

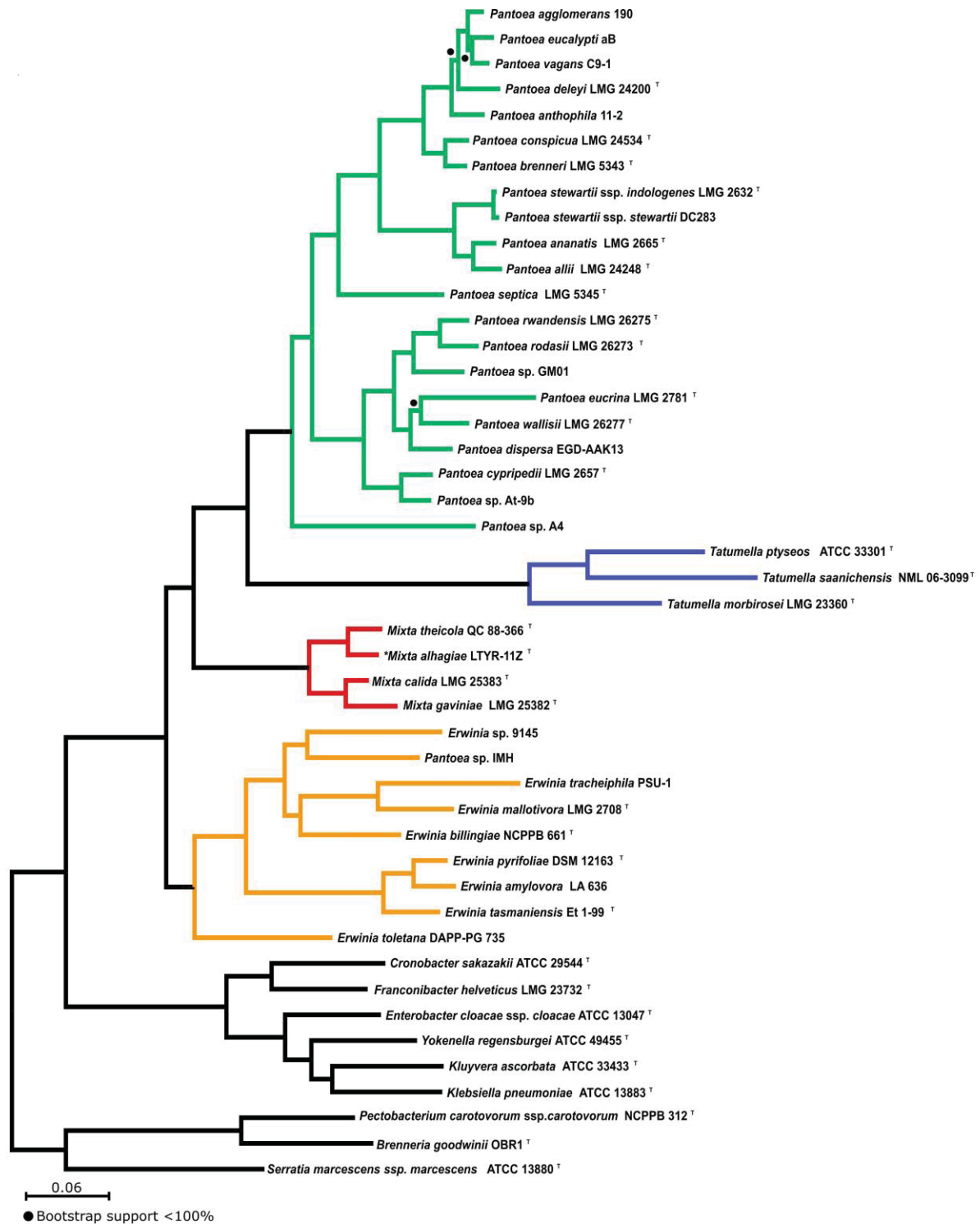
## ***Mixta* gen. nov. – A new genus in the *Erwiniaceae***

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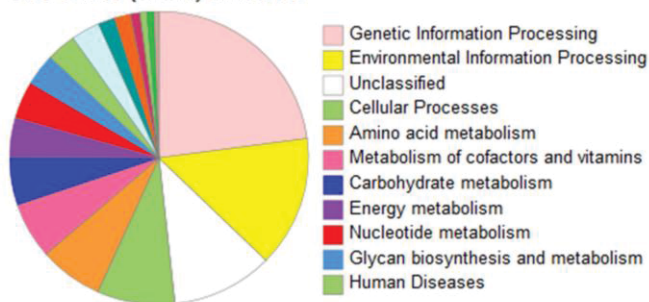


**Supplementary Figure S1.** A maximum-likelihood phylogeny for some members of *Erwinia*, *Mixta* gen. nov., *Pantoea* and *Tatumella*, with appropriate outgroup taxa, constructed from the protein sequences of all shared genes. The phylogeny was constructed from a concatenated data matrix of 1,044 sequences from 46 taxa, with partitioning, with the best-fit amino acid model of evolution applied to each partition. Branch support was inferred from 1,000 bootstrap replicates. All nodes have a bootstrap support value of 100%, except those indicated with a dot. Coloured branches correspond to *Pantoea* (green), *Tatumella* (blue), *Mixta* gen. nov. (red) and *Erwinia* (yellow). An asterisk indicates species that have not previously been validated.

*Erwinia*

Summary 1439 entries (87.5%) annotated

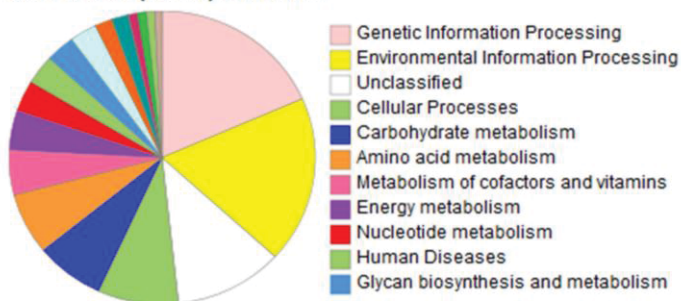
Functional category



*Mixta*

Summary 2069 entries (78.7%) annotated

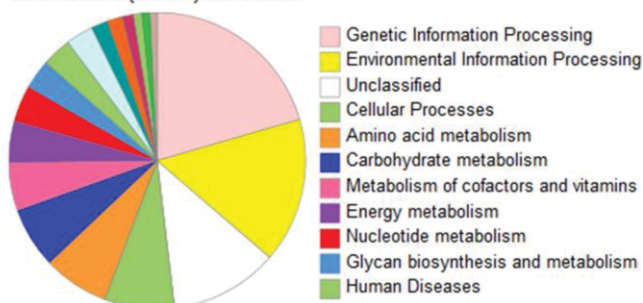
Functional category



*Pantoea*

Summary 1572 entries (84.5%) annotated

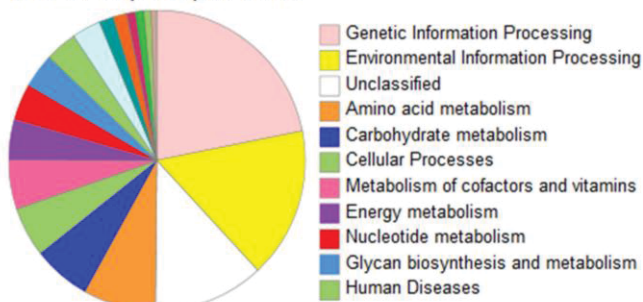
Functional category



*Tatumella*

Summary 1733 entries (79.0%) annotated

Functional category



**Supplementary Figure S2.** The number of core genes of the genera *Erwinia*, *Mixta* gen. nov., *Pantoea* and *Erwinia*, annotated with BlastKOALA. Pie charts indicate the proportion of genes involved in each functional category.



Supplementary Table S1. Average amino acid identity values for all genomes analysed in the study

	Pantoea_agglomerans_strain_190	Pantoea_sp_aB	Pantoea_vagans_C9_1	Pantoea_deleyi_LMG_24200	Pantoea_anthophila_strain_11_2	Pantoea_conspicua_LMG_24534	Pantoea_brenneri_LMG_5343	Pantoea_stewartii_subsp_indologenes_strain_LMG_2632	Pantoea_stewartii_subsp_stewartii_DC283	Pantoea_ananatis_LMG_2665	Pantoea_allii_LMG_24248	Pantoea_septica_LMG_5345	Pantoea_rwandensis_LMG_26275	Pantoea_rodasii_LMG_26273	Pantoea_sp_GM01	Pantoea_eucrina_LMG_2781	Pantoea_wallisii_LMG26277	Pantoea_dispersa_EGD_AAK13	Pantoea_cyripedii_LMG_2657	Pantoea_sp_At_9b	Pantoea_sp_A4	Tatumella_ptyoseos_ATCC_33301	Tatumella_saanichensis_NML_06_3099	Tatumella_morbirosei_strain_LMG_23360	Mixta_theicola_QC88-366	Mixta_alhagiae_LTYR_11Z	Mixta_calida_LMG_25383	Mixta_gaviniae_LMG_25382	Erwinia_sp_9145	Pantoea_sp_IMH	Erwinia_tracheiphila_PSU_1	Erwinia_mallotivora_BT_MARDI	Erwinia_billingiae_Eb661	Erwinia_pyrifoliae_DSM_12163	Erwinia_amylovora_LA636	Erwinia_tasmaniensis_Et1_99	Erwinia_toletana_DAPP_PG_735	Cronobacter_sakazakii_ATCC_29544	Franconibacter_helveticus_LMG_23732	Enterobacter_cloacae_subsp_cloacae_ATCC_13047_CP001918	Yokenella_regensburgei_ATCC_49455	Kluyvera_ascorbata_ATCC_33433	Klebsiella_pneumoniae_ATCC_13883	Pectobacterium_carotovorum_subsp_carotovorum_NCPPB_312	Brenneria_goodwinii_OBR1	Serratia_marcescens_subsp_marcescens_ATCC_13880	
Pantoea_agglomerans_strain_190	100	95.29	95.36	93.51	93.39	92.11	91.71	84.66	85.03	84.63	84.87	84.77	82.29	82.17	82.63	82.09	82.75	82.5	82.5	82.52	80.26	73.89	73.53	73.31	79.02	78.51	79.14	79.97	76.82	77.57	77.08	76.76	76.95	77.11	77	76.92	78.32	73.67	73.74	73.02	73.28	73.29	73.36	72.42	71.83	72.54	
Pantoea_sp_aB	95.29	100	95.29	93.32	93.03	91.42	91.25	84.88	85.3	85.02	85.12	84.75	82.35	82.34	82.54	82	83.01	82.69	82.77	82.66	80.38	73.98	73.6	73.49	79.12	78.75	79.32	80.1	76.97	77.78	77.33	76.89	77.13	77.37	77.2	77.15	78.48	73.56	73.86	73.32	73.44	73.34	73.26	72.73	72.1	72.83	
Pantoea_vagans_C9_1	95.36	95.29	100	93.4	93.46	91.78	91.36	84.75	85.07	84.79	85.04	84.82	82.38	82.23	82.53	82.2	82.93	82.62	82.52	82.69	80.28	73.95	73.49	73.4	78.89	78.65	79.3	80.02	77.04	77.7	77.33	76.86	77.05	77.42	77.44	77.14	78.2	73.84	73.6	73.14	73.28	73.31	73.51	72.39	71.92	72.68	
Pantoea_deleyi_LMG_24200	93.51	93.32	93.4	100	92.72	91.12	90.72	84.75	85.19	85.24	85.19	85.04	82.88	82.46	82.77	82.57	83.18	83.35	83.06	83.29	80.93	74.79	74.15	74.29	79.25	79.06	79.48	79.67	77.35	78.08	77.09	77	77.41	77.46	77.45	77.17	78.76	74.45	74.31	73.89	74.06	73.71	74.19	73.01	72.6	73.43	
Pantoea_anthophila_strain_11_2	93.39	93.03	93.46	92.72	100	91.15	91	84.89	85.51	85.06	85.1	84.91	82.42	82.25	82.54	82.16	82.99	82.73	82.77	82.81	80.67	74.2	73.79	73.58	79.04	78.64	79.3	80.05	77.06	77.77	77.43	77.03	77.03	77.47	77.27	77.1	78.44	73.77	73.75	73.51	73.5	73.63	72.54	71.97	72.92		
Pantoea_conspicua_LMG_24534	92.11	91.42	91.78	91.12	91.15	100	95.49	85.87	86.21	86.14	86.18	85.49	83.49	83.45	83.75	82.65	83.61	83.73	84.11	83.96	81.1	74.52	74.3	73.92	79.92	79.54	79.95	80.58	77.82	78.32	77.13	77.74	77.91	77.94	77.7	77.77	79.56	74.39	74.44	73.93	73.9	73.76	73.91	73.22	72.58	73.47	
Pantoea_brenneri_LMG_5343	91.71	91.25	91.36	90.72	91	95.49	100	85.58	85.96	85.47	85.52	85.41	82.96	82.9	83.35	82.88	83.59	83.43	83.37	83.66	81.07	74.62	74.26	73.93	79.83	79.49	79.84	80.38	77.77	78.42	77.98	77.61	77.76	77.81	77.89	77.64	79.31	74.46	74.4	73.76	73.87	73.95	73.88	73	72.39	73.05	
Pantoea_stewartii_subsp_indologenes_strain_LMG_2632	84.66	84.88	84.75	84.75	84.89	85.87	85.58	100	98.67	91.42	91.55	83.4	81.74	81.4	81.82	81.68	82.09	82.05	81.94	81.94	79.94	73.86	73.59	73.32	78.72	78.18	78.68	79.33	76.65	77.1	77.29	76.88	76.69	76.84	76.84	76.52	77.72	73.76	73.87	73.56	73.19	73.41	73.57	72.15	71.89	72.3	
Pantoea_stewartii_subsp_stewartii_DC283	85.04	85.3	85.07	85.19	85.51	86.21	85.96	98.67	100	91.44	91.53	83.69	82.42	82.03	82.12	81.97	82.54	82.76	82.29	82.3	80.52	74.3	73.78	73.99	78.89	78.6	79.03	79.66	77	77.29	77.19	77.11	76.83	76.97	77.07	76.56	78.72	74.03	73.92	73.76	73.92	73.43	73.69	73.86	72.35	72.22	73.01
Pantoea_ananatis_LMG_2665	84.63	85.02	84.79	85.24	85.06	86.14	85.47	91.42	91.44	100	94.16	83.47	81.72	81.37	81.82	81.67	82.44	82.08	81.85	81.84	79.91	73.94	73.37	73.24	78.67	78.22	78.79	79.51	76.67	77.17	77.13	76.64	76.56	77.07	76.98	76.47	77.63	73.81	73.63	73.28	73.42	73.4	73.41	72.31	71.91	72.42	
Pantoea_allii_LMG_24248	84.87	85.12	85.03	85.19	85.1	86.18	85.52	91.55	91.53	94.16	100	83.41	81.63	81.38	81.62	81.49	82.43	82.19	81.92	81.77	79.84	73.81	73.55	73.39	78.58	78.28	78.81	79.4	76.68	77.19	77.23	76.76	76.74	77.15	77.06	76.5	77.89	73.78	73.81	73.51	73.43	73.41	73.48	72.62	72.16	72.35	
Pantoea_septica_LMG_5345	84.77	84.75	84.82	85.04	84.91	85.49	85.41	83.4	83.69	83.47	83.41	100	83.46	83.66	83.55	83.26	84.01	84.13	83.92	84.07	81.49	74.44	74.05	73.8	79.87	79.73	80.12	80.81	77.71	78.42	77.8	77.72	77.65	77.63	77.53	77.37	79.26	74.49	74.72	73.61	74.04	74.04	74.1	73.23	72.87	73.49	
Pantoea_rwandensis_LMG_26275	82.29	82.35	82.38	82.87	82.42	83.5	82.97	81.74	82.42	81.72	81.63	83.46	100	93.2	90.4	86.1	89.49	89.15	87.26	87.23	80.69	74.11	73.57	73.51	78.75	78.36	79.03	79.59	76.95	77.58	77.73	77.22	77.09	77.34	77.18	77.21	78.54	73.65	73.62	73.21	73.09	73.01	73.03	72.33	71.86	72.43	
Pantoea_rodasii_LMG_26273	82.17	82.34	82.23	82.46	82.25	83.45	82.91	81.4	82.03	81.37	81.38	83.66	93.2	100	90.66	86	89.35	89.12	87.06	87.22	80.71	74	73.46	73.24	79.15	78.5	79.22	79.63	77.04	77.61	77.06	76.87	77.18	77.09	77.03	76.78	78.47	73.74	73.7	73.08	73.38	73.24	73.12	72.48	71.88	72.51	
Pantoea_sp_GM01	82.63	82.55	82.53	82.77	82.55	83.75	83.35	81.82	82.12	81.82	81.62	83.55	90.4	90.65	100	86.03	89.44	89.32	87.18	87.62	80.85	74.04	73.51	73.35	79.19	78.86	79.42	79.85	77.14	77.64	77.29	76.87	77.31	77.26	77.1	77.12	78.48	73.6	73.7	73.12	73.15	73.21	72.99	72.55	71.85	72.54	
Pantoea_eucrina_LMG_2781	82.08	82	82.2	82.56	82.16	82.64	82.88	81.68	81.97	81.67	81.49	83.26	86.1	86	86.03	100	87.65	87.72	85.31	85.19	80.31	74.62	74.3	74	79.28	78.93	79.34	79.94	77.64	77.68	77.72	77.33	77.22	77.07	77.41	77.29	78.72	74.21	74.27	73.73	73.81	73.78	73.88	73.07	72.73	73.32	
Pantoea_wallisii_LMG26277	82.75	83.01	82.93	83.18	82.98	83.61	83.59	82.09	82.54	82.44	82.43	84.01	89.49	89.35	89.44	87.65	100	91.12	87.55	87.56	81.07	74.76	74.2	74.23	79.45	79.04	79.6	80.11	77.44	77.84	77.7	77.4	77.42	77.85	77.79	77.37	78.82	74.39	74.26	73.91	73.84	73.77	73.89	72.96	72.59	73.12	
Pantoea_dispersa_EGD_AAK13	82.5	82.68	82.63	83.35	82.73	83.76	83.43	82.05	82.77	82.08	82.19	84.13	89.15	89.12	89.32	87.72	91.12	100	87.51	87.49	81.01	74.51	74.05	73.67	79.29	79.05	79.69	80.37	77.42	77.93	77.9	77.47	77.01	77.79	77.75	77.6	78.8	74.14	74.17	73.5	73.6	73.68	73.59	72.96	72.22	73.94	
Pantoea_cyripedii_LMG_2657	82.5	82.77	82.52	83.05	82.77	84.11	83.37	81.94	82.29	81.86	81.92	83.92	87.26	87.06	87.18	85.31	87.55	87.51	100	92.36	81	74.3	73.56	73.5	79.32	79.37	80.08	80.2	77.16	77.97	77.71	77.29	76.83	77.62	77.61	77.04	78.55	74.13	74.09	73.79	73.42	73.32	73.29	72.39	71.84	72.58	
Pantoea_sp_At_9b	82.52	82.66	82.68	83.29	82.81	83.96	83.66	81.94	82.3	81.84	81.77	84.06	87.23	87.22	87.62	85.19	87.56	87.49	92.36	100	80.95	74.17	73.71	73.65	79.35	79.49	79.88	80.54	77.33	77.93	77.99	77.5	77.3	77.62	77.6	77.29	78.86	73.91	74.1	73.53	73.62	73.31	72.31	71.65	72.52		
Pantoea_sp_A4	80.26	80.38	80.28	80.93	80.67	81.1	81.07	79.94	80.53	79.91	79.84	81.49	80.69	80.72	80.85	80.32	81.07	81.02	81	80.95	100	73.16	73.31	72.9	77.83	77.55	78.14	78.7	76.03	76.93	76.32	76	75.93	76.37	76.4	76.14	76.89	72.98	73.43	72.87	73.15	73.21	73.03	72.06	71.19	72.29	
Tatumella_ptyoseos_ATCC_33301	73.89	73.98	73.95	74.79	74.21	74.52	74.62	73.87	74.31	73.94	73.81	74.44	74.12	74.01	74.03	74.62	74.76	74.51	74.3	74.17	73.36	100	82.87	82.14	73.84	73.79	74.17	75.19	72.46	72.94	73.22	72.47	72.44	72.7	72.85												

**Supplementary Table S2. Protein sequences of genes included in datasets with alignment positions and evolu**

	Gene	Gene name	Start position	Stop position	Length (AA)	Best-fit evolutionary model
MLSA genes	rpoB	DNA-directed RNA polymerase subunit beta	1	1355	1355	JTT
	atpD	ATP synthase subunit beta	1356	1822	466	WAG
	infB	Translation initiation factor 2	1823	2743	920	JTT
	gyrB	DNA gyrase subunit B	2744	3552	808	JTT
	gene144	shikimate 5-dehydrogenase	1	607	607	JTT
	gene1013	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein	608	1961	1354	WAG
	gene520	hypothetical protein	1962	2202	241	WAG
	gene241	DNA processing protein DprA	2203	2292	90	CpREV
	gene832	peptide deformylase	2293	2589	297	LG
	gene1005	methionyl-tRNA formyltransferase	2590	2785	196	JTT
	gene45	16S rRNA methyltransferase	2786	3034	249	WAG
	gene443	potassium transporter peripheral membrane protein	3035	3261	227	JTT
	gene817	large-conductance mechanosensitive channel	3262	3624	363	WAG
	gene778	50S ribosomal protein L17	3625	3719	95	Dayhoff
	gene969	DNA-directed RNA polymerase subunit alpha	3720	3911	192	LG
	gene828	30S ribosomal protein S4	3912	3996	85	LG
	gene168	preprotein translocase subunit SecY	3997	4400	404	LG
	gene496	50S ribosomal protein L15	4401	4952	552	WAG
	gene202	50S ribosomal protein L30	4953	6359	1407	LG
	gene120	30S ribosomal protein S5	6360	6518	159	WAG
	gene1018	50S ribosomal protein L18	6519	6772	254	WAG
	gene77	50S ribosomal protein L6	6773	6974	202	Dayhoff
	gene176	30S ribosomal protein S8	6975	7216	242	WAG
	gene634	50S ribosomal protein L5	7217	7410	194	WAG
	gene490	50S ribosomal protein L24	7411	7701	291	WAG
	gene43	50S ribosomal protein L14	7702	7993	292	WAG
	gene967	30S ribosomal protein S17	7994	8134	141	LG
	gene276	50S ribosomal protein L29	8135	8268	134	JTT
	gene735	50S ribosomal protein L16	8269	8532	264	JTT
	gene507	30S ribosomal protein S3	8533	8698	166	WAG
	gene41	50S ribosomal protein L22	8699	9359	661	LG
	gene900	50S ribosomal protein L2	9360	9813	454	LG
	gene827	50S ribosomal protein L23	9814	10136	323	Dayhoff
	gene251	50S ribosomal protein L4	10137	10396	260	LG
	gene268	50S ribosomal protein L3	10397	10910	514	LG
	gene684	30S ribosomal protein S10	10911	11192	282	JTT
gene630	30S ribosomal protein S12	11193	11405	213	WAG	
gene700	sulfur transfer complex subunit TusB	11406	11624	219	LG	
gene644	hypothetical protein	11625	12072	448	JTT	

gene942	peptidyl-prolyl cis-trans isomerase	12073	12572	500	WAG
gene10	lysis protein	12573	12702	130	JTT
gene373	peptidyl-prolyl cis-trans isomerase	12703	13864	1162	WAG
gene945	potassium transporter	13865	14107	243	WAG
gene863	potassium transporter	14108	14512	405	WAG
gene849	glutathione ABC transporter ATP-binding protein	14513	15030	518	LG
gene578	hypothetical protein	15031	15254	224	WAG
gene665	phosphoribulokinase	15255	15578	324	LG
gene839	CAMP-activated global transcriptional regulator CRP	15579	15821	243	LG
gene468	anthranilate synthase component II	15822	16766	945	Dayhoff
gene1015	peptidyl-prolyl cis-trans isomerase	16767	17214	448	LG
gene702	tryptophanyl-tRNA synthetase	17215	17502	288	Dayhoff
gene561	phosphoglycolate phosphatase	17503	18112	610	Dayhoff
gene1035	ribulose-phosphate 3-epimerase	18113	18602	490	JTT
gene109	DNA adenine methylase	18603	18889	287	WAG
gene139	3-dehydroquinate synthase	18890	19125	236	WAG
gene990	shikimate kinase	19126	19652	527	JTT
gene306	porin	19653	19827	175	WAG
gene210	penicillin-binding protein 1A	19828	20153	326	LG
gene924	Intracellular growth attenuator protein igaA	20154	20587	434	WAG
gene718	ribosome-associated heat shock protein Hsp15	20588	20687	100	LG
gene600	Hsp33 chaperonin	20688	20784	97	LG
gene556	phosphoenolpyruvate carboxykinase	20785	20988	204	JTT
gene675	osmolarity sensor protein	20989	21238	250	LG
gene977	transcriptional regulatory protein OmpR	21239	21648	410	WAG
gene397	transcription elongation factor GreB	21649	21971	323	LG
gene683	carboxylesterase	21972	22311	340	LG
gene554	Fe/S biogenesis protein NfuA	22312	22506	195	JTT
gene350	transcriptional regulator	22507	22794	288	WAG
gene175	intramembrane serine protease GlpG	22795	23114	320	JTT
gene105	thiosulfate sulfurtransferase	23115	23292	178	LG
gene845	glycerol-3-phosphate dehydrogenase	23293	23500	208	LG
gene750	aspartate-semialdehyde dehydrogenase	23501	23839	339	WAG
gene712	RNA polymerase factor sigma-32	23840	23908	69	Dayhoff
gene1033	cell division protein FtsX	23909	24389	481	WAG
gene237	cell division protein FtsE	24390	24519	130	LG
gene427	cell division protein FtsY	24520	24954	435	Dayhoff
gene53	membrane protein	24955	25392	438	WAG
gene472	membrane protein	25393	25870	478	LG
gene447	sulfurtransferase	25871	26500	630	Dayhoff



gene848	membrane protein	26501	27192	692	JTT
gene98	hypothetical protein	27193	27651	459	WAG
gene211	proline/glycine betaine transporter	27652	28240	589	WAG
gene767	delta-aminolevulinic acid dehydratase	28241	28749	509	LG
gene695	membrane protein	28750	29113	364	WAG
gene1	universal stress protein A	29114	29471	358	WAG
gene420	methyltransferase	29472	29769	298	LG
gene706	hypothetical protein	29770	30018	249	WAG
gene632	glutathione reductase	30019	30230	212	WAG
gene471	camphor resistance protein CrcB	30231	30587	357	JTT
gene981	membrane protein	30588	30731	144	Dayhoff
gene654	transporter	30732	30955	224	JTT
gene569	ketol-acid reductoisomerase	30956	31289	334	LG
gene255	dihydroxy-acid dehydratase	31290	31408	119	JTT
gene142	branched-chain amino acid aminotransferase	31409	31553	145	WAG
gene1036	acetolactate synthase	31554	31752	199	WAG
gene416	acetolactate synthase catalytic subunit	31753	31955	203	WAG
gene570	hypothetical protein	31956	32175	220	WAG
gene349	tRNA(uracil-5-)-methyltransferase	32176	32534	359	JTT
gene854	transcriptional regulator	32535	32932	398	LG
gene281	soluble pyridine nucleotide transhydrogenase	32933	33092	160	WAG
gene919	transcriptional regulator	33093	33336	244	WAG
gene913	argininosuccinate lyase	33337	33502	166	WAG
gene707	acetylglutamate kinase	33503	34153	651	WAG
gene451	acetylornithine deacetylase	34154	34439	286	Dayhoff
gene698	bifunctional aspartate kinase II/homoserine dehydrogenase II	34440	34726	287	WAG
gene626	cystathionine gamma-synthase	34727	35122	396	WAG
gene955	primosome assembly protein PriA	35123	35534	412	LG
gene511	transcriptional regulator	35535	35771	237	LG
gene135	hypothetical protein	35772	36058	287	JTT
gene219	ATP-dependent protease ATP-binding subunit HslU	36059	36573	515	LG
gene568	ribonuclease activity regulator protein RraA	36574	36772	199	JTT
gene641	septal ring assembly protein ZapB	36773	37092	320	WAG
gene899	glycerol uptake facilitator GlpF	37093	37275	183	JTT
gene192	glycerol kinase	37276	37509	234	JTT
gene716	fructose 1,6-bisphosphatase	37510	37678	169	WAG
gene842	ferredoxin-NADP reductase	37679	38237	559	LG
gene410	hypothetical protein	38238	38376	139	LG
gene701	triosephosphate isomerase	38377	38485	109	WAG
gene325	sulfate transporter subunit	38486	38802	317	WAG
gene250	6-phosphofructokinase	38803	39133	331	LG
gene337	iron transporter	39134	40051	918	WAG
gene242	transcriptional regulator	40052	40341	290	LG
gene102	histidine kinase	40342	40745	404	WAG

gene758	rRNA methyltransferase	40746	41055	310	WAG
gene796	serine acetyltransferase	41056	41506	451	LG
gene330	glycerol-3-phosphate dehydrogenase	41507	41946	440	WAG
gene364	preprotein translocase subunit SecB	41947	42361	415	WAG
gene245	peptidase M37	42362	42602	241	Dayhoff
gene136	ADP-L-glycero-D-mannoheptose-6-epimerase	42603	42856	254	WAG
gene160	ADP-heptose:LPS heptosyl transferase	42857	43289	433	JTT
gene922	3-deoxy-D-manno-octulosonic acid transferase	43290	43411	122	WAG
gene815	phosphopantetheine adenyltransferase	43412	43597	186	WAG
gene145	formamidopyrimidine-DNA glycosylase	43598	44066	469	LG
gene697	50S ribosomal protein L33	44067	44604	538	JTT
gene553	hypothetical protein	44605	45237	633	JTT
gene424	deoxyuridine 5-triphosphate nucleotidohydrolase	45238	45567	330	WAG
gene446	division inhibitor protein	45568	45768	201	Dayhoff
gene366	ribonuclease PH	45769	46053	285	JTT
gene163	hypothetical protein	46054	46433	380	WAG
gene1010	guanylate kinase	46434	46617	184	LG
gene226	DNA-directed RNA polymerase subunit omega	46618	46723	106	LG
gene218	bifunctional (p)ppGpp synthetase II/ guanosine-3,5-bis pyrophosphate 3-pyrophosphohydrolase	46724	47052	329	WAG
gene769	tRNA methyltransferase	47053	47355	303	WAG
gene30	hypothetical protein	47356	47556	201	LG
gene216	hypothetical protein	47557	47731	175	Dayhoff
gene851	D-tyrosyl-tRNA(Tyr) deacylase	47732	48257	526	WAG
gene571	alpha-D-glucose-1-phosphatase	48258	48430	173	JTT
gene764	GTP-binding protein TypA	48431	48667	237	JTT
gene476	glutamine synthetase	48668	49052	385	WAG
gene826	nitrogen regulation protein NR(II)	49053	49343	291	LG
gene224	nitrogen regulation protein NR(I)	49344	49969	626	WAG
gene558	coproporphyrinogen III oxidase	49970	50080	111	Dayhoff
gene209	Der GTPase activator	50081	50611	531	WAG
gene91	GTP-binding protein YsxC	50612	50704	93	JTT
gene119	DNA polymerase I	50705	51194	490	LG
gene398	DSBA oxidoreductase	51195	51606	412	WAG
gene272	serine/threonine protein kinase	51607	51695	89	JTT
gene32	molybdopterin-guanine dinucleotide biosynthesis protein MobA	51696	51798	103	LG
gene736	potassium transporter Kup	51799	52025	227	LG
gene968	C4-dicarboxylate ABC transporter	52026	52295	270	WAG
gene676	hypothetical protein	52296	52498	203	LG
gene853	ATP-dependent DNA helicase Rep	52499	53022	524	WAG



gene803	guanosine polyphosphate pyrophosphohydrolase	53023	53173	151	JTT
gene824	RNA helicase	53174	53522	349	WAG
gene314	thioredoxin	53523	54490	968	WAG
gene935	transcription termination factor Rho	54491	54567	77	WAG
gene515	UDP-N-acetylglucosamine 2-epimerase	54568	55345	778	WAG
gene541	TDP-4-oxo-6-deoxy-D-glucose aminotransferase	55346	55548	203	LG
gene172	O-antigen translocase	55549	56406	858	JTT
gene518	4-alpha-L-fucosyltransferase	56407	56525	119	JTT
gene643	common antigen polymerase	56526	56837	312	Dayhoff
gene926	protoheme IX biogenesis protein	56838	57137	300	WAG
gene247	uroporphyrinogen III C-methyltransferase	57138	57334	197	WAG
gene273	uroporphyrinogen-III synthase	57335	58074	740	Dayhoff
gene358	porphobilinogen deaminase	58075	58204	130	JTT
gene352	adenylate cyclase	58205	58355	151	JTT
gene348	diaminopimelate epimerase	58356	58555	200	WAG
gene500	hypothetical protein	58556	58905	350	WAG
gene946	tyrosine recombinase XerC	58906	59216	311	LG
gene86	flavin mononucleotide phosphatase	59217	59588	372	WAG
gene597	magnesium/nickel/cobalt transporter CorA	59589	59786	198	Dayhoff
gene662	phospholipase A	59787	59892	106	Dayhoff
gene155	ATP-dependent DNA helicase RecQ	59893	60526	634	LG
gene970	threonine transporter RhtB	60527	60912	386	WAG
gene620	lysophospholipase L2	60913	61135	223	WAG
gene483	transcriptional regulator	61136	61294	159	WAG
gene882	uridine phosphorylase	61295	62168	874	LG
gene567	DNA recombination protein RmuC	62169	62420	252	LG
gene856	ubiquinone/menaquinone biosynthesis methyltransferase	62421	62856	436	JTT
gene405	membrane protein	62857	63238	382	WAG
gene1014	ubiquinone biosynthesis protein UbiB	63239	63887	649	LG
gene584	twin-arginine protein translocation system subunit TatC	63888	64080	193	LG
gene126	DNase TatD	64081	64447	367	WAG
gene671	transcriptional activator RfaH	64448	64978	531	WAG
gene441	3-polyprenyl-4-hydroxybenzoate decarboxylase	64979	66031	1053	LG
gene372	FMN reductase	66032	66280	249	WAG
gene355	proline dipeptidase	66281	66396	116	Dayhoff
gene267	hypothetical protein	66397	66556	160	JTT
gene615	protoporphyrinogen oxidase	66557	66656	100	JTT
gene593	UDP-N-acetylenolpyruvoylglucosamine reductase	66657	67042	386	WAG

gene426	bifunctional biotin--[acetyl-CoA-carboxylase] synthetase/biotin operon repressor	67043	67147	105	Dayhoff
gene786	pantothenate kinase	67148	67909	762	WAG
gene505	50S ribosomal protein L1	67910	68249	340	WAG
gene835	50S ribosomal protein L10	68250	68438	189	LG
gene819	DNA-directed RNA polymerase subunit beta	68439	68661	223	WAG
gene151	DNA-directed RNA polymerase subunit beta	68662	69596	935	WAG
gene562	NADH pyrophosphatase	69597	69778	182	LG
gene508	uroporphyrinogen decarboxylase	69779	69860	82	Dayhoff
gene328	endonuclease VIII	69861	70314	454	WAG
gene598	hypothetical protein	70315	70678	364	Dayhoff
gene365	DNA-binding protein HU-alpha	70679	70932	254	JTT
gene137	phosphoribosylamine--glycine ligase	70933	71023	91	JTT
gene886	phosphoribosylaminoimidazolecarboxamide formyltransferase	71024	71203	180	LG
gene290	homoserine O-succinyltransferase	71204	71324	121	JTT
gene725	glucose-6-phosphate isomerase	71325	71499	175	JTT
gene27	aspartate kinase	71500	71609	110	JTT
gene375	chorismate pyruvate lyase	71610	71740	131	WAG
gene423	diacylglycerol kinase	71741	72415	675	LG
gene667	LexA repressor	72416	72765	350	LG
gene308	transcriptional regulator	72766	72890	125	JTT
gene143	tRNA-dihydrouridine synthase A	72891	73093	203	WAG
gene225	quinone oxidoreductase	73094	73356	263	LG
gene638	DNA helicase	73357	73485	129	LG
gene588	aromatic amino acid aminotransferase	73486	73900	415	WAG
gene96	excinuclease ABC subunit A	73901	74368	468	LG
gene341	proton glutamate symport protein	74369	74877	509	JTT
gene450	N-acetylmuramic acid-6-phosphate etherase	74878	75046	169	Dayhoff
gene46	thiol:disulfide interchange protein precursor	75047	75240	194	JTT
gene859	exclusion suppressor FxsA	75241	75397	157	LG
gene789	co-chaperonin GroES	75398	75900	503	LG
gene184	molecular chaperone GroEL	75901	76471	571	JTT
gene336	membrane protein	76472	76860	389	JTT
gene1007	lysine 2,3-aminomutase	76861	77103	243	WAG
gene257	elongation factor P	77104	77467	364	WAG
gene726	lysyl-tRNA synthetase	77468	77715	248	LG
gene203	serine endoprotease	77716	78001	286	WAG
gene432	serine endoprotease	78002	78660	659	Dayhoff
gene880	cytochrome D ubiquinol oxidase subunit III	78661	78945	285	WAG
gene470	hypothetical protein	78946	79106	161	DCMut
gene618	50S ribosomal protein L13	79107	79494	388	LG
gene738	30S ribosomal protein S9	79495	79986	492	WAG
gene307	stringent starvation protein A	79987	80296	310	WAG

gene535	Clp protease ClpP	80297	80356	60	JTT
gene920	monofunctional biosynthetic peptidoglycan transglycosylase	80357	80957	601	LG
gene872	phosphohistidinoprotein-hexose phosphotransferase	80958	81207	250	Dayhoff
gene672	glmZ(sRNA)-inactivating NTPase	81208	81672	465	WAG
gene149	PTS sugar transporter subunit IIA	81673	81865	193	WAG
gene249	RNA polymerase factor sigma-54	81866	82228	363	WAG
gene519	lipopolysaccharide ABC transporter ATP-binding protein	82229	83055	827	JTT
gene951	sugar ABC transporter substrate-binding protein	83056	83426	371	WAG
gene157	sugar ABC transporter substrate-binding protein	83427	83940	514	JTT
gene180	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	83941	84147	207	LG
gene840	D-arabinose 5-phosphate isomerase	84148	84498	351	Dayhoff
gene406	sodium:proton antiporter	84499	84610	112	JTT
gene715	ABC transporter permease	84611	85296	686	WAG
gene657	phospholipid ABC transporter substrate-binding protein	85297	85592	296	LG
gene167	organic solvent ABC transporter substrate-binding protein	85593	86057	465	JTT
gene322	anti-sigma B factor antagonist	86058	86230	173	JTT
gene927	hypothetical protein	86231	86384	154	LG
gene459	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	86385	86616	232	WAG
gene891	octaprenyl diphosphate synthase	86617	86942	326	Dayhoff
gene579	50S ribosomal protein L21	86943	87211	269	WAG
gene234	50S ribosomal protein L27	87212	87355	144	JTT
gene799	GTPase CgtA	87356	87581	226	LG
gene215	D-alanyl-D-alanine carboxypeptidase	87582	87785	204	LG
gene300	transcription elongation factor GreA	87786	88101	316	WAG
gene779	RNA-binding protein YhbY	88102	88453	352	Dayhoff
gene359	23S rRNA methyltransferase	88454	88737	284	LG
gene847	ATP-dependent metalloprotease	88738	88955	218	WAG
gene781	phosphoglucosamine mutase	88956	89553	598	Dayhoff
gene40	ribosome maturation protein RimP	89554	89774	221	JTT
gene70	transcription termination factor NusA	89775	90131	357	LG
gene1002	translation initiation factor IF-2	90132	90235	104	LG
gene668	ribosome-binding factor A	90236	90519	284	WAG
gene296	tRNA pseudouridine synthase B	90520	91160	641	Dayhoff
gene885	30S ribosomal protein S15	91161	91308	148	Dayhoff
gene720	polynucleotide phosphorylase/polyadenylase	91309	91799	491	LG
gene904	lipoprotein Nlpl	91800	91860	61	RtREV
gene901	N-acetyltransferase	91861	92154	294	LG
gene502	endoribonuclease L-PSP	92155	92513	359	WAG
gene624	aspartate carbamoyltransferase regulatory subunit	92514	92662	149	WAG

gene228	aspartate carbamoyltransferase catalytic subunit	92663	92807	145	WAG
gene347	RNase E inhibitor protein	92808	92937	130	LG
gene934	valyl-tRNA synthetase	92938	93246	309	LG
gene193	DNA polymerase III subunit chi	93247	93689	443	WAG
gene938	multifunctional aminopeptidase A	93690	94040	351	CpREV
gene1022	lipopolysaccharide ABC transporter permease	94041	94285	245	LG
gene56	alanine acetyltransferase	94286	94443	158	JTT
gene1031	gluconolactonase	94444	94815	372	WAG
gene59	phosphoserine phosphatase	94816	95273	458	JTT
gene1029	DNA repair protein RadA	95274	95434	161	WAG
gene345	ABC transporter ATP-binding protein	95435	96094	660	Dayhoff
gene393	lytic murein transglycosylase	96095	96512	418	WAG
gene1020	Trp operon repressor	96513	96587	75	LG
gene357	phosphoglycerate mutase	96588	97116	529	WAG
gene67	transcriptional regulator	97117	97644	528	WAG
gene367	homoserine kinase	97645	98096	452	LG
gene374	threonine synthase	98097	98415	319	JTT
gene811	molybdenum cofactor biosynthesis protein MogA	98416	98700	285	WAG
gene788	chaperone protein DnaK	98701	98789	89	JTT
gene878	molecular chaperone DnaJ	98790	99019	230	JTT
gene704	sodium:proton antiporter	99020	99425	406	WAG
gene246	30S ribosomal protein S20	99426	99618	193	WAG
gene988	bifunctional riboflavin kinase/FMN adenylyltransferase	99619	99812	194	LG
gene834	lipoprotein signal peptidase	99813	100035	223	WAG
gene156	peptidyl-prolyl cis-trans isomerase	100036	100488	453	CpREV
gene682	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	100489	100793	305	Dayhoff
gene642	dihydrodipicolinate reductase	100794	101115	322	WAG
gene173	carbamoyl phosphate synthase large subunit	101116	101398	283	WAG
gene773	dihydrofolate reductase	101399	101588	190	LG
gene253	diadenosine tetraphosphatase	101589	101817	229	LG
gene453	cobalt transporter	101818	102060	243	WAG
gene664	dimethyladenosine transferase	102061	102260	200	WAG
gene526	4-hydroxythreonine-4-phosphate dehydrogenase	102261	102691	431	LG
gene656	peptidyl-prolyl cis-trans isomerase	102692	103012	321	LG
gene596	molecular chaperone DnaJ	103013	103112	100	CpREV
gene327	23S rRNA pseudouridylate synthase	103113	103607	495	WAG
gene411	ATP-dependent helicase	103608	103981	374	WAG
gene631	DNA polymerase II	103982	104227	246	WAG
gene78	thiamine ABC transporter ATP-binding protein	104228	104735	508	LG
gene959	isopropylmalate isomerase	104736	105059	324	WAG



gene678	3-isopropylmalate dehydratase large subunit	105060	105545	486	LG
gene687	3-isopropylmalate dehydrogenase	105546	105730	185	WAG
gene498	2-isopropylmalate synthase	105731	106086	356	WAG
gene844	acetolactate synthase	106087	106546	460	LG
gene494	acetolactate synthase	106547	106728	182	Dayhoff
gene1037	transcriptional regulator	106729	106892	164	LG
gene262	cell division protein MraZ	106893	107052	160	LG
gene428	16S rRNA methyltransferase	107053	107288	236	LG
gene691	cell division protein FtsL	107289	107620	332	WAG
gene661	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	107621	108010	390	JTT
gene1012	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	108011	108188	178	WAG
gene100	phospho-N-acetylmuramoyl-pentapeptide- transferase	108189	108640	452	LG
gene342	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	108641	108795	155	Dayhoff
gene497	cell division protein FtsW	108796	109045	250	LG
gene265	UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	109046	109697	652	JTT
gene440	UDP-N-acetylmuramate--alanine ligase	109698	109826	129	JTT
gene207	cell division protein FtsQ	109827	109917	91	JTT
gene12	cell division protein FtsA	109918	110123	206	LG
gene36	peptidase M23	110124	110487	364	Dayhoff
gene998	preprotein translocase subunit SecA	110488	111103	616	LG
gene304	nucleoside triphosphate pyrophosphohydrolase	111104	111376	273	WAG
gene335	DNA gyrase inhibitor	111377	111796	420	JTT
gene481	hypothetical protein	111797	112044	248	LG
gene340	transporter HofB	112045	112294	250	JTT
gene734	major pilin subunit	112295	112888	594	WAG
gene989	transcriptional regulator	112889	113163	275	WAG
gene1001	pyruvate dehydrogenase	113164	113299	136	JTT
gene523	pyruvate dehydrogenase	113300	113509	210	JTT
gene116	dihydrolipoamide dehydrogenase	113510	113850	341	LG
gene291	hypothetical protein	113851	114068	218	WAG
gene963	hypoxanthine phosphoribosyltransferase	114069	114298	230	WAG
gene1034	multidrug ABC transporter ATP-binding protein	114299	115593	1295	WAG
gene1024	pantoate--beta-alanine ligase	115594	116039	446	WAG
gene233	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	116040	116506	467	LG
gene201	transcriptional regulator	116507	117861	1355	LG
gene723	transcriptional regulator	117862	118113	252	Dayhoff
gene830	iron-hydroxamate transporter substrate-binding subunit	118114	118447	334	WAG

gene877	iron-sulfur cluster insertion protein ErpA	118448	118775	328	JTT
gene132	5-methylthioadenosine/S- adenosylhomocysteine nucleosidase	118776	118927	152	Dayhoff
gene793	deoxyguanosinetriphosphate triphosphohydrolase	118928	119115	188	WAG
gene724	hypothetical protein	119116	119377	262	LG
gene997	2,3,4,5-tetrahydropyridine-2,6- carboxylate N-succinyltransferase	119378	119525	148	WAG
gene449	methionine aminopeptidase	119526	119813	288	WAG
gene159	30S ribosomal protein S2	119814	120316	503	JTT
gene200	elongation factor Ts	120317	120483	167	JTT
gene804	uridylate kinase	120484	120884	401	LG
gene545	1-deoxy-D-xylulose 5-phosphate reductoisomerase	120885	121292	408	WAG
gene931	UDP pyrophosphate synthase	121293	121780	488	JTT
gene897	CDP-diglyceride synthase	121781	121900	120	LG
gene15	zinc metallopeptidase RseP	121901	121959	59	CpREV
gene805	outer membrane protein assembly factor YaeT	121960	122678	719	JTT
gene635	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	122679	122877	199	LG
gene693	hydroxymyristoyl-ACP dehydratase	122878	123521	644	JTT
gene1027	UDP-N-acetylglucosamine acyltransferase	123522	123962	441	LG
gene279	ribonuclease HII	123963	124134	172	JTT
gene339	DNA polymerase III subunit alpha	124135	124204	70	JTT
gene791	acetyl-CoA carboxylase subunit alpha	124205	124820	616	LG
gene467	lyase	124821	125031	211	WAG
gene898	prolyl-tRNA synthetase	125032	125309	278	JTT
gene996	outer membrane lipoprotein	125310	125538	229	Dayhoff
gene809	methionine ABC transporter substrate- binding protein	125539	125865	327	JTT
gene762	methionine ABC transporter permease	125866	126125	260	WAG
gene312	hypothetical protein	126126	126436	311	LG
gene197	murein transglycosylase	126437	126759	323	WAG
gene408	hypothetical protein	126760	126911	152	JTT
gene1040	ribonuclease H	126912	127259	348	LG
gene499	DNA polymerase III subunit epsilon	127260	127652	393	WAG
gene101	phosphoheptose isomerase	127653	128464	812	JTT
gene285	glutamine amidotransferase	128465	128713	249	WAG
gene177	transpeptidase	128714	129032	319	JTT
gene754	DNA polymerase IV	129033	129225	193	WAG
gene679	aminoacyl-histidine dipeptidase	129226	129335	110	LG
gene401	xanthine phosphoribosyltransferase	129336	129776	441	LG
gene404	fermentation/respiration switch protein	129777	130160	384	WAG
gene390	gamma-glutamyl kinase	130161	130320	160	JTT

gene381	gamma-glutamyl phosphate reductase	130321	130795	475	JTT
gene921	hypothetical protein	130796	131408	613	Dayhoff
gene334	shikimate kinase	131409	131703	295	JTT
gene589	hypothetical protein	131704	132016	313	WAG
gene435	recombinase	132017	132612	596	WAG
gene911	exonuclease SbcD	132613	133097	485	JTT
gene838	PhoB family transcriptional regulator	133098	133167	70	LG
gene1021	phosphate regulon sensor protein	133168	133299	132	LG
gene485	branched-chain amino acid ABC transporter substrate-binding protein	133300	133887	588	WAG
gene807	proline-specific permease	133888	134393	506	LG
gene283	ACP phosphodiesterase	134394	134753	360	LG
gene383	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	134754	134911	158	WAG
gene106	queuine tRNA-ribosyltransferase	134912	135357	446	Dayhoff
gene746	preprotein translocase subunit YajC	135358	135569	212	WAG
gene952	preprotein translocase subunit SecD	135570	135973	404	WAG
gene71	NrdR family transcriptional regulator	135974	136197	224	JTT
gene825	6,7-dimethyl-8-ribityllumazine synthase	136198	136881	684	WAG
gene487	transcription antitermination protein NusB	136882	137820	939	WAG
gene628	thiamine monophosphate kinase	137821	138259	439	WAG
gene385	1-deoxy-D-xylulose-5-phosphate synthase	138260	138453	194	LG
gene862	geranyl transferase	138454	138892	439	WAG
gene8	exodeoxyribonuclease VII small subunit	138893	139350	458	LG
gene760	tRNA s(4)U8 sulfurtransferase	139351	140058	708	WAG
gene719	oxidative-stress-resistance chaperone	140059	140550	492	WAG
gene313	2-dehydropantoate 2-reductase	140551	140776	226	WAG
gene68	nucleotide-binding protein	140777	141145	369	Dayhoff
gene221	membrane protein	141146	142090	945	WAG
gene610	protoheme IX farnesyltransferase	142091	142333	243	LG
gene24	cytochrome O ubiquinol oxidase	142334	142396	63	LG
gene756	cytochrome O ubiquinol oxidase	142397	142856	460	WAG
gene843	cytochrome O ubiquinol oxidase	142857	143118	262	JTT
gene808	cytochrome O ubiquinol oxidase	143119	143439	321	WAG
gene150	hypothetical protein	143440	143695	256	WAG
gene866	BolA family transcriptional regulator	143696	144141	446	LG
gene543	trigger factor	144142	144539	398	WAG
gene269	Clp protease proteolytic subunit ClpP	144540	145459	920	JTT
gene527	ATP-dependent protease	145460	145878	419	LG
gene166	peptidase	145879	146308	430	WAG
gene303	transcriptional regulator	146309	146625	317	WAG

gene961	folding chaperone	146626	147287	662	WAG
gene748	hypothetical protein	147288	147583	296	WAG
gene1023	queuosine biosynthesis protein QueC	147584	148454	871	WAG
gene752	multidrug ABC transporter ATP-binding protein	148455	149195	741	LG
gene301	multidrug ABC transporter ATP-binding protein	149196	149368	173	LG
gene660	nitrogen regulatory protein P-II 2	149369	149641	273	WAG
gene581	ammonium transporter	149642	149870	229	JTT
gene544	gene expression modulator	149871	150336	466	LG
gene820	hypothetical protein	150337	150562	226	WAG
gene721	multidrug transporter	150563	150917	355	WAG
gene831	multidrug transporter	150918	151320	403	WAG
gene617	transcriptional regulator	151321	151805	485	WAG
gene115	adenine phosphoribosyltransferase	151806	152184	379	WAG
gene547	hypothetical protein	152185	152421	237	JTT
gene903	recombinase RecR	152422	152958	537	WAG
gene530	heat shock protein 90	152959	153194	236	Dayhoff
gene378	adenylate kinase	153195	153466	272	LG
gene559	hypothetical protein	153467	153686	220	LG
gene48	transcriptional regulator	153687	153944	258	WAG
gene616	hypothetical protein	153945	154105	161	LG
gene816	oxidoreductase	154106	154377	272	LG
gene133	UDP-2,3-diacetylglucosamine hydrolase	154378	154575	198	JTT
gene740	peptidyl-prolyl cis-trans isomerase	154576	154854	279	WAG
gene23	cysteinyl-tRNA synthetase	154855	154938	84	Blosum62
gene531	ribosome-associated protein	154939	155511	573	LG
gene422	methenyltetrahydrofolate cyclohydrolase	155512	155718	207	Dayhoff
gene323	lipoyl synthase	155719	156055	337	WAG
gene434	lipoate--protein ligase	156056	156305	250	WAG
gene28	hypothetical protein	156306	156579	274	JTT
gene457	D-alanyl-D-alanine carboxypeptidase	156580	156867	288	WAG
gene154	cell wall shape-determining protein	156868	157086	219	WAG
gene380	penicillin-binding protein 2	157087	157416	330	JTT
gene572	50S rRNA methyltransferase	157417	157872	456	JTT
gene573	ribosome-associated protein	157873	158189	317	WAG
gene61	DNA polymerase III subunit delta	158190	158357	168	WAG
gene297	LPS-assembly lipoprotein RlpB	158358	158740	383	Dayhoff
gene802	leucyl-tRNA synthetase	158741	158942	202	LG
gene733	cobalt transporter	158943	159145	203	WAG
gene727	16S rRNA maturation RNase YbeY	159146	159294	149	JTT
gene2	nucleoside triphosphate hydrolase	159295	159502	208	WAG
gene394	(dimethylallyl)adenosine tRNA methylthiotransferase	159503	159682	180	WAG
gene319	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	159683	160047	365	WAG



gene907	asparagine synthetase B	160048	160245	198	WAG
gene1017	transcriptional regulator	160246	160495	250	WAG
gene985	N-acetylglucosamine-6-phosphate deacetylase	160496	160742	247	LG
gene770	glutamate--tRNA ligase	160743	161323	581	WAG
gene592	ferric uptake regulator	161324	161779	456	LG
gene461	flavodoxin	161780	162209	430	LG
gene277	LexA regulated protein	162210	162385	176	JTT
gene893	metal-binding protein	162386	162498	113	JTT
gene438	type II citrate synthase	162499	162932	434	LG
gene1032	succinate dehydrogenase	162933	163283	351	WAG
gene829	succinate dehydrogenase cytochrome b556 small membrane subunit	163284	163452	169	JTT
gene548	succinate dehydrogenase flavoprotein subunit	163453	164177	725	LG
gene351	succinate dehydrogenase iron-sulfur subunit	164178	164358	181	WAG
gene190	2-oxoglutarate dehydrogenase E1	164359	164545	187	JTT
gene582	dihydrolipoamide succinyltransferase	164546	164896	351	WAG
gene933	malate--CoA ligase subunit beta	164897	165263	367	JTT
gene751	succinyl-CoA synthetase subunit alpha	165264	165565	302	WAG
gene974	colicin transporter	165566	165656	91	WAG
gene651	colicin transporter	165657	166040	384	WAG
gene709	membrane protein	166041	166122	82	Dayhoff
gene775	peptidoglycan-associated outer membrane lipoprotein	166123	166547	425	LG
gene896	tol-pal system protein	166548	166909	362	WAG
gene252	zinc transporter ZitB	166910	167108	199	Dayhoff
gene852	phosphoglyceromutase	167109	167596	488	WAG
gene1041	galactose-1-epimerase	167597	167826	230	LG
gene111	galactokinase	167827	168162	336	WAG
gene248	galactose-1-phosphate uridylyltransferase	168163	168351	189	WAG
gene39	pyridoxal phosphate phosphatase	168352	168958	607	JTT
gene429	6-phosphogluconolactonase	168959	169382	424	Dayhoff
gene344	excinuclease ABC subunit B	169383	170273	891	LG
gene732	hypothetical protein	170274	170542	269	WAG
gene986	molybdenum cofactor biosynthesis protein A	170543	171307	765	LG
gene206	molybdopterin biosynthesis protein B	171308	171503	196	JTT
gene995	molybdenum cofactor biosynthesis protein MoaC	171504	171954	451	WAG
gene669	molybdopterin synthase small subunit	171955	172323	369	Dayhoff
gene532	molybdopterin guanine dinucleotide biosynthesis protein MoaE	172324	172427	104	Dayhoff
gene906	lipoprotein	172428	172787	360	DCMut
gene388	membrane protein	172788	173149	362	WAG
gene417	tRNA-dihydrouridine synthase C	173150	173464	315	JTT

## Shared genes

gene230	D-alanyl-D-alanine endopeptidase	173465	173652	188	JTT
gene699	beta-D-glucoside glucohydrolase	173653	173828	176	WAG
gene917	ATP-dependent DNA helicase DinG	173829	174318	490	WAG
gene183	glycosyl transferase	174319	174596	278	WAG
gene696	N-acetylmuramoyl-L-alanine amidase amid	174597	175038	442	WAG
gene528	ATP-dependent Clp protease adaptor protein ClpS	175039	175400	362	WAG
gene633	ATP-dependent Clp protease ATP- binding protein	175401	175764	364	LG
gene761	leucyl/phenylalanyl-tRNA--protein transferase	175765	176330	566	WAG
gene25	amino acid ABC transporter permease	176331	176466	136	LG
gene18	thioredoxin reductase	176467	176643	177	Dayhoff
gene14	AsnC family transcriptional regulator	176644	176787	144	JTT
gene305	lipoprotein chaperone	176788	177871	1084	WAG
gene458	recombinase RarA	177872	178192	321	Dayhoff
gene1003	seryl-tRNA synthetase	178193	178344	152	LG
gene188	MFS transporter	178345	178608	264	LG
gene199	3- phosphoserine/phosphohydroxythreo nine aminotransferase	178609	178842	234	JTT
gene73	3-phosphoshikimate 1- carboxyvinyltransferase	178843	178938	96	LG
gene108	cytidylate kinase	178939	179019	81	JTT
gene164	30S ribosomal protein S1	179020	179395	376	WAG
gene222	integration host factor subunit beta	179396	179881	486	LG
gene887	ATP-binding protein	179882	180782	901	WAG
gene343	tetraacyldisaccharide 4-kinase	180783	181041	259	JTT
gene612	hypothetical protein	181042	181686	645	JTT
gene813	3-deoxy-manno-octulosonate cytidyltransferase	181687	182095	409	WAG
gene914	hypothetical protein	182096	182352	257	WAG
gene771	condesin subunit F	182353	182666	314	WAG
gene673	condesin subunit E	182667	183064	398	WAG
gene152	cell division protein MukB	183065	183281	217	LG
gene293	hypothetical protein	183282	183599	318	WAG
gene129	hypothetical protein	183600	183870	271	WAG
gene92	aromatic amino acid aminotransferase	183871	184419	549	WAG
gene976	asparaginyl-tRNA synthetase	184420	184664	245	WAG
gene640	nicotinate phosphoribosyltransferase	184665	184933	269	JTT
gene694	dihydroorotate dehydrogenase	184934	185360	427	WAG
gene649	cell division protein ZapC	185361	185751	391	WAG
gene317	23S rRNA methyltransferase	185752	185952	201	WAG
gene384	ABC transporter ATPase	185953	186208	256	LG
gene399	paraquat-inducible protein B	186209	186437	229	LG
gene674	lipoprotein	186438	186709	272	WAG
gene493	3-hydroxydecanoyl-ACP dehydratase	186710	187221	512	WAG

gene860	Lon protease	187222	187530	309	WAG
gene595	Ter macrodomain organizer mats-binding protein	187531	187964	434	WAG
gene686	membrane protein	187965	188616	652	Dayhoff
gene444	cell division protein	188617	188814	198	WAG
gene517	DNA helicase IV	188815	189115	301	WAG
gene580	sulfur transfer protein TusE	189116	189255	140	LG
gene563	HflBKC-binding inner membrane protein	189256	189778	523	LG
gene910	alanine glycine permease	189779	190641	863	JTT
gene837	excinuclease ABC subunit C	190642	191016	375	LG
gene737	phosphatidylglycerophosphate synthetase	191017	191147	131	JTT
gene550	glucan biosynthesis protein G	191148	191707	560	WAG
gene227	glucosyltransferase	191708	192260	553	LG
gene957	lipid A biosynthesis lauroyl acyltransferase	192261	192532	272	Dayhoff
gene984	sulfurtransferase	192533	192753	221	LG
gene187	lipoprotein	192754	193299	546	LG
gene973	alanine acetyltransferase	193300	193680	381	WAG
gene196	23S rRNA pseudouridylate synthase C	193681	194026	346	WAG
gene918	septum formation protein Maf	194027	194356	330	WAG
gene107	hypothetical protein	194357	194573	217	JTT
gene744	phosphate acyltransferase	194574	194818	245	WAG
gene540	3-oxoacyl-ACP synthase	194819	196325	1507	JTT
gene766	3-ketoacyl-ACP reductase	196326	196612	287	WAG
gene564	acyl carrier protein	196613	197551	939	WAG
gene158	3-oxoacyl-ACP synthase	197552	198231	680	JTT
gene191	aminodeoxychorismate lyase	198232	198735	504	LG
gene522	thymidylate kinase	198736	199060	325	WAG
gene475	DNAse	199061	199472	412	JTT
gene198	purine nucleoside phosphoramidase	199473	199791	319	WAG
gene379	penicillin-binding protein activator LpoB	199792	200008	217	LG
gene873	beta-hexosaminidase	200009	200313	305	JTT
gene402	NADH dehydrogenase	200314	200803	490	WAG
gene966	hypothetical protein	200804	201018	215	Dayhoff
gene745	transcription-repair coupling factor	201019	201276	258	WAG
gene363	outer membrane-specific lipoprotein transporter subunit LolC	201277	201519	243	LG
gene795	peptide ABC transporter ATP-binding protein	201520	201845	326	LG
gene462	transporter	201846	202217	372	LG
gene576	NAD-dependent deacetylase	202218	202630	413	LG
gene941	sensor protein PhoQ	202631	202896	266	WAG
gene714	PhoP family transcriptional regulator	202897	203191	295	LG
gene1026	adenylosuccinate lyase	203192	203624	433	JTT

gene510	tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase	203625	204025	401	WAG
gene504	23S rRNA pseudouridylate synthase	204026	204341	316	LG
gene850	isocitrate dehydrogenase	204342	204633	292	WAG
gene994	membrane protein	204634	205611	978	Dayhoff
gene69	molecular chaperone	205612	205924	313	JTT
gene148	GTP-binding protein YchF	205925	206381	457	WAG
gene590	peptidyl-tRNA hydrolase	206382	206910	529	JTT
gene287	membrane protein	206911	207373	463	JTT
gene637	ribose-phosphate pyrophosphokinase	207374	207693	320	WAG
gene821	kinase	207694	208000	307	LG
gene594	outer membrane lipoprotein LolB	208001	208229	229	WAG
gene999	glutamyl-tRNA reductase	208230	208610	381	WAG
gene503	peptide chain release factor 1	208611	209294	684	LG
gene731	hypothetical protein	209295	209629	335	WAG
gene629	2-dehydro-3-deoxyphosphooctonate aldolase	209630	209932	303	WAG
gene469	sodium:proton antiporter	209933	210248	316	JTT
gene286	transcriptional regulator	210249	210573	325	WAG
gene717	membrane protein	210574	210699	126	LG
gene549	yfeABCD regulator yfeE	210700	211347	648	Dayhoff
gene110	threonyl-tRNA synthetase	211348	211854	507	LG
gene460	translation initiation factor IF-3	211855	211942	88	JTT
gene220	phenylalanyl-tRNA synthetase subunit beta	211943	212345	403	WAG
gene627	integration host factor subunit alpha	212346	212597	252	Dayhoff
gene488	endopeptidase	212598	213010	413	Dayhoff
gene857	hypothetical protein	213011	213384	374	LG
gene368	hypothetical protein	213385	214219	835	LG
gene20	pyruvate kinase	214220	214398	179	LG
gene258	riboflavin synthase subunit alpha	214399	214501	103	LG
gene83	transcriptional regulator	214502	214781	280	WAG
gene923	endopeptidase	214782	215055	274	WAG
gene356	ribonuclease T	215056	215289	234	WAG
gene21	glyoxalase I	215290	215393	104	LG
gene609	outer membrane lipoprotein pcp	215394	215515	122	WAG
gene346	anhydro-N-acetylmuramic acid kinase	215516	215992	477	WAG
gene613	pyridoxamine 5-phosphate oxidase	215993	216199	207	LG
gene943	tyrosyl-tRNA synthetase	216200	216707	508	LG
gene49	pyridoxamine kinase	216708	216935	228	LG
gene50	endonuclease IV	216936	217227	292	WAG
gene944	elongation factor G	217228	217821	594	WAG
gene780	electron transport complex protein RsxA	217822	217935	114	LG
gene909	electron transporter RnfG	217936	218313	378	WAG
gene392	electron transporter RnfB	218314	218720	407	WAG
gene915	electron transport complex RsxE subunit	218721	218855	135	JTT



gene138	DNA replication terminus site-binding protein	218856	219568	713	JTT
gene890	malonic semialdehyde reductase	219569	219851	283	WAG
gene448	hypothetical protein	219852	220084	233	WAG
gene908	membrane protein	220085	220212	128	Dayhoff
gene236	fumarate/nitrate reduction transcriptional regulator	220213	220359	147	LG
gene486	universal stress protein E	220360	220615	256	WAG
gene51	hypothetical protein	220616	220981	366	WAG
gene513	transcriptional regulator	220982	221347	366	WAG
gene1030	sensor protein RstB	221348	221545	198	WAG
gene44	serine protease	221546	221755	210	LG
gene93	azoreductase	221756	221867	112	LG
gene174	hypothetical protein	221868	222107	240	JTT
gene329	hypothetical protein	222108	222467	360	CpREV
gene55	tRNA 2-thiocytidine biosynthesis protein TtcA	222468	223197	730	JTT
gene611	transcriptional regulator	223198	223383	186	LG
gene477	membrane protein	223384	223940	557	Dayhoff
gene774	hypothetical protein	223941	224138	198	Dayhoff
gene38	phage-shock protein	224139	224349	211	Dayhoff
gene439	phage-shock protein	224350	224421	72	JTT
gene263	ABC transporter substrate-binding protein	224422	224532	111	JTT
gene506	peptide ABC transporter permease	224533	224705	173	LG
gene833	peptide ABC transporter permease	224706	224992	287	LG
gene141	peptide ABC transporter ATP-binding protein	224993	225328	336	JTT
gene179	translation initiation factor Sui1	225329	225962	634	JTT
gene413	orotidine 5-phosphate decarboxylase	225963	226271	309	WAG
gene76	tetratricopeptide repeat protein	226272	226496	225	LG
gene89	membrane protein	226497	227112	616	WAG
gene22	phosphatidylglycerophosphatase	227113	227235	123	FLU
gene127	GTP cyclohydrolase II	227236	227674	439	LG
gene650	CysB family transcriptional regulator	227675	228204	530	JTT
gene975	topoisomerase I	228205	228572	368	LG
gene123	peptidase	228573	228743	171	JTT
gene239	oxoacyl-ACP reductase	228744	228943	200	Dayhoff
gene777	23S rRNA pseudouridylate synthase B	228944	229566	623	WAG
gene205	hypothetical protein	229567	229795	229	WAG
gene729	anthranilate phosphoribosyltransferase	229796	230099	304	WAG
gene790	indole-3-glycerol phosphate synthase	230100	230613	514	LG
gene730	tryptophan synthase subunit beta	230614	230881	268	WAG
gene739	tryptophan synthase subunit alpha	230882	231339	458	LG
gene31	membrane protein	231340	231555	216	Dayhoff
gene338	intracellular septation protein A	231556	231693	138	WAG
gene623	hypothetical protein	231694	231972	279	Dayhoff

gene645	cardiolipin synthetase	231973	232262	290	WAG
gene7	dsDNA-mimic protein	232263	232706	444	WAG
gene361	thymidine kinase	232707	232986	280	JTT
gene625	DNA-binding protein	232987	233141	155	LG
gene95	UTP--glucose-1-phosphate uridylyltransferase subunit GalU	233142	233393	252	JTT
gene295	response regulator	233394	233629	236	WAG
gene542	formyltetrahydrofolate deformylase	233630	233847	218	WAG
gene583	exodeoxyribonuclease III	233848	234282	435	WAG
gene66	DNA topoisomerase III	234283	234444	162	WAG
gene889	oxidoreductase	234445	235303	859	LG
gene299	protease	235304	235390	87	LG
gene409	cytoplasmic asparaginase I	235391	235549	159	JTT
gene298	transcriptional regulator	235550	236014	465	LG
gene655	glyceraldehyde-3-phosphate dehydrogenase	236015	236605	591	WAG
gene377	glucose-6-phosphate 1-epimerase	236606	236743	138	JTT
gene525	PrkA family serine protein kinase	236744	237210	467	WAG
gene171	hypothetical protein	237211	237550	340	Dayhoff
gene565	alanine racemase	237551	237903	353	LG
gene128	D-amino acid dehydrogenase small subunit	237904	238067	164	WAG
gene728	SpoVR family protein	238068	238679	612	WAG
gene622	fatty acid metabolism regulator	238680	238998	319	WAG
gene797	hypothetical protein	238999	239183	185	Dayhoff
gene801	hypothetical protein	239184	239614	431	LG
gene6	hypothetical protein	239615	239932	318	WAG
gene254	cell division inhibitor MinD	239933	240033	101	WAG
gene431	cell division topological specificity factor MinE	240034	240147	114	Dayhoff
gene972	ribonuclease D	240148	240386	239	Dayhoff
gene670	membrane protein	240387	240601	215	JTT
gene812	hypothetical protein	240602	240996	395	WAG
gene884	ATP-dependent helicase	240997	241105	109	WAG
gene360	endoribonuclease L-PSP	241106	241369	264	WAG
gene131	hypothetical protein	241370	241601	232	LG
gene113	membrane protein	241602	241850	249	JTT
gene647	23S rRNA methyltransferase	241851	241934	84	JTT
gene124	cold-shock protein	241935	242423	489	JTT
gene35	hypothetical protein	242424	242668	245	JTT
gene320	heat shock protein HtpX	242669	243201	533	LG
gene680	carboxyl-terminal processing protease	243202	243427	226	WAG
gene433	hypothetical protein	243428	243581	154	VT
gene240	hypothetical protein	243582	243835	254	LG
gene229	DNA polymerase III subunit theta	243836	244202	367	Dayhoff
gene749	glucose-6-phosphate 1- dehydrogenase	244203	244602	400	WAG
gene421	pyruvate kinase	244603	244715	113	JTT
gene509	lipid A biosynthesis (KDO)2-(lauroyl)- lipid IVA acyltransferase	244716	244874	159	Dayhoff

gene846	zinc ABC transporter substrate-binding protein	244875	245243	369	WAG
gene591	zinc ABC transporter ATPase	245244	245473	230	JTT
gene681	zinc transporter	245474	245656	183	JTT
gene278	Holliday junction resolvase	245657	245967	311	LG
gene302	hypothetical protein	245968	246124	157	Dayhoff
gene87	dihydroneopterin triphosphate pyrophosphatase	246125	246578	454	LG
gene16	aspartyl-tRNA synthetase	246579	246745	167	Dayhoff
gene1042	hypothetical protein	246746	246918	173	WAG
gene646	rRNA cytosine-C5-methyltransferase	246919	247119	201	WAG
gene118	tRNA methyltransferase	247120	247365	246	JTT
gene947	copper homeostasis protein CutC	247366	247569	204	JTT
gene1008	hypothetical protein	247570	247878	309	LG
gene316	arginyl-tRNA synthetase	247879	248122	244	WAG
gene982	hypothetical protein	248123	248479	357	DCMut
gene282	amino acid ABC transporter permease	248480	248982	503	JTT
gene794	hypothetical protein	248983	249162	180	LG
gene425	exonuclease I	249163	249354	192	LG
gene546	putrescine/spermidine ABC transporter	249355	249690	336	LG
gene217	hypothetical protein	249691	250074	384	WAG
gene13	ATP phosphoribosyltransferase	250075	250517	443	CpREV
gene902	imidazoleglycerol-phosphate dehydratase	250518	250732	215	WAG
gene956	imidazole glycerol phosphate synthase	250733	250953	221	WAG
gene147	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	250954	251428	475	JTT
gene178	imidazole glycerol phosphate synthase	251429	251741	313	LG
gene516	phosphoribosyl-ATP pyrophosphatase	251742	252070	329	WAG
gene533	6-phosphogluconate dehydrogenase	252071	252653	583	WAG
gene940	glucose-1-phosphate thymidyltransferase	252654	252830	177	JTT
gene991	dTDP-glucose 4,6-dehydratase	252831	253444	614	JTT
gene463	UDP-glucose 4-epimerase	253445	254078	634	LG
gene663	UTP--glucose-1-phosphate uridylyltransferase subunit GalU	254079	254371	293	WAG
gene953	tyrosine kinase	254372	254763	392	WAG
gene689	polysaccharide export protein Wza	254764	255129	366	WAG
gene414	deoxycytidine triphosphate deaminase	255130	255224	95	Dayhoff
gene608	uridine/cytidine kinase	255225	255594	370	LG
gene747	multidrug transporter	255595	256066	472	Dayhoff
gene983	transcriptional regulator	256067	256499	433	WAG
gene1016	lipid kinase	256500	256584	85	CpREV
gene703	antiporter	256585	256677	93	JTT

gene436	methionine--tRNA ligase	256678	257273	596	WAG
gene607	malate dehydrogenase	257274	257571	298	WAG
gene992	vancomycin high temperature exclusion protein	257572	257789	218	WAG
gene875	membrane protein	257790	258114	325	WAG
gene407	GTP cyclohydrolase I	258115	258729	615	LG
gene784	S-(hydroxymethyl)glutathione dehydrogenase	258730	259623	894	Dayhoff
gene765	S-formylglutathione hydrolase	259624	260001	378	WAG
gene473	lysine transporter	260002	260398	397	WAG
gene452	transcriptional regulator	260399	260670	272	LG
gene238	endonuclease V	260671	260883	213	JTT
gene960	PTS system fructose-specific transporter subunits IIBC	260884	261242	359	WAG
gene980	1-phosphofructokinase	261243	261451	209	WAG
gene170	PTS fructose transporter subunit IIA	261452	261721	270	WAG
gene688	elongation factor Ts	261722	262378	657	LG
gene311	membrane protein	262379	262826	448	LG
gene289	multidrug transporter	262827	263473	647	WAG
gene223	16S rRNA pseudouridylate synthase	263474	263798	325	WAG
gene710	hypothetical protein	263799	264335	537	WAG
gene395	50S ribosomal protein L25	264336	264512	177	WAG
gene333	nucleoid-associated protein NdpA	264513	265005	493	JTT
gene806	hypothetical protein	265006	265209	204	LG
gene601	membrane protein	265210	265550	341	WAG
gene1011	thiamine biosynthesis lipoprotein	265551	265887	337	WAG
gene274	transcriptional regulator	265888	266193	306	JTT
gene557	DNA gyrase subunit A	266194	266910	717	WAG
gene868	bifunctional 3-demethylubiquinone-9 3-methyltransferase/ 2-octaprenyl-6-hydroxy phenol methylase	266911	268209	1299	WAG
gene881	ribonucleotide-diphosphate reductase subunit alpha	268210	268415	206	Dayhoff
gene585	ribonucleotide-diphosphate reductase subunit beta	268416	269578	1163	JTT
gene54	2Fe-2S ferredoxin	269579	270432	854	WAG
gene370	NADH:ubiquinone oxidoreductase subunit N	270433	270583	151	WAG
gene948	NADH:ubiquinone oxidoreductase subunit M	270584	270922	339	Dayhoff
gene474	NADH:ubiquinone oxidoreductase subunit L	270923	271479	557	WAG
gene186	NADH:ubiquinone oxidoreductase subunit K	271480	271690	211	LG
gene396	NADH:ubiquinone oxidoreductase subunit J	271691	271788	98	Dayhoff
gene993	NADH dehydrogenase subunit I	271789	272266	478	WAG
gene403	NADH:ubiquinone oxidoreductase subunit H	272267	272469	203	WAG
gene72	NADH dehydrogenase subunit F	272470	273171	702	WAG
gene636	NADH dehydrogenase subunit E	273172	273490	319	WAG



gene753	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	273491	273904	414	LG
gene79	NADH dehydrogenase subunit B	273905	274251	347	LG
gene512	transcriptional regulator	274252	274585	334	WAG
gene1028	aminotransferase AlaT	274586	274948	363	WAG
gene855	5-nucleotidase	274949	275154	206	LG
gene538	hypothetical protein	275155	275595	441	JTT
gene954	acetate kinase	275596	275794	199	JTT
gene1039	phosphate acetyltransferase	275795	276148	354	JTT
gene555	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	276149	276529	381	WAG
gene332	amidophosphoribosyltransferase	276530	276893	364	WAG
gene722	cell division protein DedD	276894	277266	373	WAG
gene204	acetyl-CoA carboxylase subunit beta	277267	277623	357	WAG
gene65	membrane protein	277624	277903	280	LG
gene534	tRNA pseudouridine synthase A	277904	278240	337	WAG
gene930	erythronate-4-phosphate dehydrogenase	278241	278530	290	WAG
gene464	3-oxoacyl-ACP synthase	278531	278686	156	JTT
gene741	hypothetical protein	278687	278985	299	LG
gene653	hypothetical protein	278986	279063	78	Dayhoff
gene88	membrane protein	279064	279556	493	WAG
gene964	chorismate synthase	279557	279800	244	JTT
gene189	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	279801	280074	274	WAG
gene552	peptidase S10	280075	280246	172	Dayhoff
gene134	phosphohistidine phosphatase	280247	280484	238	WAG
gene445	membrane protein	280485	280613	129	LG
gene822	manganese transporter	280614	281030	417	LG
gene19	glutamyl-tRNA ligase	281031	281160	130	JTT
gene566	hypothetical protein	281161	281529	369	WAG
gene400	NAD-dependent DNA ligase LigA	281530	281975	446	JTT
gene759	sulfate transporter	281976	282345	370	LG
gene711	cysteine synthase A	282346	282648	303	WAG
gene74	PTS sugar transporter	282649	282886	238	LG
gene85	PTS glucose transporter subunit IIA	282887	283017	131	LG
gene315	cysteine synthase	283018	283824	807	WAG
gene537	sulfate/thiosulfate transporter subunit	283825	284107	283	LG
gene213	sulfate/thiosulfate transporter permease subunit	284108	284290	183	WAG
gene602	sulfate/thiosulfate transporter subunit	284291	284586	296	WAG
gene768	RpoE-regulated lipoprotein	284587	284893	307	WAG
gene743	acetyltransferase	284894	285097	204	WAG
gene841	reductase	285098	285392	295	WAG
gene437	succinyl-diaminopimelate desuccinylase	285393	285504	112	LG
gene231	membrane protein	285505	285829	325	LG

gene376	phosphoribosylaminoimidazole-succinocarboxamide synthase	285830	286404	575	WAG
gene47	lipoprotein	286405	286740	336	Dayhoff
gene705	dihydrodipicolinate synthase	286741	286992	252	WAG
gene260	hypothetical protein	286993	287388	396	WAG
gene99	DNA replication initiation factor	287389	287647	259	WAG
gene60	uracil transporter	287648	287932	285	VT
gene81	uracil phosphoribosyltransferase	287933	288080	148	Dayhoff
gene310	phosphoribosylaminoimidazole synthetase	288081	288414	334	WAG
gene858	phosphoribosylglycinamide formyltransferase	288415	288830	416	WAG
gene495	polyphosphate kinase	288831	289105	275	Dayhoff
gene9	exopolyphosphatase	289106	289244	139	LG
gene84	tellurite resistance protein TehB	289245	289699	455	WAG
gene104	GMP synthase	289700	290046	347	JTT
gene103	inosine 5-monophosphate dehydrogenase	290047	290778	732	LG
gene876	ribosome-associated GTPase EngA	290779	290937	159	LG
gene386	membrane biogenesis protein	290938	291204	267	WAG
gene382	membrane protein	291205	291450	246	JTT
gene165	histidyl-tRNA synthetase	291451	291867	417	LG
gene892	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	291868	292143	276	JTT
gene874	50S rRNA methyltransferase	292144	292382	239	JTT
gene430	nucleoside diphosphate kinase	292383	293175	793	JTT
gene412	3-mercaptopyruvate sulfurtransferase	293176	293809	634	WAG
gene603	enhanced serine sensitivity protein SseB	293810	294035	226	WAG
gene925	aminopeptidase B	294036	294580	545	LG
gene454	cysteine desulfurase	294581	294764	184	WAG
gene869	transcriptional regulator	294765	295324	560	WAG
gene82	tRNA (cytidine/uridine-2-O)-methyltransferase	295325	295609	285	WAG
gene879	serine hydroxymethyltransferase	295610	295801	192	JTT
gene321	nitrogen regulatory protein P-II	295802	296389	588	WAG
gene708	phosphoribosylformylglycinamide synthase	296390	296526	137	WAG
gene90	membrane protein	296527	296838	312	WAG
gene52	hypothetical protein	296839	297037	199	LG
gene776	4-phosphopantetheinyl transferase	297038	297282	245	WAG
gene489	DNA repair protein RecO	297283	297670	388	Dayhoff
gene181	GTPase Era	297671	298299	629	WAG
gene971	ribonuclease III	298300	298551	252	WAG
gene75	signal peptidase	298552	298663	112	JTT
gene11	SoxR reducing system protein RseC	298664	298992	329	LG
gene212	anti-sigma E factor	298993	299456	464	WAG
gene586	anti-RNA polymerase sigma factor SigE	299457	299856	400	WAG
gene659	RNA polymerase sigma factor AlgU	299857	299967	111	Dayhoff
gene58	SAM-dependent methyltransferase	299968	300566	599	WAG

gene354	co-chaperone GrpE	300567	300882	316	WAG
gene465	recombination and repair protein	300883	301066	184	JTT
gene214	outer membrane biogenesis protein BamE	301067	301225	159	LG
gene962	hypothetical protein	301226	301638	413	JTT
gene1004	hypothetical protein	301639	301774	136	JTT
gene114	single-stranded DNA-binding protein	301775	302030	256	WAG
gene648	protein lysine acetyltransferase	302031	302128	98	JTT
gene112	phosphatidylserine synthase	302129	302390	262	WAG
gene757	protein disaggregation chaperone	302391	302650	260	JTT
gene117	hypothetical protein	302651	302953	303	WAG
gene284	23S rRNA pseudouridine synthase D	302954	303103	150	WAG
gene606	outer membrane biogenesis protein BamD	303104	303377	274	JTT
gene466	cold-shock protein	303378	303721	344	LG
gene17	bifunctional chorismate mutase/prephenate dehydratase	303722	303838	117	CpREV
gene501	T-protein	303839	304135	297	WAG
gene521	phospho-2-dehydro-3-deoxyheptonate aldolase	304136	304756	621	WAG
gene888	50S ribosomal protein L19	304757	305209	453	LG
gene492	tRNA (guanine-N1)-methyltransferase	305210	305353	144	WAG
gene456	16S rRNA-processing protein M	305354	305423	70	DCMut
gene818	signal recognition particle protein	305424	305761	338	WAG
gene783	membrane protein	305762	305978	217	JTT
gene823	S-ribosylhomocysteinase	305979	306452	474	Dayhoff
gene491	glutamate--cysteine ligase	306453	306684	232	JTT
gene256	carbon storage regulator	306685	307110	426	LG
gene1009	RecX family transcriptional regulator	307111	307560	450	WAG
gene97	recombinase RecA	307561	307868	308	JTT
gene331	hypothetical protein	307869	308297	429	LG
gene867	hypothetical protein	308298	308442	145	JTT
gene326	murein hydrolase B	308443	308570	128	LG
gene1019	DNA mismatch repair protein MutS	308571	308720	150	WAG
gene713	peptidase	308721	308825	105	JTT
gene33	protein-L-isoaspartate O-methyltransferase	308826	308949	124	JTT
gene987	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	308950	309580	631	LG
gene5	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	309581	309754	174	JTT
gene605	cell division protein FtsB	309755	310115	361	LG
gene415	adenylylsulfate kinase	310116	310625	510	WAG
gene324	sulfate adenylyltransferase subunit 1	310626	310777	152	Dayhoff
gene785	sulfate adenylyltransferase subunit 2	310778	311026	249	WAG
gene153	phosphoadenosine phosphosulfate reductase	311027	311364	338	JTT

gene871	sulfite reductase subunit beta	311365	311494	130	WAG
gene4	sulfite reductase subunit alpha	311495	311876	382	WAG
gene1025	6-carboxy-5,6,7,8-tetrahydropterin synthase	311877	312215	339	LG
gene1000	coenzyme PQQ biosynthesis protein	312216	312320	105	LG
gene514	enolase	312321	313091	771	WAG
gene146	CTP synthase	313092	313440	349	LG
gene614	nucleoside triphosphate hydrolase	313441	314235	795	Dayhoff
gene280	flavodoxin	314236	315198	963	Dayhoff
gene604	tRNA pseudouridine synthase C	315199	315670	472	Dayhoff
gene261	secretion protein	315671	316174	504	LG
gene1044	7-cyano-7-deazaguanine reductase	316175	316521	347	WAG
gene264	LOG family protein	316522	316744	223	JTT
gene161	endonuclease	316745	316854	110	Dayhoff
gene275	23S rRNA methyltransferase	316855	317047	193	WAG
gene905	transcriptional regulator	317048	317237	190	WAG
gene621	hypothetical protein	317238	317631	394	WAG
gene208	N-acetylglutamate synthase	317632	318064	433	WAG
gene965	thymidylate synthase	318065	318383	319	WAG
gene235	prolipoprotein diacylglyceryl transferase	318384	318769	386	WAG
gene479	phosphoenolpyruvate-protein phosphotransferase	318770	318970	201	WAG
gene742	RNA pyrophosphohydrolase	318971	319325	355	WAG
gene94	DNA mismatch repair protein	319326	319693	368	WAG
gene3	diaminopimelate decarboxylase	319694	319852	159	JTT
gene362	lysyl-tRNA synthetase	319853	320137	285	JTT
gene539	ssDNA exonuclease RecJ	320138	320384	247	Dayhoff
gene387	protein disulfide isomerase II DsbC	320385	320659	275	JTT
gene755	tyrosine recombinase XerD	320660	320918	259	LG
gene1038	flavodoxin FldB	320919	321364	446	JTT
gene162	global regulator	321365	321783	419	LG
gene185	glycine dehydrogenase	321784	322043	260	LG
gene772	glycine cleavage system protein H	322044	322455	412	Dayhoff
gene978	glycine cleavage system aminomethyltransferase T	322456	322744	289	WAG
gene259	oxidoreductase	322745	322829	85	CpREV
gene782	2-octaprenyl-6-methoxyphenyl hydroxylase	322830	323185	356	WAG
gene125	hypothetical protein	323186	323509	324	WAG
gene482	3-phosphoglycerate dehydrogenase	323510	323944	435	WAG
gene895	ribose 5-phosphate isomerase A	323945	324317	373	WAG
gene244	hypothetical protein	324318	324799	482	JTT
gene575	arginine exporter protein	324800	324879	80	WAG
gene763	mechanosensitive channel MscS	324880	325290	411	LG
gene292	fructose-bisphosphate aldolase	325291	325529	239	JTT
gene912	arginine decarboxylase	325530	325738	209	JTT
gene939	S-adenosylmethionine synthetase	325739	326487	749	JTT
gene29	hypothetical protein	326488	326587	100	JTT

gene685	16S rRNA methyltransferase	326588	326863	276	WAG
gene182	glutathione synthetase	326864	327187	324	JTT
gene524	hypothetical protein	327188	327392	205	LG
gene369	Holliday junction resolvase	327393	327733	341	WAG
gene865	hypothetical protein	327734	328005	272	WAG
gene658	hypothetical protein	328006	328336	331	JTT
gene949	HemN family oxidoreductase	328337	329318	982	WAG
gene243	hypothetical protein	329319	329502	184	JTT
gene560	tRNA (guanine-N(7)-methyltransferase	329503	329982	480	WAG
gene353	adenine glycosylase	329983	330222	240	WAG
gene619	oxidative damage protection protein	330223	330695	473	WAG
gene551	murein transglycosylase	330696	330895	200	JTT
gene34	purine nucleoside phosphorylase	330896	330990	95	WAG
gene442	phosphopentomutase	330991	331408	418	WAG
gene194	deoxyribose-phosphate aldolase	331409	331619	211	WAG
gene309	deoxyribonuclease	331620	331900	281	WAG
gene1043	periplasmic protein	331901	332061	161	JTT
gene536	biopolymer transporter ExbD	332062	332313	252	WAG
gene371	biopolymer transporter ExbB	332314	332575	262	LG
gene195	cystathionine beta-lyase	332576	332760	185	WAG
gene652	membrane protein	332761	333249	489	LG
gene883	1-acyl-sn-glycerol-3-phosphate acyltransferase	333250	333367	118	Dayhoff
gene932	DNA topoisomerase IV subunit A	333368	333662	295	Dayhoff
gene169	DNA topoisomerase IV subunit B	333663	334067	405	JTT
gene639	esterase	334068	334171	104	JTT
gene894	3,5-cyclic-nucleotide phosphodiesterase	334172	334648	477	LG
gene810	outer membrane channel protein	334649	334873	225	LG
gene318	hypothetical protein	334874	335345	472	WAG
gene130	3,4-dihydroxy-2-butanone 4-phosphate synthase	335346	335400	55	LG
gene814	heptose 1-phosphate adenylyltransferase	335401	335506	106	WAG
gene26	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	335507	335739	233	HIVb
gene1006	adenylate cyclase	335740	335932	193	LG
gene391	hypothetical protein	335933	336352	420	JTT
gene64	dihydroneopterin triphosphate 2-epimerase	336353	336619	267	LG
gene121	RNA polymerase sigma factor RpoD	336620	336910	291	JTT
gene787	23S rRNA methyltransferase	336911	337286	376	WAG
gene266	membrane protein	337287	337732	446	WAG
gene666	membrane protein	337733	338633	901	WAG
gene480	membrane protein	338634	338754	121	LG
gene484	membrane protein	338755	338870	116	LG
gene37	hypothetical protein	338871	338970	100	LG
gene574	DnaA initiator-associating protein DiaA	338971	339214	244	Dayhoff



gene587	outer membrane lipoprotein	339215	339450	236	WAG
gene979	pirin	339451	339738	288	WAG
gene950	LysR family transcripitolnal regulator	339739	339868	130	WAG
gene677	peptidase PmbA	339869	339966	98	LG
gene958	hypothetical protein	339967	340184	218	LG
gene42	fructose-1,6-bisphosphatase	340185	340264	80	JTT
gene529	inorganic pyrophosphatase	340265	340693	429	WAG
gene478	translocation and assembly module TamB	340694	340845	152	WAG
gene792	membrane protein	340846	340945	100	MtREV
gene577	membrane protein	340946	341288	343	WAG
gene140	hypothetical protein	341289	341868	580	LG
gene916	3-5-bisphosphate nucleotidase	341869	342075	207	WAG
gene798	peptidyl-prolyl cis-trans isomerase	342076	342678	603	LG
gene80	50S ribosomal protein L9	342679	343088	410	WAG
gene57	30S ribosomal protein S18	343089	343384	296	Dayhoff
gene928	30S ribosomal protein S6	343385	343650	266	WAG
gene232	23S rRNA (guanosine-2-O-)-methyltransferase	343651	344051	401	JTT
gene122	exoribonuclease R	344052	344390	339	JTT
gene836	adenylosuccinate synthetase	344391	344542	152	WAG
gene294	cell division protein FtsH	344543	344973	431	WAG
gene861	cell division protein FtsH	344974	345254	281	WAG
gene419	GTPase HflX	345255	345713	459	LG
gene929	tRNA delta(2)-isopentenylpyrophosphate transferase	345714	345946	233	WAG
gene692	ADP-binding protein	345947	346249	303	WAG
gene389	oligoribonuclease	346250	346784	535	WAG
gene62	GTPase RsgA	346785	347045	261	WAG
gene270	phosphatidylserine decarboxylase	347046	347202	157	JTT
gene63	protease TldD	347203	347401	199	LG
gene936	hypothetical protein	347402	347853	452	WAG
gene271	ribonuclease G	347854	348175	322	WAG
gene937	septum formation protein Maf	348176	348505	330	Dayhoff
gene288	rod shape-determining protein MreD	348506	349060	555	JTT
gene418	rod shape-determining protein MreC	349061	349234	174	LG
gene870	rod shape-determining protein Mbl	349235	349478	244	WAG
gene800	TMAO/DMSO reductase	349479	349814	336	JTT
gene455	sulfite oxidase subunit YedZ	349815	350277	463	WAG
gene599	3-dehydroquinate dehydratase	350278	350475	198	LG
gene690	acetyl-CoA carboxylase biotin carboxyl carrier protein	350476	350571	96	Dayhoff
gene864	methionine ABC transporter ATP-binding protein	350572	350738	167	Dayhoff

**Supplementary Table S3. Genome inferred reactions conserved in the respective genera**

Reaction	Gene/Enzyme	<i>Pantoea</i>	<i>Tatumella</i>	<i>Mixta</i>	<i>Erwinia</i>
Butyryl-[acp] + NAD+ <=> But-2-enoyl-[acyl-	FASN (fabK)	+	+	+	-
UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine + H2O <=> UDP-3-O-(3-hydroxytetradecanoyl)-D-glucosamine + Acetate	lpxC	+	+	+	-
ATP + D-Gluconic acid <=> ADP + 6-Phospho-D-gluconate	gntK	+	+	+	-
D-Gluconic acid + NADP+ <=> 2-Keto-D-gluconic acid + NADPH + H+	gluconate 2-dehydrogenase (alpha chain) - E1.1.99.3A	+	+	+	-
ATP + D-Mannose <=> ADP + D-Mannose 6-phosphate	HK (hexokinase) (manX)	+	+	+	-
D-Mannose 6-phosphate <=> beta-D-Fructose 6-phosphate	manA	+	+	+	-
L-Alanine + 3-Oxopropanoate <=> Pyruvate + beta-Alanine	ABAT	+	+	+	-
beta-Alanine + 2-Oxoglutarate <=> 3-Oxopropanoate + L-Glutamate	ABAT	+	+	+	-
ATP + H2O + H+in = ADP + phosphate +	ATPF1B (atpD)	+	+	+	-
Thymidine + Orthophosphate <=> Thymine + 2-Deoxy-D-ribose 1-phosphate	deoA	+	+	+	-
ATP + acetate + CoA = AMP + diphosphate + acetyl-CoA	ACSS (acs)	+	+	+	-
L-Aspartate <=> N-Acetyl-L-aspartate	NAT8L	+	+	+	-
L-Aspartate <=> Fumarate + Ammonia	aspA	+	+	+	-
quinol + 2 ferricytochrome c = quinone + 2 ferrocycytochrome c + 2 H+	fbcH	+	+	+	-
Succinate semialdehyde <=> Succinate	gabD	+	+	+	-
an acyl-[acyl-carrier protein] + NADP+ = a trans-2,3-dehydroacyl-[acyl-carrier protein] + NADPH + H+	fabI	+	+	+	-
Betaine aldehyde + NAD+ + H2O <=> Betaine + NADH + 2 H+	betB	+	+	+	-
(S)-Allantoin + H2O <=> Allantoate	allB	+	+	+	-
Adenosine + H2O <=> Inosine + Ammonia	add	+	+	+	-
NAD+ + Glycine + Sulfur donor <=> ADP-5-ethyl-4-methylthiazole-2-carboxylate + Nicotinamide + 3 H2O	THI4, THI1	+	+	+	-
Reduced FMN + NAD+ <=> FMN + NADH + H+	hpaC	+	+	+	-
Succinyl-CoA + L-Arginine <=> CoA + N2-Succinyl-L-arginine	astA	+	+	+	-
N2-Succinyl-L-arginine + 2 H2O <=> N2-Succinyl-L-ornithine + CO2 + 2 Ammonia	astB	+	+	+	-

Nicotinamide + H2O <=> Nicotinate + Ammonia	PNC1	+	+	+	-
4-(Cytidine 5'-diphospho)-2-C-methyl-D-erythritol + ATP <=> 2-Phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol + ADP	ispE	+	+	-	+
5-Carboxyamino-1-(5-phospho-D-ribosyl)imidazole <=> 1-(5-Phospho-D-ribosyl)-5-amino-4-imidazolecarboxylate	purE	+	+	-	+
3-Amino-2-oxopropyl phosphate + 1-Deoxy-D-xylulose 5-phosphate <=> Pyridoxine phosphate + Orthophosphate + 2 H2O	pdxJ	+	+	-	+
Putrescine + Oxygen + H2O <=> 4-Aminobutyraldehyde + Ammonia + Hydrogen peroxide	AOC1	+	+	-	+
Biuret + H2O <=> Urea-1-carboxylate + Ammonia	atzE	+	+	-	-
N-Succinyl-L-glutamate + H2O <=> L-Glutamate + Succinate	astE	+	+	-	-
L-Glutamate <=> 4-Aminobutanoate + CO2	gadB	+	+	-	-
L-1-Pyrroline-3-hydroxy-5-carboxylate + NADP+ + 2 H2O <=> L-erythro-4-Hydroxyglutamate + NADPH + H+	E 1.2.1.88	+	+	-	-
(S)-1-Pyrroline-5-carboxylate + NADP+ + 2 H2O <=> L-Glutamate + NADPH + H+	E 1.2.1.88	+	+	-	-
cis-2-Chloro-4-carboxymethylenebut-2-en-1,4-olide + H2O <=> 2-Chloromaleylacetate	E 3.1.1.45	+	-	+	+
4-Fluoromuconolactone + H2O <=> 2-Maleylacetate + Hydrofluoric acid	E 3.1.1.45	+	-	+	+
(S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+	MDH1	+	-	+	+
beta-D-Fructose 6-phosphate + D-Glyceraldehyde 3-phosphate <=> D-Erythrose 4-phosphate + D-Xylulose 5-phosphate	tktA, tktB	+	-	+	+
2-Dehydro-3-deoxy-6-phospho-D-galactonate <=> Pyruvate + D-Glyceraldehyde 3-phosphate	dgoA	+	-	+	+
Sedoheptulose 7-phosphate + D-Glyceraldehyde 3-phosphate <=> D-Ribose 5-phosphate + D-Xylulose 5-phosphate	tktA, tktB	+	-	+	+
L-Aspartate <=> beta-Alanine + CO2	panD	+	-	+	+
L-Selenocysteine + Reduced acceptor <=> Hydrogen selenide + L-Alanine + Acceptor	SCLY	+	-	+	+

2,5-Dichloro-carboxymethylenebut-2-en-4-olide + H2O <=> 2,5-Dichloro-4-oxohex-2-enedioate	E 3.1.1.45	+	-	+	+
S-Adenosyl-L-methionine + Malonyl-[acyl-carrier protein] <=> S-Adenosyl-L-homocysteine + Malonyl-[acp] methyl ester	bioC	+	-	+	+
Dethiobiotin + Sulfur donor + 2 S-Adenosyl-L-methionine + 2 e- + 2 H+ <=> Biotin + 2 L-Methionine + 2 5'-Deoxyadenosine	bioB	+	-	+	+
L-Lysine + 8-Amino-7-oxononanoate <=> L-2-Amino adipate 6-semialdehyde + 7,8-Diaminononanoate	bioA	+	-	+	+
Acyl-[acyl-carrier protein] + S-Adenosyl-L-methionine <=> Acyl-carrier protein + 5'-Methylthioadenosine + N-Acyl-L-homoserine lactone	lasI	+	-	+	+
Aminoimidazole ribotide + S-Adenosyl-L-methionine <=> 4-Amino-2-methyl-5-(phosphoxymethyl)pyrimidine + 5'-Deoxyadenosine + L-Methionine + Formate + CO	thiC	+	-	+	+
ATP + 4-Amino-2-methyl-5-(phosphoxymethyl)pyrimidine <=> ADP + 4-Amino-5-hydroxymethyl-2-methylpyrimidine diphosphate	THI20	+	-	+	+
ATP + 4-Amino-5-hydroxymethyl-2-methylpyrimidine <=> ADP + 4-Amino-2-methyl-5-(phosphoxymethyl)pyrimidine	THI20	+	-	+	+
4-Amino-5-hydroxymethyl-2-methylpyrimidine diphosphate + 4-Methyl-5-(2-phosphoxyethyl)thiazole <=> Diphosphate + Thiamin monophosphate	thiE	+	-	+	+
4-Amino-5-hydroxymethyl-2-methylpyrimidine diphosphate + 2-(2-Carboxy-4-methylthiazol-5-yl)ethyl phosphate <=> Thiamin monophosphate + Diphosphate + CO2	thiE	+	-	+	+
ATP + Nicotinamide-beta-riboside <=> ADP + Nicotinamide D-ribonucleotide	NRK1_2	+	-	+	+
OPC4-CoA + Acetyl-CoA <=> CoA + 3-Oxo-OPC6-CoA	fadA	+	-	+	-
OPC6-CoA + Acetyl-CoA <=> CoA + 3-Oxo-OPC8-CoA	fadA	+	-	+	-
OPC6-CoA + Acetyl-CoA <=> CoA + 3-Oxo-OPC8-CoA	fadA	+	-	+	-

(3S)-3-Hydroxyacyl-CoA + NAD+ $\rightleftharpoons$ 3-Oxoacyl-CoA + NADH + H+	HADH (3-hydroxyacyl-CoA dehydrogenase)	+	-	+	-
(3S)-3-Hydroxyadipyl-CoA + NAD+ $\rightleftharpoons$ 3-Oxoadipyl-CoA + NADH + H+	HADH (3-hydroxyacyl-CoA dehydrogenase)	+	-	+	-
(3S)-3-Hydroxyacyl-CoA $\rightleftharpoons$ trans-2,3-Dehydroacyl-CoA + H <sub>2</sub> O	echA (enoyl-CoA hydratase)	+	-	+	-
5-Carboxy-2-pentenoyl-CoA + H <sub>2</sub> O $\rightleftharpoons$ (3S)-3-Hydroxyadipyl-CoA	echA (enoyl-CoA hydratase)	+	-	+	-
Acyl-CoA + Oxygen $\rightleftharpoons$ trans-2,3-Dehydroacyl-CoA + Hydrogen peroxide	ACOX1/3 (E 1.3.3.5)	+	-	+	-
2 Acetyl-CoA $\rightleftharpoons$ CoA + Acetoacetyl-CoA	atoB	+	-	+	-
ATP + Long-chain carboxylate + CoA $\rightleftharpoons$ AMP + Diphosphate + Acyl-CoA	fadD	+	-	+	-
Sedoheptulose 7-phosphate + D-Glyceraldehyde 3-phosphate $\rightleftharpoons$ D-Ribose 5-phosphate + D-Xylulose 5-phosphate	tktA, tktB	+	-	+	-
Starch + n H <sub>2</sub> O $\rightleftharpoons$ (n+1) Maltodextrin	treX	+	-	+	-
Maltodextrin $\rightleftharpoons$ 1-alpha-D-[(1->4)-alpha-D-Glucosyl](n-1)-alpha-D-glucopyranoside	treY	+	-	+	-
Starch + Orthophosphate $\rightleftharpoons$ Amylose + D-Glucose 1-phosphate	glgP	+	-	+	-
ADP-glucose + D-Glucose 1-phosphate $\rightleftharpoons$ ADP + alpha-Maltose 1-phosphate	glgM	+	-	+	-
ADP-glucose + D-Glucose $\rightleftharpoons$ alpha,alpha-Trehalose + ADP	treT	+	-	+	-
2-Dehydro-3-deoxy-6-phospho-D-gluconate $\rightleftharpoons$ D-Glyceraldehyde 3-phosphate + Pyruvate	eda	+	-	+	-
myo-Inositol $\rightleftharpoons$ 2,4,6/3,5-Pentahydroxycyclohexanone $\rightleftharpoons$ 3D-3,5/4-Trihydroxycyclohexane-1,2-dione $\rightleftharpoons$ 5-Deoxy-D-gluconate $\rightleftharpoons$ 2-Deoxy-5-keto-D-gluconic acid $\rightleftharpoons$ 2-Deoxy-5-keto-D-gluconic acid 6-phosphate	iolB,C,D,E,G	+	-	+	-
3-Oxopropanoate + CoA $\rightleftharpoons$ Acetyl-CoA + CO <sub>2</sub>	mmsA (iolA)	+	-	+	-
2-methyl-3-oxopropanoate + CoA + H <sub>2</sub> O = propanoyl-CoA + HCO <sub>3</sub> <sup>-</sup>	mmsA (iolA)	+	-	+	-
3-Hydroxypropionyl-CoA $\rightleftharpoons$ Propenoyl-CoA + H <sub>2</sub> O	paaf (echA)	+	-	+	-
(2S,3S)-3-Hydroxy-2-methylbutanoyl-CoA + NAD+ $\rightleftharpoons$ 2-Methylacetoacetyl-CoA + NADH + H+	HADH	+	-	+	-
(2S,3S)-3-Hydroxy-2-methylbutanoyl-CoA $\rightleftharpoons$ 2-Methylbut-2-enoyl-CoA + H <sub>2</sub> O	paaf (echA)	+	-	+	-



Propanoyl-CoA + Acetyl-CoA $\rightleftharpoons$ CoA + 2-Methylacetoacetyl-CoA	fadA	+	-	+	-
L-Lysine $\rightleftharpoons$ Cadaverine + CO <sub>2</sub>	ldcC (E 4.1.1.18)	+	-	+	-
N-Succinyl-L-glutamate 5-semialdehyde + NAD <sup>+</sup> + H <sub>2</sub> O $\rightleftharpoons$ N-Succinyl-L-glutamate + NADH + H <sup>+</sup>	astD	+	-	+	-
Cob(I)yrinate a,c diamide + ATP $\rightleftharpoons$ Adenosyl cobyryinate a,c diamide + Triphosphate	MMAB (pduO)	+	-	+	-
ATP + Cob(I)alamin $\rightleftharpoons$ Triphosphate + Cobamide coenzyme	MMAB (pduO)	+	-	+	-
N <sup>2</sup> -Succinyl-L-ornithine + 2-Oxoglutarate $\rightleftharpoons$ N-Succinyl-L-glutamate 5-semialdehyde + L-Glutamate	astC	+	-	+	-
ATP + L-Glutamate + Putrescine $\rightleftharpoons$ ADP + Orthophosphate + gamma-L-Glutamylputrescine	puuA	+	-	+	-
gamma-L-Glutamylputrescine + H <sub>2</sub> O + Oxygen $\rightleftharpoons$ gamma-Glutamyl-gamma-aminobutyraldehyde + Ammonia + Hydrogen peroxide	puuB	+	-	+	-
D-Glucose 1-phosphate $\rightleftharpoons$ alpha-D-Glucose 6-phosphate	pgm (phosphoglucomutase)	+	-	-	+
D-Glycerate + ATP $\rightleftharpoons$ 2-Phospho-D-glycerate + ADP	gck	+	-	-	+
alpha,alpha'-Trehalose 6-phosphate + H <sub>2</sub> O $\rightleftharpoons$ alpha,alpha'-Trehalose + Orthophosphate	otsB	+	-	-	-
ATP + L-Ribulose $\rightleftharpoons$ ADP + L-Ribulose 5-phosphate	araB	+	-	-	-
Aminoacrylate + H <sub>2</sub> O $\rightleftharpoons$ 3-Oxopropanoate + Ammonia	rutD	+	-	-	-
(Z)-3-Peroxyaminoacrylate $\rightleftharpoons$ Aminoacrylate	rutC	+	-	-	-
(S)-Malate + CoA $\rightleftharpoons$ Acetyl-CoA + H <sub>2</sub> O + Glyoxylate	aceB	+	-	-	-
4-Aminobutanoate + Acetate $\rightleftharpoons$ 4-Acetamidobutanoate + H <sub>2</sub> O	E 3.5.1.63	+	-	-	-
4-Coumaryl alcohol $\rightleftharpoons$ p-Hydroxyphenyl lignin	E 1.11.1.7	+	-	-	-
4-(L-gamma-Glutamylamino)butanoate + H <sub>2</sub> O $\rightleftharpoons$ 4-Aminobutanoate + L-Glutamate	puuD	+	-	-	-
Malonyl-CoA + Acyl-carrier protein $\rightleftharpoons$ CoA + Malonyl-[acyl-carrier protein]	FASN (fabD)	-	+	+	+

D-glycero-beta-D-manno-Heptose 1,7-bisphosphate + H <sub>2</sub> O $\rightleftharpoons$ D-glycero-beta-D-manno-Heptose 1-phosphate + Orthophosphate	gmhB	-	+	+	+
ATP + Aminoimidazole ribotide + HCO <sub>3</sub> <sup>-</sup> $\rightleftharpoons$ ADP + Orthophosphate + 5-Carboxyamino-1-(5-phospho-D-ribosyl)imidazole	purK	-	+	+	+
alpha-D-Glucose $\rightleftharpoons$ alpha-D-Glucose 6-phosphate	HK (hexokinase)	-	+	+	+
ATP + 3-Phospho-D-glycerate $\rightleftharpoons$ ADP + 3-Phospho-D-glyceroyl phosphate	PGK	-	+	+	+
(S)-Dihydroorotate + H <sub>2</sub> O $\rightleftharpoons$ N-Carbamoyl-L-aspartate	CAD	-	+	+	+
S-Adenosylmethioninamine + Spermidine $\rightleftharpoons$ 5'-Methylthioadenosine + Spermine	speE	-	+	+	+
S-Adenosyl-L-methionine + H <sup>+</sup> $\rightleftharpoons$ S-Adenosylmethioninamine + CO <sub>2</sub>	speD	-	+	+	+
S-Adenosylmethioninamine + Putrescine $\rightleftharpoons$ 5'-Methylthioadenosine + Spermidine	speE	-	+	+	+
L-Histidinol phosphate + 2-Oxoglutarate $\rightleftharpoons$ 3-(Imidazol-4-yl)-2-oxopropyl phosphate + L-Glutamate	hisC	-	+	+	+
ATP + Dihydropteroate + L-Glutamate $\rightleftharpoons$ ADP + Orthophosphate + Dihydrofolate	FPGS	-	+	+	+
2-Amino-7,8-dihydro-4-hydroxy-6-(diphosphooxymethyl)pteridine + 4-Aminobenzoate $\rightleftharpoons$ Diphosphate + Dihydropteroate	FOL1	-	+	+	+
Fe-coproporphyrin III + 2 H <sup>+</sup> $\rightleftharpoons$ Coproporphyrin III + Fe <sup>2+</sup>	hemH	-	+	+	+
Carbamoyl phosphate + L-Ornithine $\rightleftharpoons$ Orthophosphate + L-Citrulline	OTC	-	+	+	+
5'-Methylthioadenosine + H <sub>2</sub> O $\rightleftharpoons$ 5'-S-Methyl-5'-thioinosine + Ammonia	mtaD	-	+	+	+
Spermidine + Oxygen + H <sub>2</sub> O $\rightleftharpoons$ 1,3-Diaminopropane + 4-Aminobutyraldehyde + Hydrogen peroxide	MPAO	-	+	+	+
CTP $\rightleftharpoons$ dCTP	rtpR	-	+	+	-
D-Erythrose 4-phosphate + NAD <sup>+</sup> + H <sub>2</sub> O $\rightleftharpoons$ 4-Phospho-D-erythronate + NADH + H <sup>+</sup>	epd	-	+	+	-
ATP + N-Acetyl-D-glucosamine $\rightleftharpoons$ ADP + N-Acetyl-D-glucosamine 6-phosphate	NAGK	-	+	+	-
Propanoyl-CoA $\rightleftharpoons$ Propenoyl-CoA	ACADM (acd)	-	+	+	-
D-Glycerate $\rightleftharpoons$ Hydroxypyruvate	gyaR	-	+	+	-

Glycolate <=> Glyoxylate	gyaR	-	+	+	-
Nicotinate D-ribonucleotide + Diphosphate + CO2 <=> Quinolinate + 5-Phospho-alpha-D-ribose 1-diphosphate	nadC	-	+	+	-
Succinyl-CoA + NADPH + H+ <=> Succinate semialdehyde + NADP+ + CoA	sucD	-	+	+	-
Biotin sulfoxide + NADPH + H+ <=> Biotin + NADP+ + H2O	bisC	-	+	+	-
2,3-Diketo-5-methylthiopentyl-1-phosphate + H2O <=> 1,2-Dihydroxy-5-(methylthio)pent-1-en-3-one + Orthophosphate	mtnC	-	+	+	-
1,2-Dihydroxy-5-(methylthio)pent-1-en-3-one + Oxygen <=> 3-(Methylthio)propanoate + Formate + CO	mtnD	-	+	+	-
1,2-Dihydroxy-5-(methylthio)pent-1-en-3-one + Oxygen <=> 4-Methylthio-2-oxobutanoic acid + Formate	mtnD	-	+	+	-
S-Methyl-5-thio-D-ribulose 1-phosphate <=> 2,3-Diketo-5-methylthiopentyl-1-phosphate + H2O	mtnB	-	+	+	-
L-Allothreonine <=> Glycine + Acetaldehyde	ltaE	-	+	+	-
5-Hydroxyisourate + H2O <=> 5-Hydroxy-2-oxo-4-ureido-2,5-dihydro-1H-imidazole-5-carboxylate	uraH	-	+	+	-
Urate + Oxygen + H2O <=> 5-Hydroxyisourate + Hydrogen peroxide	uaZ	-	+	+	-
1,4-Dihydroxy-2-naphthoyl-CoA + H2O <=> 1,4-Dihydroxy-2-naphthoate + CoA	E 3.1.2.28 (menI)	-	+	+	-
trans-Cinnamate + Oxygen + NADPH + H+ <=> 4-Coumarate + NADP+ + H2O	CYP73A	-	+	+	-
Guanine + H2O <=> Xanthine + Ammonia	guaD	-	+	+	-
UDP-2,3-bis(3-hydroxytetradecanoyl)glucosamine + Lipid X <=> UDP + Lipid A disaccharide	lpxB	-	+	-	+
Orotidine 5'-phosphate + Diphosphate <=> Orotate + 5-Phospho-alpha-D-ribose 1-diphosphate	UMPS (uridine onophosphate synthetase)	-	+	-	+
L-Histidinal + H2O + NAD+ <=> L-Histidine + NADH + H+	hisD	-	+	-	+
L-Histidinol + NAD+ <=> L-Histidinal + NADH + H+	hisD	-	+	-	+
Choline + Oxygen <=> Betaine aldehyde + Hydrogen peroxide	betA	-	+	-	+
Adenylated molybdopterin + Molybdate <=> Molybdoenzyme molybdenum cofactor + AMP + H2O	moeA	-	+	-	+

2,5-Diamino-6-(5-phospho-D-ribose)pyrimidin-4(3H)-one + H2O $\rightleftharpoons$ 5-Amino-6-(5'-phosphoribosylamino)uracil + Ammonia	ribD1	-	+	-	+
5-Amino-6-(5'-phospho-D-ribitylamino)uracil + NADP+ $\rightleftharpoons$ 5-Amino-6-(5'-phosphoribosylamino)uracil + NADPH + H+	ribD2	-	+	-	+
Phosphatidylglycerol + Diglycosyldiacylglycerol $\rightleftharpoons$ 1,2-Diacyl-sn-glycerol + Glycerophosphoglycolipid	mdoB	-	+	-	-
Pectate + H2O $\rightleftharpoons$ Digalacturonate + Pectate	polygalacturonase (E 3.2.1.15)	-	+	-	-
Pectate + H2O $\rightleftharpoons$ D-Galacturonate + Pectate	polygalacturonase (E 3.2.1.15)	-	+	-	-
Sucrose + H2O $\rightleftharpoons$ D-Fructose + D-Glucose	MGAM (malZ)	-	+	-	-
ATP + Glycerone $\rightleftharpoons$ ADP + Glycerone phosphate	DAK (triose/dihydroxy acetone kinase/FAD-AMP lyase)	-	+	-	-
D-Arabitol + NADP+ $\rightleftharpoons$ D-Xylulose + NADPH + H+	dalD	-	+	-	-
(R)-3-Ureidoisobutyrate + H2O $\rightleftharpoons$ (R)-3-Amino-2-methylpropanoate + CO2 + Ammonia	UPB1 (pydC)	-	+	-	-
Glutaminyl-tRNA + L-Glutamate + Orthophosphate + ADP $\rightleftharpoons$ L-Glutamyl-tRNA(Gln) + L-Glutamine + ATP + H2O	gatA	-	+	-	-
5-Hydroxy-2-oxo-4-ureido-2,5-dihydro-1H-imidazole-5-carboxylate $\rightleftharpoons$ (S)-Allantoin + CO2	PRHOXNB	-	+	-	-
gamma-Glutamyl-gamma-aminobutyraldehyde + NADP+ + H2O $\rightleftharpoons$ 4-(L-gamma-Glutamylamino)butanoate + NADPH + H+	puuC	-	+	-	-
Formate + NAD+ $\rightleftharpoons$ H+ + CO2 + NADH	FDH	-	-	+	-
(S)-Malate + NAD+ $\rightleftharpoons$ Pyruvate + CO2 + NADH + H+	MDH (E 1.1.1.39)	-	-	+	-
D-Galacturonate $\rightleftharpoons$ D-Tagaturonate	uxaC	-	-	+	-
L-Gulonate + NAD+ $\rightleftharpoons$ D-Fructuronate + NADH + H+	rspB	-	-	+	-
D-Tagaturonate $\rightleftharpoons$ D-Fructuronate	uxaE	-	-	+	-
D-Glucuronate $\rightleftharpoons$ D-Fructuronate	uxaC	-	-	+	-
D-Mannonate + NAD+ $\rightleftharpoons$ D-Fructuronate + NADH + H+	uxuB	-	-	+	-
D-Mannonate $\rightleftharpoons$ 2-Dehydro-3-deoxy-D-gluconate + H2O	uxuA	-	-	+	-

D-Altronate $\rightleftharpoons$ 2-Dehydro-3-deoxy-D-gluconate + H <sub>2</sub> O	uxaA	-	-	+	-
L-Galactono-1,4-lactone + Oxygen $\rightleftharpoons$ Ascorbate + Hydrogen peroxide	GLDH	-	-	+	-
1-alpha-D-[(1->4)-alpha-D-Glucosyl](n-1)-alpha-D-glucopyranoside + H <sub>2</sub> O $\rightleftharpoons$ alpha,alpha-Trehalose + Maltodextrin	treZ	-	-	+	-
UDP-glucose + Cellulose $\rightleftharpoons$ UDP + Cellulose	bcsA	-	-	+	-
Amylose $\rightleftharpoons$ Starch	glgB	-	-	+	-
ADP-glucose + Amylose $\rightleftharpoons$ ADP + Amylose	glgA	-	-	+	-
alpha-D-Glucose $\rightleftharpoons$ D-Fructose	xylA	-	-	+	-
L-Ribulose 5-phosphate $\rightleftharpoons$ D-Xylulose 5-phosphate	araD	-	-	+	+
L-Arabinose $\rightleftharpoons$ L-Ribulose	araA	-	-	+	-
ATP + 2-Dehydro-3-deoxy-D-gluconate $\rightleftharpoons$ ADP + 2-Dehydro-3-deoxy-6-phospho-D-gluconate	kdgK	-	-	+	-
Protein N(pi)-phospho-L-histidine + Ascorbate $\rightleftharpoons$ Protein histidine + L-Ascorbate 6-phosphate	ulaC	-	-	+	-
L-Histidine $\rightleftharpoons$ Urocanate + Ammonia	hutH	-	-	+	-
4-Imidazolone-5-propanoate $\rightleftharpoons$ Urocanate + H <sub>2</sub> O	hutU	-	-	+	-
4-Imidazolone-5-propanoate + H <sub>2</sub> O $\rightleftharpoons$ N-Formimino-L-glutamate	hutI	-	-	+	-
N-Formimino-L-glutamate + H <sub>2</sub> O $\rightleftharpoons$ L-Glutamate + Formamide	hutG	-	-	+	-
D-Xylulose 5-phosphate + Orthophosphate $\rightleftharpoons$ Acetyl phosphate + D-Glyceraldehyde 3-phosphate + H <sub>2</sub> O	xfp	-	-	+	-
D-Glycerate $\rightleftharpoons$ 2-Hydroxy-3-oxopropanoate	garR	-	-	+	-
L-Aspartate + H <sub>2</sub> O + Oxygen $\rightleftharpoons$ Oxaloacetate + Ammonia + Hydrogen peroxide	nadB	-	-	+	-
Quinolinate + 2 H <sub>2</sub> O + Orthophosphate $\rightleftharpoons$ Iminoaspartate + Glycerone phosphate	nadA	-	-	+	-
Acetyl-CoA + Putrescine $\rightleftharpoons$ CoA + N-Acetylputrescine	speG	-	-	+	-
Indolepyruvate $\rightleftharpoons$ Indole-3-acetaldehyde + CO <sub>2</sub>	ipdC	-	-	+	-
2-Succinylbenzoyl-CoA $\rightleftharpoons$ 1,4-Dihydroxy-2-naphthoyl-CoA + H <sub>2</sub> O	menB	-	-	+	-
1,4-Dihydroxy-2-naphthoate + all-trans-Octaprenyl diphosphate $\rightleftharpoons$ 2-Demethylmenaquinone + Diphosphate + CO <sub>2</sub>	menA	-	-	+	-



1,4-Dihydroxy-2-naphthoate + Phytyl diphosphate $\rightleftharpoons$ 2-Phytyl-1,4-naphthoquinone + CO <sub>2</sub> + Diphosphate	menA	-	-	+	-
L-Tyrosine + S-Adenosyl-L-methionine + Reduced acceptor $\rightleftharpoons$ Iminoglycine + 4-Cresol + 5'-Deoxyadenosine + L-Methionine + Acceptor	thiH	-	-	+	-
Hypoxanthine $\rightleftharpoons$ Xanthine	XDH	-	-	+	-
7,8-Dihydroneopterin 3'-triphosphate + 3 H <sub>2</sub> O $\rightleftharpoons$ 2-Amino-4-hydroxy-6-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine + 3 Orthophosphate	phoA,phoB	-	-	+	-
Sulfur-carrier protein + ATP $\rightleftharpoons$ Adenylyl-[sulfur-carrier protein] + Diphosphate	thiF	-	-	+	-
Dextrin + H <sub>2</sub> O $\rightleftharpoons$ D-Glucose + Dextrin	MGAM (susB)	-	-	-	+
Pimeloyl-[acyl-carrier protein] + L-Alanine $\rightleftharpoons$ 8-Amino-7-oxononanoate + Acyl-carrier protein + CO <sub>2</sub>	bioF	-	-	-	+
6-Carboxyhexanoyl-CoA + L-Alanine $\rightleftharpoons$ 8-Amino-7-oxononanoate + CoA + CO <sub>2</sub>	bioF	-	-	-	+

+ Present

- Absent















