpyrophosphate synthetase	ATP + D-ribose-5-phosphate = AMP + 5-phosphoribosyl-1-pyrophosphate
	R-0076	0	R-0076	0.0133	R-0076	phosphopentomutase	alpha-D-ribose-1-phosphate = D-ribose-5-phosphate
	R-0077	0.0007	R-0077	0.0004	R-0077	1-deoxy-D-xylulose-5-phosphate synthase	pyruvate + D-glyceraldehyde-3-phosphate = 1-deoxy-D-xylulose-5-phos
	R-0078	0	R-0078	0	R-0078	2-deoxyribose-5-phosphate aldolase	2-deoxy-D-ribose-5-phosphate = D-glyceraldehyde-3-phosphate + aceta
	R-0079	0	R-0079	0	R-0079	6-phosphogluconate dehydratase	6-phospho-D-gluconate = 2-dehydro-3-deoxy-D-gluconate-6-phosphate
	R-0080	0	R-0080	0	R-0080	2-keto-3-deoxygluconate 6-phosphate aldolase	2-dehydro-3-deoxy-D-gluconate-6-phosphate = pyruvate + D-glyceraldel
	R-0081	0	R-0081	0	R-0081	2-keto-4-hydroxyglutarate aldolase	4-hydroxy-2-oxoglutarate = pyruvate + glyoxylate
	R-0082	0	R-0082	0	R-0082	bisphosphoglycerate mutase	3-phospho-D-glyceroylphosphate = 2,3-bisphospho-D-glycerate
	R-0083	0	R-0083	0	R-0083	cob(I)alamin adenosyltransferase	ATP + cobinamide = triphosphate + adenosylcobinamide
	R-0086	0	R-0086	0	R-0086	glyoxylate reductase	glyoxylate + NADH + H+ = glycolate + NAD+
	R-0089	0.0483	R-0089	0.0285	R-0089	succinyl-CoA synthetase	ATP + succinate + CoA = ADP + phosphate + succinyl-CoA
	R-0090	0	R-0090	0	R-0090	malate dehydrogenase, FAD/NAD(P)-binding domain	(S)-malate + UQ = oxaloacetate + UQH2
	R-0094	0	R-0094	0	R-0094	pyruvate phosphate dikinase	ATP + pyruvate + phosphate = AMP + phosphoenolpyruvate + diphosph
	R-0095	0	R-0095	23.2254	R-0095	formate dehydrogenase (cytochrome-linked) periplasmic	formate[p] + 2 oxidized-cytochrome-c = CO2[p] + 2 reduced-cytochrome
	R-0097	0.0025	R-0097	0.0015	R-0097	(R)-3-hydroxybutyryl-CoA dehydratase	(R)-3-hydroxybutanoyl-CoA = crotonyl-CoA + H2O
	R-0098	0	R-0098	0	R-0098	ethylmalonyl-CoA epimerase	(2S)-ethylmalonyl-CoA = (2R)-ethylmalonyl-CoA
	R-0099	-0.6042	R-0099	-0.3571	R-0099	pyruvate kinase	ATP + pyruvate = ADP + phosphoenolpyruvate
	R-0101	0	R-0101	0	R-0101	acetyl-CoA synthetase	ATP + acetate + CoA = AMP + diphosphate + acetyl-CoA
	R-0102	0	R-0102	0	R-0102	S-lactoylglutathione hydrolase	S-lactoylglutathione + H2O = glutathione + D-lactate
	R-0105	0	R-0105	0	R-0105	pyruvate dehydrogenase/oxidase	pyruvate + H2O + 2 oxidized-cytochrome-c = acetate + CO2 + 2 reduced
	R-0106	0	R-0106	0	R-0106	phosphate acetyltransferase 1	acetyl-CoA + phosphate = CoA + acetylphosphate
	R-0107	0.0136	R-0107	0.008	R-0107	acetate kinase	acetate + ATP = acetylphosphate + ADP
	R-0108	0	R-0108	0	R-0108	propionate kinase	propanoate + ATP = ADP + propionylphosphate
	R-0109	0	R-0109	0	R-0109	lactaldehyde dehydrogenase	(S)-lactaldehyde + NAD+ + H2O = (S)-lactate + NADH + 2 H+
	R-0110	0	R-0110	0	R-0110	glycolaldehyde dehydrogenase	glycolaldehyde + NAD+ + H2O = glycolate + NADH + H+
	R-0111	0	R-0111	0	R-0111	lactoylglutathione lyase	S-lactoylglutathione = glutathione + methylglyoxal
	R-0112	0	R-0112	0	R-0112	phosphopentomutase 2	deoxyribose-1-phosphate = 2-deoxy-D-ribose-5-phosphate
	R-0113	0.074	R-0113	0.0438	R-0113	amino acid transferase (leucine)	4-methyl-2-oxopentanoate + L-glutamate = L-leucine + 2-oxoglutarate
	R-0114	0.0782	R-0114	0.0462	R-0114	amino acid transferase (valine)	3-methyl-2-oxobutanoate + L-glutamate = L-valine + 2-oxoglutarate
	R-0115	0.039	R-0115	0.023	R-0115	amino acid transferase (isoleucine)	2-keto-3-methyl-valerate + L-glutamate = L-isoleucine + 2-oxoglutarate
	R-0116	0.0782	R-0116	0.0462	R-0116	valine tRNA synthetase	ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valyl-tRNA(Val)
	R-0117	0.0739	R-0117	0.0437	R-0117	leucine tRNA synthetase	ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu)
	R-0118	0.0388	R-0118	0.0229	R-0118	isoleucine tRNA synthetase	ATP + L-isoleucine + tRNA(Ile) = AMP + diphosphate + L-isoleucyl-tRNA
	R-0119	0.074	R-0119	0.0438	R-0119	2-isopropylmalate synthase	acetyl-CoA + 3-methyl-2-oxobutanoate + H2O = (2S)-2-isopropylmalate
	R-0120	0.074	R-0120	0.0438	R-0120	3-isopropylmalate dehydrogenase	3-isopropylmalate + NAD+ = 2-isopropyl-3-oxosuccinate + NADH + H+
	R-0121	0.074	R-0121	0.0438	R-0121	2-isopropyl-3-oxosuccinate decarboxylase	2-isopropyl-3-oxosuccinate = 4-methyl-2-oxopentanoate + CO2
	R-0122	0.155	R-0122	0.0916	R-0122	2,3-dihydroxy-isovalerate dehydratase	2,3-dihydroxy-isovalerate = 3-methyl-2-oxobutanoate + H2O
	R-0123	0.039	R-0123	0.023	R-0123	2,3-dihydroxy-3-methylvalerate dehydratase	2,3-dihydroxy-3-methylvalerate = 2-keto-3-methyl-valerate + H2O
	R-0124	0.155	R-0124	0.0916	R-0124	acetolactate synthase	2 pyruvate = 2-acetolactate + CO2
	R-0125	0.039	R-0125	0.023	R-0125	2-aceto-2-hydroxy-butyrate synthase	pyruvate + 2-oxobutanoate + H+ = 2-aceto-2-hydroxy-butyrate + CO2
	R-0126	0.155	R-0126	0.0916	R-0126	2-acetolactate reductoisomerase	2-acetolactate + NADPH + H+ = 2,3-dihydroxy-isovalerate + NADP+
	R-0127	0.039	R-0127	0.023	R-0127	2-aceto-2-hydroxy-butyrate reductoisomerase	2-aceto-2-hydroxy-butyrate + NADPH + H+ = 2,3-dihydroxy-3-methylval
	R-0128	0.074	R-0128	0.0438	R-0128	3-isopropylmalate isomerase	isopropylmaleate + H2O = 3-isopropylmalate
	R-0129	-0.074	R-0129	-0.0438	R-0129	2-isopropylmalate isomerase	isopropylmaleate + H2O = (2S)-2-isopropylmalate
	R-0130	-0.1847	R-0130	-0.1092	R-0130	phosphoglucomutase	D-glucose-1-phosphate = D-glucose-6-phosphate
	R-0131	0	R-0131	0	R-0131	phosphomannomutase	D-mannose-1-phosphate = D-mannose-6-phosphate
	R-0132	0	R-0132	0	R-0132	beta phosphoglucomutase	b-D-glucose-1-phosphate = b-D-glucose-6-phosphate
	R-0133	0.0711	R-0133	0.042	R-0133	glucose-1-phosphate uridylyltransferase	UTP + D-glucose-1-phosphate = diphosphate + UDP-glucose
	R-0134	0	R-0134	0	R-0134	UDP-glucose 4-epimerase	UDP-glucose = UDP-galactose
	R-0135	0	R-0135	0	R-0135	UDP-glucose-6-dehydrogenase	UDP-glucose + 2 NAD+ + H2O = UDP-glucuronate + 2 NADH + 2 H+
	R-0136	0	R-0136	0	R-0136	GDP-L-fucose synthase	GDP-4-dehydro-6-deoxy-D-mannose + NADPH + H+ = GDP-fucose + N
	R-0137	0	R-0137	0	R-0137	mannose-1-phosphate guanylyltransferase	GTP + D-mannose-1-phosphate = GDP-mannose + diphosphate
	R-0138	0	R-0138	0	R-0138	mannose-6-phosphate isomerase	D-fructose-6-phosphate = D-mannose-6-phosphate
	R-0139	1000	R-0139	1000	R-0139	GDP-mannose 3,5-epimerase 1	GDP-mannose = GDP-galactose
	R-0140	-1000	R-0140	-1000	R-0140	GDP-mannose 3,5-epimerase 2	GDP-mannose = GDP-gulose
	R-0141	-1000	R-0141	-1000	R-0141	GDP-mannose 3,5-epimerase 3	GDP-gulose = GDP-galactose
	R-0142	0	R-0142	0	R-0142	GDP-mannose 4,6-dehydratase	GDP-mannose = GDP-4-dehydro-6-deoxy-D-mannose + H2O
	R-0143	0	R-0143	0	R-0143	gluconate 2-dehydrogenase (periplasmic)	D-gluconate[p] + 2 oxidized-cytochrome-c = 2-dehydro-D-gluconate[p] +
	R-0145	0	R-0145	0	R-0145	gluconokinase	ATP + D-gluconate = ADP + 6-phospho-D-gluconate
	R-0146	0	R-0146	0	R-0146	galactose mutarotase	D-galactose[p] = b-D-galactose[p]
	R-0147	0	R-0147	0	R-0147	aldose sugar dehydrogenase	D-glucose[p] + 2 oxidized-cytochrome-c = glucono-d-lactone[p] + 2 H+[p
	R-0148	0	R-0148	0	R-0148	L-fuculose-1-phosphate aldolase	L-fuculose-1-phosphate = glycerone-phosphate + (S)-lactaldehyde
	R-0149	0.0066	R-0149	0.0039	R-0149	trehalose-6-phosphate synthase	UDP-glucose + D-glucose-6-phosphate = UDP + trehalose-6-phosphate
	R-0150	0.0066	R-0150	0.0039	R-0150	trehalose-6-phosphate phosphatase	trehalose-6-phosphate + H2O = trehalose + phosphate
	R-0151	0	R-0151	0	R-0151	maltose alpha-D-glucosyltransferase	maltose = trehalose
	R-0152	0	R-0152	0	R-0152	maltooligosyltrehalose trehalohydrolase	maltooligosyl-trehalose = maltodextrin + trehalose
	R-0153	0.0645	R-0153	0.0381	R-0153	cellulose synthase	UDP-glucose + (1,4-beta-D-glucosyl)(n) = UDP + (1,4-beta-D-glucosyl)(
	R-0154	0	R-0154	0	R-0154	glycogen synthase	ADP-glucose + (1,4-alpha-D-glucosyl)(n) = ADP + (1,4-alpha-D-glucosyl
	R-0155	0	R-0155	0	R-0155	1,4-alpha-glucan branching enzyme	(1,4-alpha-D-glucosyl)(n+1) = glycogen
	R-0156	0	R-0156	0	R-0156	4-a-glucanotransferase	limit-dextrin = limit-dextrin-with-short-branches
	R-0157	0	R-0157	0	R-0157	amylo-a-1,6-glucosidase	limit-dextrin-with-short-branches + H2O = debranched-limit-dextrin + b-D
	R-0158	0	R-0158	0	R-0158	glycogen phosphorylase	glycogen + phosphate = limit-dextrin + D-glucose-1-phosphate
	R-0159	0	R-0159	0	R-0159	glucoamylase	debranched-limit-dextrin + n H2O = n b-D-glucose
	R-0160	0	R-0160	0	R-0160	alpha-D-glucose-1-phosphate cytidylyltransferase	CTP + D-glucose-1-phosphate = diphosphate + CDP-glucose
	R-0161	0	R-0161	0	R-0161	cdp-glucose 4,6-dehydratase	CDP-glucose = CDP-4-dehydro-6-deoxy-D-glucose + H2O
	R-0162	0	R-0162	0	R-0162	CDP-4-dehydro-6-deoxy-D-gulose 4-reductase	CDP-4-dehydro-6-deoxy-D-glucose + NADPH + H+ = CDP-4-dehydro-3,
	R-0163	0.1136	R-0163	0.0671	R-0163	dTDP-4-dehydrorhamnose 3,5-epimerase	dTDP-4-dehydro-6-deoxy-D-glucose = dTDP-4-dehydro-6-deoxy-L-man
	R-0164	0.1136	R-0164	0.0671	R-0164	dTDP-glucose 4,6-dehydratase	dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-glucose + H2O
	R-0165	0.1136	R-0165	0.0671	R-0165	dTDP-4-dehydrorhamnose reductase	dTDP-4-dehydro-6-deoxy-L-mannose + NADPH + H+ = dTDP-a-L-rham
	R-0166	0.1136	R-0166	0.0671	R-0166	glucose-1-phosphate thymidylyltransferase	dTTP + D-glucose-1-phosphate = diphosphate + dTDP-glucose
	R-0167	0	R-0167	0	R-0167	endo-1,4-D-glucanase	(1,4-alpha-D-glucosyl)(n+1) + H2O = (1,4-alpha-D-glucosyl)(x) + short-g
	R-0168	-0.0395	R-0168	-0.0233	R-0168	shikimate 5-dehydrogenase	shikimate + NADP+ = 3-dehydroshikimate + NADPH + H+
	R-0169	0.0253	R-0169	0.015	R-0169	prephenate dehydratase	prephenate = phenylpyruvate + H2O + CO2
	R-0170	0	R-0170	0	R-0170	malonyl-CoA decarboxylase	malonyl-CoA = acetyl-CoA + CO2
	R-0171	0.1643	R-0171	0.0971	R-0171	acetyl-CoA carboxylase	ATP + acetyl-CoA + HCO3- + H+ = ADP + phosphate + malonyl-CoA
	R-0174	0	R-0174	0	R-0174	propionyl-CoA synthetase	ATP + propanoate + CoA = AMP + diphosphate + propionyl-CoA
	R-0175	0	R-0175	0	R-0175	malonate decarboxylase	malonate = acetate + CO2
	R-0176	0	R-0176	0	R-0176	phosphate acetyltransferase 2	propionyl-CoA + phosphate = propionylphosphate + CoA
	R-0177	0.0395	R-0177	0.0233	R-0177	2-dehydro-3-deoxyphosphoheptonate aldolase	phosphoenolpyruvate + D-erythrose-4-phosphate + H2O = 3-deoxy-D-ar
	R-0178	0.0395	R-0178	0.0233	R-0178	5-enolpyruvylshikimate-3-phosphate synthetase	phosphoenolpyruvate + shikimate-3-phosphate = phosphate + 5-enolpyr
	R-0179	0.0001	R-0179	0.0001	R-0179	anthranilate phosphoribosyltransferase	anthranilate + 5-phosphoribosyl-1-pyrophosphate = N-(5-phospho-beta-I
	R-0180	0.0001	R-0180	0.0001	R-0180	phosphoribosylanthranilate isomerase	N-(5-phospho-beta-D-ribosyl)-anthranilate = 1-(2-carboxyphenylamino)-
	R-0181	0.0001	R-0181	0.0001	R-0181	anthranilate synthase	chorismate + L-glutamine = anthranilate + pyruvate + L-glutamate
	R-0182	0	R-0182	0	R-0182	tryptophan synthase	L-serine + indole-3-glycerol-phosphate = L-tryptophan + D-glyceraldehy
	R-0183	0.0001	R-0183	0.0001	R-0183	tryptophan synthase A	indole-3-glycerol-phosphate = indole + D-glyceraldehyde-3-phosphate
	R-0184	0.0001	R-0184	0.0001	R-0184	tryptophan synthase B	indole + L-serine = L-tryptophan + H2O
	R-0185	0.0394	R-0185	0.0233	R-0185	chorismate mutase	chorismate = prephenate
	R-0186	0	R-0186	0	R-0186	aminodeoxychorismate synthase	chorismate + L-glutamine = 4-amino-4-deoxychorismate + L-glutamate
	R-0187	0.014	R-0187	0.0083	R-0187	tyrosine tRNA synthetase	ATP + L-tyrosine + tRNA(Tyr) = AMP + diphosphate + L-tyrosyl-tRNA(Ty
	R-0188	0.0253	R-0188	0.015	R-0188	phenylalanine tRNA synthetase	ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylal
	R-0189	0.0395	R-0189	0.0233	R-0189	chorismate synthase	5-enolpyruvylshikimate-3-phosphate = chorismate + phosphate
	R-0190	0.0395	R-0190	0.0233	R-0190	3-dehydroquinate dehydratase	3-dehydroquinate = 3-dehydroshikimate + H2O
	R-0191	0.0001	R-0191	0.0001	R-0191	indole-3-glycerol phosphate synthase	1-(2-carboxyphenylamino)-1-deoxy-D-ribulose-5-phosphate = indole-3-g
	R-0192	0	R-0192	0	R-0192	cyclohexadienyl dehydrogenase	L-arogenate + NAD+ = L-tyrosine + CO2 + NADH + H+
	R-0193	0.0126	R-0193	0.0075	R-0193	histidinol-phosphate aminotransferase	imidazol-acetol-phosphate + L-glutamate = L-histidinol-phosphate + 2-o
	R-0194	0.0395	R-0194	0.0233	R-0194	shikimate kinase	shikimate + ATP = shikimate-3-phosphate + ADP
	R-0195	0.0395	R-0195	0.0233	R-0195	3-dehydroquinate synthase	3-deoxy-D-arabino-heptulosonate-7-phosphate = 3-dehydroquinate + ph
	R-0196	0	R-0196	0	R-0196	UDP-glucuronate 5'-epimerase	UDP-glucuronate = UDP-L-iduronate
	R-0197	0	R-0197	0	R-0197	homoserine O-succinyltransferase	succinyl-CoA + L-homoserine = CoA + O-succinyl-L-homoserine

R-0198	0	R-0198	0	R-0198	5'-methylthioadenosine phosphorylase	(S)-methyl-5'-thioadenosine + phosphate = adenine + (S)-methyl-5-thio-a
R-0199	0	R-0199	0	R-0199	spermidine synthase	(S)-adenosylmethioninamine + putrescine = (S)-methyl-5'-thioadenosine
R-0200	0.0003	R-0200	0.0002	R-0200	S-adenosylhomocysteine hydrolase	(S)-adenosyl-L-homocysteine + H2O = L-homocysteine + adenosine
R-0201	0.0105	R-0201	0.0062	R-0201	O-acetylhomoserine sulfhydrylase	O-acetyl-L-homoserine + H2S = L-homocysteine + acetate
R-0202	0	R-0202	0	R-0202	cystathionine gamma-synthase	O-succinyl-L-homoserine + L-cysteine = L-cystathionine + succinate
R-0203	0	R-0203	0	R-0203	cystathionine beta-lyase	L-cystathionine + H2O = L-homocysteine + NH3 + pyruvate
R-0204	0.0105	R-0204	0.0062	R-0204	methionyl-tRNA synthetase	ATP + L-methionine + tRNA(Met) = AMP + diphosphate + L-methionyl-tR
R-0205	0.0003	R-0205	0.0002	R-0205	methionine adenosyltransferase	ATP + L-methionine + H2O = phosphate + diphosphate + (S)-adenosyl-L
R-0206	0.0105	R-0206	0.0062	R-0206	homoserine O-acetyltransferase	acetyl-CoA + L-homoserine = CoA + O-acetyl-L-homoserine
R-0207	0.0108	R-0207	0.0064	R-0207	homocysteine transmethylase	5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methio
R-0208	0.0108	R-0208	0.0064	R-0208	5,10-methylenetetrahydrofolate reductase	5,10-methylenetetrahydrofolate + NADPH + H+ = 5-methyltetrahydrofola
R-0209	0	R-0209	0	R-0209	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltrar	10-formyltetrahydrofolate + L-methionyl-tRNA(fMet) = tetrahydrofolate +
R-0210	0.0479	R-0210	0.0283	R-0210	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	succinyl-CoA + tetrahydrodipicolinate + H2O = CoA + N-succinyl-2-amin
R-0211	0.0479	R-0211	0.0283	R-0211	N-succinyl-L-diaminopimelate desuccinylase	N-succinyl-L,L-2,6-diaminopimelate + H2O = LL-2,6-diaminoheptanedioa
R-0212	0.0479	R-0212	0.0283	R-0212	diaminopimelate decarboxylase	meso-diaminoheptanedioate = L-lysine + CO2
R-0213	0.0479	R-0213	0.0283	R-0213	diaminopimelate epimerase	LL-2,6-diaminoheptanedioate = meso-diaminoheptanedioate
R-0214	0.0479	R-0214	0.0283	R-0214	dihydrodipicolinate synthase	L-aspartate-4-semialdehyde + pyruvate = dihydrodipicolinate + 2 H2O
R-0215	0.0479	R-0215	0.0283	R-0215	lysyl tRNA synthetase	ATP + L-lysine + tRNA(Lys) = AMP + diphosphate + L-lysyl-tRNA(Lys)
R-0216	0.0479	R-0216	0.0283	R-0216	dihydrodipicolinate reductase	dihydrodipicolinate + NADPH + H+ = tetrahydrodipicolinate + NADP+
R-0217	-0.0533	R-0217	-0.0315	R-0217	acetylornithine aminotransferase	N-acetyl-L-ornithine + 2-oxoglutarate = L-glutamate + N-acetyl-L-glutam
R-0218	0	R-0218	0	R-0218	succinylornithine transaminase	N2-succinyl-L-ornithine + 2-oxoglutarate = L-glutamate + N2-succinyl-L-
R-0219	0.0126	R-0219	0.0075	R-0219	histidinal dehydrogenase	histidinal + NAD+ + H2O = L-histidine + NADH + H+
R-0220	0.0126	R-0220	0.0075	R-0220	histidinol dehydrogenase	L-histidinol + NAD+ = histidinal + NADH + H+
R-0221	0.0126	R-0221	0.0075	R-0221	imidazoleglycerol-phosphate dehydratase	D-erythro-imidazole-glycerol-phosphate = imidazol-acetol-phosphate + H
R-0222	0.0126	R-0222	0.0075	R-0222	histidyl-tRNA synthetase	ATP + L-histidine + tRNA(His) = AMP + diphosphate + L-histidyl-tRNA(H
R-0223	0.0126	R-0223	0.0075	R-0223	imidazole glycerol phosphate synthase	phosphoribulosylformimino-AICAR-phosphate + L-glutamine = L-glutam
R-0224	0.0126	R-0224	0.0075	R-0224	phosphoribosyl-ATP pyrophosphatase	phosphoribosyl-ATP + H2O = phosphoribosyl-AMP + diphosphate
R-0225	0.0126	R-0225	0.0075	R-0225	phosphoribosyl-AMP cyclohydrolase	phosphoribosyl-AMP + H2O = phosphoribosylformimino-AICAR-phosph
R-0226	0.0126	R-0226	0.0075	R-0226	N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'-phosphoribo	phosphoribosylformimino-AICAR-phosphate = phosphoribulosylformimin
R-0227	0.0126	R-0227	0.0075	R-0227	ATP phosphoribosyltransferase	ATP + 5-phosphoribosyl-1-pyrophosphate = phosphoribosyl-ATP + diph
R-0228	31.6734	R-0228	32.5431	R-0228	oxalyl-CoA decarboxylase	oxalyl-CoA = formyl-CoA + CO2
R-0229	31.6734	R-0229	32.5431	R-0229	formyl-CoA transferase	formyl-CoA + oxalate = formate + oxalyl-CoA
R-0230	0	R-0230	0	R-0230	hydroxypyruvate isomerase	hydroxypyruvate = tartronate-semialdehyde
R-0231	-2.1266	R-0231	-1.2569	R-0231	glyoxylate dehydrogenase	glyoxylate + CoA + NADP+ = oxalyl-CoA + NADPH + H+
R-0232	0	R-0232	0	R-0232	phosphoglycolate phosphatase	2-phosphoglycolate + H2O = glycolate + phosphate
R-0233	0	R-0233	0	R-0233	2-hydroxy-3-oxopropionate reductase (NAD)	D-glycerate + NAD+ = tartronate-semialdehyde + NADH + H+
R-0234	0	R-0234	0	R-0234	2-hydroxy-3-oxopropionate reductase (NADP)	D-glycerate + NADP+ = tartronate-semialdehyde + NADPH + H+
R-0235	0	R-0235	0	R-0235	formamide amidohydrolase	formamide + H2O = formate + NH3
R-0236	0.0003	R-0236	0.0002	R-0236	5-aminolevulinate synthase	succinyl-CoA + glycine = 5-aminolevulinate + CoA + CO2
R-0237	0.0001	R-0237	0.0001	R-0237	porphobilinogen synthase	2 5-aminolevulinate = porphobilinogen + 2 H2O
R-0238	0	R-0238	0	R-0238	porphobilinogen deaminase	4 porphobilinogen + H2O = 4 NH3 + hydroxymethylbilane
R-0239	0	R-0239	0	R-0239	uroporphyrinogen III synthase	hydroxymethylbilane = uroporphyrinogen-III + H2O
R-0240	0	R-0240	0	R-0240	sarcosine oxidase	sarcosine + O2 + H2O = H2O2 + formaldehyde + glycine
R-0241	0.1552	R-0241	0.0918	R-0241	aspartate-semialdehyde dehydrogenase	L-aspartyl-4-phosphate + NADPH + H+ = phosphate + L-aspartate-4-se
R-0242	0	R-0242	0	R-0242	glycine amidinotransferase	glycine + L-arginine = guanidinoacetate + L-ornithine
R-0243	0	R-0243	0	R-0243	glycine decarboxylase	H-Gcv-protein-(lipoyl)lysine + glycine = H-protein-S-(aminomethyldihydro
R-0244	0	R-0244	0	R-0244	H-protein-lipoamide dehydrogenase	H-Gcv-protein-(dihydrolipoyl)lysine + NAD+ = H-Gcv-protein-(lipoyl)lysin
R-0245	0	R-0245	0	R-0245	H-protein-aminomethyltransferase	H-protein-S-(aminomethyldihydrolipoyl)lysine + tetrahydrofolate = H-Gcv
R-0249	0.0968	R-0249	0.0572	R-0249	threonine synthase	O-phospho-L-homoserine + H2O = L-threonine + phosphate
R-0251	0	R-0251	0	R-0251	phosphoserine phosphatase (D)	O-phospho-D-serine + H2O = D-serine + phosphate
R-0252	0	R-0252	0	R-0252	L-threonine aldolase	L-threonine = glycine + acetaldehyde
R-0253	0	R-0253	0	R-0253	L-allo-threonine aldolase	L-allo-threonine = glycine + acetaldehyde
R-0254	0	R-0254	0	R-0254	phenylserine aldolase	L-threo-3-phenylserine = benzaldehyde + glycine
R-0255	0.039	R-0255	0.023	R-0255	threonine deaminase	L-threonine = 2-oxobutanoate + NH3 + H+
R-0256	0	R-0256	0	R-0256	L-serine deaminase	L-serine = pyruvate + NH3
R-0257	0.1073	R-0257	0.0634	R-0257	homoserine dehydrogenase	L-aspartate-4-semialdehyde + NADPH + H+ = L-homoserine + NADP+
R-0258	0.0573	R-0258	0.0338	R-0258	threonine tRNA synthetase	ATP + L-threonine + tRNA(Thr) = AMP + diphosphate + L-threonyl-tRNA
R-0259	0.0577	R-0259	0.0341	R-0259	serine tRNA synthetase	ATP + L-serine + tRNA(Ser) = AMP + diphosphate + L-seryl-tRNA(Ser)
R-0260	0.0968	R-0260	0.0572	R-0260	homoserine kinase	L-homoserine + ATP = O-phospho-L-homoserine + ADP
R-0261	0.1552	R-0261	0.0918	R-0261	aspartokinase	L-aspartate + ATP = L-aspartyl-4-phosphate + ADP
R-0262	0.2182	R-0262	0.129	R-0262	glycine tRNA synthetase	ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyl-tRNA(Gly)
R-0263	0.3288	R-0263	0.1943	R-0263	D-3-phosphoglycerate dehydrogenase	3-phospho-D-glycerate + NAD+ = 3-phospho-hydroxypyruvate + NADH
R-0264	0.3288	R-0264	0.1943	R-0264	phosphoserine aminotransferase	L-glutamate + 3-phospho-hydroxypyruvate = 3-phospho-L-serine + 2-oxo
R-0265	0.3288	R-0265	0.1943	R-0265	phosphoserine phosphatase	3-phospho-L-serine + H2O = L-serine + phosphate
R-0266	0	R-0266	0	R-0266	phosphohydroxythreonine aminotransferase	2-oxo-3-hydroxy-4-phosphobutanoate + L-glutamate = 4-(phosphonooxy
R-0267	0	R-0267	0	R-0267	a-ketoglutarate reductase	2-hydroxyglutarate + NAD+ = 2-oxoglutarate + NADH + H+
R-0268	0.015	R-0268	0.0089	R-0268	glycerol-3-phosphate dehydrogenase	glycerone-phosphate + NADPH + H+ = sn-glycerol-3-phosphate + NADP+
R-0269	0	R-0269	0	R-0269	glycerol-3-phosphate dehydrogenase	glycerone-phosphate + NADH + H+ = sn-glycerol-3-phosphate + NAD+
R-0270	0	R-0270	0	R-0270	ethanolamine ammonia-lyase	ethanolamine = acetaldehyde + NH3
R-0272	0.0006	R-0272	0.0004	R-0272	CDP-diacylglycerol synthetase (n-16:0)	CTP + 1,2-dihexadecanoyl-sn-glycerol-3-phosphate = diphosphate + CD
R-0273	0.0006	R-0273	0.0004	R-0273	CDP-diacylglycerol synthetase (n-16:1)	CTP + 1,2-dihexadec-9-enoyl-sn-glycerol-3-phosphate = diphosphate +
R-0274	0.0006	R-0274	0.0004	R-0274	CDP-diacylglycerol synthetase (n-18:0)	CTP + 1,2-dioctadecanoyl-sn-glycerol-3-phosphate = diphosphate + CD
R-0275	0.0097	R-0275	0.0057	R-0275	CDP-diacylglycerol synthetase (n-18:1)	CTP + 1,2-dioctadec-9-enoyl-sn-glycerol-3-phosphate = diphosphate + C
R-0276	0	R-0276	0	R-0276	phosphatidylethanolamine-N-methyltransferase (n-16:0)	(S)-adenosyl-L-methionine + phosphatidylethanolamine(dihexadecanoyl
R-0277	0	R-0277	0	R-0277	phosphatidylethanolamine-N-methyltransferase (n-16:1)	(S)-adenosyl-L-methionine + phosphatidylethanolamine(dihexadec-9-en
R-0278	0	R-0278	0	R-0278	phosphatidylethanolamine-N-methyltransferase (n-18:0)	(S)-adenosyl-L-methionine + phosphatidylethanolamine(dioctadecanoyl)
R-0279	0	R-0279	0	R-0279	phosphatidylethanolamine-N-methyltransferase (n-18:1)	(S)-adenosyl-L-methionine + phosphatidylethanolamine(dioctadec-9-enc
R-0280	0.0004	R-0280	0.0002	R-0280	phosphatidylserine decarboxylase (n-16:0)	phosphatidyl-L-serine(dihexadecanoyl) = phosphatidylethanolamine(dihe
R-0281	0.0004	R-0281	0.0003	R-0281	phosphatidylserine decarboxylase (n-16:1)	phosphatidyl-L-serine(dihexadec-9-enoyl) = phosphatidylethanolamine(d
R-0282	0.0004	R-0282	0.0002	R-0282	phosphatidylserine decarboxylase (n-18:0)	phosphatidyl-L-serine(dioctadecanoyl) = phosphatidylethanolamine(dioc
R-0283	0.0066	R-0283	0.0039	R-0283	phosphatidylserine decarboxylase (n-18:1)	phosphatidyl-L-serine(dioctadec-9-enoyl) = phosphatidylethanolamine(d
R-0284	0.0004	R-0284	0.0003	R-0284	phosphatidylserine synthase (n-16:0)	CDP-1,2-dihexadecanoyl-glycerol + L-serine = CMP + phosphatidyl-L-se
R-0285	0.0004	R-0285	0.0003	R-0285	phosphatidylserine synthase (n-16:1)	CDP-1,2-dihexadec-9-enoyl-glycerol + L-serine = CMP + phosphatidyl-L
R-0286	0.0004	R-0286	0.0002	R-0286	phosphatidylserine synthase (n-18:0)	CDP-1,2-dioctadecanoyl-glycerol + L-serine = CMP + phosphatidyl-L-se
R-0287	0.0068	R-0287	0.004	R-0287	phosphatidylserine synthase (n-18:1)	CDP-1,2-dioctadec-9-enoyl-glycerol + L-serine = CMP + phosphatidyl-L-
R-0289	0.0002	R-0289	0.0001	R-0289	phosphatidylglycerophosphate synthetase (n-16:0)	CDP-1,2-dihexadecanoyl-glycerol + sn-glycerol-3-phosphate = CMP + p
R-0290	0.0002	R-0290	0.0001	R-0290	phosphatidylglycerophosphate synthetase (n-16:1)	CDP-1,2-dihexadec-9-enoyl-glycerol + sn-glycerol-3-phosphate = CMP +
R-0291	0.0002	R-0291	0.0001	R-0291	phosphatidylglycerophosphate synthetase (n-18:0)	CDP-1,2-dioctadecanoyl-glycerol + sn-glycerol-3-phosphate = CMP + ph
R-0292	0.0029	R-0292	0.0017	R-0292	phosphatidylglycerophosphate synthetase (n-18:1)	CDP-1,2-dioctadec-9-enoyl-glycerol + sn-glycerol-3-phosphate = CMP +
R-0294	0	R-0294	0	R-0294	sn-Glycero-3-phosphocholine glycerophosphohydrolase	sn-glycero-3-phosphocholine + H2O = sn-glycerol-3-phosphate + choline
R-0295	0	R-0295	0	R-0295	sn-Glycero-3-phosphoethanolamine glycerophosphohydrolase	sn-glycero-3-phosphoethanolamine + H2O = sn-glycerol-3-phosphate +
R-0298	0	R-0298	0	R-0298	lysophospholipase C1 (n-16:0)	1-hexadecanoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-pho
R-0299	0	R-0299	0	R-0299	lysophospholipase C2 (n-16:0)	2-hexadecanoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-pho
R-0300	0	R-0300	0	R-0300	lysophospholipase C1 (n-16:1)	1-hexadec-9-enoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-p
R-0301	0	R-0301	0	R-0301	lysophospholipase C2 (n-16:1)	2-hexadec-9-enoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-p
R-0302	0	R-0302	0	R-0302	lysophospholipase C1 (n-18:0)	1-octadecanoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-pho
R-0303	0	R-0303	0	R-0303	lysophospholipase C2 (n-18:0)	2-octadecanoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-pho
R-0304	0	R-0304	0	R-0304	lysophospholipase C1 (n-18:1)	1-octadec-9-enoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-p
R-0305	0	R-0305	0	R-0305	lysophospholipase C2 (n-18:1)	2-octadec-9-enoyl-sn-glycero-3-phosphocholine + H2O = sn-glycero-3-p
R-0308	0	R-0308	0	R-0308	lysophospholipase E1 (n-16:0)	1-hexadecanoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glycero
R-0309	0	R-0309	0	R-0309	lysophospholipase E2 (n-16:0)	2-hexadecanoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glycero
R-0310	0	R-0310	0	R-0310	lysophospholipase E1 (n-16:1)	1-hexadec-9-enoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glyc
R-0311	0	R-0311	0	R-0311	lysophospholipase E2 (n-16:1)	2-hexadec-9-enoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glyc
R-0312	0	R-0312	0	R-0312	lysophospholipase E1 (n-18:0)	1-octadecanoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glycero-
R-0313	0	R-0313	0	R-0313	lysophospholipase E2 (n-18:0)	2-octadecanoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glycero-
R-0314	0	R-0314	0	R-0314	lysophospholipase E1 (n-18:1)	1-octadec-9-enoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glyce
R-0315	0	R-0315	0	R-0315	lysophospholipase E2 (n-18:1)	2-octadec-9-enoyl-sn-glycero-3-phosphoethanolamine + H2O = sn-glyce
R-0317	0	R-0317	0	R-0317	2-acylglycerophosphoethanolamine acyltransferase (n-16:0)	hexadecanoyl-[acyl-carrier-protein] + 2-hexadecanoyl-sn-glycero-3-phos
R-0318	0	R-0318	0	R-0318	2-acylglycerophosphoethanolamine acyltransferase (n-16:1)	hexadec-9-enoyl-[acyl-carrier-protein] + 2-hexadec-9-enoyl-sn-glycero-3
R-0319	0	R-0319	0	R-0319	2-acylglycerophosphoethanolamine acyltransferase (n-18:0)	octadecanoyl-[acyl-carrier-protein] + 2-octadecanoyl-sn-glycero-3-phosp
R-0320	0	R-0320	0	R-0320	2-acylglycerophosphoethanolamine acyltransferase (n-18:1)	octadec-9-enoyl-[acyl-carrier-protein] + 2-octadec-9-enoyl-sn-glycero-3-p
R-0322	0.0012	R-0322	0.0007	R-0322	acyl-acyl carrier protein synthetase (n-16:0)	ATP + hexadecanoate + [acyl-carrier-protein] = AMP + diphosphate + he
R-0323	0	R-0323	0	R-0323	acyl-acyl carrier protein synthetase (n-16:1)	ATP + 9-hexadecenoate + [acyl-carrier-protein] = AMP + diphosphate +
R-0324	0.0012	R-0324	0.0007	R-0324	acyl-acyl carrier protein synthetase (n-18:0)	ATP + octadecanoate + [acyl-carrier-protein] = AMP + diphosphate + oc
R-0325	0	R-0325	0	R-0325	acyl-acyl carrier protein synthetase (n-18:1)	ATP + 9-octadecenoate + [acyl-carrier-protein] = AMP + diphosphate + c
R-0327	0	R-0327	0	R-0327	diacylglycerol kinase (n-16:0)	ATP + 1,2-dihexadecanoyl-glycerol = ADP + 1,2-dihexadecanoyl-sn-glyc
R-0328	0	R-0328	0	R-0328	diacylglycerol kinase (n-16:1)	ATP + 1,2-dihexadec-9-enoyl-glycerol = ADP + 1,2-dihexadec-9-enoyl-s
R-0329	0	R-0329	0	R-0329	diacylglycerol kinase (n-18:0)	ATP + 1,2-dioctadecanoyl-glycerol = ADP + 1,2-dioctadecanoyl-sn-glyce
R-0330	0	R-0330	0	R-0330	diacylglycerol kinase (n-18:1)	ATP + 1,2-dioctadec-9-enoyl-glycerol = ADP + 1,2-dioctadec-9-enoyl-sn
R-0331	0	R-0331	0	R-0331	dihydroxyacetone kinase	ATP + glycerone = ADP + glycerone-phosphate
R-0332	0	R-0332	0	R-0332	glycerol kinase	ATP + glycerol = ADP + sn-glycerol-3-phosphate
R-0334	0.0006	R-0334	0.0004	R-0334	lysophosphatidic acid acyltransferase (n-16:0)	hexadecanoyl-[acyl-carrier-protein] + 1-hexadecanoyl-sn-glycerol-3-phos
R-0335	0.0006	R-0335	0.0004	R-0335	lysophosphatidic acid acyltransferase (n-16:1)	hexadec-9-enoyl-[acyl-carrier-protein] + 1-hexadec-9-enoyl-sn-glycerol-3
R-0336	0.0006	R-0336	0.0004	R-0336	lysophosphatidic acid acyltransferase (n-18:0)	octadecanoyl-[acyl-carrier-protein] + 1-octadecanoyl-sn-glycerol-3-phosp

	R-0337	0.0097	R-0337	0.0057	R-0337	lysophosphatidic acid acyltransferase (n-18:1)	octadec-9-enoyl-[acyl-carrier-protein] + 1-octadec-9-enoyl-sn-glycerol-3-
	R-0338	0.1643	R-0338	0.0971	R-0338	malonyl-CoA-[acyl-carrier-protein] transacylase	malonyl-CoA + [acyl-carrier-protein] = CoA + malonyl-[acyl-carrier-protei
	R-0339	0.0207	R-0339	0.0122	R-0339	acetyl-CoA:ACP transacylase	acetyl-CoA + [acyl-carrier-protein] = acetyl-[acyl-carrier-protein] + CoA
	R-0340	0.0207	R-0340	0.0122	R-0340	3-oxoacyl-[acyl-carrier-protein] synthase (n-4:0)	acetyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = acetoacetyl
	R-0341	0.0207	R-0341	0.0122	R-0341	3-oxoacyl-[acyl-carrier-protein] synthase (n-6:0)	butyryl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-oxohexa
	R-0342	0.0207	R-0342	0.0122	R-0342	3-oxoacyl-[acyl-carrier-protein] synthase (n-8:0)	hexanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-oxooct
	R-0343	0.0207	R-0343	0.0122	R-0343	3-oxoacyl-[acyl-carrier-protein] synthase (n-10:0)	octanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-oxodec
	R-0344	0.0001	R-0344	0.0001	R-0344	3-oxoacyl-[acyl-carrier-protein] synthase (n-12:0)	decanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-oxodo
	R-0345	0.0001	R-0345	0	R-0345	3-oxoacyl-[acyl-carrier-protein] synthase (n-14:0)	dodecanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-oxo
	R-0346	0	R-0346	0	R-0346	3-oxoacyl-[acyl-carrier-protein] synthase (n-16:0)	tetradecanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-o
	R-0347	0	R-0347	0	R-0347	3-oxoacyl-[acyl-carrier-protein] synthase (n-18:0)	hexadecanoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-o
	R-0348	0.0206	R-0348	0.0122	R-0348	3-oxoacyl-[acyl-carrier-protein] synthase (n-12:1)	cis-dec-3-enoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3-
	R-0349	0.0206	R-0349	0.0122	R-0349	3-oxoacyl-[acyl-carrier-protein] synthase (n-14:1)	cis-dodec-5-enoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] =
	R-0350	0.0206	R-0350	0.0122	R-0350	3-oxoacyl-[acyl-carrier-protein] synthase (n-16:1)	cis-tetradec-7-enoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein]
	R-0351	0.0194	R-0351	0.0115	R-0351	3-oxoacyl-[acyl-carrier-protein] synthase (n-18:1)	hexadec-9-enoyl-[acyl-carrier-protein] + malonyl-[acyl-carrier-protein] = 3
	R-0352	0.0207	R-0352	0.0122	R-0352	3-oxoacyl-[acyl-carrier-protein] reductase (n-4:0)	acetoacetyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydroxybutano
	R-0353	0.0207	R-0353	0.0122	R-0353	3-oxoacyl-[acyl-carrier-protein] reductase (n-6:0)	3-oxohexanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydroxyhe
	R-0354	0.0207	R-0354	0.0122	R-0354	3-oxoacyl-[acyl-carrier-protein] reductase (n-8:0)	3-oxooctanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydroxyoct
	R-0355	0.0207	R-0355	0.0122	R-0355	3-oxoacyl-[acyl-carrier-protein] reductase (n-10:0)	3-oxodecanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydroxyde
	R-0356	0.0001	R-0356	0.0001	R-0356	3-oxoacyl-[acyl-carrier-protein] reductase (n-12:0)	3-oxododecanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydroxy
	R-0358	0.0001	R-0358	0	R-0358	3-oxoacyl-[acyl-carrier-protein] reductase (n-14:0)	3-oxotetradecanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydro
	R-0359	0	R-0359	0	R-0359	3-oxoacyl-[acyl-carrier-protein] reductase (n-16:0)	3-oxohexadecanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydro
	R-0360	0	R-0360	0	R-0360	3-oxoacyl-[acyl-carrier-protein] reductase (n-18:0)	3-oxooctadecanoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-hydro
	R-0361	0.0206	R-0361	0.0122	R-0361	3-oxoacyl-[acyl-carrier-protein] reductase (n-12:1)	3-oxo-cis-dodec-5-enoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3-h
	R-0362	0.0206	R-0362	0.0122	R-0362	3-oxoacyl-[acyl-carrier-protein] reductase (n-14:1)	3-oxo-cis-tetradec-7-enoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3
	R-0363	0.0206	R-0363	0.0122	R-0363	3-oxoacyl-[acyl-carrier-protein] reductase (n-16:1)	3-oxo-cis-hexadec-9-enoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-3
	R-0364	0.0194	R-0364	0.0115	R-0364	3-oxoacyl-[acyl-carrier-protein] reductase (n-18:1)	3-oxo-cis-octadec-11-enoyl-[acyl-carrier-protein] + NADPH + H+ = (3R)-
	R-0365	0.0207	R-0365	0.0122	R-0365	B-hydroxydecanoyl thioester dehydrase	(3R)-3-hydroxydecanoyl-[acyl-carrier-protein] = trans-dec-2-enoyl-[acyl-c
	R-0366	0.0206	R-0366	0.0122	R-0366	trans-2-decenoyl-ACP isomerase	trans-dec-2-enoyl-[acyl-carrier-protein] = cis-dec-3-enoyl-[acyl-carrier-pr
	R-0367	0.0207	R-0367	0.0122	R-0367	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-4:0)	(3R)-3-hydroxybutanoyl-[acyl-carrier-protein] = crotonyl-[acyl-carrier-prot
	R-0368	0.0207	R-0368	0.0122	R-0368	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-6:0)	(3R)-3-hydroxyhexanoyl-[acyl-carrier-protein] = trans-hex-2-enoyl-[acyl-c
	R-0369	0.0207	R-0369	0.0122	R-0369	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-8:0)	(3R)-3-hydroxyoctanoyl-[acyl-carrier-protein] = trans-oct-2-enoyl-[acyl-ca
	R-0370	0.0001	R-0370	0.0001	R-0370	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-12:0)	(3R)-3-hydroxydodecanoyl-[acyl-carrier-protein] = trans-dodec-2-enoyl-[a
	R-0371	0	R-0371	0	R-0371	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-14:0)	(3R)-3-hydroxytetradecanoyl-[acyl-carrier-protein] = trans-tetradec-2-enc
	R-0372	0	R-0372	0	R-0372	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-16:0)	(3R)-3-hydroxyhexadecanoyl-[acyl-carrier-protein] = trans-hexadec-2-en
	R-0373	0	R-0373	0	R-0373	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-18:0)	(3R)-3-hydroxyoctadecanoyl-[acyl-carrier-protein] = trans-octadec-2-eno
	R-0374	0.0206	R-0374	0.0122	R-0374	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-12:1)	(3R)-3-hydroxy-cis-dodec-5-enoyl-[acyl-carrier-protein] = trans-3-cis-5-d
	R-0375	0.0206	R-0375	0.0122	R-0375	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-14:1)	(3R)-3-hydroxy-cis-tetradec-7-enoyl-[acyl-carrier-protein] = trans-3-cis-7-
	R-0376	0.0206	R-0376	0.0122	R-0376	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-16:1)	(3R)-3-hydroxy-cis-hexadec-9-enoyl-[acyl-carrier-protein] = trans-3-cis-9
	R-0377	0.0194	R-0377	0.0115	R-0377	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-18:1)	(3R)-3-hydroxy-cis-octadec-11-enoyl-[acyl-carrier-protein] = trans-3-cis-
	R-0378	0.0207	R-0378	0.0122	R-0378	enoyl-[acyl-carrier-protein] reductase (n-4:0)	crotonyl-[acyl-carrier-protein] + NADPH + H+ = butyryl-[acyl-carrier-prote
	R-0379	0.0207	R-0379	0.0122	R-0379	enoyl-[acyl-carrier-protein] reductase (n-6:0)	trans-hex-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = hexanoyl-[acyl-
	R-0380	0.0207	R-0380	0.0122	R-0380	enoyl-[acyl-carrier-protein] reductase (n-8:0)	trans-oct-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = octanoyl-[acyl-c
	R-0381	0.0001	R-0381	0.0001	R-0381	enoyl-[acyl-carrier-protein] reductase (n-10:0)	trans-dec-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = decanoyl-[acyl-
	R-0382	0.0001	R-0382	0.0001	R-0382	enoyl-[acyl-carrier-protein] reductase (n-12:0)	trans-dodec-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = dodecanoyl-
	R-0383	0	R-0383	0	R-0383	enoyl-[acyl-carrier-protein] reductase (n-14:0)	trans-tetradec-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = tetradecan
	R-0384	0	R-0384	0	R-0384	enoyl-[acyl-carrier-protein] reductase (n-16:0)	trans-hexadec-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = hexadecan
	R-0385	0	R-0385	0	R-0385	enoyl-[acyl-carrier-protein] reductase (n-18:0)	trans-octadec-2-enoyl-[acyl-carrier-protein] + NADPH + H+ = octadecan
	R-0386	0.0206	R-0386	0.0122	R-0386	enoyl-[acyl-carrier-protein] reductase (n-12:1)	trans-3-cis-5-dodecenoyl-[acyl-carrier-protein] + NADPH + H+ = cis-dode
	R-0387	0.0206	R-0387	0.0122	R-0387	enoyl-[acyl-carrier-protein] reductase (n-14:1)	trans-3-cis-7-tetradecenoyl-[acyl-carrier-protein] + NADPH + H+ = cis-te
	R-0388	0.0206	R-0388	0.0122	R-0388	enoyl-[acyl-carrier-protein] reductase (n-16:1)	trans-3-cis-9-hexadecenoyl-[acyl-carrier-protein] + NADPH + H+ = hexac
	R-0389	0.0194	R-0389	0.0115	R-0389	enoyl-[acyl-carrier-protein] reductase (n-18:1)	trans-3-cis-11-octadecenoyl-[acyl-carrier-protein] + NADPH + H+ = octac
	R-0390	0	R-0390	0	R-0390	glutaminase	L-glutamine + H2O = L-glutamate + NH3
	R-0391	0.0063	R-0391	0.0037	R-0391	L-glutamine:D-fructose-6-phosphate aminotransferase	L-glutamine + D-fructose-6-phosphate = L-glutamate + D-glucosamine-6
	R-0392	0.2066	R-0392	0.1221	R-0392	glutamate racemase	L-glutamate = D-glutamate
	R-0393	-0.352	R-0393	-0.2081	R-0393	aspartate aminotransferase	L-aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate
	R-0394	0	R-0394	0	R-0394	GMP synthetase	ATP + XMP + L-glutamine + H2O = AMP + diphosphate + GMP + L-glu
	R-0395	0.0224	R-0395	0	R-0395	GMP synthetase (ammonia dependent)	NH3 + XMP + ATP = AMP + diphosphate + GMP
	R-0396	0.0512	R-0396	0.0303	R-0396	glutamyl-tRNA synthetase	ATP + L-glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamyl-tRN
	R-0397	1.7103	R-0397	1.0109	R-0397	glutamine synthetase	ATP + L-glutamate + NH3 = ADP + phosphate + L-glutamine
	R-0398	0	R-0398	0	R-0398	gamma-glutamylcysteine synthetase	ATP + L-glutamate + L-cysteine = ADP + phosphate + gamma-L-glutam
	R-0399	0	R-0399	0	R-0399	glutathione synthetase	ATP + gamma-L-glutamyl-L-cysteine + glycine = ADP + phosphate + glu
	R-0400	0	R-0400	0	R-0400	glutamine-dependent NAD(+) synthetase	ATP + nicotinate-adenine-dinucleotide + L-glutamine + H2O = AMP + di
	R-0401	0.0386	R-0401	0.0228	R-0401	amidophosphoribosyltransferase (PRPP amidotransferase)	L-glutamine + 5-phosphoribosyl-1-pyrophosphate + H2O = 5-phospho-b
	R-0402	0	R-0402	0	R-0402	glutamate synthase 1	NH3 + 2-oxoglutarate + NADPH + H+ = L-glutamate + NADP+ + H2O
	R-0403	1.4582	R-0403	0.8619	R-0403	glutamate synthase 2	L-glutamine + 2-oxoglutarate + NADPH + H+ = 2 L-glutamate + NADP+
	R-0404	0.0327	R-0404	0.0193	R-0404	carbamoyl phosphate synthetase	2 ATP + L-glutamine + HCO3- + H+ + H2O = 2 ADP + phosphate + L-glu
	R-0405	0.003	R-0405	0.0018	R-0405	cysteine synthase	O-acetyl-L-serine + H2S = L-cysteine + acetate
	R-0406	0.003	R-0406	0.0018	R-0406	serine acetyltransferase	acetyl-CoA + L-serine = CoA + O-acetyl-L-serine
	R-0407	0	R-0407	0	R-0407	D-cysteine desulfhydrase	D-cysteine + H2O = H2S + NH3 + pyruvate
	R-0408	0.0002	R-0408	0.0001	R-0408	cysteine tRNA synthetase	ATP + L-cysteine + tRNA(Cys) = AMP + diphosphate + L-cysteinyl-tRNA
	R-0409	0	R-0409	0	R-0409	3-mercaptopyruvate sulfurtransferase	3-mercaptopyruvate + cyanide = pyruvate + thiocyanate
	R-0410	0.0763	R-0410	0.0451	R-0410	pyrroline-5-carboxylate reductase	(S)-1-pyrroline-5-carboxylate + NADPH + H+ = L-proline + NADP+
	R-0411	0.0182	R-0411	0.0107	R-0411	proline dehydrogenase	L-proline + FAD = (S)-1-pyrroline-5-carboxylate + FADH2
	R-0412	0	R-0412	0	R-0412	1-pyrroline-5-carboxylate dehydrogenase	(S)-1-pyrroline-5-carboxylate + NAD+ + 2 H2O = L-glutamate + NADH +
	R-0413	0	R-0413	0	R-0413	ornithine cyclodeaminase	L-ornithine = L-proline + NH3
	R-0414	-0.0449	R-0414	-0.0265	R-0414	arginase	L-arginine + H2O = L-ornithine + urea
	R-0415	0	R-0415	0	R-0415	ornithine carbamoyltransferase	carbamoyl-phosphate + L-ornithine = phosphate + L-citrulline
	R-0416	0.0579	R-0416	0.0342	R-0416	proline-tRNA ligase	ATP + L-proline + tRNA(Pro) = AMP + diphosphate + L-prolyl-tRNA(Pro)
	R-0417	0.0449	R-0417	0.0265	R-0417	arginyl-tRNA synthetase	ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(A
	R-0418	0	R-0418	0	R-0418	UDP-N-acetylenolpyruvoylglucosamine reductase	UDP-N-acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH + H+ = UD
	R-0419	0	R-0419	0	R-0419	N-acetylglucosamine-6-phosphate deacetylase	N-acetyl-D-glucosamine-6-phosphate + H2O = D-glucosamine-6-phosph
	R-0420	0	R-0420	0	R-0420	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	phosphoenolpyruvate + UDP-N-acetyl-D-glucosamine = phosphate + UD
	R-0421	0	R-0421	0	R-0421	beta N-acetyl-glucosaminidase	GlcNAc-1,6-anhMurNAc + H2O = 1,6-anhydro-N-acetylmuramate + N-ac
	R-0422	0.0063	R-0422	0.0037	R-0422	N-acetylglucosamine-1-phosphate uridyltransferase	N-acetyl-glucosamine-1-phosphate + UTP = UDP-N-acetyl-D-glucosami
	R-0423	0.0063	R-0423	0.0037	R-0423	glucosamine-1-phosphate acetyltransferase	D-glucosamine-1-phosphate + acetyl-CoA = N-acetyl-glucosamine-1-pho
	R-0424	-0.0063	R-0424	-0.0037	R-0424	phosphoglucosamine mutase	D-glucosamine-1-phosphate = D-glucosamine-6-phosphate
	R-0425	0	R-0425	0	R-0425	aspartate ammonia-lyase	L-aspartate = fumarate + NH3 + H+
	R-0426	0.0013	R-0426	0.0008	R-0426	L-aspartate oxidase	L-aspartate + O2 = a-iminosuccinate + H2O2 + H+
	R-0427	0.0013	R-0427	0.0008	R-0427	quinolinate synthetase	a-iminosuccinate + glycerone-phosphate = quinolinate + phosphate + 2
	R-0428	0.0013	R-0428	0.0008	R-0428	quinolinate phosphoribosyltransferase	5-phosphoribosyl-1-pyrophosphate + quinolinate = CO2 + diphosphate +
	R-0429	0	R-0429	0	R-0429	L-asparaginase	L-asparagine + H2O = L-aspartate + NH3
	R-0430	-0.2066	R-0430	-0.1221	R-0430	alanine racemase	L-alanine = D-alanine
	R-0431	0.0288	R-0431	0.017	R-0431	adenylosuccinate synthetase	GTP + IMP + L-aspartate = GDP + phosphate + adenylo-succinate
	R-0432	0.0327	R-0432	0.0193	R-0432	aspartate carbamoyltransferase	carbamoyl-phosphate + L-aspartate = phosphate + N-carbamoyl-L-aspa
	R-0433	0	R-0433	0	R-0433	argininosuccinate synthase	ATP + L-citrulline + L-aspartate = AMP + diphosphate + L-arginino-succi
	R-0434	0.0461	R-0434	0.0273	R-0434	aspartate tRNA synthetase	ATP + L-aspartate + tRNA(Asp) = AMP + diphosphate + L-aspartyl-tRNA
	R-0435	0	R-0435	0	R-0435	asparagine synthase	L-glutamine + L-aspartate + ATP + H2O = L-glutamate + L-asparagine +
	R-0436	0.2054	R-0436	0.1214	R-0436	alanyl-tRNA synthetase	ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala)
	R-0437	0	R-0437	0	R-0437	argininosuccinate lyase	L-arginino-succinate = L-arginine + fumarate
	R-0438	0.0288	R-0438	0.017	R-0438	adenylosuccinate lyase	adenylo-succinate = fumarate + AMP
	R-0439	0.0386	R-0439	0.0228	R-0439	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazol	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole = fumar
	R-0440	0	R-0440	0	R-0440	succinate-semialdehyde dehydrogenase	succinate-semialdehyde + NADP+ + H2O = succinate + NADPH + H+
	R-0441	0	R-0441	0.0133	R-0441	guanine phosphoribosyltransferase	5-phosphoribosyl-1-pyrophosphate + guanine = diphosphate + GMP
	R-0442	0	R-0442	0	R-0442	hypoxanthine phosphoribosyltransferase	5-phosphoribosyl-1-pyrophosphate + hypoxanthine = diphosphate + IMP
	R-0443	35.4245	R-0443	24.8228	R-0443	ATP synthase	ADP + phosphate + 4 H+[p] = ATP + H2O + 4 H+
	R-0444	0	R-0444	24.7037	R-0444	cytochrome c oxidase	2 reduced-cytochrome-c + 0.5 O2 + 4 H+ = 2 oxidized-cytochrome-c + 1
	R-0445	18.41	R-0445	0	R-0445	cytochrome o ubiquinol oxidase	1 UQH2 + 0.5 O2 + 4 H+ = 1 UQ + 1 H2O + 4 H+[p]
	R-0446	0	R-0446	1.4783	R-0446	ubiquinol-cytochrome c reductase	2 oxidized-cytochrome-c + UQH2 = 2 reduced-cytochrome-c + UQ + 2 H
	R-0447	18.4107	R-0447	1.4787	R-0447	NADH:ubiquinone oxidoreductase I	NADH + UQ + 5 H+ = NAD+ + UQH2 + 4 H+[p]
	R-0448	7.1852	R-0448	4.2468	R-0448	NAD(P) transhydrogenase	NADP+ + NADH + H+[p] = NADPH + NAD+ + H+
	R-0449	0.0386	R-0449	0.0228	R-0449	phosphoribosylglycinamide synthetase	5-phospho-beta-D-ribosylamine + ATP + glycine = ADP + phosphate + 5
	R-0450	0.0386	R-0450	0.0228	R-0450	phosphoribosylglycinamide formyltransferase	5-phospho-ribosyl-glycineamide + 10-formyltetrahydrofolate = 5'-phosph
	R-0451	0.0386	R-0451	0.0228	R-0451	phosphoribosylformylglycinamide synthetase	ATP + 5'-phosphoribosyl-N-formylglycineamide + L-glutamine + H2O = L
	R-0452	0.0386	R-0452	0.0228	R-0452	phosphoribosylaminoimidazole synthetase	ATP + 5-phosphoribosyl-N-formylglycineamidine = ADP + phosphate + 5
	R-0453	0.0386	R-0453	0.0228	R-0453	phosphoribosylaminoimidazole carboxylase	5-aminoimidazole-ribonucleotide + CO2 = 4-carboxyaminoimidazole-ribo
	R-0454	0.0386	R-0454	0.0228	R-0454	phosphoribosylaminoimidazole-succinocarboxamide synthetase	ATP + 4-carboxyaminoimidazole-ribonucleotide + L-aspartate = ADP + p
	R-0455	0.0512	R-0455	0.0303	R-0455	phosphoribosylaminoimidazolecarboxamide formyltransferase	aminoimidazole-carboxamide-ribonucleotide + 10-formyltetrahydrofolate
	R-0456	0.0512	R-0456	0.0303	R-0456	inosine monophosphate cyclohydrolase	phosphoribosyl-formamido-carboxamide = IMP + H2O
	R-0457	0.0224	R-0457	0.0133	R-0457	IMP dehydrogenase	IMP + NAD+ + H2O = XMP + NADH + H+
	R-0458	0.0224	R-0458	0.0133	R-0458	guanylate kinase	GMP + ATP = GDP + ADP
	R-0459	0	R-0459	0	R-0459	deoxyguanylate kinase	dGMP + ATP = dGDP + ADP
	R-0460	0.1072	R-0460	0.0634	R-0460	UDP kinase	UDP + ATP = UTP + ADP
	R-0461	0.0089	R-0461	0.0053	R-0461	CDP kinase	CDP + ATP = CTP + ADP

R-0462	0.0028	R-0462	0.0017	R-0462	dUDP kinase	dUDP + ATP = dUTP + ADP
R-0463	0.0062	R-0463	0.0037	R-0463	dCDP kinase	dCDP + ATP = dCTP + ADP
R-0464	0.1164	R-0464	0.0688	R-0464	dTDP kinase	dTDP + ATP = dTTP + ADP
R-0465	0.0028	R-0465	0.0017	R-0465	dADP kinase	dADP + ATP = dATP + ADP
R-0466	0.0062	R-0466	0.0037	R-0466	dGDP kinase	dGDP + ATP = dGTP + ADP
R-0467	0.045	R-0467	0.0266	R-0467	GDP kinase	GDP + ATP = GTP + ADP
R-0469	0.0224	R-0469	0.0132	R-0469	CTP synthetase	ATP + UTP + L-glutamine + H2O = ADP + phosphate + CTP + L-glutam
R-0470	0.0028	R-0470	0.0017	R-0470	UDP reductase	UDP + reduced-thioredoxin = dUDP + oxidized-thioredoxin + H2O
R-0471	0.0062	R-0471	0.0037	R-0471	CDP reductase	CDP + reduced-thioredoxin = dCDP + oxidized-thioredoxin + H2O
R-0472	0.0028	R-0472	0.0017	R-0472	ADP reductase	ADP + reduced-thioredoxin = dADP + oxidized-thioredoxin + H2O
R-0474	0.0062	R-0474	0.0037	R-0474	GDP reductase	GDP + reduced-thioredoxin = dGDP + oxidized-thioredoxin + H2O
R-0475	0.0316	R-0475	0.0187	R-0475	thioredoxin reductase	oxidized-thioredoxin + NADPH + H+ = reduced-thioredoxin + NADP+
R-0476	3.4191	R-0476	2.0209	R-0476	adenylate kinase	AMP + ATP = 2 ADP
R-0477	0.0327	R-0477	0.0193	R-0477	dihydroorotase	N-carbamoyl-L-aspartate = dihydroorotate + H2O
R-0478	0.0327	R-0478	0.0193	R-0478	dihydroorotate dehydrogenase	dihydroorotate + O2 = orotate + H2O2
R-0479	0.0327	R-0479	0.0193	R-0479	orotate phosphoribosyltransferase	5-phosphoribosyl-1-pyrophosphate + orotate = orotidine-5'-phosphate +
R-0480	0.0327	R-0480	0.0193	R-0480	orotidine 5'-phosphate decarboxylase	orotidine-5'-phosphate = CO2 + UMP
R-0481	0.0151	R-0481	0.0089	R-0481	cytidylate kinase	CMP + ATP = CDP + ADP
R-0482	0.0327	R-0482	0.0193	R-0482	uridylate kinase	UMP + ATP = UDP + ADP
R-0483	0	R-0483	0	R-0483	dCTP deaminase	dCTP + H2O = NH3 + dUTP
R-0484	0.0028	R-0484	0.0017	R-0484	thymidylate synthetase	dUMP + 5,10-methylenetetrahydrofolate = dTMP + 7,8-dihydrofolate
R-0485	0.0029	R-0485	0.0017	R-0485	dihydrofolate reductase	NADPH + 7,8-dihydrofolate + H+ = NADP+ + tetrahydrofolate
R-0486	0.0028	R-0486	0.0017	R-0486	deoxyuridine 5'-triphosphate nucleotidohydrolase	dUTP + H2O = dUMP + diphosphate
R-0487	0	R-0487	0	R-0487	nucleoside triphosphate pyrophosphohydrolase (ATP)	ATP + H2O = AMP + diphosphate
R-0489	0	R-0489	0	R-0489	nucleoside triphosphate pyrophosphohydrolase (GTP)	GTP + H2O = GMP + diphosphate
R-0490	0	R-0490	0	R-0490	nucleoside triphosphate pyrophosphohydrolase (CTP)	CTP + H2O = CMP + diphosphate
R-0491	0	R-0491	0	R-0491	nucleoside triphosphate pyrophosphohydrolase (UTP)	UTP + H2O = UMP + diphosphate
R-0492	0	R-0492	0	R-0492	5'-nucleotidase (GMP)	GMP + H2O = guanosine + phosphate
R-0493	-0.0003	R-0493	-0.0002	R-0493	5'-nucleotidase (AMP)	AMP + H2O = adenosine + phosphate
R-0494	0	R-0494	0	R-0494	5'-nucleotidase (IMP)	IMP + H2O = inosine + phosphate
R-0495	0	R-0495	0.0133	R-0495	5'-nucleotidase (XMP)	XMP + H2O = xanthosine + phosphate
R-0496	0	R-0496	0	R-0496	GTP cyclohydrolase I	GTP + H2O = formate + 7,8-dihydroneopterin-triphosphate
R-0497	0	R-0497	0	R-0497	dihydroneopterin triphosphate pyrophosphohydrolase	7,8-dihydroneopterin-triphosphate + H2O = dihydroneopterin-phosphate
R-0498	0	R-0498	0	R-0498	dihydroneopterin aldolase	7,8-dihydro-D-neopterin = glycolaldehyde + 6-hydroxymethyl-7,8-dihydro
R-0499	0	R-0499	0	R-0499	dihydroneopterin monophosphate dephosphorylase	dihydroneopterin-phosphate + H2O = 7,8-dihydro-D-neopterin + phosph
R-0500	0	R-0500	0	R-0500	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophos	6-hydroxymethyl-7,8-dihydropterin + ATP = 6-hydroxymethyl-dihydropte
R-0501	0	R-0501	0	R-0501	dihydropteroate synthase	p-aminobenzoate + 6-hydroxymethyl-dihydropterin-diphosphate = dipho
R-0502	0	R-0502	0	R-0502	folylpolyglutamate synthase 1	L-glutamate + ATP + methylene-tetrahydropteroyl-[gamma-Glu](n) = AD
R-0503	0	R-0503	0	R-0503	dihydrofolate synthetase 1	L-glutamate + ATP + 7,8-dihydropteroate = phosphate + ADP + 7,8-dihy
R-0504	0	R-0504	0	R-0504	folylpolyglutamate synthase 2	L-glutamate + ATP + 10-formyl-tetrahydropteroyl-[gamma-Glu](n) = ADP
R-0505	0	R-0505	0	R-0505	folylpolyglutamate synthase 3	L-glutamate + ATP + tetrahydropteroyl-[gamma-Glu](n) = ADP + phosph
R-0506	0.0001	R-0506	0	R-0506	dihydromethanopterin reductase	NADPH + 7,8-dihydromethanopterin + H+ = NADP+ + tetrahydromethan
R-0507	0.0007	R-0507	0.0004	R-0507	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1-deoxy-D-xylulose-5-phosphate + NADPH + H+ = 2-C-methyl-D-erythrit
R-0508	0.0007	R-0508	0.0004	R-0508	4-diphosphocytidyl-2C- methyl-D-erythritol synthase	2-C-methyl-D-erythritol-4-phosphate + CTP = 4-(cytidine-5'-diphospho)-2
R-0509	0.0007	R-0509	0.0004	R-0509	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	2-phospho-4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methy
R-0510	0.0007	R-0510	0.0004	R-0510	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol + ATP = 2-phospho-4-(
R-0511	0.0007	R-0511	0.0004	R-0511	1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase	2-C-methyl-D-erythritol-2,4-cyclodiphosphate + 2 reduced-ferredoxin + 2
R-0512	0.0002	R-0512	0.0001	R-0512	1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate reductase 1	1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate + NADPH + H+ = dimet
R-0513	0.0005	R-0513	0.0003	R-0513	1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate reductase 2	1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate + NADPH + H+ = isope
R-0514	0.0002	R-0514	0.0001	R-0514	geranyl diphosphate synthase	dimethylallyl-diphosphate + isopentenyl-diphosphate = diphosphate + ge
R-0515	0.0002	R-0515	0.0001	R-0515	farnesyl-diphosphate synthase	geranyl-diphosphate + isopentenyl-diphosphate = diphosphate + all-tran
R-0516	0.0002	R-0516	0.0001	R-0516	geranylgeranyl pyrophosphate synthase	isopentenyl-diphosphate + all-trans-farnesyl-diphosphate = all-trans-gera
R-0517	0.0001	R-0517	0	R-0517	phytoene synthase 1	2 all-trans-geranyl-geranyl-diphosphate = prephytoene-diphosphate + di
R-0518	0.0001	R-0518	0	R-0518	phytoene synthase 2	prephytoene-diphosphate = phytoene + diphosphate
R-0519	0.0001	R-0519	0	R-0519	phytoene dehydrogenase 1	phytoene + reduced-electron-acceptor + O2 = phytofluene + oxidized-ele
R-0520	0.0001	R-0520	0	R-0520	phytoene dehydrogenase 2	phytofluene + reduced-electron-acceptor + O2 = zeta-carotene + oxidize
R-0521	0.0001	R-0521	0	R-0521	zeta-carotene desaturase 1	zeta-carotene + reduced-electron-acceptor + O2 = neurosporene + oxidi
R-0522	0.0001	R-0522	0	R-0522	zeta-carotene desaturase 2	neurosporene + reduced-electron-acceptor + O2 = trans-lycopene + oxid
R-0523	0.0141	R-0523	0.0083	R-0523	prephenate dehydrogenase	prephenate + NAD+ = 4-hydroxyphenylpyruvate + CO2 + NADH + H+
R-0524	0.0253	R-0524	0.015	R-0524	aromatic-amino-acid transaminase (PHE)	phenylpyruvate + L-glutamate = L-phenylalanine + 2-oxoglutarate
R-0525	0.0141	R-0525	0.0083	R-0525	aromatic-amino-acid transaminase (TYR)	4-hydroxyphenylpyruvate + L-glutamate = L-tyrosine + 2-oxoglutarate
R-0526	0.2066	R-0526	0.1221	R-0526	D-alanine aminotransferase	pyruvate + D-glutamate = D-alanine + 2-oxoglutarate
R-0527	0.0126	R-0527	0.0075	R-0527	histidinol-phosphatase	L-histidinol-phosphate + H2O = L-histidinol + phosphate
R-0529	0.0006	R-0529	0.0004	R-0529	acyl phosphate synthase (n-16:0)	hexadecanoyl-[acyl-carrier-protein] + phosphate = hexadecanoyl-phosph
R-0530	0.0006	R-0530	0.0004	R-0530	acyl phosphate synthase (n-16:1)	hexadec-9-enoyl-[acyl-carrier-protein] + phosphate = hexadec-9-enoyl-p
R-0531	0.0006	R-0531	0.0004	R-0531	acyl phosphate synthase (n-18:0)	octadecanoyl-[acyl-carrier-protein] + phosphate = octadecanoyl-phospha
R-0532	0.0097	R-0532	0.0057	R-0532	acyl phosphate synthase (n-18:1)	octadec-9-enoyl-[acyl-carrier-protein] + phosphate = octadec-9-enoyl-ph
R-0534	0.0006	R-0534	0.0004	R-0534	glycerol-3-phosphate synthetase (n-16:0)	sn-glycerol-3-phosphate + hexadecanoyl-phosphate = 1-hexadecanoyl-s
R-0535	0.0006	R-0535	0.0004	R-0535	glycerol-3-phosphate synthetase (n-16:1)	sn-glycerol-3-phosphate + hexadec-9-enoyl-phosphate = 1-hexadec-9-e
R-0536	0.0006	R-0536	0.0004	R-0536	glycerol-3-phosphate synthetase (n-18:0)	sn-glycerol-3-phosphate + octadecanoyl-phosphate = 1-octadecanoyl-sn
R-0537	0.0097	R-0537	0.0057	R-0537	glycerol-3-phosphate synthetase (n-18:1)	sn-glycerol-3-phosphate + octadec-9-enoyl-phosphate = 1-octadec-9-en
R-0538	0.0028	R-0538	0.0017	R-0538	thymidylate kinase	dTMP + ATP = dTDP + ADP
R-0539	0	R-0539	0	R-0539	adenylate kinase 2	dAMP + ATP = ADP + dADP
R-0540	0.0516	R-0540	0.0305	R-0540	glutamyl-tRNA amidotransferase	ATP + L-glutamyl-tRNA(Gln) + L-glutamine + H2O = ADP + phosphate +
R-0541	0.0516	R-0541	0.0305	R-0541	nondiscriminating glutamyl-tRNA synthetase	ATP + L-glutamate + tRNA(Gln) = AMP + diphosphate + L-glutamyl-tRN
R-0542	0.0465	R-0542	0.0275	R-0542	nondiscriminating aspartate tRNA synthetase	ATP + L-aspartate + tRNA(Asn) = AMP + diphosphate + L-aspartyl-tRN/
R-0543	0.0465	R-0543	0.0275	R-0543	aspartyl-tRNA amidotransferase	ATP + L-aspartyl-tRNA(Asn) + L-glutamine + H2O = ADP + phosphate +
R-0544	0.0581	R-0544	0.0344	R-0544	gamma-glutamyl kinase	L-glutamate + ATP = L-glutamate-5-phosphate + ADP
R-0545	0.0581	R-0545	0.0344	R-0545	glutamate-5-semialdehyde dehydrogenase	L-glutamate-5-phosphate + NADPH + H+ = L-glutamate-gamma-semialc
R-0546	0.0581	R-0546	0.0344	R-0546	L-glutamate-gamma-semialdehyde (cyclase dehydratase)	L-glutamate-gamma-semialdehyde = (S)-1-pyrroline-5-carboxylate + H2O
R-0547	0	R-0547	0	R-0547	N-acetylglutamate synthase	L-glutamate + acetyl-CoA = N-acetyl-L-glutamate + CoA
R-0548	0.0533	R-0548	0.0315	R-0548	acetylglutamate kinase	N-acetyl-L-glutamate + ATP = N-acetylglutamyl-phosphate + ADP
R-0549	0.0533	R-0549	0.0315	R-0549	N-acetylglutamylphosphate reductase	N-acetylglutamyl-phosphate + NADPH + H+ = N-acetyl-L-glutamate-5-s
R-0550	0	R-0550	0	R-0550	acetylornithine deacetylase	N-acetyl-L-ornithine + H2O = L-ornithine + acetate
R-0551	0.0533	R-0551	0.0315	R-0551	glutamate N-acetyltransferase	L-glutamate + N-acetyl-L-ornithine = N-acetyl-L-glutamate + L-ornithine
R-0552	0	R-0552	0	R-0552	methylation	(S)-adenosyl-L-methionine + demethylated-methyl-acceptor = (S)-adeno
R-0553	0.0001	R-0553	0.0001	R-0553	tryptophanyl tRNA synthetase	ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophyl-tR
R-0554	0	R-0554	0	R-0554	phosphoglucose isomerase 2	b-D-glucose-6-phosphate = D-fructose-6-phosphate
R-0555	0	R-0555	0	R-0555	glucokinase 2	ATP + b-D-glucose = ADP + b-D-glucose-6-phosphate
R-0556	0	R-0556	0	R-0556	2'-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	dephospho-CoA + ATP = 2'-(5-triphosphoribosyl)-3'-dephospho-CoA + a
R-0557	0	R-0557	0	R-0557	phosphoribosyl-dephospho-CoA transferase	2'-(5-triphosphoribosyl)-3'-dephospho-CoA + malonate-decarboxylase-a
R-0558	0	R-0558	0	R-0558	Isoquinoline 1-oxidoreductase	isoquinoline + oxidized-electron-acceptor + H2O = isoquinolin-1(2H)-one
R-0559	0	R-0559	0	R-0559	polysulphide reductase	S(n)2- + reduced-electron-acceptor = S(n-1)2- + H2S + oxidized-electron
R-0560	0.0343	R-0560	0.0203	R-0560	potassium-transporting ATPase	K+[p] + H2O + ATP = K+ + phosphate + ADP
R-0561	0	R-0561	0	R-0561	myo-inositol-1-phosphate synthase	b-D-glucose-6-phosphate = D-myo-inositol-3-monophosphate
R-0562	0	R-0562	0	R-0562	pyridoxamine 5'-phosphate oxidase	pyridoxamine-5'-phosphate + O2 + H2O = H2O2 + NH3 + pyridoxal-5'-ph
R-0563	0	R-0563	0	R-0563	pyridoxine 5'-phosphate oxidase	pyridoxine-5'-phosphate + O2 = H2O2 + pyridoxal-5'-phosphate
R-0565	0	R-0565	0	R-0565	3-deoxy-D-manno-octulosonate cytidylyltransferase	3-deoxy-D-manno-octulosonate + CTP = CMP-3-deoxy-D-manno-octulo
R-0566	0	R-0566	0	R-0566	3-deoxy-8-phosphooctulonate synthase	D-arabinose-5-phosphate + phosphoenolpyruvate + H2O = 3-deoxy-D-m
R-0567	0	R-0567	0	R-0567	3-deoxy-D-manno-octulosonate-8-phosphate phosphatase	3-deoxy-D-manno-octulosonate-8-P + H2O = 3-deoxy-D-manno-octulos
R-0568	0	R-0568	0	R-0568	D-arabinose-5-phosphate isomerase	D-arabinose-5-phosphate = D-ribulose-5-phosphate
R-0569	0	R-0569	0	R-0569	salicylate hydroxylase	salicylate + NADH + O2 + 2 H+ = catechol + CO2 + NAD+ + H2O
R-0570	0	R-0570	0	R-0570	adenine phosphoribosyltransferase	5-phosphoribosyl-1-pyrophosphate + adenine = AMP + diphosphate
R-0571	0	R-0571	0	R-0571	inositol monophosphatase	D-myo-inositol-3-monophosphate + H2O = phosphate + myo-inositol
R-0572	0	R-0572	0	R-0572	glycerol-2-phosphatase	glycerol-2-phosphate + H2O = glycerol + phosphate
R-0573	0	R-0573	0	R-0573	thiamine phosphate synthase	4-methyl-5-(b-hydroxyethyl)thiazole-phosphate + 4-amino-5-hydroxymet
R-0574	0	R-0574	0	R-0574	thiazole synthase 1	iminoglycine + L-tyrosine + thiS-thiF-acyl-disulfide = 4-methyl-5-(b-hydro
R-0576	0	R-0576	0	R-0576	glycine oxidase 1	glycine + H2O + O2 = glyoxylate + NH3 + H2O2
R-0577	0	R-0577	0	R-0577	glycine oxidase 2	D-alanine + H2O + O2 = pyruvate + NH3 + H2O2
R-0578	0	R-0578	0	R-0578	glycine oxidase 3	sarcosine + H2O + O2 = glyoxylate + methylamine + H2O2
R-0579	0	R-0579	0	R-0579	glycine oxidase 4	N-ethylglycine + H2O + O2 = glyoxylate + ethylamine + H2O2
R-0580	0	R-0580	0	R-0580	gluconolactonase	glucono-d-lactone[p] + H2O[p] = D-gluconate[p]
R-0581	0	R-0581	0	R-0581	coproporphyrinogen III oxidase	coproporphyrinogen-III + O2 = protoporphyrinogen-IX + 2 CO2 + 2 H2O
R-0582	0	R-0582	0	R-0582	AMP nucleosidase	AMP[p] + H2O[p] = D-ribose-5-phosphate[p] + adenine[p]
R-0583	0	R-0583	0	R-0583	ceramide glucosyltransferase	UDP-glucose + ceramide = UDP + D-glucosyl-ceramide
R-0584	0	R-0584	0	R-0584	7,8-diaminopelargonic acid synthetase	(S)-adenosyl-L-methionine + 7-keto-8-aminopelargonate = (S)-adenosyl-
R-0585	0	R-0585	0	R-0585	7-keto-8-aminopelargonic acid synthetase	6-carboxyhexanoyl-CoA + L-alanine = CO2 + 7-keto-8-aminopelargonat
R-0586	0	R-0586	0	R-0586	biotin biosynthesis hypothetical reaction	malonyl-CoA + ADP + phosphate = ATP + 6-carboxyhexanoyl-CoA + HC
R-0587	0	R-0587	0	R-0587	cobalamin synthase	adenosylcobinamide-GDP + a-ribazole = coenzyme-B12 + GMP
R-0588	0	R-0588	0	R-0588	cobalamin-5'-phosphate synthase	adenosylcobinamide-GDP + a-ribazole-5'-P = adenosylcobalamin-5'-phc
R-0589	0	R-0589	0	R-0589	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosylt	nicotinate-mononucleotide + dimethylbenzimidazole = nicotinate + a-riba
R-0590	0	R-0590	0	R-0590	3-demethylubiquinone-8 3-O-methyltransferase	(S)-adenosyl-L-methionine + 3-demethylubiquinol-8 = (S)-adenosyl-L-ho
R-0591	0	R-0591	0	R-0591	2-octaprenyl-8-hydroxyphenol methylase	2-octaprenyl-6-hydroxyphenol + (S)-adenosyl-L-methionine = 2-octaprer
R-0593	0	R-0593	0	R-0593	nitric oxide dioxygenase	2 NO + NADPH + 2 O2 = 2 NO3- + NADP+ + H+

	R-0594	0	R-0594	0	R-0594	dihydropteridine reductase	5,6,7,8-tetrahydropteridine + NADP+ = 6,7-dihydropteridine + NADPH +
	R-0595	0	R-0595	0	R-0595	phosphoribulokinase	D-ribulose-5-phosphate + ATP = D-ribulose-1,5-bisphosphate + ADP
	R-0596	0.0084	R-0596	0.005	R-0596	ornithine decarboxylase	L-ornithine = CO2 + putrescine
	R-0597	0	R-0597	0	R-0597	molybdopterin guanine dinucleotide synthase	molybdenum-cofactor + GTP + 4 H+ = molybdopterin-guanine-dinucleoti
	R-0598	0	R-0598	0	R-0598	precorrin-6Y C(5,15)-methyltransferase	precorrin-6B + 2 (S)-adenosyl-L-methionine = precorrin-8x + 2 (S)-adeno
	R-0599	0	R-0599	0	R-0599	precorrin-4 C(11)-methyltransferase	(S)-adenosyl-L-methionine + precorrin-4 = (S)-adenosyl-L-homocysteine
	R-0600	0	R-0600	0	R-0600	cobyrinic acid a,c-diamide synthase	cobyrinate + 2 L-glutamine + 2 ATP + 2 H2O = cob(II)yrinate-a,c-diamid
	R-0601	0	R-0601	0	R-0601	hydrogenobyrinate a,c-diamide synthase	hydrogenobyrinate + 2 L-glutamine + 2 ATP + 2 H2O = 2 L-glutamate +
	R-0602	0	R-0602	0	R-0602	isonitrile hydratase	N-cyclohexylformamide = cyclohexyl-isocyanide + H2O
	R-0603	-0.0449	R-0603	-0.0265	R-0603	urease	urea + H2O = 2 NH3 + CO2
	R-0604	0	R-0604	0	R-0604	6-pyruvoyl tetrahydrobiopterin synthase	7,8-dihydroneopterin-triphosphate = triphosphate + 6-pyruvoyl-tetrahydr
	R-0605	0	R-0605	0	R-0605	quinoprotein ethanol dehydrogenase	ethanol[p] + 2 oxidized-cytochrome-c = 2 reduced-cytochrome-c + 2 H+[
	R-0606	0	R-0606	0	R-0606	cytochrome d terminal oxidase	2 UQH2 + O2 + 4 H+ = 2 UQ + 2 H2O + 4 H+[p]
	R-0607	0	R-0607	0	R-0607	2-octaprenylphenol hydroxylase	2-octaprenylphenol + O2 + 2 H+ = 2-octaprenyl-6-hydroxyphenol + H2O
	R-0608	0	R-0608	0	R-0608	NADPH-dependent FMN reductase	FMNH2 + NADP+ = FMN + NADPH + H+
	R-0609	0	R-0609	0	R-0609	precorrin-3B C(17)-methyltransferase	precorrin-3B + (S)-adenosyl-L-methionine = precorrin-4 + (S)-adenosyl-L
	R-0610	0	R-0610	0	R-0610	precorrin-2 C(20)-methyltransferase	precorrin-2 + (S)-adenosyl-L-methionine = (S)-adenosyl-L-homocysteine
	R-0611	0	R-0611	0	R-0611	precorrin-8X methylmutase	precorrin-8x = hydrogenobyrinate
	R-0612	0	R-0612	0	R-0612	precorrin-3B synthase	precorrin-3A + NADH + O2 + H+ = precorrin-3B + NAD+ + H2O
	R-0613	0	R-0613	0	R-0613	cobinamide phosphate guanylyltransferase	adenosyl-cobinamide-phosphate + GTP = adenosylcobinamide-GDP + d
	R-0614	0	R-0614	0	R-0614	cobinamide kinase	adenosylcobinamide + ATP = adenosyl-cobinamide-phosphate + ADP
	R-0615	0	R-0615	0	R-0615	cobalamin adenosyltransferase	ATP + cob(I)alamin = coenzyme-B12 + triphosphate + H+
	R-0616	0	R-0616	0	R-0616	ferrochelatase	Fe2+ + protoporphyrin-IX = protoheme-IX + 2 H+
	R-0617	0.0028	R-0617	0.0017	R-0617	dephospho-CoA kinase	dephospho-CoA + ATP = ADP + CoA
	R-0618	0	R-0618	0	R-0618	uroporphyrinogen decarboxylase	uroporphyrinogen-III = 4 CO2 + coproporphyrinogen-III
	R-0619	0	R-0619	0	R-0619	molybdopterin synthase sulfurylase	precursor-Z + 2 sulfurated-molybdopterin-synthase = 2 molybdopterin-s
	R-0620	0	R-0620	0	R-0620	ETF dehydrogenase	reduced-ETF + UQ = oxidized-ETF + UQH2
	R-0621	0	R-0621	0	R-0621	3-hydroxybutyryl-CoA dehydrogenase	(S)-3-hydroxybutanoyl-CoA + NADP+ = acetoacetyl-CoA + NADPH + H+
	R-0622	0	R-0622	0	R-0622	uracil phosphoribosyltransferase	diphosphate + UMP = 5-phosphoribosyl-1-pyrophosphate + uracil
	R-0623	0	R-0623	0	R-0623	glycogen phosphorylase-limit dextrin a-1,6-glucohydrolase	limit-dextrin + H2O = maltotetraose + debranched-limit-dextrin
	R-0624	0	R-0624	0	R-0624	thiamine biosynthesis protein thiC	5-aminoimidazole-ribonucleotide + (S)-adenosyl-L-methionine = hydroxy
	R-0625	0	R-0625	-0.0133	R-0625	guanine deaminase	guanine + H2O = NH3 + xanthine
	R-0626	0	R-0626	0	R-0626	ureidoglycolate amidohydrolase	(S)-ureidoglycolate + H2O = 2 NH3 + CO2 + glyoxylate
	R-0627	0.0028	R-0627	0.0017	R-0627	3-methyl-2-oxobutanoate hydroxymethyltransferase	3-methyl-2-oxobutanoate + 5,10-methylenetetrahydrofolate + H2O = 2-d
	R-0628	0	R-0628	0	R-0628	carboxymethylenebutenolidase	2-chloro-cis-dienelactone + H2O = 2-chloromaleylacetate + H+
	R-0629	0	R-0629	0	R-0629	dienelactone hydrolase (cis)	cis-dienelactone + H2O = 2-maleylacetate + H+
	R-0630	0	R-0630	0	R-0630	dienelactone hydrolase (trans)	trans-dienelactone + H2O = 2-maleylacetate + H+
	R-0631	0	R-0631	0	R-0631	4-(b-D-ribofuranosyl)aminobenzene-5'-phosphate synthase	p-aminobenzoate + 5-phosphoribosyl-1-pyrophosphate = 4-(b-D-ribofura
	R-0632	0	R-0632	0	R-0632	acyl carrier protein phosphodiesterase	[acyl-carrier-protein] + H2O = 4'-phosphopantetheine + apo-[acyl-carrier-
	R-0633	0	R-0633	0	R-0633	homospermidine synthase 1	putrescine + spermidine = 1,3-diaminopropane + sym-homospermidine
	R-0634	0	R-0634	0	R-0634	homospermidine synthase 2	2 putrescine = NH3 + sym-homospermidine
	R-0635	0	R-0635	0	R-0635	N-ethylmaleimide reductase	N-ethylmaleimide + 2 H+ = N-ethylsuccinimide
	R-0636	0	R-0636	2.1378	R-0636	inorganic pyrophosphatase	diphosphate + H2O = 2 phosphate
	R-0637	0	R-0637	0	R-0637	UDP-3-O-[3-hydroxymyristoyl]glucosamine N-acetyltransferase	(3R)-3-hydroxytetradecanoyl-[acyl-carrier-protein] + UDP-3-O-(3-hydrox
	R-0638	0	R-0638	0	R-0638	undecaprenyl diphosphate synthase 1	all-trans-farnesyl-diphosphate + isopentenyl-diphosphate = 2-cis,6-trans
	R-0639	0	R-0639	0	R-0639	undecaprenyl diphosphate synthase 2	2-cis,6-trans,10-trans-geranylgeranyl-diphosphate + isopentenyl-diphosp
	R-0640	0	R-0640	0	R-0640	undecaprenyl diphosphate synthase 3	di-trans,poly-cis-pentaprenyl-diphosphate + isopentenyl-diphosphate = d
	R-0641	0	R-0641	0	R-0641	undecaprenyl diphosphate synthase 4	di-trans,poly-cis-hexaprenyl-diphosphate + isopentenyl-diphosphate = di
	R-0642	0	R-0642	0	R-0642	undecaprenyl diphosphate synthase 5	di-trans,poly-cis-heptaprenyl-diphosphate + isopentenyl-diphosphate = d
	R-0643	0	R-0643	0	R-0643	undecaprenyl diphosphate synthase 6	di-trans,poly-cis-octaprenyl-diphosphate + isopentenyl-diphosphate = di-
	R-0644	0	R-0644	0	R-0644	undecaprenyl diphosphate synthase 7	di-trans,poly-cis-nonaprenyldiphosphate + isopentenyl-diphosphate = di-
	R-0645	0	R-0645	0	R-0645	undecaprenyl diphosphate synthase 8	di-trans,poly-cis-decaprenyldiphosphate + isopentenyl-diphosphate = di-
	R-0646	0	R-0646	0	R-0646	acyl-CoA thioesterase II (n-h6:0)	(3R)-3-hydroxyhexanoyl-CoA + H2O = (3R)-3-hydroxyhexanoate + CoA
	R-0647	0	R-0647	0	R-0647	acyl-CoA thioesterase II (n-h8:0)	(3R)-3-hydroxyoctanoyl-CoA + H2O = (3R)-3-hydroxyoctanoate + CoA
	R-0648	0	R-0648	0	R-0648	acyl-CoA thioesterase II (n-h10:0)	(3R)-3-hydroxydecanoyl-CoA + H2O = (3R)-3-hydroxydecanoate + CoA
	R-0649	0	R-0649	0	R-0649	acyl-CoA thioesterase II (n-h12:0)	(3R)-3-hydroxydodecanoyl-CoA + H2O = (3R)-3-hydroxydodecanoate +
	R-0650	0	R-0650	0	R-0650	acyl-CoA thioesterase II (n-h14:0)	(3R)-3-hydroxytetradecanoyl-CoA + H2O = (3R)-3-hydroxytetradecanoa
	R-0651	0	R-0651	0	R-0651	acyl-CoA thioesterase II (n-h16:0)	(3R)-3-hydroxyhexadecanoyl-CoA + H2O = (3R)-3-hydroxyhexadecanoa
	R-0652	0	R-0652	0	R-0652	acyl-CoA thioesterase II (n-h18:0)	(3R)-3-hydroxyoctadecanoyl-CoA + H2O = (3R)-3-hydroxyoctadecanoat
	R-0653	0	R-0653	0	R-0653	acyl-CoA thioesterase II (n-6:0)	hexanoyl-CoA + H2O = hexanoate + CoA
	R-0654	0	R-0654	0	R-0654	acyl-CoA thioesterase II (n-8:0)	octanoyl-CoA + H2O = octanoate + CoA
	R-0655	0	R-0655	0	R-0655	acyl-CoA thioesterase II (n-10:0)	decanoyl-CoA + H2O = decanoate + CoA
	R-0656	0	R-0656	0	R-0656	acyl-CoA thioesterase II (n-12:0)	dodecanoyl-CoA + H2O = dodecanoate + CoA
	R-0657	0	R-0657	0	R-0657	acyl-CoA thioesterase II (n-14:0)	tetradecanoyl-CoA + H2O = tetradecanoate + CoA
	R-0658	0	R-0658	0	R-0658	acyl-CoA thioesterase II (n-16:0)	hexadecanoyl-CoA + H2O = hexadecanoate + CoA
	R-0659	0	R-0659	0	R-0659	acyl-CoA thioesterase II (n-18:0)	octadecanoyl-CoA + H2O = octadecanoate + CoA
	R-0660	0	R-0660	0	R-0660	creatininase	creatinine + H2O = creatine
	R-0661	0	R-0661	0	R-0661	fumarylacetoacetate hydrolase	4-fumaryl-acetoacetate + H2O = fumarate + acetoacetate
	R-0662	0.0028	R-0662	0.0017	R-0662	2-dehydropantoate 2-reductase	2-dehydropantoate + NADPH + H+ = L-pantoate + NADP+
	R-0663	0.0135	R-0663	0.008	R-0663	sulfate adenylyltransferase	SO42- + ATP + 2 H+ = adenosine-5'-phosphosulfate + diphosphate
	R-0664	0.0135	R-0664	0.008	R-0664	phosphoadenosine phosphosulfate reductase	phosphoadenosine-5'-phosphosulfate + reduced-thioredoxin = adenosin
	R-0665	0.0135	R-0665	0.008	R-0665	sulfite reductase-(NADPH)	HSO3- + 3 NADPH + 4 H+ = H2S + 3 NADP+ + 3 H2O
	R-0666	0	R-0666	0	R-0666	pyridoxine 5'-phosphate synthase	1-deoxy-D-xylulose-5-phosphate + 1-amino-propan-2-one-3-phosphate
	R-0667	0	R-0667	0	R-0667	holo-[acyl-carrier-protein] synthase	apo-[acyl-carrier-protein] + CoA = adenosine-3',5'-bisphosphate + [acyl-c
	R-0669	0	R-0669	0	R-0669	glutathione reductase	glutathione-disulfide + NADPH + H+ = 2 glutathione + NADP+
	R-0670	0.0007	R-0670	0.0004	R-0670	NADPH-ferredoxin oxidoreductase 1	2 oxidized-ferredoxin + NADPH = 2 reduced-ferredoxin + NADP+ + H+
	R-0671	0	R-0671	0	R-0671	dethiobiotin synthetase	CO2 + 7,8-diaminopelargonate + ATP = dethiobiotin + phosphate + ADP
	R-0672	0	R-0672	0	R-0672	undecaprenyl pyrophosphate phosphatase	di-trans,poly-cis-undecaprenyl-diphosphate + H2O = di-trans,poly-cis-un
	R-0673	0	R-0673	0	R-0673	peptidoglycan glycosyltransferase	diphosphoundecaprenyl-[GlcNAc-MurNAc-pentapeptide](n) + peptidogly
	R-0674	0.0028	R-0674	0.0017	R-0674	pantothenate kinase	(R)-pantothenate + ATP = (D)-4'-phosphopantothenate + ADP
	R-0675	0	R-0675	0	R-0675	methylamine dehydrogenase	methylamine[p] + oxidized-amicyanin + H2O[p] = formaldehyde[p] + NH3
	R-0676	0	R-0676	0	R-0676	maleylacetoacetate isomerase	4-maleyl-acetoacetate = 4-fumaryl-acetoacetate
	R-0677	0	R-0677	0	R-0677	NADH:ubiquinone oxidoreductase II	UQ + NADH + H+ = UQH2 + NAD+
	R-0679	0	R-0679	0	R-0679	pyridoxal kinase	ATP + pyridoxal = ADP + pyridoxal-5'-phosphate
	R-0680	0	R-0680	0	R-0680	pyridoxamine kinase	ATP + pyridoxamine = ADP + pyridoxamine-5'-phosphate
	R-0681	0	R-0681	0	R-0681	trans-2,3-dihydro-3-hydroxy-anthranilate isomerase	trans-2,3-dihydro-3-hydroxyanthranilate = 2,3-dihydro-3-hydroxy-anthran
	R-0682	0	R-0682	0	R-0682	L-Ala-D/L-Glu epimerase	L-Ala-y-D-Glu = L-Ala-L-Glu
	R-0683	0	R-0683	0	R-0683	spermidine acetyltransferase	acetyl-CoA + spermidine = N-acetylspermidine + CoA
	R-0684	0	R-0684	0	R-0684	methoxyneurosporene dehydrogenase 1	hydroxyneurosporene + oxidized-electron-acceptor = demethylspheroide
	R-0685	0.0001	R-0685	0	R-0685	methoxyneurosporene dehydrogenase 2	rhodopin + oxidized-electron-acceptor = 3,4-dehydrorhodopin + reduced
	R-0686	0.0001	R-0686	0	R-0686	methoxyneurosporene dehydrogenase 3	rhodovibrin + oxidized-electron-acceptor = hydroxyspirilloxanthin + reduc
	R-0687	0	R-0687	0	R-0687	hydroxyneurosporene methyltransferase 1	demethylspheroidene + (S)-adenosyl-L-methionine = spheroidene + (S)-
	R-0688	0	R-0688	0	R-0688	hydroxyneurosporene methyltransferase 2	hydroxyneurosporene + (S)-adenosyl-L-methionine = methoxyneurospo
	R-0689	0	R-0689	0	R-0689	hydroxyneurosporene methyltransferase 3	rhodopin + (S)-adenosyl-L-methionine = 3,4-dihydroanhydrorhodovibrin
	R-0690	0	R-0690	0	R-0690	hydroxyneurosporene methyltransferase 4	3',4'-dihydrorhodovibrin + (S)-adenosyl-L-methionine = 3,4,3',4'-tetrahyd
	R-0691	0.0001	R-0691	0	R-0691	hydroxyneurosporene methyltransferase 5	3,4-dehydrorhodopin + (S)-adenosyl-L-methionine = anhydrorhodovibrin
	R-0692	0.0001	R-0692	0	R-0692	hydroxyneurosporene methyltransferase 6	hydroxyspirilloxanthin + (S)-adenosyl-L-methionine = spirilloxanthin + (S
	R-0693	0	R-0693	0	R-0693	2-desacetyl-2-hydroxyethyl bacteriochlorophyllide a dehydrog	2-desacetyl-2-hydroxyethyl-bacteriochlorophyllidea = bacteriochlorophyl
	R-0694	0	R-0694	0	R-0694	chlorophyllide a reductase	chlorophyllidea + ATP + H2O = 3-vinyl-bacteriochlorophyllidea + ADP +
	R-0695	0	R-0695	0	R-0695	3-hydroxyethylchlorophyllide a reductase	3-hydroxyethylchlorophyllidea + 2 H+ = 2-desacetyl-2-hydroxyethyl-bact
	R-0696	0	R-0696	0	R-0696	cyanase	cyanate + HCO3- + H+ = carbamate + CO2
	R-0697	0	R-0697	0	R-0697	di-haem cytochrome c peroxidase	H2O2[p] + 2 reduced-cytochrome-c + 2 H+ = 2 oxidized-cytochrome-c +
	R-0698	0	R-0698	0	R-0698	L-sorbosone dehydrogenase	L-sorbosone-2,6-lactone + reduced-electron-acceptor + H2O = 2-keto-L-
	R-0699	0	R-0699	0	R-0699	xanthine dehydrogenase 1	xanthine + NAD+ + H2O = urate + NADH + H+
	R-0700	0.197	R-0700	0.1164	R-0700	carbonic anhydrase	CO2 + H2O = HCO3- + H+
	R-0701	0	R-0701	0	R-0701	molybdenum::molybdopterin ligase	molybdopterin-AMP + molybdate + H+ = molybdenum-cofactor + AMP +
	R-0702	0.0013	R-0702	0.0008	R-0702	nicotinate nucleotide adenylyltransferase	ATP + nicotinate-mononucleotide = diphosphate + nicotinate-adenine-di
	R-0703	0	R-0703	0	R-0703	acetyl-CoA:acetoacetyl-CoA transferase	acetoacetate + acetyl-CoA = acetoacetyl-CoA + acetate
	R-0704	0	R-0704	0	R-0704	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) p	N-acetylmuramoyl-pentapeptide-diphosphoundecaprenol + UDP-N-acety
	R-0705	0	R-0705	0	R-0705	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) p	N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelyl-D-alany
	R-0706	0	R-0706	0	R-0706	UDP-N-acetylmuramate-alanine ligase	L-alanine + UDP-N-acetylmuramate + ATP = UDP-N-acetylmuramoyl-L-
	R-0707	0	R-0707	0	R-0707	D-alanine-D-alanine ligase B	2 D-alanine + ATP = D-alanyl-D-alanine + phosphate + ADP
	R-0708	0	R-0708	0	R-0708	UDP-3-O-acyl-N-acetylglucosamine deacetylase	UDP-3-O-(3-hydroxymyristoyl)-N-acetylglucosamine + H2O = UDP-3-O-
	R-0709	0	R-0709	0	R-0709	thymidine phosphorylase	phosphate + thymidine = deoxyribose-1-phosphate + thymine
	R-0710	0	R-0710	0	R-0710	uracil phosphorylase	phosphate + deoxyuridine = deoxyribose-1-phosphate + uracil
	R-0711	0	R-0711	0.0133	R-0711	xanthosine phosphorylase	xanthosine + phosphate = alpha-D-ribose-1-phosphate + xanthine
	R-0712	0	R-0712	0	R-0712	cytidine deaminase 1	cytidine + H2O = uridine + NH3
	R-0713	0	R-0713	0	R-0713	cytidine deaminase 2	deoxycytidine + H2O = deoxyuridine + NH3
	R-0714	0	R-0714	0	R-0714	tetraacyldisaccharide 4'-kinase	lipid-A-disaccharide + ATP = lipid-IVA + ADP
	R-0715	0	R-0715	0	R-0715	3-deoxy-D-manno-octulosonic acid transferase 1	(KDO)-lipid-IVA + CMP-3-deoxy-D-manno-octulosonate = KDO2-lipid-IV
	R-0716	0	R-0716	0	R-0716	3-deoxy-D-manno-octulosonic acid transferase 2	lipid-IVA + CMP-3-deoxy-D-manno-octulosonate = (KDO)-lipid-IVA + CM
	R-0717	0	R-0717	0	R-0717	GTP cyclohydrolase II	GTP + 3 H2O = diphosphate + 2,5-diamino-6-(ribosylamino)-4-(3H)-pyri
	R-0718	0	R-0718	0	R-0718	acylphosphatase (n-16:0)	hexadecanoyl-phosphate + H2O = hexadecanoate + phosphate
	R-0719	0	R-0719	0	R-0719	acylphosphatase (n-16:1)	hexadec-9-enoyl-phosphate + H2O = 9-hexadecenoate + phosphate

R-0720	0	R-0720	0	R-0720	acylphosphatase (n-18:0)	octadecanoyl-phosphate + H2O = octadecanoate + phosphate
R-0721	0	R-0721	0	R-0721	acylphosphatase (n-18:1)	octadec-9-enoyl-phosphate + H2O = 9-octadecenoate + phosphate
R-0722	0	R-0722	0	R-0722	magnesium chelatase	ATP + protoporphyrin-IX + Mg2+ + H2O = Mg-protoporphyrin + phospha
R-0724	3.6169	R-0724	0	R-0724	H(+)-translocating pyrophosphatases	diphosphate + H2O + H+ = 2 phosphate + H+[p]
R-0725	0	R-0725	0	R-0725	octaprenyl diphosphate synthase 1	isopentenyl-diphosphate + all-trans-geranyl-geranyl-diphosphate = gera
R-0726	0	R-0726	0	R-0726	octaprenyl diphosphate synthase 2	geranylfarnesyl-diphosphate + isopentenyl-diphosphate = all-trans-hexa
R-0727	0	R-0727	0	R-0727	octaprenyl diphosphate synthase 3	all-trans-hexaprenyl-diphosphate + isopentenyl-diphosphate = all-trans-h
R-0728	0	R-0728	0	R-0728	octaprenyl diphosphate synthase 4	all-trans-heptaprenyl-diphosphate + isopentenyl-diphosphate = diphosph
R-0729	0	R-0729	0	R-0729	thiamine monophosphate kinase	thiamine-phosphate + ATP = thiamine-diphosphate + ADP
R-0730	0	R-0730	0	R-0730	6,7-dimethyl-8-ribityllumazine synthase	5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinedione + L-3,4-dihydroxybut
R-0731	0	R-0731	0	R-0731	riboflavin synthase	2 6,7-dimethyl-8-(1-D-ribityl)lumazine = 5-amino-6-ribitylamino-2,4(1H,3H
R-0732	0	R-0732	0	R-0732	diaminohydroxyphosphoribosylaminopyrimidine deaminase	2,5-diamino-6-(ribosylamino)-4-(3H)-pyrimidinone-5'-phosphate + H2O =
R-0733	0	R-0733	0	R-0733	5-amino-6-(5-phosphoribosylamino)uracil reductase	5-amino-6-(5'-phosphoribosylamino)uracil + NADPH + H+ = 5-amino-6-r
R-0736	0.017	R-0736	0.01	R-0736	hydroperoxidase	2 H2O2 = 2 H2O + O2
R-0737	0	R-0737	0	R-0737	heme d synthase	protoheme-IX + H2O2 = heme-d
R-0738	0	R-0738	0	R-0738	nitrate reductase (periplasmic)	NO3-[p] + 2 reduced-cytochrome-c + 2 H+[p] = NO2-[p] + 2 oxidized-cyt
R-0739	0	R-0739	0	R-0739	uroporphyrin III C-methyltransferase 2	(S)-adenosyl-L-methionine + precorrin-1 = (S)-adenosyl-L-homocysteine
R-0740	0	R-0740	0	R-0740	uroporphyrin III C-methyltransferase 1	(S)-adenosyl-L-methionine + uroporphyrinogen-III = (S)-adenosyl-L-hom
R-0741	0	R-0741	0	R-0741	precorrin-2 dehydrogenase	precorrin-2 + NAD+ = sirohydrochlorin + NADH + H+
R-0742	0	R-0742	0	R-0742	sirohydrochlorin ferrochelatase	sirohydrochlorin + Fe2+ = siroheme + 2 H+
R-0743	0	R-0743	0	R-0743	cobaltochelatase	hydrogenobyrinate-a,c-diamide + Co2+ + ATP + H2O = cob(II)yrinate-a,
R-0744	-0.0024	R-0744	-0.0014	R-0744	acyl-CoA dehydrogenase (n-4:0)	butyryl-CoA + FAD = crotonyl-CoA + FADH2
R-0745	-0.0024	R-0745	-0.0014	R-0745	acyl-CoA dehydrogenase (n-6:0)	hexanoyl-CoA + FAD = trans-hex-2-enoyl-CoA + FADH2
R-0746	-0.0024	R-0746	-0.0014	R-0746	acyl-CoA dehydrogenase (n-8:0)	octanoyl-CoA + FAD = trans-oct-2-enoyl-CoA + FADH2
R-0747	-0.0024	R-0747	-0.0014	R-0747	acyl-CoA dehydrogenase (n-10:0)	decanoyl-CoA + FAD = trans-dec-2-enoyl-CoA + FADH2
R-0748	-0.0024	R-0748	-0.0014	R-0748	acyl-CoA dehydrogenase (n-12:0)	dodecanoyl-CoA + FAD = trans-dodec-2-enoyl-CoA + FADH2
R-0749	-0.0024	R-0749	-0.0014	R-0749	acyl-CoA dehydrogenase (n-14:0)	tetradecanoyl-CoA + FAD = trans-tetradec-2-enoyl-CoA + FADH2
R-0750	-0.0024	R-0750	-0.0014	R-0750	acyl-CoA dehydrogenase (n-16:0)	hexadecanoyl-CoA + FAD = trans-hexadec-2-enoyl-CoA + FADH2
R-0751	-0.0012	R-0751	-0.0007	R-0751	acyl-CoA dehydrogenase (n-18:0)	octadecanoyl-CoA + FAD = trans-octadec-2-enoyl-CoA + FADH2
R-0752	0	R-0752	0	R-0752	acyl-CoA dehydrogenase (n-12:1)	cis-dodec-5-enoyl-CoA + FAD = trans-3-cis-5-dodecenoyl-CoA + FADH2
R-0753	0	R-0753	0	R-0753	acyl-CoA dehydrogenase (n-14:1)	cis-tetradec-7-enoyl-CoA + FAD = trans-3-cis-7-tetradecenoyl-CoA + FA
R-0754	0	R-0754	0	R-0754	acyl-CoA dehydrogenase (n-16:1)	hexadec-9-enoyl-CoA + FAD = trans-3-cis-9-hexadecenoyl-CoA + FADH
R-0755	0	R-0755	0	R-0755	acyl-CoA dehydrogenase (n-18:1)	octadec-9-enoyl-CoA + FAD = trans-3-cis-11-octadecenoyl-CoA + FADH
R-0756	0	R-0756	0	R-0756	heme O synthase	protoheme-IX + all-trans-farnesyl-diphosphate + H2O = heme-o + diphos
R-0757	0	R-0757	0	R-0757	N-formylglutamate amidohydrolase	N-formyl-L-glutamate + H2O = L-glutamate + formate
R-0758	0	R-0758	0	R-0758	haloacid dehalogenase	chloroacetate + H2O = glycolate + HCl
R-0759	0	R-0759	0	R-0759	superoxide dismutase	2 superoxide + 2 H+ = H2O2 + O2
R-0760	0	R-0760	0	R-0760	sulfite oxidase	HSO3- + O2 + H2O = H2O2 + SO42- + H+
R-0762	0	R-0762	0	R-0762	2-hydroxychromene-2-carboxylate isomerase	2-hydroxychromene-2-carboxylate = trans-O-hydroxybenzylidenepyruvate
R-0763	0	R-0763	0	R-0763	precorrin-5 (C1)-methyltransferase	precorrin-5 + (S)-adenosyl-L-methionine + H2O = precorrin-6A + (S)-ade
R-0764	0	R-0764	0	R-0764	fatty acyl-CoA synthetase (n-4:0)	butyrate + ATP + CoA = butyryl-CoA + AMP + diphosphate
R-0765	0	R-0765	0	R-0765	fatty acyl-CoA synthetase (n-6:0)	hexanoate + ATP + CoA = hexanoyl-CoA + AMP + diphosphate
R-0766	0	R-0766	0	R-0766	fatty acyl-CoA synthetase (n-8:0)	octanoate + ATP + CoA = octanoyl-CoA + AMP + diphosphate
R-0767	0	R-0767	0	R-0767	fatty acyl-CoA synthetase (n-10:0)	decanoate + ATP + CoA = decanoyl-CoA + AMP + diphosphate
R-0768	0	R-0768	0	R-0768	fatty acyl-CoA synthetase (n-12:0)	dodecanoate + ATP + CoA = dodecanoyl-CoA + AMP + diphosphate
R-0769	0	R-0769	0	R-0769	fatty acyl-CoA synthetase (n-14:0)	tetradecanoate + ATP + CoA = tetradecanoyl-CoA + AMP + diphosphate
R-0770	-0.0012	R-0770	-0.0007	R-0770	fatty acyl-CoA synthetase (n-16:0)	hexadecanoate + ATP + CoA = hexadecanoyl-CoA + AMP + diphosphate
R-0771	-0.0012	R-0771	-0.0007	R-0771	fatty acyl-CoA synthetase (n-18:0)	octadecanoate + ATP + CoA = octadecanoyl-CoA + AMP + diphosphate
R-0772	0	R-0772	0	R-0772	fatty acyl-CoA synthetase (n-12:1)	5-dodecenoate + ATP + CoA = cis-dodec-5-enoyl-CoA + AMP + diphosp
R-0773	0	R-0773	0	R-0773	fatty acyl-CoA synthetase (n-14:1)	7-tetradecenoate + ATP + CoA = cis-tetradec-7-enoyl-CoA + AMP + dip
R-0774	0	R-0774	0	R-0774	fatty acyl-CoA synthetase (n-16:1)	9-hexadecenoate + ATP + CoA = hexadec-9-enoyl-CoA + AMP + diphos
R-0775	0	R-0775	0	R-0775	fatty acyl-CoA synthetase (n-18:1)	9-octadecenoate + ATP + CoA = octadec-9-enoyl-CoA + AMP + diphosp
R-0776	0	R-0776	0	R-0776	adenine deaminase	adenine + H2O = NH3 + hypoxanthine
R-0777	0	R-0777	0	R-0777	exopolyphosphatase	polyphosphate(n) + H2O = polyphosphate(n-1) + phosphate
R-0778	0	R-0778	0	R-0778	lauroyl acyltransferase	dodecanoyl-[acyl-carrier-protein] + KDO2-lipid-IVA = KDO2-(lauroyl)-lipid
R-0779	0	R-0779	0	R-0779	alcohol dehydrogenase (isopropanol)	isopropanol + NAD+ = acetone + NADH + H+
R-0780	0	R-0780	0	R-0780	alcohol dehydrogenase (acetaldehyde)	acetaldehyde + NADH + H+ = ethanol + NAD+
R-0781	0	R-0781	0	R-0781	acetoin reductase	acetoin + NADH + H+ = 2,3-butanediol + NAD+
R-0782	0	R-0782	0	R-0782	diacetyl reductase	diacetyl + NADH + H+ = acetoin + NAD+
R-0783	0	R-0783	0	R-0783	3,4-dihydroxy-2-butanone-4-phoshate synthase	D-ribulose-5-phosphate = formate + L-3,4-dihydroxybutan-2-one-4-phos
R-0784	0	R-0784	0	R-0784	pyrimidine phosphatase	5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinedione-5'-phosphate + H2O
R-0785	0	R-0785	0	R-0785	2,3-dihydro-3-hydroxy-anthranilate oxidation (spontaneous)	2,3-dihydro-3-hydroxy-anthranilate = 2,3-dihydro-3-oxo-anthranilate + 4
R-0786	0	R-0786	0	R-0786	2,3-dihydro-3-oxo-anthranilate condensation (hypothetical)	2 2,3-dihydro-3-oxo-anthranilate = phenazine-1-carboxylate + CO2 + O2
R-0787	0.0013	R-0787	0.0008	R-0787	NH3-dependent NAD(+) synthetase	ATP + nicotinate-adenine-dinucleotide + NH3 = AMP + diphosphate + N
R-0788	0	R-0788	0	R-0788	anhydro-N-acetylmuramoyl-L-alanine amidase	GlcNAc-1,6-anhMurNAc-L-Ala-gamma-D-Glu-DAP-D-Ala + H2O = GlcN
R-0789	0	R-0789	0	R-0789	4-hydroxybenzoate octaprenyltransferase	all-trans-octaprenyl-diphosphate + 4-hydroxybenzoate = 3-octaprenyl-4-
R-0790	0	R-0790	0	R-0790	chorismate lyase	chorismate = 4-hydroxybenzoate + pyruvate
R-0791	0	R-0791	0	R-0791	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	3-octaprenyl-4-hydroxybenzoate = 2-octaprenylphenol + CO2
R-0792	0	R-0792	0	R-0792	molybderin biosynthesis protein	GTP + H2O = precursor-Z + diphosphate
R-0793	0	R-0793	0	R-0793	4-hydroxy-L-threonine phosphate dehydrogenase, NAD-deper	4-(phosphonooxy)-threonine + NAD+ = (2S)-2-amino-3-oxo-4-phosphon
R-0794	0	R-0794	0	R-0794	xanthine dehydrogenase 2	hypoxanthine + H2O = xanthine + 2 H+
R-0795	0	R-0795	0	R-0795	urea carboxylase	ATP + urea + CO2 + H2O = ADP + phosphate + urea-1-carboxylate
R-0796	0	R-0796	0	R-0796	allophanate hydrolase	urea-1-carboxylate + H2O = 2 NH3 + 2 CO2
R-0797	0	R-0797	0	R-0797	putative n-methylproline demethylase	monomethyl-proline + demethylated-methyl-acceptor = L-proline + meth
R-0798	0	R-0798	0	R-0798	choline kinase	choline + ATP = phosphoryl-choline + ADP + 2 H+
R-0799	0	R-0799	0	R-0799	ethanolamine kinase	ethanolamine + ATP = phosphoryl-ethanolamine + ADP
R-0800	0	R-0800	0	R-0800	hydantoinase	dihydrouracil + H2O = 3-ureidopropionate
R-0801	0	R-0801	0	R-0801	UDP-N-acetylglucosamine 2-epimerase	UDP-N-acetyl-D-glucosamine + H2O = N-acetyl-D-mannosamine + UDP
R-0802	0	R-0802	0	R-0802	nigerose hydrolase	nigerose + H2O = 2 D-glucose
R-0803	0	R-0803	0	R-0803	2-octaprenyl-6-methoxyphenol hydroxylase	2-octaprenyl-6-methoxyphenol + O2 + 4 H+ = 2-octaprenyl-6-methoxy-1
R-0804	0	R-0804	0	R-0804	nicotinamidase	nicotinamide + H2O = NH3 + nicotinate
R-0805	0	R-0805	0	R-0805	agmatinase	agmatine + H2O = urea + putrescine
R-0806	0.0028	R-0806	0.0017	R-0806	phosphopantothenoylcysteine decarboxylase	(R)-4'-phosphopantothenoyl-L-cysteine = 4'-phosphopantetheine + CO2
R-0807	0.0028	R-0807	0.0017	R-0807	phosphopantothenoylcysteine synthetase	(D)-4'-phosphopantothenate + L-cysteine + CTP = (R)-4'-phosphopantot
R-0808	0	R-0808	0	R-0808	(S)-adenosylmethionine:2-DMK methyltransferase	(S)-adenosyl-L-methionine + demethylmenaquinone-8 = (S)-adenosyl-L-
R-0809	0	R-0809	0	R-0809	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase	(S)-adenosyl-L-methionine + 2-octaprenyl-6-methoxy-1,4-benzoquinol =
R-0810	0	R-0810	0	R-0810	biotin synthase	sulfurated-sulfur-donor + dethiobiotin + 2 (S)-adenosyl-L-methionine = b
R-0811	0	R-0811	0	R-0811	5-carboxymethyl-2-oxo-hex-3-ene-1,7-dioate decarboxylase	5-carboxy-2-oxohept-3-enedioate = 2-hydroxyhepta-2,4-dienedioate + C
R-0812	0	R-0812	0	R-0812	5-carboxymethyl-2-hydroxymuconate isomerase	5-carboxymethyl-2-hydroxymuconate = 5-carboxy-2-oxohept-3-enedioate
R-0813	0	R-0813	0	R-0813	rubredoxin NAD+ reductase	oxidized-rubredoxin + NADH = reduced-rubredoxin + NAD+
R-0814	0.0001	R-0814	0.0001	R-0814	pyridine nucleotide-disulphide oxidoreductase	oxidized-electron-acceptor + NADH + H+ = reduced-electron-acceptor +
R-0815	0	R-0815	0	R-0815	catalase	ethanol + H2O2 = acetaldehyde + 2 H2O
R-0816	0	R-0816	0	R-0816	maltose acetyltransferase	maltose + acetyl-CoA = acetylmaltose + CoA
R-0817	0	R-0817	0	R-0817	D-lactate dehydrogenase	D-lactate + NAD+ = pyruvate + NADH + H+
R-0819	-0.0024	R-0819	-0.0014	R-0819	enoyl-CoA hydratase (n-6:0)	trans-hex-2-enoyl-CoA + H2O = (3S)-3-hydroxyhexanoyl-CoA
R-0820	-0.0024	R-0820	-0.0014	R-0820	enoyl-CoA hydratase (n-8:0)	trans-oct-2-enoyl-CoA + H2O = (3S)-3-hydroxyoctanoyl-CoA
R-0821	-0.0024	R-0821	-0.0014	R-0821	enoyl-CoA hydratase (n-12:0)	trans-dodec-2-enoyl-CoA + H2O = (3S)-3-hydroxydodecanoyl-CoA
R-0822	-0.0024	R-0822	-0.0014	R-0822	enoyl-CoA hydratase (n-14:0)	trans-tetradec-2-enoyl-CoA + H2O = (3S)-3-hydroxytetradecanoyl-CoA
R-0823	-0.0024	R-0823	-0.0014	R-0823	enoyl-CoA hydratase (n-16:0)	trans-hexadec-2-enoyl-CoA + H2O = (3S)-3-hydroxyhexadecanoyl-CoA
R-0824	-0.0012	R-0824	-0.0007	R-0824	enoyl-CoA hydratase (n-18:0)	trans-octadec-2-enoyl-CoA + H2O = (3S)-3-hydroxyoctadecanoyl-CoA
R-0825	0	R-0825	0	R-0825	enoyl-CoA hydratase (n-12:1)	trans-3-cis-5-dodecenoyl-CoA + H2O = (3S)-3-hydroxy-cis-dodec-5-eno
R-0826	0	R-0826	0	R-0826	enoyl-CoA hydratase (n-14:1)	trans-3-cis-7-tetradecenoyl-CoA + H2O = (3S)-3-hydroxy-cis-tetradec-7-
R-0827	0	R-0827	0	R-0827	enoyl-CoA hydratase (n-16:1)	trans-3-cis-9-hexadecenoyl-CoA + H2O = (3S)-3-hydroxy-cis-hexadec-9
R-0828	0	R-0828	0	R-0828	enoyl-CoA hydratase (n-18:1)	trans-3-cis-11-octadecenoyl-CoA + H2O = (3S)-3-hydroxy-cis-octadec-1
R-0829	0	R-0829	0	R-0829	cardiolipin synthase (n-16:0)	phosphatidylglycerol(dihexadecanoyl) = cardiolipin(dihexadecanoyl) + gl
R-0830	0	R-0830	0	R-0830	cardiolipin synthase (n-16:1)	phosphatidylglycerol(dihexadec-9-enoyl) = cardiolipin(dihexadec-9-enoy
R-0831	0	R-0831	0	R-0831	cardiolipin synthase (n-18:0)	phosphatidylglycerol(dioctadecanoyl) = cardiolipin(dioctadecanoyl) + gly
R-0832	0	R-0832	0	R-0832	cardiolipin synthase (n-18:1)	phosphatidylglycerol(dioctadec-9-enoyl) = cardiolipin(dioctadec-9-enoyl)
R-0833	0	R-0833	0	R-0833	hydroxymethylpyrimidine kinase	ATP + hydroxymethylpyrimidine = ADP + hydroxymethylpyrimidine-phos
R-0834	0	R-0834	0	R-0834	phosphohydroxymethylpyrimidine kinase	hydroxymethylpyrimidine-phosphate + ATP = 4-amino-5-hydroxymethyl-
R-0835	0	R-0835	0	R-0835	ferredoxin--nitrite reductase	NO2- + 6 reduced-ferredoxin + 7 H+ = NH3 + 6 oxidized-ferredoxin + 2 H
R-0837	0	R-0837	0	R-0837	saccharopine dehydrogenase (NADP+, L-glutamate-forming)	saccharopine + NADP+ + H2O = L-glutamate + 2-aminoadipate-6-semia
R-0838	0	R-0838	0	R-0838	nicotinate phosphoribosyltransferase	nicotinate-mononucleotide + diphosphate = nicotinate + 5-phosphoribos
R-0839	0.0028	R-0839	0.0017	R-0839	pantetheine-phosphate adenylyltransferase	4'-phosphopantetheine + ATP = dephospho-CoA + diphosphate
R-0840	0	R-0840	0	R-0840	UDP-N-acetylmuramoylalanine--D-glutamate ligase	UDP-N-acetylmuramoyl-L-alanine + D-glutamate + ATP = UDP-N-acetyl
R-0841	0	R-0841	0	R-0841	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate
R-0842	0	R-0842	0	R-0842	phospho-N-acetylmuramoyl-pentapeptide-transferase 1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelyl-D
R-0843	0	R-0843	0	R-0843	phospho-N-acetylmuramoyl-pentapeptide-transferase 2	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine +
R-0844	0	R-0844	0	R-0844	UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimela	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate + meso-diaminoheptanedi
R-0845	0	R-0845	0	R-0845	UDP-N-acetylglucosamine acyltransferase	(3R)-3-hydroxytetradecanoyl-[acyl-carrier-protein] + UDP-N-acetyl-D-glu
R-0846	0	R-0846	0	R-0846	lipid-A-disaccharide synthase	2,3-bis(3-hydroxymyristoyl)-b-D-glucosaminyl-1-phosphate + UDP-2,3-b
R-0847	0	R-0847	0	R-0847	tartrate dehydrogenase	L-tartrate + NAD+ = 2-hydroxy-3-oxosuccinate + NADH + H+
R-0848	0	R-0848	0	R-0848	tartrate decarboxylase	L-tartrate = D-glycerate + CO2
R-0849	0	R-0849	0	R-0849	D-malate dehydrogenase [decarboxylating]	(R)-malate + NAD+ = CO2 + pyruvate + NADH + H+

	R-0850	0	R-0850	0	R-0850	precorrin-6A reductase	precorrin-6A + NADPH + H+ = precorrin-6B + NADP+
	R-0851	0	R-0851	0	R-0851	adenosyl-cobyric acid synthase	adenosyl-cobyrinate-a,c-diamide + 4 L-glutamine + 4 ATP + 4 H2O = 4 L
	R-0852	0	R-0852	0	R-0852	adenosylcobinamide-phosphate synthase	ATP + adenosyl-cobyrate + (R)-1-amino-2-propanol-O-2-phosphate = Al
	R-0853	0	R-0853	0	R-0853	L-threonine-O-3-phosphate decarboxylase	L-threonine-O-3-phosphate = (R)-1-amino-2-propanol-O-2-phosphate +
	R-0854	0	R-0854	0	R-0854	2-nitropropane dioxygenase	2 2-nitropropane + O2 = 2 NO2- + 2 acetone + 2 H+
	R-0855	0	R-0855	0	R-0855	aerobic magnesium-protoporphyrin IX monomethyl ester cycla	131-oxo-magnesium-protoporphyrin-IX-13-monomethyl-ester + NADPH
	R-0856	0	R-0856	0	R-0856	aerobic magnesium-protoporphyrin IX monomethyl ester cycla	131-hydroxy-magnesium-protoporphyrin-IX-13-monomethyl-ester + NAD
	R-0857	0	R-0857	0	R-0857	magnesium protoporphyrin IX methyltransferase	Mg-protoporphyrin + (S)-adenosyl-L-methionine = (S)-adenosyl-L-homoc
	R-0858	0	R-0858	0	R-0858	protochlorophyllide reductase	monovinyl-protochlorophyllidea + NADPH + H+ = chlorophyllidea + NAD
	R-0859	0	R-0859	0	R-0859	3-vinyl bacteriochlorophyllide a hydratase	3-vinyl-bacteriochlorophyllidea + H2O = 2-desacetyl-2-hydroxyethyl-bact
	R-0860	0	R-0860	0	R-0860	chlorophyllide hydratase	chlorophyllidea + H2O = 3-hydroxyethylchlorophyllidea
	R-0861	0	R-0861	0	R-0861	bacteriochlorophyll a synthase	bacteriochlorophyllidea + all-trans-geranyl-geranyl-diphosphate = geran
	R-0862	0	R-0862	0	R-0862	geranylgeranyl reductase 1	geranylgeranyl-bacteriochlorophylla + NADPH + H+ = dihydrogeranylge
	R-0863	0	R-0863	0	R-0863	geranylgeranyl reductase 2	dihydrogeranylgeranyl-bacteriochlorophylla + NADPH + H+ = tetrahydro
	R-0864	0	R-0864	0	R-0864	geranylgeranyl reductase 3	tetrahydrogeranylgeranyl-bacteriochlorophylla + NADPH + H+ = bacteric
	R-0865	0	R-0865	0	R-0865	arsenate reductase	arsenate + reduced-glutaredoxin = arsenite + oxidized-glutaredoxin + H2O
	R-0866	0	R-0866	0	R-0866	phosphonate dehydrogenase	phosphonate + NAD+ + H2O = phosphate + NADH + H+
	R-0867	0	R-0867	0	R-0867	methylglyoxal reductase	methylglyoxal + NADPH + H+ = acetol + NADP+
	R-0868	0	R-0868	0	R-0868	b-keto ester reductase	ethyl-2-methylacetoacetate + NADPH + H+ = ethyl-(2R)-methyl-(3S)-hyc
	R-0869	0	R-0869	0	R-0869	2,5-didehydro-D-gluconate + NADPH + H+ = 2-keto-L-gluconate + NADI
	R-0870	0	R-0870	0	R-0870	chromate reductase	Cr6+ + 2 NADPH + O2 = Cr3+ + H2O2 + 2 NADP+
	R-0871	0	R-0871	0	R-0871	nitrilase	indole-3-acetonitrile + 2 H2O = NH3 + indole-3-acetate + H+
	R-0872	0	R-0872	0	R-0872	neurosporene dehydratase	neurosporene + H2O = hydroxyneurosporene
	R-0873	0.0001	R-0873	0	R-0873	hydroxyneurosporene synthase 1	trans-lycopene + H2O = rhodopin
	R-0874	0.0001	R-0874	0	R-0874	hydroxyneurosporene synthase 2	anhydrorhodovibrin + H2O = rhodovibrin
	R-0875	0	R-0875	0	R-0875	hydroxyneurosporene synthase 3	3,4-dihydroanhydrorhodovibrin + H2O = 3',4'-dihydrorhodovibrin
	R-0876	0	R-0876	0	R-0876	aerobic magnesium-protoporphyrin IX monomethyl ester cycla	Mg-protoporphyrin-monomethyl-ester + NADPH + O2 + H+ = 131-hydro
	R-0877	0	R-0877	0	R-0877	3,8-divinyl protochlorophyllide 8-vinyl reductase	divinyl-protochlorophyllidea + NADPH + H+ = monovinyl-protochlorophyl
	R-0878	0	R-0878	0	R-0878	molybdopterin adenylyltransferase	ATP + molybdopterin = molybdopterin-AMP + diphosphate
	R-0879	0	R-0879	0	R-0879	3-hydroxyacyl-CoA epimerase (n-4:0)	(S)-3-hydroxybutanoyl-CoA = (R)-3-hydroxybutanoyl-CoA
	R-0880	0	R-0880	0	R-0880	3-hydroxyacyl-CoA epimerase (n-6:0)	(3S)-3-hydroxyhexanoyl-CoA = (3R)-3-hydroxyhexanoyl-CoA
	R-0881	0	R-0881	0	R-0881	3-hydroxyacyl-CoA epimerase (n-8:0)	(3S)-3-hydroxyoctanoyl-CoA = (3R)-3-hydroxyoctanoyl-CoA
	R-0882	0	R-0882	0	R-0882	3-hydroxyacyl-CoA epimerase (n-12:0)	(3S)-3-hydroxydodecanoyl-CoA = (3R)-3-hydroxydodecanoyl-CoA
	R-0883	0	R-0883	0	R-0883	3-hydroxyacyl-CoA epimerase (n-14:0)	(3S)-3-hydroxytetradecanoyl-CoA = (3R)-3-hydroxytetradecanoyl-CoA
	R-0884	0	R-0884	0	R-0884	3-hydroxyacyl-CoA epimerase (n-16:0)	(3S)-3-hydroxyhexadecanoyl-CoA = (3R)-3-hydroxyhexadecanoyl-CoA
	R-0885	0	R-0885	0	R-0885	3-hydroxyacyl-CoA epimerase (n-18:0)	(3S)-3-hydroxyoctadecanoyl-CoA = (3R)-3-hydroxyoctadecanoyl-CoA
	R-0886	0	R-0886	0	R-0886	3-hydroxyacyl-CoA epimerase (n-12:1)	(3S)-3-hydroxy-cis-dodec-5-enoyl-CoA = (3R)-3-hydroxy-cis-dodec-5-en
	R-0887	0	R-0887	0	R-0887	3-hydroxyacyl-CoA epimerase (n-14:1)	(3S)-3-hydroxy-cis-tetradec-7-enoyl-CoA = (3R)-3-hydroxy-cis-tetradec-7
	R-0888	0	R-0888	0	R-0888	3-hydroxyacyl-CoA epimerase (n-16:1)	(3S)-3-hydroxy-cis-hexadec-9-enoyl-CoA = (3R)-3-hydroxy-cis-hexadec-
	R-0889	0	R-0889	0	R-0889	3-hydroxyacyl-CoA epimerase (n-18:1)	(3S)-3-hydroxy-cis-octadec-11-enoyl-CoA = (3R)-3-hydroxy-cis-octadec-
	R-0890	0	R-0890	0	R-0890	3-hydroxyacyl-CoA dehydrogenase (n-4:0)	(S)-3-hydroxybutanoyl-CoA + NAD+ = acetoacetyl-CoA + NADH + H+
	R-0891	-0.0024	R-0891	-0.0014	R-0891	3-hydroxyacyl-CoA dehydrogenase (n-6:0)	(3S)-3-hydroxyhexanoyl-CoA + NAD+ = 3-oxohexanoyl-CoA + NADH +
	R-0892	-0.0024	R-0892	-0.0014	R-0892	3-hydroxyacyl-CoA dehydrogenase (n-8:0)	(3S)-3-hydroxyoctanoyl-CoA + NAD+ = 3-oxooctanoyl-CoA + NADH + H+
	R-0893	-0.0024	R-0893	-0.0014	R-0893	3-hydroxyacyl-CoA dehydrogenase (n-12:0)	(3S)-3-hydroxydodecanoyl-CoA + NAD+ = 3-oxododecanoyl-CoA + NAD
	R-0894	-0.0024	R-0894	-0.0014	R-0894	3-hydroxyacyl-CoA dehydrogenase (n-14:0)	(3S)-3-hydroxytetradecanoyl-CoA + NAD+ = 3-oxotetradecanoyl-CoA +
	R-0895	-0.0024	R-0895	-0.0014	R-0895	3-hydroxyacyl-CoA dehydrogenase (n-16:0)	(3S)-3-hydroxyhexadecanoyl-CoA + NAD+ = 3-oxohexadecanoyl-CoA +
	R-0896	-0.0012	R-0896	-0.0007	R-0896	3-hydroxyacyl-CoA dehydrogenase (n-18:0)	(3S)-3-hydroxyoctadecanoyl-CoA + NAD+ = 3-oxooctadecanoyl-CoA + N
	R-0897	0	R-0897	0	R-0897	3-hydroxyacyl-CoA dehydrogenase (n-12:1)	(3S)-3-hydroxy-cis-dodec-5-enoyl-CoA + NAD+ = 3-oxo-cis-dodec-5-enc
	R-0898	0	R-0898	0	R-0898	3-hydroxyacyl-CoA dehydrogenase (n-14:1)	(3S)-3-hydroxy-cis-tetradec-7-enoyl-CoA + NAD+ = 3-oxo-cis-tetradec-7
	R-0899	0	R-0899	0	R-0899	3-hydroxyacyl-CoA dehydrogenase (n-16:1)	(3S)-3-hydroxy-cis-hexadec-9-enoyl-CoA + NAD+ = 3-oxo-cis-hexadec-9
	R-0900	0	R-0900	0	R-0900	3-hydroxyacyl-CoA dehydrogenase (n-18:1)	(3S)-3-hydroxy-cis-octadec-11-enoyl-CoA + NAD+ = 3-oxo-cis-octadec-
	R-0901	0	R-0901	0	R-0901	enoyl-CoA isomerase (n-6:0)	trans-hex-2-enoyl-CoA = cis-hex-3-enoyl-CoA
	R-0902	0	R-0902	0	R-0902	enoyl-CoA isomerase (n-8:0)	trans-oct-2-enoyl-CoA = cis-oct-3-enoyl-CoA
	R-0903	0	R-0903	0	R-0903	enoyl-CoA isomerase (n-12:0)	trans-dodec-2-enoyl-CoA = cis-dodec-3-enoyl-CoA
	R-0904	0	R-0904	0	R-0904	enoyl-CoA isomerase (n-14:0)	trans-tetradec-2-enoyl-CoA = cis-tetradec-3-enoyl-CoA
	R-0905	0	R-0905	0	R-0905	enoyl-CoA isomerase (n-16:0)	trans-hexadec-2-enoyl-CoA = cis-hexadec-3-enoyl-CoA
	R-0906	0	R-0906	0	R-0906	enoyl-CoA isomerase (n-18:0)	trans-octadec-2-enoyl-CoA = cis-octadec-3-enoyl-CoA
	R-0907	0	R-0907	0	R-0907	enoyl-CoA isomerase (n-12:1)	trans-2-cis-5-dodecenoyl-CoA = cis-3-cis-5-dodecenoyl-CoA
	R-0908	0	R-0908	0	R-0908	enoyl-CoA isomerase (n-14:1)	trans-2-cis-7-tetradecenoyl-CoA = cis-3-cis-7-tetradecenoyl-CoA
	R-0909	0	R-0909	0	R-0909	enoyl-CoA isomerase (n-16:1)	trans-2-cis-9-hexadecenoyl-CoA = cis-3-cis-9-hexadecenoyl-CoA
	R-0910	0	R-0910	0	R-0910	enoyl-CoA isomerase (n-18:1)	trans-2-cis-11-octadecenoyl-CoA = cis-3-cis-11-octadecenoyl-CoA
	R-0911	0	R-0911	0	R-0911	enoyl-CoA isomerase (n-4:0)	crotonyl-CoA = vinylacetyl-CoA
	R-0913	-0.0024	R-0913	-0.0014	R-0913	3-ketoacyl-CoA thiolase (n-6:0)	3-oxohexanoyl-CoA + CoA = acetyl-CoA + butyryl-CoA
	R-0914	-0.0024	R-0914	-0.0014	R-0914	3-ketoacyl-CoA thiolase (n-8:0)	3-oxooctanoyl-CoA + CoA = acetyl-CoA + hexanoyl-CoA
	R-0915	-0.0024	R-0915	-0.0014	R-0915	3-ketoacyl-CoA thiolase (n-10:0)	3-oxodecanoyl-CoA + CoA = acetyl-CoA + octanoyl-CoA
	R-0916	-0.0024	R-0916	-0.0014	R-0916	3-ketoacyl-CoA thiolase (n-12:0)	3-oxododecanoyl-CoA + CoA = acetyl-CoA + decanoyl-CoA
	R-0917	-0.0024	R-0917	-0.0014	R-0917	3-ketoacyl-CoA thiolase (n-14:0)	3-oxotetradecanoyl-CoA + CoA = acetyl-CoA + dodecanoyl-CoA
	R-0918	-0.0024	R-0918	-0.0014	R-0918	3-ketoacyl-CoA thiolase (n-16:0)	3-oxohexadecanoyl-CoA + CoA = acetyl-CoA + tetradecanoyl-CoA
	R-0919	-0.0012	R-0919	-0.0007	R-0919	3-ketoacyl-CoA thiolase (n-18:0)	3-oxooctadecanoyl-CoA + CoA = acetyl-CoA + hexadecanoyl-CoA
	R-0920	0	R-0920	0	R-0920	3-ketoacyl-CoA thiolase (n-12:1)	3-oxo-cis-dodec-5-enoyl-CoA + CoA = acetyl-CoA + cis-dec-3-enoyl-CoA
	R-0921	0	R-0921	0	R-0921	3-ketoacyl-CoA thiolase (n-14:1)	3-oxo-cis-tetradec-7-enoyl-CoA + CoA = acetyl-CoA + cis-dodec-5-enoy
	R-0922	0	R-0922	0	R-0922	3-ketoacyl-CoA thiolase (n-16:1)	3-oxo-cis-hexadec-9-enoyl-CoA + CoA = acetyl-CoA + cis-tetradec-7-en
	R-0923	0	R-0923	0	R-0923	3-ketoacyl-CoA thiolase (n-18:1)	3-oxo-cis-octadec-11-enoyl-CoA + CoA = acetyl-CoA + hexadec-9-enoy
	R-0924	0	R-0924	0	R-0924	enoyl-CoA isomerase (n-10:0)	trans-dec-2-enoyl-CoA = cis-dec-2-enoyl-CoA
	R-0925	-0.0024	R-0925	-0.0014	R-0925	3-hydroxyacyl-CoA dehydrogenase (n-10:0)	(3S)-3-hydroxydecanoyl-CoA + NAD+ = 3-oxodecanoyl-CoA + NADH +
	R-0926	0	R-0926	0	R-0926	3-hydroxyacyl-CoA epimerase (n-10:0)	(3S)-3-hydroxydecanoyl-CoA = (3R)-3-hydroxydecanoyl-CoA
	R-0927	-0.0024	R-0927	-0.0014	R-0927	enoyl-CoA hydratase (n-10:0)	trans-dec-2-enoyl-CoA + H2O = (3S)-3-hydroxydecanoyl-CoA
	R-0928	0	R-0928	0	R-0928	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxyla	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol + O2 + H+ = 3-demet
	R-0929	0	R-0929	0	R-0929	L-sorbosone to L-sorbosone-2,6-lactone (spontaneously)	L-sorbosone = L-sorbosone-2,6-lactone
	R-0930	0.0028	R-0930	0.0017	R-0930	pantothenate synthetase	b-alanine + L-pantoate + ATP = (R)-pantothenate + diphosphate + AMP
	R-0933	0.0002	R-0933	0.0001	R-0933	phosphatidylglycerophosphatase (n-16:0)	phosphatidylglycerolphosphate(dihexadecanoyl) + H2O = phosphate + p
	R-0934	0.0002	R-0934	0.0001	R-0934	phosphatidylglycerophosphatase (n-16:1)	phosphatidylglycerolphosphate(dihexadec-9-enoyl) + H2O = phosphate
	R-0935	0.0002	R-0935	0.0001	R-0935	phosphatidylglycerophosphatase (n-18:0)	phosphatidylglycerolphosphate(dioctadecanoyl) + H2O = phosphate + p
	R-0936	0.0029	R-0936	0.0017	R-0936	phosphatidylglycerophosphatase (n-18:1)	phosphatidylglycerolphosphate(dioctadec-9-enoyl) + H2O = phosphate +
	R-0937	0	R-0937	0	R-0937	protoporphyrinogen IX oxidase	protoporphyrinogen-IX + 3 O2 = protoporphyrin-IX + 3 H2O2
	R-0938	0	R-0938	0	R-0938	1-amino-propan-2-one-3-phosphate synthesis	(2S)-2-amino-3-oxo-4-phosphonooxybutanoate = 1-amino-propan-2-one
	R-0939	0	R-0939	0	R-0939	riboflavin kinase	riboflavin + ATP = ADP + FMN
	R-0940	0	R-0940	0	R-0940	FMN adenylyltransferase	ATP + FMN = diphosphate + FAD
	R-0941	0	R-0941	0	R-0941	UDP-2,3-diacylglucosamine hydrolase	UDP-2,3-bis(3-hydroxymyristoyl)glucosamine + H2O = 2,3-bis(3-hydroxy
	R-0942	0	R-0942	0	R-0942	cob(I)yrinic acid a,c-diamide adenosyltransferase	cob(I)yrinate-a,c-diamide + ATP = adenosyl-cobyrinate-a,c-diamide + tri
	R-0943	0	R-0943	0	R-0943	cob(II)yrinate a,c-diamide reductase	cob(II)yrinate-a,c-diamide + FMNH2 = cob(I)yrinate-a,c-diamide + FMN
	R-0944	0	R-0944	0	R-0944	a-ribazole-5'-phosphate phosphatase	a-ribazole-5'-P + H2O = a-ribazole + phosphate
	R-0945	0	R-0945	0	R-0945	adenosylcobalamine-5'-phosphate phosphatase	adenosylcobalamin-5'-phosphate + H2O = coenzyme-B12 + phosphate
	R-0946	0	R-0946	0	R-0946	L-threonine kinase	L-threonine + ATP = L-threonine-O-3-phosphate + ADP
	R-0947	0	R-0947	0	R-0947	flavin destructase	FMNH2 + O2 = 2 dimethylbenzimidazole + D-erythrose-4-phosphate + H
	R-0965	0.0479	R-0965	0.0283	R-0965	N-succinyldiaminopimelate-aminotransferase	L-glutamate + N-succinyl-2-amino-6-ketopimelate = 2-oxoglutarate + N-s
	R-0966	0	R-0966	0	R-0966	L-asparaginase (periplasm)	L-asparagine[p] + H2O[p] = L-aspartate[p] + NH3[p]
	R-0967	0	R-0967	0	R-0967	superoxide dismutase (periplasm)	2 superoxide[p] + 2 H+[p] = H2O2[p] + O2[p]
	R-0968	0	R-0968	0	R-0968	galactose oxidase (extracellular)	D-galactose[e] + O2[e] = D-galacto-hexodialdose[e] + H2O2[e]
	R-0969	0	R-0969	0	R-0969	phytoene dehydrogenase 1 (extracellular)	phytoene[e] + reduced-electron-acceptor[e] + O2[e] = phytofluene[e] + o
	R-0970	0	R-0970	0	R-0970	phytoene dehydrogenase 2 (extracellular)	phytofluene[e] + reduced-electron-acceptor[e] + O2[e] = zeta-carotene[e
	R-0971	0	R-0971	0	R-0971	zeta-carotene desaturase 1 (extracullular)	zeta-carotene[e] + reduced-electron-acceptor[e] + O2[e] = neurosporene
	R-0972	0	R-0972	0	R-0972	zeta-carotene desaturase 2 (extracellular)	neurosporene[e] + reduced-electron-acceptor[e] + O2[e] = trans-lycopen
	R-0973	0	R-0973	0	R-0973	deoxynucleoside triphosphate pyrophosphohydrolase (dATP)	dATP + H2O = dAMP + diphosphate
	R-0974	0	R-0974	0	R-0974	deoxynucleoside triphosphate pyrophosphohydrolase (dTTP)	dTTP + H2O = dTMP + diphosphate
	R-0975	0	R-0975	0	R-0975	deoxynucleoside triphosphate pyrophosphohydrolase (dGTP)	dGTP + H2O = dGMP + diphosphate
	R-0976	0	R-0976	0	R-0976	deoxynucleoside triphosphate pyrophosphohydrolase (dCTP)	dCTP + H2O = dCMP + diphosphate
	R-0977	0	R-0977	0	R-0977	NADH-azoreductase	methyl-red + 2 NADH + 2 H+ = anthranilate + N,N'-dimethyl-p-phenylene
	R-0978	0	R-0978	0	R-0978	acetyldehyde dehydrogenase	acetaldehyde + NADP+ + H2O = acetate + NADPH + H+
	R-0979	0	R-0979	0	R-0979	beta-glucosidase	short-glucan(y) + y H2O = y b-D-glucose
	R-0980	0	R-0980	0	R-0980	2-acetolactate decarboxylation	2-acetolactate = CO2 + 2 H+ + diacetyl
	R-0981	0	R-0981	0	R-0981	5-methylthioribose-1-phosphate isomerase	(S)-methyl-5-thio-alpha-D-ribose-1-phosphate = (S)-methyl-5-thio-D-ribu
	R-0982	0	R-0982	0	R-0982	S-adenosylmethionine decarboxylase	(S)-adenosyl-L-methionine = CO2 + (S)-adenosylmethioninamine
	R-0983	0.0135	R-0983	0.008	R-0983	adenylylsulfate kinase	adenosine-5'-phosphosulfate + ATP = phosphoadenosine-5'-phosphosu
	R-0984	0	R-0984	0	R-0984	nitrate reductase assimilatory	NO3- + NADPH + H+ = NO2- + NADP+ + H2O
	R-0985	0.0135	R-0985	0.008	R-0985	adenosine-3'(2'),5'-bisphosphate nucleotidase	adenosine-3',5'-bisphosphate + H2O = phosphate + AMP
	R-0988	0	R-0988	0	R-0988	5-keto-D-gluconate 5-reductase (inferred from physiology)	NADPH + 5-dehydro-D-gluconate + H+ = NADP+ + D-gluconate
	R-0989	0	R-0989	0	R-0989	malyl-CoA thioesterase	(S)-malyl-CoA + H2O = (S)-malate + CoA
	R-0990	0	R-0990	0	R-0990	triphosphate phosphohydrolase (inferred from gap)	triphosphate + H2O = diphosphate + phosphate
	R-0991	0	R-0991	0	R-0991	NADPH oxidoreductase (OYE)	NADPH + H+ + O2 = NADP+ + H2O2
	R-0992	0	R-0992	0	R-0992	glutathione peroxidase (periplasmic)	H2O2[p] + 2 glutathione = glutathione-disulfide + 2 H2O[p]
	R-0993	0	R-0993	0	R-0993	5'-deoxyadenosine phosphorylase	5'-deoxyadenosine + phosphate = adenine + 5'-deoxyribose-1-phosphate
	R-0994	0	R-0994	0	R-0994	aminodeoxychorismate lyase	4-amino-4-deoxychorismate = p-aminobenzoate + pyruvate
	R-0995	0	R-0995	0	R-0995	sulfur donor activation	unsulfurated-sulfur-acceptor + H2S = sulfurated-sulfur-donor

R-0996	0.0028	R-0996	0.0017	R-0996	aspartate 1-decarboxylase	L-aspartate = b-alanine + CO2
R-0997	0	R-0997	0	R-0997	molybdopterin-synthase activations	sulfurated-sulfur-donor + molybdopterin-synthase = sulfurated-molybdop
R-0998	0	R-0998	0	R-0998	erythronate-4-phosphate dehydrogenase	erythronate-4-phosphate + NAD+ = 2-oxo-3-hydroxy-4-phosphobutanoa
R-0999	0	R-0999	0	R-0999	erythrose 4-phosphate dehydrogenase	D-erythrose-4-phosphate + NAD+ + H2O = erythronate-4-phosphate + N
R-1000	0	R-1000	0	R-1000	glycine oxidase 5	glycine + O2 = iminoglycine + H2O2
R-1001	0	R-1001	0	R-1001	thiamin biosynthesis 1	thiS + ATP = adenylated-thiS + diphosphate
R-1002	0	R-1002	0	R-1002	thiamin biosynthesis 2	thiI + L-cysteine = thiI-persulfide + L-alanine
R-1003	0	R-1003	0	R-1003	thiamin biosynthesis 3	adenylated-thiS + thiI-persulfide = thiS-thiI-acyl-disulfide + AMP
R-1004	0	R-1004	0	R-1004	thiamin biosynthesis 4	thiS-thiI-acyl-disulfide + thiF = thiS-thiF-acyl-disulfide + thiI
R-1005	0	R-1005	0	R-1005	debranched limit dextrin phosphorylase	debranched-limit-dextrin + n phosphate = n D-glucose-1-phosphate
R-1006	0.0005	R-1006	0.0003	R-1006	NAD kinase	NAD+ + ATP = NADP+ + ADP
R-1007	0	R-1007	0	R-1007	photosystem I	2 oxidized-ferredoxin + 2 reduced-cytochrome-c + photon = 2 reduced-fe
R-1008	0	R-1008	0	R-1008	sulfur oxidation enzyme system	thiosulfate[p] + 5 H2O[p] + oxidized-cytochrome-c = 2 SO42-[p] + 10 H+
R-1009	0	R-1009	0	R-1009	formaldehyde dehydrogenase	formaldehyde[p] + 2 oxidized-cytochrome-c = formate[p] + 2 H+[p] + 2 re
R-1010	0	R-1010	0	R-1010	aldose sugar dehydrogenase (D-arabinose)	D-arabinose[p] + 2 oxidized-cytochrome-c = D-arabinono-1,4-lactone[p]
R-1011	0	R-1011	0	R-1011	aldose sugar dehydrogenase (L-arabinose)	L-arabinose[p] + 2 oxidized-cytochrome-c = L-arabinono-1,4-lactone[p] +
R-1012	0	R-1012	0	R-1012	D-arabinolactonase	D-arabinono-1,4-lactone[p] + H2O[p] = D-arabinonate[p]
R-1013	0	R-1013	0	R-1013	L-arabinolactonase	L-arabinono-1,4-lactone[p] + H2O[p] = L-arabinonate[p]
R-1014	0	R-1014	0	R-1014	aldose sugar dehydrogenase (L-lyxose)	L-lyxose[p] + 2 oxidized-cytochrome-c = L-lyxono-1,4-lactone[p] + 2 H+[p
R-1015	0	R-1015	0	R-1015	L-lyxolactonase	L-lyxono-1,4-lactone[p] + H2O[p] = L-lyxonate[p]
R-1016	0	R-1016	0	R-1016	aldose sugar dehydrogenase (D-xylose)	D-xylose[p] + 2 oxidized-cytochrome-c = D-xylono-1,4-lactone[p] + 2 H+
R-1017	0	R-1017	0	R-1017	D-xylolactonase	D-xylono-1,4-lactone[p] + H2O[p] = D-xylonate[p]
R-1018	0	R-1018	0	R-1018	aldose sugar dehydrogenase (D-ribose)	D-ribose[p] + 2 oxidized-cytochrome-c = D-ribono-1,4-lactone[p] + 2 H+[
R-1019	0	R-1019	0	R-1019	D-ribolactonase	D-ribono-1,4-lactone[p] + H2O[p] = D-ribonate[p]
R-1020	0	R-1020	0	R-1020	aldose sugar dehydrogenase (2-deoxy-D-ribose)	2-deoxy-D-ribose[p] + 2 oxidized-cytochrome-c = 2-deoxy-D-ribono-1,4-
R-1021	0	R-1021	0	R-1021	2-deoxy-D-ribolactonase	2-deoxy-D-ribono-1,4-lactone[p] + H2O[p] = 2-deoxy-D-ribonate[p]
R-1022	0	R-1022	0	R-1022	aldose sugar dehydrogenase (3-O-b-D-galactopyranosyl-D-ar	3-O-b-D-galactopyranosyl-D-arabinose[p] + 2 oxidized-cytochrome-c = 3
R-1023	0	R-1023	0	R-1023	3-O-b-D-galactopyranosyl-D-arabinolactonase	3-O-b-D-galactopyranosyl-D-arabinono-1,4-lactone[p] + H2O[p] = 3-O-b-
R-1024	0	R-1024	0	R-1024	ethylamine dehydrogenase	ethylamine[p] + oxidized-amicyanin + H2O[p] = acetaldehyde[p] + NH3[p
R-1025	0	R-1025	0	R-1025	amicyanin oxidation	2 oxidized-cytochrome-c + reduced-amicyanin = 2 reduced-cytochrome-
R-1026	0	R-1026	0	R-1026	photosystem I cyclic	2 reduced-ferredoxin + 2 H+ + UQ = 2 oxidized-ferredoxin + UQH2
R-1027	0	R-1027	0	R-1027	2-amino-2-deoxyisochorismate synthase	chorismate + L-glutamine = 2-amino-2-deoxy-isochorismate + L-glutamate
R-1028	0	R-1028	0	R-1028	2-amino-2-deoxyisochorismate hydrolase	2-amino-2-deoxy-isochorismate + H2O = trans-2,3-dihydro-3-hydroxyant
R-1029	0	R-1029	0	R-1029	carbamate degradation (spontaneous)	carbamate + H+ = NH3 + CO2
R-1030	0	R-1030	0	R-1030	D-lactate dehydrogenase (cytochrome)	D-lactate + 2 oxidized-cytochrome-c = pyruvate + 2 H+ + 2 reduced-cyto
R-1031	0	R-1031	0	R-1031	S-lactate dehydrogenase	(S)-lactate + NAD+ = pyruvate + NADH + H+
R-1032	0	R-1032	0	R-1032	1,2-propanediol dehydrogenase	1,2-propanediol[p] + 4 oxidized-cytochrome-c = (S)-lactate[p] + 4 H+[p] +
R-5001	0	R-5001	0	R-5001	methanol transport via diffusion (extracellular to periplasm)	methanol[e] = methanol[p]
R-5002	0	R-5002	0	R-5002	formaldehyde transport via diffusion (periplasm to cytoplasm)	formaldehyde[p] = formaldehyde
R-5003	-60.1211	R-5003	-63.1796	R-5003	CO2 transport via diffusion (extracellular to periplasm)	CO2[e] = CO2[p]
R-5004	-60.1211	R-5004	-39.9542	R-5004	CO2 transport via diffusion (periplasm to cytoplasm)	CO2[p] = CO2
R-5005	9.2224	R-5005	12.3621	R-5005	O2 transport via diffusion (extracellular to periplasm)	O2[e] = O2[p]
R-5006	9.2224	R-5006	12.3621	R-5006	O2 transport via diffusion (periplasm to cytoplasm)	O2[p] = O2
R-5007	0	R-5007	0	R-5007	formaldehyde transport via diffusion (extracellular to periplasm	formaldehyde[e] = formaldehyde[p]
R-5008	0.2256	R-5008	0.1333	R-5008	phosphate transport via diffusion (extracellular to periplasm)	phosphate[e] = phosphate[p]
R-5009	0	R-5009	0	R-5009	phosphate ABC transporter	phosphate[p] + ATP + H2O = 2 phosphate + ADP
R-5010	1.7869	R-5010	1.0561	R-5010	NH3 transport via diffusion (extracellular to periplasm)	NH3[e] = NH3[p]
R-5011	1.7869	R-5011	1.0561	R-5011	NH3 transport (periplasm to cytoplasm)	NH3[p] + H+[p] = NH3 + H+
R-5012	0	R-5012	0	R-5012	succinate transport via diffusion (extracellular to periplasm)	succinate[e] = succinate[p]
R-5013	0	R-5013	0	R-5013	succinate symport (periplasm to cytoplasm)	succinate[p] = succinate
R-5014	0	R-5014	0	R-5014	fumarate transport via diffusion (extracellular to periplasm)	fumarate[e] = fumarate[p]
R-5015	0	R-5015	0	R-5015	fumarate symport (periplasm to cytoplasm)	fumarate[p] = fumarate
R-5016	0	R-5016	0	R-5016	citrate transport via diffusion (extracellular to periplasm)	citrate[e] = citrate[p]
R-5017	0	R-5017	0	R-5017	citrate symport (periplasm to cytoplasm)	citrate[p] = citrate
R-5018	0	R-5018	0	R-5018	glycolate transport via diffusion (extracellular to periplasm)	glycolate[e] = glycolate[p]
R-5019	0	R-5019	0	R-5019	glycolate symport (periplasm to cytoplasm)	glycolate[p] = glycolate
R-5020	0	R-5020	0	R-5020	formate transport via diffusion (extracellular to periplasm)	formate[e] = formate[p]
R-5021	33.8	R-5021	10.5746	R-5021	formate symport (periplasm to cytoplasm)	formate[p] = formate
R-5022	33.8	R-5022	33.8	R-5022	oxalate transport via diffusion (extracellular to periplasm)	oxalate[e] = oxalate[p]
R-5023	33.8	R-5023	33.8	R-5023	oxalate/formate antiporter (periplasm to cytoplasm)	oxalate[p] + formate = oxalate + formate[p]
R-5024	0	R-5024	0	R-5024	acetate transport via diffusion (extracellular to periplasm)	acetate[e] = acetate[p]
R-5025	0	R-5025	0	R-5025	sodium/acetate symporter (periplasm to cytoplasm)	acetate[p] = acetate
R-5026	0	R-5026	0	R-5026	D-gluconate transport via diffusion (extracellular to periplasm)	D-gluconate[e] = D-gluconate[p]
R-5027	0	R-5027	0	R-5027	H+/gluconate symporter	D-gluconate[p] = D-gluconate
R-5028	0	R-5028	0	R-5028	putrescine transport via diffusion (extracellular to periplasm)	putrescine[e] = putrescine[p]
R-5029	0	R-5029	0	R-5029	putrescine ABC transporter	putrescine[p] + ATP + H2O = putrescine + ADP + phosphate
R-5030	0	R-5030	0	R-5030	a-ketoglutarate transport via diffusion (extracellular to periplasm	2-oxoglutarate[e] = 2-oxoglutarate[p]
R-5031	0	R-5031	0	R-5031	a-ketoglutarate MFS transporter	2-oxoglutarate[p] = 2-oxoglutarate
R-5032	0.2256	R-5032	0.1333	R-5032	PiT phosphate transporter	phosphate[p] + H+[p] = phosphate + H+
R-5033	0.0143	R-5033	0.0084	R-5033	sulfate transport via diffusion (extracellular to periplasm)	SO42-[e] = SO42-[p]
R-5034	0.0143	R-5034	0.0084	R-5034	sodium/sulphate symporter	SO42-[p] + Na+[p] = SO42- + Na+
R-5035	0.0008	R-5035	0.0004	R-5035	sodium transport via diffusion (extracellular to periplasm)	Na+[e] = Na+[p]
R-5036	0	R-5036	0	R-5036	thiosulfate transport via diffusion (extracellular to periplasm)	thiosulfate[e] = thiosulfate[p]
R-5037	0	R-5037	0	R-5037	sulfate ABC transporter	SO42-[p] + ATP + H2O = SO42- + phosphate + ADP
R-5038	0	R-5038	0	R-5038	thiosulfate ABC transporter	thiosulfate[p] + ATP + H2O = thiosulfate + phosphate + ADP
R-5039	0.0135	R-5039	0.008	R-5039	sodium-proton antiporter	Na+ + 2 H+[p] = Na+[p] + 2 H+
R-5040	0	R-5040	0	R-5040	nitrate ABC transporter	NO3-[p] + ATP + H2O = NO3- + phosphate + ADP
R-5041	0	R-5041	0	R-5041	nitrate transport via diffusion (extracellular to periplasm)	NO3-[e] = NO3-[p]
R-5042	0	R-5042	0	R-5042	glutamate transport via diffusion (extracellular to periplasm)	L-glutamate[e] = L-glutamate[p]
R-5043	0	R-5043	0	R-5043	aspartate transport via diffusion (extracellular to periplasm)	L-aspartate[e] = L-aspartate[p]
R-5044	0	R-5044	0	R-5044	aspartate ABC transporter	L-aspartate[p] + ATP + H2O = L-aspartate + phosphate + ADP
R-5045	0	R-5045	0	R-5045	glutamate ABC transporter	L-glutamate[p] + ATP + H2O = L-glutamate + phosphate + ADP
R-5046	-30.5264	R-5046	-31.8651	R-5046	H2O transport via diffusion (extracellular to periplasm)	H2O[e] = H2O[p]
R-5047	-30.5264	R-5047	-31.8651	R-5047	H2O transport via aquaporin	H2O[p] = H2O
R-5048	0	R-5048	0	R-5048	ethanolamine transport via diffusion (extracellular to periplasm	ethanolamine[e] = ethanolamine[p]
R-5049	0	R-5049	0	R-5049	ethanolamine transporter (permease)	ethanolamine[p] = ethanolamine
R-5050	0	R-5050	0	R-5050	malate transport via diffusion (extracellular to periplasm)	(S)-malate[e] = (S)-malate[p]
R-5051	0	R-5051	0	R-5051	malate symport (periplasm to cytoplasm)	(S)-malate[p] = (S)-malate
R-5052	0	R-5052	0	R-5052	pyruvate transport via diffusion (extracellular to periplasm)	pyruvate[e] = pyruvate[p]
R-5053	0	R-5053	0	R-5053	pyruvate symport (periplasm to cytoplasm)	pyruvate[p] = pyruvate
R-5055	0	R-5055	0	R-5055	glucose porin B (extracellular to periplasm)	D-glucose[e] = D-glucose[p]
R-5056	0	R-5056	0	R-5056	D-ribose transport via diffusion (extracellular to periplasm)	D-ribose[e] = D-ribose[p]
R-5058	0	R-5058	0	R-5058	2-deoxy-D-ribose transport via diffusion (extracellular to peripl	2-deoxy-D-ribose[e] = 2-deoxy-D-ribose[p]
R-5060	0	R-5060	0	R-5060	5-dehydro-D-gluconate transporter (inferred from physiology)	5-dehydro-D-gluconate[p] = 5-dehydro-D-gluconate
R-5061	0	R-5061	0	R-5061	5-dehydro-D-gluconate transport via diffusion (extracellular to	5-dehydro-D-gluconate[e] = 5-dehydro-D-gluconate[p]
R-5062	0	R-5062	0	R-5062	Co2+ transport via diffusion (extracellular to periplasm)	Co2+[e] = Co2+[p]
R-5063	0	R-5063	0	R-5063	Cobalt transporter (periplasm to cytoplasm)	Co2+[p] = Co2+
R-5064	0.0252	R-5064	0.0149	R-5064	H+ transport via diffusion (extracellular to periplasm)	H+[e] = H+[p]
R-5065	0	R-5065	0	R-5065	H2O2 transport via diffusion (extracellular to periplasm)	H2O2[e] = H2O2[p]
R-5066	0	R-5066	0	R-5066	H2O2 transport via diffusion (periplasm to cytoplasm)	H2O2[p] = H2O2
R-5067	0	R-5067	0	R-5067	iron ABC transporter	Fe2+[p] + ATP + H2O = Fe2+ + phosphate + ADP
R-5068	0.0014	R-5068	0.0008	R-5068	iron transport via diffusion (extracellular to periplasm)	Fe2+[e] = Fe2+[p]
R-5069	0.0006	R-5069	0.0004	R-5069	molybdate ABC transporter	molybdate[p] + ATP + H2O = molybdate + phosphate + ADP
R-5070	0.0006	R-5070	0.0004	R-5070	molybdate transport via diffusion (extracellular to periplasm)	molybdate[e] = molybdate[p]
R-5071	0	R-5071	0	R-5071	potassium:proton antiporter	K+ + H+[p] = K+[p] + H+
R-5072	0.0343	R-5072	0.0203	R-5072	potassium transport via diffusion (extracellular to periplasm)	K+[e] = K+[p]
R-5073	0.0015	R-5073	0.0009	R-5073	magnesium transport via diffusion (extracellular to periplasm)	Mg2+[e] = Mg2+[p]
R-5074	0.0015	R-5074	0.0009	R-5074	magnesium ABC transporter	Mg2+[p] + ATP + H2O = Mg2+ + phosphate + ADP
R-5075	0.0009	R-5075	0.0005	R-5075	calcium transport via diffusion (extracellular to periplasm)	Ca2+[e] = Ca2+[p]
R-5076	0.0009	R-5076	0.0005	R-5076	calcium ABC transporter	Ca2+[p] + ATP + H2O = Ca2+ + phosphate + ADP
R-5077	0.0006	R-5077	0.0004	R-5077	copper transport via diffusion (extracellular to periplasm)	Cu2+[e] = Cu2+[p]
R-5078	0.0006	R-5078	0.0004	R-5078	copper ABC transporter	Cu2+[p] + ATP + H2O = Cu2+ + phosphate + ADP
R-5079	0	R-5079	0	R-5079	copper-exporting ATPase	Cu2+ + ATP + H2O = Cu2+[p] + phosphate + ADP
R-5080	0.0006	R-5080	0.0004	R-5080	manganese transport via diffusion (extracellular to periplasm)	Mn2+[e] = Mn2+[p]
R-5081	0.0006	R-5081	0.0004	R-5081	manganese:proton symport	Mn2+[p] + H+[p] = Mn2+ + H+
R-5082	0.0014	R-5082	0.0008	R-5082	iron:proton symport	Fe2+[p] + H+[p] = Fe2+ + H+
R-5083	0	R-5083	0	R-5083	cobalt-exporting ATPase	Co2+ + ATP + H2O = Co2+[p] + phosphate + ADP
R-5084	0	R-5084	0	R-5084	zinc-exporting ATPase	Zn2+ + ATP + H2O = Zn2+[p] + phosphate + ADP
R-5085	0	R-5085	0	R-5085	cadmium-exporting ATPase	Cd2+ + ATP + H2O = Cd2+[p] + phosphate + ADP
R-5086	0.0006	R-5086	0.0004	R-5086	zinc transport via diffusion (extracellular to periplasm)	Zn2+[e] = Zn2+[p]
R-5087	0.0006	R-5087	0.0004	R-5087	zinc ABC transporter	Zn2+[p] + ATP + H2O = Zn2+ + phosphate + ADP
R-5088	0.0009	R-5088	0.0005	R-5088	chloride transport via diffusion (extracellular to periplasm)	Cl-[e] = Cl-[p]
R-5089	0.0009	R-5089	0.0005	R-5089	chloride channel	Cl-[p] = Cl-
R-5090	0	R-5090	0	R-5090	sodium/calcium exchanger	Na+[p] + Ca2+ = Na+ + Ca2+[p]

R-5091	0	R-5091	0	R-5091	D-arabinose transport via diffusion (extracellular to periplasm)	D-arabinose[e] = D-arabinose[p]
R-5092	0	R-5092	0	R-5092	L-arabinose transport via diffusion (extracellular to periplasm)	L-arabinose[e] = L-arabinose[p]
R-5093	0	R-5093	0	R-5093	D-arabinonate transport via diffusion (extracellular to periplasm)	D-arabinonate[e] = D-arabinonate[p]
R-5094	0	R-5094	0	R-5094	L-arabinonate transport via diffusion (extracellular to periplasm)	L-arabinonate[e] = L-arabinonate[p]
R-5095	0	R-5095	0	R-5095	L-lyxose transport via diffusion (extracellular to periplasm)	L-lyxose[e] = L-lyxose[p]
R-5096	0	R-5096	0	R-5096	D-xylose transport via diffusion (extracellular to periplasm)	D-xylose[e] = D-xylose[p]
R-5097	0	R-5097	0	R-5097	D-xylonate transport via diffusion (extracellular to periplasm)	D-xylonate[e] = D-xylonate[p]
R-5098	0	R-5098	0	R-5098	L-lyxonate transport via diffusion (extracellular to periplasm)	L-lyxonate[e] = L-lyxonate[p]
R-5099	0	R-5099	0	R-5099	D-ribonate transport via diffusion (extracellular to periplasm)	D-ribonate[e] = D-ribonate[p]
R-5100	0	R-5100	0	R-5100	2-deoxy-D-ribonate transport via diffusion (extracellular to peri	2-deoxy-D-ribonate[e] = 2-deoxy-D-ribonate[p]
R-5101	0	R-5101	0	R-5101	acetoacetate symport (periplasm to cytoplasm)	acetoacetate[p] = acetoacetate
R-5102	0	R-5102	0	R-5102	acetoacetate transport via diffusion (extracellular to periplasm)	acetoacetate[e] = acetoacetate[p]
R-5103	0	R-5103	0	R-5103	propanoate symport (periplasm to cytoplasm)	propanoate[p] = propanoate
R-5104	0	R-5104	0	R-5104	propanoate transport via diffusion (extracellular to periplasm)	propanoate[e] = propanoate[p]
R-5105	0	R-5105	0	R-5105	3-O-b-D-galactopyranosyl-D-arabinose transport via diffusion	3-O-b-D-galactopyranosyl-D-arabinose[e] = 3-O-b-D-galactopyranosyl-D
R-5106	0	R-5106	0	R-5106	3-O-b-D-galactopyranosyl-D-arabinonate transport via diffusio	3-O-b-D-galactopyranosyl-D-arabinonate[e] = 3-O-b-D-galactopyranosyl
R-5107	0	R-5107	0	R-5107	short-chain fatty acid (decanoate) transporter (periplasm to cy	decanoate[p] = decanoate
R-5108	0	R-5108	0	R-5108	decanoate transport via diffusion (extracellular to periplasm)	decanoate[e] = decanoate[p]
R-5109	0	R-5109	0	R-5109	methylamine transport via diffusion (extracellular to periplasm)	methylamine[e] = methylamine[p]
R-5110	0	R-5110	0	R-5110	ethylamine transport via diffusion (extracellular to periplasm)	ethylamine[e] = ethylamine[p]
R-5111	0	R-5111	0	R-5111	acetaldehyde transport via diffusion (periplasm to cytoplasm)	acetaldehyde[p] = acetaldehyde
R-5112	0	R-5112	0	R-5112	ethanol transport via diffusion (extracellular to periplasm)	ethanol[e] = ethanol[p]
R-5113	0	R-5113	0	R-5113	L-tartrate transport via diffusion (extracellular to periplasm)	L-tartrate[e] = L-tartrate[p]
R-5114	0	R-5114	0	R-5114	L-tartrate transporter	L-tartrate[p] = L-tartrate
R-5115	0	R-5115	0	R-5115	glycerone transport via diffusion (extracellular to periplasm)	glycerone[e] = glycerone[p]
R-5116	0	R-5116	0	R-5116	glycerone transport via diffusion (periplasm to cytoplasm)	glycerone[p] = glycerone
R-5117	0	R-5117	0	R-5117	1,2-propanediol transport via diffusion (extracellular to periplas	1,2-propanediol[e] = 1,2-propanediol[p]
R-5118	0	R-5118	0	R-5118	(S)-lactate transport via diffusion (extracellular to periplasm)	(S)-lactate[e] = (S)-lactate[p]
R-5119	0	R-5119	0	R-5119	(S)-lactate transport (periplasm to cytoplasm)	(S)-lactate[p] = (S)-lactate
R-oxs	2.1266	R-oxs	1.2569	R-oxs	oxalyl-CoA synthase	ATP + oxalate + CoA = AMP + diphosphate + oxalyl-CoA
A-GAM	9.994	A-GAM	5.907			
mue	0.1861	mue	0.11			
NGAM	9.5	NGAM	9.5			
COFAC	0.0005	COFAC	0.0005			
SECMET	0.0002	SECMET	0.0002			
POLYN	0.004	POLYN	0.004			
PROTEIN	0.5913	PROTEIN	0.5913			
RNA	0.082	RNA	0.082			
DNA	0.03	DNA	0.03			
Fatty	0.0362	Fatty	0.0362			
Carbohydrate	0.1643	Carbohydrate	0.1643			
PHB	0.0236	PHB	0.0236			
intra-metabolite	0.0264	intra-metabolite	0.0264			
GAM	0.01	GAM	0.01			
NOQUANTY	0.001	NOQUANTY	0.001			
Inorganic	0.011	Inorganic	0.011			