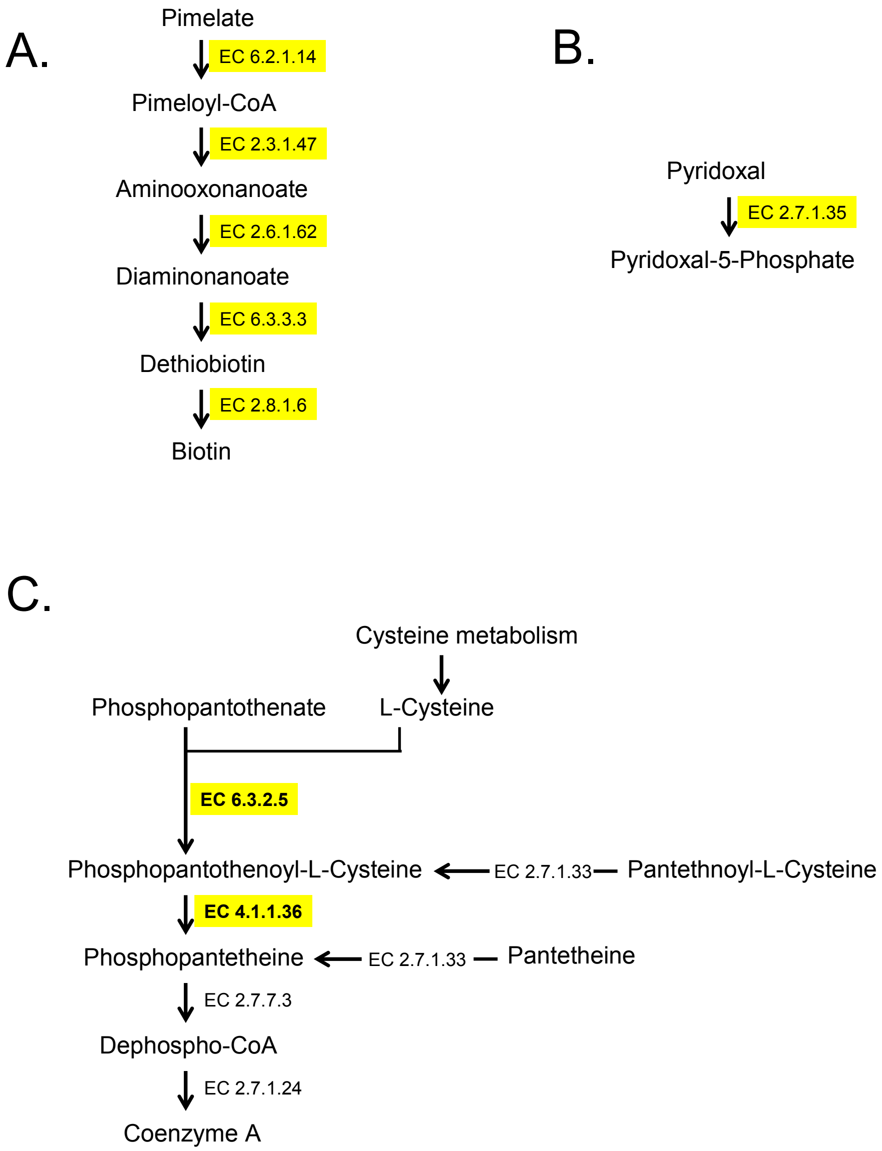
Supplementary Figure 1



Supplementary Tables 1-4:

T. primitia genes up in coculture

Gene Annotation	TREPR #	Start	End	Pure Culture	Co Culture	Ratio
NAD-reducing hydrogenase subunit HoxE (EC 1.12.1.2)	3286	874002	874493	183.30	2230.55	12.17
1.12.7.2)	3288	870374	872107	80.78	864.46	10.70
NAD-reducing hydrogenase subunit HoxF (EC 1.12.1.2)	3287	872126	874009	97.19	1030.81	10.61
carboxylesterase type B	1338	2968291	2969916	263.38	1929.71	7.33
Methionine biosynthesis and transport regulator MtaR, LysR family	3284	874786	875715	26.91	161.26	5.99
L-arabinose-binding periplasmic protein precursor araF (TC 3.A.1.2.2)	3001	1166292	1167440	669.45	4007.11	5.99
4.1.3.27)	382	3961274	3962782	10.61	62.94	5.93
Transcriptional regulator, MerR family	3853	321299	321640	8.80	51.85	5.89
para-nitrobenzyl esterase (intracellular esterase B)	1337	2970016	2971620	337.28	1963.68	5.82
hypothetical protein	3536	631219	631452	17.17	87.86	5.12
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	3283	875727	877490	39.14	194.76	4.98
hypothetical protein	3282	877487	878695	47.19	229.54	4.86
Methylcobalamin:coenzyme M methyltransferase, methylamine-specific	2998	1170460	1171461	37.96	183.13	4.82
Prephenate and/or arogenate dehydrogenase (unknown specificity)	3227	927783	928649	117.78	495.34	4.21
Tryptophan synthase beta chain like (EC 4.2.1.20)	456	3882792	3884171	151.56	624.16	4.12
Carboxylesterase, type B precursor	1599	2692216	2693931	362.10	1452.99	4.01
L-arabinose transport system permease protein (TC 3.A.1.2.2)	2999	1169115	1170308	52.41	199.05	3.80
hypothetical protein		537570	537692	15.87	59.08	3.72
Conserved domain protein	3310	849023	849433	17.07	61.28	3.59
L-arabinose transport ATP-binding protein araG (TC 3.A.1.2.2)	3000	1167547	1169073	105.37	333.36	3.16
2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta	3226	928662	929687	155.12	486.58	3.14
RNA polymerase sigma factor RpoD	3818	354130	355032	29.93	93.88	3.14
Spermidine Putrescine ABC transporter permease component potB	568	3757692	3758525	26.41	78.19	2.96
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	384	3959654	3960709	23.70	69.68	2.94
hypothetical protein	1822	2428503	2428907	17.33	50.67	2.92
Branched-chain amino acid transport ATP-binding protein livG	435	3902047	3902817	31.17	90.63	2.91
Phosphoribosylanthranilate isomerase (EC 5.3.1.24)		3958024	3958767	49.80	134.00	2.69
Phosphoglycerate mutase family	2955	1219843	1220697	26.93	71.91	2.67
ClpB protein	638	3685111	3687729	29.43	78.25	2.66
Two-component response regulator yvqC	3518	648537	649157	19.35	51.03	2.64
Cytidine deaminase (EC 3.5.4.5)	1802	2450915	2451313	25.13	65.46	2.61
Pyrimidine ABC transporter, substrate-binding component	427	3908904	3909986	26.80	69.66	2.60
hypothetical protein		3530451	3530573	65.57	160.17	2.44
ABC transporter, periplasmic spermidine putrescine-bind protein potD	570	3755719	3756759	336.54	807.92	2.40
Homolog of plant auxin-responsive GH3-like protein	1121	3194547	3196250	28.84	67.91	2.35
Heat shock protein 60 family chaperone GroEL	596	3728822	3730468	1335.42	3105.94	2.33
Lysine 2,3-aminomutase (EC 5.4.3.2)	566	3759958	3761019	32.99	76.30	2.31
Acetoin utilization protein AcuB	1127	3189210	3189854	66.77	153.16	2.29
Endoribonuclease L-PSP	2961	1215000	1215377	47.75	108.60	2.27
Cell division transporter, ATP-binding protein ftsE (TC 3.A.5.1.1)		2861251	2861931	27.94	62.95	2.25
Glutamine transport ATP-binding protein glnQ (TC 3.A.1.3.2)	953	3376499	3377248	38.04	84.71	2.23
Chaperone protein HtpG	3196	957207	959114	142.63	315.70	2.21
Hypothetical protein YaeJ with similarity to translation release factor	1030	3290592	3291017	44.71	98.52	2.20

Methyltransferase small	1456	2830844	2832103	47.66	104.95	2.20
Kynurenine formamidase, bacterial (EC 3.5.1.9)	3197	956537	957205	32.93	72.43	2.20
Branched-chain amino acid ABC transporter, amino acid-binding protein	432	3904910	3906109	236.03	516.86	2.19
Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)	3147	1018648	1019817	57.49	125.63	2.19
4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	3620	539625	539942	192.43	416.82	2.17
hypothetical protein	2494	1708273	1709193	36.96	79.90	2.16
Uncharacterized protein TP_0983 precursor	459	3881265	3881951	24.78	52.90	2.13
Cell division protein	3138	1027529	1028272	410.50	862.87	2.10
hypothetical protein	694	3622768	3622908	171.43	352.26	2.05
hypothetical protein	766	3546689	3548152	24.61	50.25	2.04

T. primitia genes up in pure culture

Gene Annotation	**TREPR #**	**Start**	**End**	**Pure Culture**	**Co Culture**	**Ratio**
Formate dehydrogenase chain D (EC 1.2.1.2)	3093	1070856	1071467	62.19	1.52	40.84
hypothetical protein	3096	1068556	1068936	286.84	7.35	39.05
Formate dehydrogenase chain D (EC 1.2.1.2)	3097	1067822	1068559	398.91	21.46	18.59
Electron transport protein hydN	3098	1067277	1067795	1100.39	59.28	18.56
Formate dehydrogenase H (EC 1.2.1.2); selenocysteine-containing	3099	1065082	1067280	601.46	33.44	17.98
DNA polymerase III alpha subunit (EC 2.7.7.7)	3289	869227	869886	95.60	5.65	16.93
hypothetical protein	3290	1569215	1569355	107.14	6.65	16.12
hypothetical protein	2615	868868	869035	269.46	16.72	16.12
1.12.7.2)	3094	1069499	1070863	494.87	31.38	15.77
Fe-S-cluster-containing hydrogenase components 2	3095	1068951	1069496	552.29	39.27	14.06
hypothetical protein		668548	668670	90.16	7.63	11.82
hypothetical protein		78581	78751	58.82	5.47	10.75
Periplasmic binding protein precursor	3273	885955	887037	697.78	77.40	9.02
hypothetical protein		3272279	3272416	58.39	6.79	8.60
hypothetical protein	3847	325023	325166	104.90	13.01	8.06
hypothetical protein		1335569	1335694	56.00	7.44	7.52
Transport system permease protein precursor	3272	887030	888097	359.89	47.96	7.50
Ubiquinone biosynthesis SAM-dependent O-methyltransferase	3278	881732	882385	1356.81	183.82	7.38
hypothetical protein		881534	881680	226.03	31.87	7.09
Cobalamin biosynthesis protein CbiG	522	3809375	3810166	99.87	15.29	6.53
hypothetical protein	3558	609833	610060	52.86	8.20	6.45
Formylmethanofuran dehydrogenase subunit E	3274	885421	885945	692.75	111.87	6.19
Periplasmic binding protein precursor	3277	882407	883468	1388.31	256.96	5.40
2.1.1.133)	521	3810163	3810915	98.40	19.80	4.97
hypothetical protein	763	3550294	3550488	231.96	47.96	4.84
hypothetical protein	438	3900273	3900569	60.81	12.57	4.84
Phage-related protein	774	3542127	3542432	72.13	15.25	4.73
Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	531	3800567	3801205	235.11	51.05	4.61
Cobalt-precorrin-6 synthase, anaerobic	520	3810912	3812117	131.12	28.57	4.59
hypothetical protein	3033	1134458	1134580	98.36	22.88	4.30
Ferric siderophore transport system, periplasmic binding protein TonB	519	3812121	3812810	136.43	33.76	4.04
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	1325	2985738	2986022	52.82	13.11	4.03
Iron(III) dicitrate transport system permease protein fecD (TC 3.A.1.14.1)	3276	883461	884558	506.84	127.23	3.98
Cobyrinic acid A,C-diamide synthase	526	3805166	3806659	97.12	24.93	3.90
Vitamin B12 ABC transporter, ATPase component BtuD	3275	884552	885319	447.20	116.46	3.84
Glycosyl transferase, family 2	2389	1836405	1837325	54.35	14.16	3.84

Cobalt-precorrin-6x reductase (EC 1.3.1.54)		3807912	3808658	95.17	24.95	3.82
Sirohydrochlorin cobaltochelatase CbiK (EC 4.99.1.3)	516	3815334	3816242	286.34	75.83	3.78
TonB-dependent receptor; Outer membrane receptor for ferrienterochelin	518	3812807	3814774	82.87	22.23	3.73
hypothetical protein		3796685	3796810	328.00	89.33	3.67
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	3268	891497	892330	429.77	122.88	3.50
hypothetical protein		3335858	3336019	80.75	23.12	3.49
hypothetical protein	990	1407341	1407556	60.47	17.31	3.49
ABC-type cobalamin/Fe3+-siderophores transport systems	3271	888094	888861	232.07	69.15	3.36
hypothetical protein		2258891	2259022	213.74	63.93	3.34
hypothetical protein		3542927	3543043	51.72	16.04	3.22
Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	530	3801205	3801708	105.37	33.30	3.16
Cobalt-precorrin-3b C17-methyltransferase	523	3808651	3809382	80.71	26.73	3.02
hypothetical protein	2720	3796129	3796686	879.71	292.35	3.01
hypothetical protein	536	1462944	1463141	71.07	23.62	3.01
Dipeptide-binding ABC transporter, periplasmic substrate-binding comp.	3270	888911	890509	1202.75	406.44	2.96
DNA-damage-inducible protein J	1440	2845993	2846259	82.71	27.98	2.96
Helix-turn-helix domain protein	1430	2857398	2857748	62.86	21.27	2.96
Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-)	525	3806656	3807915	76.25	25.87	2.95
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	3269	890514	891500	775.86	265.18	2.93
Dipeptide transport ATP-binding protein dppF (TC 3.A.1.5.2)	3266	893251	893922	697.47	242.68	2.87
hypothetical protein		3409480	3409626	54.79	19.12	2.87
hypothetical protein		4041243	4041416	260.12	91.44	2.84
Virulence associated protein B	605	3721600	3721875	105.45	37.22	2.83
hypothetical protein	3503	662654	662770	181.03	64.17	2.82
hypothetical protein	646	3676334	3677143	80.35	28.75	2.79
L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	528	3803164	3804219	60.66	22.05	2.75
hypothetical protein	361	3984083	3984316	98.71	35.94	2.75
hypothetical protein		3285304	3285438	149.25	55.55	2.69
hypothetical protein	2251	2786862	2787296	357.14	132.93	2.69
hypothetical protein	1516	1987378	1987521	139.86	52.06	2.69
hypothetical protein	3880	291840	292043	349.75	132.93	2.63
Transcriptional regulator, ArsR family	2793	1376031	1376321	134.48	51.34	2.62
D,D-heptose 7-phosphate kinase	2396	1828711	1829745	51.26	19.80	2.59
Plasmid maintenance system killer	3322	836035	836316	110.32	43.05	2.56
PAP2 family protein	419	3918046	3918837	68.27	27.06	2.52
Vitamin B12 ABC transporter, permease component BtuC	532	3799488	3800570	51.76	20.64	2.51
predicted protein	3281	879668	880534	83.14	33.31	2.50
carboxylesterase type B		3895004	3895147	468.53	188.70	2.48
hypothetical protein	2778	1402807	1403109	99.34	40.05	2.48
L-2-haloalkanoic acid dehalogenase	1977	2284492	2285262	77.92	31.42	2.48
Dephospho-CoA kinase (EC 2.7.1.24)	3267	1028278	1028919	308.89	124.84	2.47
Dipeptide transport ATP-binding protein dppD (TC 3.A.1.5.2)	3137	892335	893267	531.12	214.65	2.47
Multi antimicrobial extrusion protein (Na(+)/drug antiporter)	1569	2731914	2733287	56.81	23.04	2.47
hypothetical protein		78818	79132	130.57	53.34	2.45
Uncharacterized protein TP_0753	1731	2532485	2532817	75.30	30.83	2.44
hypothetical protein		2815446	2815541	3336.84	1381.06	2.42
hypothetical protein	2440	1770337	1770753	74.52	31.31	2.38

predicted metal-dependent hydrolase	1688	2573507	2573977	195.74	85.13	2.30
dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	202	75026	75928	89.80	39.20	2.29
hypothetical protein	3516	649678	649911	218.88	95.85	2.28
Transcription antitermination protein NusG	2355	1875071	1875613	302.58	135.63	2.23
Outer membrane vitamin B12 receptor BtuB	537	3794074	3796101	192.40	86.30	2.23
1.2.7.7)	3422	732798	733028	1052.17	473.34	2.22
hypothetical protein	328	4015961	4016398	70.94	31.94	2.22
Ubiquinone biosynthesis SAM-dependent O-methyltransferase		4015438	4015665	105.73	49.19	2.15
hypothetical protein	751	3558743	3558886	139.86	65.07	2.15
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase)	3471	1883010	1883387	137.93	64.17	2.15
hypothetical protein	2347	690256	690429	115.61	53.79	2.15
Amino acid transporter	3564	603721	605130	1449.25	674.93	2.15
Core component NikM of nickel ECF transporter	3292	867358	868365	283.02	132.14	2.14
hypothetical protein		345083	345220	284.67	135.84	2.10
hypothetical protein	3218	937348	937512	225.61	107.80	2.09
hypothetical protein	2805	1366237	1366476	405.86	194.67	2.08
Uroporphyrinogen-III decarboxylase	514	3817849	3818976	106.48	51.19	2.08
hypothetical protein		1500570	1500749	324.02	155.95	2.08
Nitrogenase iron protein (EC 1.18.6.1)	541	3789166	3791367	112.22	54.54	2.06
Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	543	3787352	3787882	126.42	61.45	2.06
hypothetical protein		4017052	4017225	121.39	59.16	2.05
Serine phosphatase RsbU, regulator of sigma subunit		2011343	2011795	92.92	45.29	2.05
Phosphinothricin N-acetyltransferase	2912	1274940	1275449	82.51	40.22	2.05
hypothetical protein		178749	178934	91.89	45.27	2.03
COG0523: Putative GTPases (G3E family)		2735711	2736307	78.86	39.03	2.02
Cobyric acid synthase	529	3801705	3803180	109.15	54.25	2.01

T. azotonutricium genes up in coculture

Gene Annotation	TREAZ #	Start	End	Pure Culture	Co Culture	Ratio
ABC transporter substrate-binding protein - sugar transport	1577	794228	795781	38.31	547.65	14.29
putative membrane protein	1575	798115	799464	6.67	75.06	11.25
hypothetical protein	558	1917883	1917996	8.85	79.65	9.00
hypothetical protein	1576	795901	798039	23.85	203.11	8.51
Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)	1574	799701	800621	23.37	100.27	4.29
maltose/maltodextrin transport permease	1578	793317	794204	22.55	88.78	3.94
hypothetical protein	3021	3171453	3172115	224.32	832.70	3.71
hypothetical protein	2253	92597	92782	59.46	206.76	3.48
hypothetical protein	2447	3750238	3750360	16.39	55.33	3.38
HtrA protease/chaperone protein	3421	2764903	2766411	1613.73	5425.07	3.36
Ferredoxin	2914	3274324	3275586	494.06	1565.37	3.17
Collagen binding protein Cna	714	1767659	1769179	163.16	513.65	3.15
Collagen binding protein Cna	1765	593572	595089	152.93	468.69	3.06
LSU ribosomal protein L6p (L9e)	2666	3537428	3537967	709.65	2149.81	3.03
Uncharacterized protein TP_0214	2678	3531176	3531397	622.17	1802.04	2.90
hypothetical protein		2751730	2751873	27.97	78.67	2.81
LSU ribosomal protein L24p (L26e)	2662	3539135	3539461	960.12	2622.70	2.73
hypothetical protein		1303994	1304119	20.00	54.00	2.70
hypothetical protein	1930	437899	438171	82.72	223.35	2.70

hypothetical protein	1138	3503057	3503263	97.09	262.14	2.70
SSU ribosomal protein S21p	1214	1201828	1202001	526.01	1417.63	2.70
LSU ribosomal protein L17p	2676	3531398	3531856	1042.58	2775.66	2.66
LSU ribosomal protein L14p (L23e)	2661	3539471	3539842	394.88	1024.93	2.60
SSU ribosomal protein S17p (S11e)	2660	3539858	3540130	900.74	2332.72	2.59
hypothetical protein	1105	1349558	1349728	20.59	52.94	2.57
SSU ribosomal protein S19p (S15e)	2655	3541887	3542168	485.77	1249.11	2.57
SSU ribosomal protein S8p (S15Ae)	2665	3537980	3538378	468.19	1190.84	2.54
hypothetical protein	1690	681256	682269	131.29	333.17	2.54
hypothetical protein	2359	3836956	3837180	35.71	90.40	2.53
Preprotein translocase secY subunit (TC 3.A.5.1.1)	2671	3534522	3535850	335.36	839.91	2.50
hypothetical protein	3420	2763773	2764906	301.85	754.63	2.50
SSU ribosomal protein S14p (S29e)	2664	3538388	3538573	505.46	1241.80	2.46
hypothetical protein	629	1855804	1856811	166.34	406.65	2.44
DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)	2675	3531846	3532901	849.13	2073.74	2.44
LSU ribosomal protein L22p (L17e)	2656	3541507	3541875	720.11	1754.76	2.44
Phosphomannomutase (EC 5.4.2.8) / Phosphoglucosamine mutase (EC 5.4.2.10)	254	2220429	2222225	104.12	250.56	2.41
3-isopropylmalate dehydrogenase (EC 1.1.1.85)	3029	3161729	3162880	162.47	390.96	2.41
LSU ribosomal protein L5p (L11e)	2663	3538584	3539135	954.63	2294.92	2.40
Recombination inhibitory protein MutS2	3464	2718721	2719116	315.19	751.90	2.39
Outer membrane protein H precursor	551	1928159	1928686	304.55	717.27	2.36
LSU ribosomal protein L2p (L8e)	2654	3542180	3543007	1026.60	2415.96	2.35
hypothetical protein	1691	680503	681153	774.62	1810.38	2.34
LSU ribosomal protein L29p (L35e)	2659	3540134	3540361	1171.81	2735.68	2.33
SSU ribosomal protein S5p (S2e)		3536467	3537048	1213.43	2823.15	2.33
LSU ribosomal protein L16p (L10e)	2658	3540371	3540796	862.35	1990.59	2.31
LSU ribosomal protein L18p (L5e)	2667	3537057	3537419	864.64	1995.17	2.31
LSU ribosomal protein L3p (L3e)	2651	3544001	3544636	788.19	1782.28	2.26
precursor	552	1925611	1928148	383.72	867.36	2.26
SSU ribosomal protein S11p (S14e)	2673	3533563	3533946	1214.10	2743.47	2.26
Dihydroxy-acid dehydratase (EC 4.2.1.9)	3030	3160069	3161727	131.18	294.48	2.24
DNA mismatch repair protein MutS	550	1928727	1931381	133.76	299.27	2.24
COG0779: clustered with transcription termination protein NusA	547	1934486	1934980	175.10	391.70	2.24
Serine protease precursor MucD/AlgY associated with sigma factor RpoE	3508	2677520	2679364	220.99	491.73	2.23
Transcription termination protein NusB	3447	2736466	2736933	240.90	534.80	2.22
SSU ribosomal protein S7p (S5e)	2647	3546788	3547258	975.53	2163.83	2.22
LSU ribosomal protein L23p (L23Ae)	2653	3543014	3543301	611.50	1348.43	2.21
Plasmid maintenance system antidote protein, XRE family	2077	292355	292777	2131.52	4697.27	2.20
Uncharacterized protein TP_0374	3507	2679377	2681053	391.11	861.87	2.20
LSU ribosomal protein L4p (L1e)	2652	3543298	3543996	1344.56	2962.39	2.20
LSU ribosomal protein L34p	2143	223628	223783	619.35	1364.52	2.20
Flagellar hook-basal body complex protein fliE	892	1568194	1568502	152.60	336.04	2.20
hypothetical protein	626	1858949	1859245	128.38	281.25	2.19
Cell division protein ftsQ	904	1556017	1556835	56.85	123.78	2.18
Transcriptional regulator, DeoR family	1971	400460	401221	219.45	476.02	2.17
Transcription antitermination protein NusG	1288	1114129	1114686	468.58	1009.87	2.16
COG1801: Uncharacterized conserved protein	1049	1409475	1410308	93.64	201.04	2.15
SSU ribosomal protein S3p (S3e)	2657	3540799	3541506	1106.53	2358.66	2.13
hypothetical protein	2292	51148	52395	81.40	173.22	2.13

Acetolactate synthase large subunit (EC 2.2.1.6)	3031	3158316	3160067	159.05	337.95	2.12
YidD	2141	224180	224398	160.55	340.60	2.12
tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)	2468	3729183	3729983	171.25	362.81	2.12
Ribosome recycling factor	619	1865960	1866514	562.27	1189.98	2.12
SSU ribosomal protein S4p (S9e)	2674	3532911	3533546	829.62	1748.41	2.11
hypothetical protein	1275	1130118	1131407	4907.29	10307.41	2.10
Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	620	1865238	1865948	260.56	545.07	2.09
2-isopropylmalate synthase (EC 2.3.3.13)	3027	3164497	3166035	280.56	580.79	2.07
2.7.7.6)	1283	1117146	1120781	497.37	1028.91	2.07
Preprotein translocase subunit YajC (TC 3.A.5.1.1)	3376	2804757	2805155	413.32	853.64	2.07
hypothetical protein	3157	3025153	3025599	105.38	216.93	2.06
hypothetical protein	615	1869218	1869424	169.90	349.51	2.06
hypothetical protein	1060	1399684	1399899	25.58	52.33	2.05
Endoribonuclease L-PSP	572	1902509	1902895	174.87	355.57	2.03
cell division protein FtsL, putative	908	1552063	1552338	274.55	556.36	2.03
2-isopropylmalate synthase (EC 2.3.3.13)	3448	3162892	3164493	127.15	257.47	2.03
Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8)	3028	2735423	2736463	548.08	1109.86	2.03
SSU ribosomal protein S10p (S20e)	2650	3544761	3545165	2334.59	4719.92	2.02
Methyl-accepting chemotaxis protein	1310	1094976	1095431	179.12	360.99	2.02
2.7.7.6)	1282	1120792	1125546	545.80	1093.02	2.00
LSU ribosomal protein L7/L12 (L23e)	1284	1116613	1116993	1002.63	2007.24	2.00
hypothetical protein	252	2222249	2222650	132.17	263.72	2.00
Glycerol-3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94)	963	1500264	1501625	224.11	444.34	1.98

T. azotonutricium genes up in pure culture

Gene Annotation	TREAZ #	Start	End	Pure Culture	Co Culture	Ratio
hypothetical protein	791	2215870	2216097	77.09	0.00	#DIV/0!
hypothetical protein	262	1688613	1688729	77.59	0.00	#DIV/0!
hypothetical protein	2728	3720529	3720648	63.03	0.00	#DIV/0!
hypothetical protein	2483	3464837	3465133	59.12	0.00	#DIV/0!
FeMo cofactor biosynthesis protein NifB	1489	896526	897446	58.15	2.45	23.78
Transmembrane component of general energizing module of ECF transporters	444	2038340	2038981	78.78	3.51	22.44
Sulfate-binding protein sbp	1737	631985	633055	228.04	10.51	21.69
hypothetical protein	1093	1366629	1366850	214.95	10.51	20.44
Aspartate carbamoyltransferase regulatory chain (pyrI)	2117	250702	251148	304.93	25.22	12.09
hypothetical protein	2343	3851733	3852158	55.29	5.29	10.44
Aspartate carbamoyltransferase (EC 2.1.3.2)	2116	251161	252084	297.40	29.25	10.17
Maltose/maltodextrin ABC transporter, permease protein MalG	2114	252627	253481	52.69	5.27	10.00
Nicotinamide-nucleotide adenylyltransferase, NadR family (EC 2.7.7.1) / Ribosylnicotinamide kinase (EC 2.7.1.22)		1662636	1663007	59.30	6.06	9.78
ATPase component CbiO of energizing module of cobalt ECF transporter	445	2037595	2038347	202.79	20.94	9.68
Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor	447	2035955	2036974	447.01	50.79	8.80
Mlc, transcriptional repressor of MalT (the transcriptional activator of maltose regulon) and manXYZ operon	2081	288645	289799	50.26	5.85	8.59
hypothetical protein	1418	967746	967916	97.06	13.24	7.33
hypothetical protein	2610	3593260	3593469	76.56	10.77	7.11
Transposase		1891141	1891443	51.32	7.45	6.89
hypothetical protein	523	1962257	1962655	1070.35	158.29	6.76

ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1484	899596	900666	56.07	8.41	6.67
D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	527	1959307	1959813	205.53	31.13	6.60
Dihydroorotase (EC 3.5.2.3)	2118	249418	250695	180.89	28.19	6.42
Core component BioY of biotin ECF transporter	446	2037027	2037605	141.00	23.36	6.04
hypothetical protein	2745	3448277	3448525	54.44	9.07	6.00
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	2881	3308376	3309554	2071.73	353.35	5.86
RTX toxin, putative	522	1962657	1964027	1202.92	205.29	5.86
hypothetical protein	1148	1292431	1292628	65.99	11.42	5.78
Cysteine synthase (EC 2.5.1.47)	1486	898388	899338	94.21	16.58	5.68
Zinc ABC transporter, inner membrane permease protein ZnuB	526	1959915	1960754	343.27	61.68	5.57
Sulfate and thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)	1734	634751	635824	103.45	18.87	5.48
Zinc ABC transporter, ATP-binding protein ZnuC	525	1960747	1961478	563.61	107.73	5.23
Phosphoserine aminotransferase (EC 2.6.1.52)	2880	3309588	3310691	1266.09	242.75	5.22
TonB-dependent receptor		1966243	1968273	250.25	48.77	5.13
hypothetical protein	2361	3836209	3836343	85.82	16.79	5.11
Nitrogenase iron protein (EC 1.18.6.1)	1487	897462	898340	154.33	30.75	5.02
hypothetical protein	2495	3717043	3717477	51.84	10.37	5.00
hypothetical protein	1958	415639	416046	54.05	11.06	4.89
hypothetical protein	2489	3718605	3718880	74.55	16.36	4.56
anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	3130	3053986	3054339	86.40	19.12	4.52
hypothetical protein	1543	1428039	1428173	74.63	16.79	4.44
hypothetical protein	1030	840328	840699	54.50	12.26	4.44
transposase, mutator family	2687	3522440	3523681	87.43	19.94	4.38
Endonuclease/exonuclease/phosphatase family protein	1972	399357	400457	53.64	12.27	4.37
Glutamine synthetase type III, GlnN (EC 6.3.1.2)	2961	3230164	3232305	197.18	45.42	4.34
serine/threonine kinase	518	1965188	1966228	676.92	157.93	4.29
Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	2879	3310743	3311315	899.48	212.41	4.23
hypothetical protein		3831876	3832310	108.29	25.92	4.18
Integrase domain protein	2915	3272902	3274137	53.04	12.75	4.16
ABC transporter, periplasmic substrate-binding protein	2007	366260	367774	123.51	29.72	4.16
Alkanesulfonates transport system permease protein	1500	885440	886441	91.91	22.48	4.09
Periplasmic solute binding protein precursor	524	1961479	1962249	1031.17	254.22	4.06
Cysteine synthase (EC 2.5.1.47)	3538	2646421	2647341	1936.41	481.79	4.02
Probable AAA family ATPase	2168	192289	194463	57.27	14.49	3.95
Response regulator	883	1578143	1579243	56.36	14.32	3.94
hypothetical protein	65	2416901	2417056	54.84	14.52	3.78
ABC transporter, ATP-binding protein	945	1515538	1516515	59.88	16.12	3.71
hypothetical protein	3514	2670183	2670407	73.66	20.09	3.67
Phosphonopyruvate decarboxylase (EC 4.1.1.82)	2215	128641	129825	197.21	55.11	3.58
Transcriptional regulator, LuxR family	1633	743966	744580	51.30	14.66	3.50
hypothetical protein	1215	1200918	1201808	52.81	15.17	3.48
hypothetical protein	783	1696186	1696551	63.01	18.49	3.41
hypothetical protein	1606	767235	767453	105.50	30.96	3.41
hypothetical protein	519	1964464	1965210	513.40	150.80	3.40
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1) / Molybdenum transport system permease protein modB (TC 3.A.1.8.1)		2954491	2955156	57.14	16.92	3.38
hypothetical protein	482	2003758	2003928	129.41	39.71	3.26
Cell surface protein	3591	2580069	2583068	52.02	16.51	3.15
Threonyl-tRNA synthetase (EC 6.1.1.3)	1969	401992	403776	864.91	276.21	3.13

hypothetical protein	556	2217022	2217135	123.89	39.82	3.11
Integrase domain protein	308	2160815	2162050	51.01	16.40	3.11
Helix-turn-helix domain protein	260	1919420	1919767	40.35	12.97	3.11
hypothetical protein	1517	926271	926387	60.34	19.40	3.11
hypothetical protein	1459	867432	867587	90.32	29.03	3.11
Putative ABC transport system ATP-binding protein	2826	3370491	3371162	52.16	16.77	3.11
Spermidine Putrescine ABC transporter permease component potB (TC_3.A.1.11.1)	3005	3182812	3183687	63.43	20.57	3.08
Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	1732	636520	637422	100.00	32.50	3.08
Integration host factor beta subunit	2492	3717890	3718210	129.69	42.19	3.07
Sensory box histidine kinase	2984	3203998	3205086	107.08	35.16	3.05
Histone acetyltransferase HPA2 and related acetyltransferases	2776	3415136	3415642	52.37	17.79	2.94
Phosphoenolpyruvate phosphomutase (EC 5.4.2.9)	2217	125737	127035	315.87	107.47	2.94
Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor	51	2429845	2430624	50.06	17.33	2.89
Site-specific tyrosine recombinase	3403	3708494	3709720	74.23	25.69	2.89
V-type ATP synthase subunit K (EC 3.6.3.14)	2505	2776024	2776341	123.03	42.59	2.89
hypothetical protein	373	2107487	2107972	52.58	18.56	2.83
hypothetical protein	1128	1323574	1323696	209.02	73.77	2.83
DNA-binding protein	2370	3827749	3828018	70.63	25.09	2.81
hypothetical protein	798	1679057	1680868	52.46	18.64	2.81
2-aminoethylphosphonate:pyruvate aminotransferase (EC 2.6.1.37)	2216	127046	128641	245.14	87.46	2.80
hypothetical protein	1954	421513	421878	121.88	43.63	2.79
amino acid ABC transporter, amino acid-binding protein		1912200	1913033	1003.00	359.24	2.79
transposase, mutator family	2408	3789549	3790433	92.19	33.09	2.79
hypothetical protein	2291	52469	52981	60.55	21.97	2.76
Predicted L-rhamnose ABC transporter, substrate-binding component	28	2454433	2455506	75.02	27.26	2.75
Sugar ABC transporter, periplasmic sugar-binding protein USSDB1B	2109	257351	258661	117.56	42.94	2.74
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1499	886456	887469	188.06	68.85	2.73
Cell surface protein IsdA, transfers heme from hemoglobin to apo-IsdC	1119	1333594	1335216	411.84	151.20	2.72
Neuraminidase NanP	869	1594078	1595892	63.67	23.57	2.70
Ferric iron ABC transporter, iron-binding protein	649	1840118	1841098	577.04	215.82	2.67
hypothetical protein	1716	774604	774723	50.42	18.91	2.67
transcriptional regulator, Cro/CI family	1597	653636	653932	60.81	22.80	2.67
ABC-type polar amino acid transport system, ATPase component	562	1913775	1914530	102.65	38.74	2.65
2.4.1.25)	2460	3733124	3735151	170.62	64.54	2.64
Ferric iron ABC transporter, permease protein	647	1841886	1843454	64.41	24.39	2.64
Phosphate transport system permease protein pstA (TC 3.A.1.7.1)	2299	44130	44978	56.01	21.23	2.64
Sensor histidine kinase	1661	713925	715127	54.08	20.59	2.63
hypothetical protein	2701	3508369	3509283	103.39	39.39	2.63
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.-)	152	2332757	2333392	64.57	24.80	2.60
hypothetical protein	712	1769654	1770256	58.14	22.43	2.59
Methyl-accepting chemotaxis protein	2582	3621777	3623627	62.70	24.32	2.58
hypothetical protein	3330	2851364	2851744	76.32	29.61	2.58
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2)	2946	3242602	3244017	130.74	50.88	2.57
hypothetical protein	1348	1056627	1057235	65.79	25.90	2.54
4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-)	2927	3264142	3265005	79.37	31.29	2.54
Voltage-gated chloride channel		952873	953292	53.70	21.48	2.50

hypothetical protein	3309	2870079	2870615	52.24	20.99	2.49
6-phosphofructokinase (EC 2.7.1.11)	3452	2730120	2731226	176.76	71.20	2.48
RNA polymerase sigma factor RpoE	1623	752159	752761	73.92	29.90	2.47
CRISPR-associated protein Cas2	2809	3385765	3386040	60.00	24.55	2.44
hypothetical protein	521	1964041	1964163	90.16	36.89	2.44
hypothetical protein	3119	3720038	3720241	54.19	22.17	2.44
Uracil-DNA glycosylase (EC 3.2.2.-)	2485	3065182	3065931	73.43	30.04	2.44
hypothetical protein	658	1832850	1833341	122.20	50.41	2.42
hypothetical protein	1986	386122	387522	77.86	32.14	2.42
Probable lipoprotein nlpC precursor	1588	780084	781226	51.66	21.67	2.38
Sucrose transport protein	1316	1085710	1087008	74.35	31.20	2.38
Nitroreductase family protein	2844	3348824	3349330	74.11	31.13	2.38
hypothetical protein	3545	2637363	2638052	92.89	39.19	2.37
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2)	2947	3241283	3242605	92.66	39.15	2.37
hypothetical protein	3666	2493800	2494207	104.42	44.23	2.36
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	2856	3336747	3338282	51.79	21.99	2.36
hypothetical protein	2569	3636939	3638072	56.05	23.83	2.35
hypothetical protein	793	1686598	1687713	118.39	50.45	2.35
Transcriptional repressor of the arabinose operon	2764	3425137	3426192	54.98	23.46	2.34
Periplasmic sugar-binding proteins	1964	483585	484562	64.48	27.64	2.33
ABC transporter, ATP-binding protein	1872	408652	409353	89.87	38.52	2.33
hypothetical protein	2917	3270393	3270566	150.29	65.03	2.31
FOG: WD40 repeat	1751	618744	621686	56.25	24.47	2.30
Oxidoreductase, aldo/keto reductase family	1109	1346635	1347555	229.89	100.27	2.29
Radical SAM domain protein	2539	3669908	3670894	62.37	27.38	2.28
possible Bacterial Ig-like domain (group 1)	2635	3558194	3559915	138.58	61.45	2.26
Sugar diacid utilization regulator SdaR	2281	64777	65955	60.27	26.74	2.25
tRNA:Cm32/Um32 methyltransferase	2707	3503657	3504457	150.00	67.50	2.22
Integrase domain protein	2017	356321	357556	52.23	23.68	2.21
Phosphate transport system regulatory protein PhoU	2301	42719	43375	83.08	37.73	2.20
Rhomboid family protein	2227	118384	119025	84.24	38.61	2.18
hypothetical protein	794	1684166	1686637	59.49	27.32	2.18
Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	2949	3239784	3240872	85.02	39.29	2.16
Uracil-DNA glycosylase (EC 3.2.2.-)	1702	670578	670787	162.68	75.36	2.16
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10)	1733	635814	636512	138.97	64.47	2.16
hypothetical protein	2005	370696	371445	1176.90	549.73	2.14
hypothetical protein	2434	3765078	3765419	98.24	46.19	2.13
Protease IV	2523	3688680	3690314	67.32	31.67	2.13
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25)	1731	637422	638783	101.76	47.94	2.12
Outer membrane autotransporter barrel	3471	2711398	2712405	75.47	35.75	2.11
Outer membrane autotransporter barrel	2107	259158	261098	61.08	28.99	2.11
Mlr3463 protein	3592	2578651	2580054	57.38	27.26	2.10
Amino acid ABC transporter, permease protein	563	1913062	1913778	328.21	157.12	2.09
DNA polymerase IV (EC 2.7.7.7)	1159	1268245	1269414	56.03	26.95	2.08
hypothetical protein	1548	836763	837005	115.70	55.79	2.07
Ribose 5-phosphate isomerase B (EC 5.3.1.6)	191	2294942	2295400	141.92	68.78	2.06
Glycine cleavage system H protein	2948	3240902	3241273	87.60	42.45	2.06
Probable membrane protein	2087	281376	282638	55.07	26.74	2.06

Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis, PTPS-III		2405466	2405840	98.93	48.13	2.06
Transposase IS4 family protein	75	3786399	3786647	74.60	36.29	2.06
hypothetical protein	751	1733113	1733274	142.86	69.88	2.04
Multiple polyol-specific dehydrogenase (EC 1.1.1.-)	1998	377087	378619	257.83	126.31	2.04
hypothetical protein	978	1486119	1487501	149.42	73.26	2.04
Putative sugar transporter	1117	1336737	1338146	55.36	27.15	2.04
Expressed protein	3345	2832902	2834002	70.91	34.77	2.04
Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB	2471	3727547	3727822	214.55	106.36	2.02
Mov34/MPN/PAD-1	1739	631201	631605	201.73	100.25	2.01
hypothetical protein		1453041	1453355	57.32	28.66	2.00
Inosose dehydratase (EC 4.2.1.44)	2189	716262	717086	87.38	43.69	2.00
hypothetical protein	1660	155208	155345	65.69	32.85	2.00
hypothetical protein	1008	3711218	3711727	61.89	30.94	2.00
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	157	3698576	3699868	111.46	55.73	2.00
Putative pheromone precursor lipoprotein	2517	2326125	2326586	68.33	34.16	2.00

T. primitia genes not expressed in either condition

Gene Annotation	TREPR #	Start	End
hypothetical protein		30	161
hypothetical protein		7658	7780
hypothetical protein		73023	73145
hypothetical protein		106760	106957
hypothetical protein	128	145544	145657
hypothetical protein		147530	147646
hypothetical protein	103	173083	173208
hypothetical protein		184218	184370
hypothetical protein		191008	191130
hypothetical protein	48	228903	229043
hypothetical protein		255438	255599
hypothetical protein		255731	255898
hypothetical protein		256006	256146
hypothetical protein	25	256579	256734
hypothetical protein		258205	258354
Transporter	18	261890	262258
hypothetical protein	16	262987	263124
hypothetical protein	15	263087	263563
Acetyltransferase	3889	283286	284350
hypothetical protein	3885	287603	287728
hypothetical protein	3884	287708	287842
hypothetical protein		303050	303172
hypothetical protein	3865	306802	307545
hypothetical protein		341829	342008
Iron-sulfur cluster-binding protein	3830	341995	342807
hypothetical protein		405639	405773
hypothetical protein		427534	427674
hypothetical protein		434604	434732
hypothetical protein	3741	436464	437312
hypothetical protein		440532	440726
putative protein family member (5Q829)	3736	440746	441336
Alpha-1,2-fucosyltransferase	3735	441373	442269
Maltose O-acetyltransferase (EC 2.3.1.79)	3733	443190	443801
hypothetical protein		449427	449543
hypothetical protein		465706	465858
hypothetical protein		469531	469746
hypothetical protein		471126	471245
hypothetical protein	3686	481547	482122
hypothetical protein	3675	487699	488451
hypothetical protein	3666	498068	498187
hypothetical protein	3658	504668	504820
hypothetical protein	3647	516099	516812
hypothetical protein	3646	516799	517347
hypothetical protein	3645	517388	517780
hypothetical protein	3631	531804	531962
hypothetical protein	3628	536985	537122
hypothetical protein		576489	576620
hypothetical protein		581904	582074
Oligopeptide transport system permease protein oppB	3542	624245	625225

hypothetical protein	3539	628867	629118
hypothetical protein		723582	723695
hypothetical protein	3436	723789	723938
hypothetical protein		784264	784377
hypothetical protein	3380	787773	787889
amino acid ABC transporter, permease protein	3346	814269	814967
amino acid ABC transporter, ATP-binding protein	3337	821623	822381
hypothetical protein		874542	874673
hypothetical protein	3246	911792	912013
hypothetical protein		912101	912235
hypothetical protein		921188	921370
hypothetical protein	3231	922468	922587
hypothetical protein		929981	930226
hypothetical protein		951703	951843
hypothetical protein	3199	954695	954895
hypothetical protein	3195	959256	959384
hypothetical protein	3128	1037378	1037512
hypothetical protein	3106	1061036	1061209
hypothetical protein	3085	1076276	1076404
hypothetical protein	3019	1149448	1149540
hypothetical protein		1237088	1237201
hypothetical protein	2892	1293760	1293888
hypothetical protein		1293903	1294022
hypothetical protein		1311493	1311648
hypothetical protein	2802	1367736	1367996
hypothetical protein		1396746	1396886
hypothetical protein	2752	1426040	1426207
hypothetical protein	2748	1429972	1430109
hypothetical protein	2713	1466276	1466614
hypothetical protein	2703	1477034	1477240
hypothetical protein	2664	1512784	1513290
hypothetical protein		1589540	1590019
hypothetical protein	2593	1592674	1592817
hypothetical protein	2592	1592932	1593168
hypothetical protein	2591	1593161	1593586
Exonuclease SbcC	2590	1593849	1594610
hypothetical protein	2577	1608181	1608327
hypothetical protein		1722807	1722929
hypothetical protein	2304	1927527	1927649
hypothetical protein	2293	1942558	1942677
hypothetical protein	2284	1950800	1951021
ATPase	2271	1965740	1965997
hypothetical protein	2272	1965994	1966125
hypothetical protein	2266	1973172	1973393
hypothetical protein	2262	1976879	1977214
hypothetical protein	2261	1977204	1977425
hypothetical protein		1983527	1983667
hypothetical protein	2246	1991844	1991969
hypothetical protein		2032504	2032671
hypothetical protein		2038758	2038895
hypothetical protein	2197	2040638	2040976

hypothetical protein	2194	2043079	2043630
hypothetical protein	2193	2043631	2043912
hypothetical protein	2192	2043872	2044159
hypothetical protein	2190	2044429	2044596
hypothetical protein	2189	2044599	2045153
hypothetical protein	2188	2045275	2045541
hypothetical protein	2184	2048338	2048946
hypothetical protein		2054605	2054760
hypothetical protein		2054991	2055116
hypothetical protein	2170	2057000	2057131
hypothetical protein	2167	2058030	2058143
hypothetical protein		2059682	2059807
probable methyltransferase	2164	2059780	2060406
Plasmid stabilization system protein	2159	2061994	2062329
hypothetical protein		2075840	2075953
hypothetical protein	2132	2088512	2088625
hypothetical protein	2119	2099859	2100074
hypothetical protein	2118	2100543	2100677
hypothetical protein	2117	2100720	2100836
hypothetical protein		2100860	2101660
hypothetical protein		2111964	2112083
hypothetical protein	2107	2112721	2113329
hypothetical protein	2106	2113361	2113807
hypothetical protein	2103	2116166	2116393
hypothetical protein		2118258	2118389
hypothetical protein	2093	2122946	2123059
hypothetical protein		2123260	2123388
hypothetical protein	2090	2123916	2124044
hypothetical protein	2088	2124457	2124657
hypothetical protein	2087	2124746	2125018
ORF009	2085	2125575	2126795
Phage portal protein, HK97	2084	2126792	2128021
Probable prohead protease	2082	2128720	2129388
Major capsid protein, HK97 family	2081	2129457	2130758
Phage integrase	2080	2130883	2132121
hypothetical protein	2058	2184901	2185020
hypothetical protein	2055	2185960	2186085
hypothetical protein		2186124	2186282
hypothetical protein	2051	2188032	2188367
hypothetical protein	2047	2191584	2191967
hypothetical protein	2041	2195534	2195968
hypothetical protein	2040	2195992	2196588
hypothetical protein		2196673	2196831
hypothetical protein	2036	2198728	2199282
hypothetical protein	2035	2199304	2199582
hypothetical protein	2034	2199809	2200576
hypothetical protein		2200786	2200938
hypothetical protein	2032	2201133	2201549
hypothetical protein		2202080	2202214
hypothetical protein	2021	2215828	2215953
hypothetical protein		2216482	2216640

hypothetical protein	2019	2216641	2216970
hypothetical protein	2018	2217029	2217448
ORF009	2013	2221495	2222730
hypothetical protein		2225626	2225766
hypothetical protein		2277938	2278078
hypothetical protein		2353763	2353894
hypothetical protein	1899	2353882	2354517
hypothetical protein	1896	2358212	2358688
hypothetical protein		2365134	2365304
hypothetical protein	1888	2365308	2365517
hypothetical protein	1887	2365565	2365750
hypothetical protein	1886	2365803	2366042
Flagellar motor switch protein fliM	1885	2366044	2366628
hypothetical protein	1883	2369624	2370436
hypothetical protein		2371901	2372035
hypothetical protein	1874	2377801	2377938
hypothetical protein		2379059	2379190
hypothetical protein	1870	2379788	2379907
hypothetical protein	1869	2380202	2380645
hypothetical protein		2380700	2380822
hypothetical protein		2384580	2384699
hypothetical protein		2410420	2410527
hypothetical protein		2478720	2478875
hypothetical protein		2559089	2559232
hypothetical protein	1706	2559235	2559414
hypothetical protein	1697	2566847	2566966
hypothetical protein	1674	2590171	2590293
hypothetical protein		2673814	2673930
hypothetical protein		2694453	2694605
hypothetical protein		2741398	2741547
hypothetical protein	1536	2761830	2761958
hypothetical protein		2787281	2787394
hypothetical protein	1436	2854711	2854950
hypothetical protein	1433	2856340	2856606
hypothetical protein	1432	2856966	2857139
hypothetical protein		2857119	2857247
hypothetical protein	1429	2857787	2858029
Leader peptidase (Prepilin peptidase) (EC 3.4.23.43)	1398	2898642	2899076
General secretion pathway protein E	1396	2901255	2902757
Type 4 fimbrial assembly protein pilC	1395	2902757	2903812
hypothetical protein	1393	2904278	2904505
hypothetical protein	1391	2905016	2906020
hypothetical protein	1390	2905998	2907152
hypothetical protein	1389	2907172	2907660
hypothetical protein	1387	2908225	2908890
hypothetical protein	1327	2984646	2984771
hypothetical protein		3007994	3008113
hypothetical protein		3017845	3017988
hypothetical protein		3048769	3048906
aminoglycoside 6-adenylyltransferase	1245	3083514	3083774
hypothetical protein	1244	3083782	3084093

hypothetical protein	1242	3084517	3085089
hypothetical protein	1187	3132410	3132550
hypothetical protein	1137	3177664	3177795
5'-nucleotidase (EC 3.1.3.5)	1134	3180348	3182177
hypothetical protein	1113	3203606	3203863
hypothetical protein		3241610	3241732
hypothetical protein	1045	3275215	3275850
hypothetical protein	1042	3277673	3277840
hypothetical protein		3319904	3320152
hypothetical protein		3320163	3320324
hypothetical protein	992	3334892	3335011
hypothetical protein	951	3377624	3377755
hypothetical protein	947	3382231	3382392
hypothetical protein	909	3421167	3422387
hypothetical protein	908	3422537	3422725
hypothetical protein	907	3423523	3423699
hypothetical protein		3424581	3424718
DNA repair protein RadC	898	3433297	3433764
hypothetical protein	895	3435542	3435766
hypothetical protein	894	3435756	3436004
hypothetical protein	891	3437378	3437587
hypothetical protein	888	3439198	3439968
Single-stranded DNA-binding protein	887	3440033	3440428
hypothetical protein	885	3441316	3441705
hypothetical protein	880	3443465	3444061
hypothetical protein	876	3445955	3446086
hypothetical protein	877	3446059	3446307
hypothetical protein	863	3457088	3457390
hypothetical protein		3509185	3509301
hypothetical protein	752	3558501	3558662
Gsl2900 protein	742	3572877	3573077
hypothetical protein		3576080	3576268
hypothetical protein	712	3604228	3604353
Oligopeptide transport ATP-binding protein oppD	674	3642310	3643341
hypothetical protein	654	3667715	3667828
Type II restriction enzyme BsuBI (EC 3.1.21.4)	652	3668937	3669338
hypothetical protein		3681307	3681543
hypothetical protein		3705357	3705491
hypothetical protein	618	3705845	3706693
Bacterial regulatory proteins, AsnC family	576	3751484	3751720
hypothetical protein	458	3882029	3882406
hypothetical protein	457	3882409	3882678
hypothetical protein		3906199	3906342
hypothetical protein		3918834	3918953
hypothetical protein	415	3921264	3921494

T. azotonutricium **genes not expressed in either condition**

Gene Annotation	TREAZ #	Start	End
hypothetical protein	2311	32157	32477
hypothetical protein	1995	380204	380326
hypothetical protein	1748	623360	623500
hypothetical protein	1695	677905	678018

hypothetical protein	1693	680380	680502
hypothetical protein	1671	708742	708867
hypothetical protein	1670	708870	709061
hypothetical protein	1664	712461	712595
hypothetical protein	1646	733842	733964
hypothetical protein	1485	899391	899528
hypothetical protein		940960	941085
hypothetical protein	1443	941158	941277
hypothetical protein	1244	1163639	1163770
hypothetical protein	1183	1239332	1239541
hypothetical protein	1161	1267167	1267298
hypothetical protein	1056	1406968	1407099
hypothetical protein	977	1487534	1487647
hypothetical protein	813	1661588	1661716
hypothetical protein	812	1661762	1662304
hypothetical protein	778	1702265	1702399
hypothetical protein	713	1769399	1769518
hypothetical protein	604	1872659	1872850
hypothetical protein	597	1878392	1878595
hypothetical protein		1884397	1884531
hypothetical protein	560	1916445	1916558
hypothetical protein	520	1964271	1964387
hypothetical protein	499	1983160	1983306
hypothetical protein	497	1985482	1985613
hypothetical protein	374	2107329	2107487
hypothetical protein	362	2114030	2114272
hypothetical protein	358	2117205	2117591
hypothetical protein	319	2149442	2149684
hypothetical protein	313	2154900	2155031
hypothetical protein	309	2160286	2160408
Transposase IS4 family		2363437	2363610
hypothetical protein	3444	2739039	2739155
hypothetical protein	3363	2816088	2816225
hypothetical protein	3120	3064981	3065142
hypothetical protein	3070	3124117	3124284
hypothetical protein	3069	3124659	3124784
hypothetical protein	2988	3201792	3201938
hypothetical protein	2936	3254441	3254605
hypothetical protein	2685	3524255	3524380
hypothetical protein	2564	3640681	3640803
hypothetical protein	2419	3780402	3780608

	T. primitia sample A	*T. primitia* sample B	*T. azotonutricium* sample A	*T. azotonutricium* sample B	co-culture sample A	co-culture sample B
Total sequences	15151014	14267420	13194946	13523348	13878935	12565943
Mapped sequences	13633119	11749745	11215221	11661398	11882471	11379324
Sequences mapping to non 16S or 23S genes	427444	595988	380752	519125	789755	594670

T. primitia				**Normalized Avg. RNA-Seq**		
	TREPR #	**Start**	**End**	**Single Culture**	**Co-Culture**	**Ratio**
hypothetical protein		30	161	0	0	#DIV/0!
Chromosomal replication initiator protein dnaA	277	301	1740	66.71299514	62.7230716	0.94019
hypothetical protein	276	1755	1925	11.76470588	5.47352941	0.46525
DNA polymerase III beta subunit (EC 2.7.7.7)	275	1938	3041	208.5222121	124.010426	0.59471
DNA recombination and repair protein RecF	274	3065	4174	85.66275924	62.0892696	0.72481
Uncharacterized protein TP_0004	273	4171	4749	77.85467128	88.5423875	1.13728
hypothetical protein	272	4753	5961	106.7880795	70.865894	0.66361
hypothetical protein	271	6003	6791	121.8274112	164.136421	1.34729
UPF0088 protein TP_0032	270	6801	7661	51.1627907	58.4267442	1.14198
hypothetical protein		7658	7780	0	0	#DIV/0!
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	268	7765	9312	29.73497091	19.8490627	0.66753
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	267	9328	10293	25.90673575	15.4279793	0.59552
Ribose ABC transporter, periplasmic ribose-binding protein rbsB (TC 3.A.1.2.1)	266	10349	11290	195.5366631	105.806057	0.54111
Ribose operon repressor	265	11325	12350	18.53658537	25.4185366	1.37126
Threonine synthase (EC 4.2.3.1)	264	12439	13743	124.2331288	74.2116564	0.59736
Mechanosensitive ion channel family protein	263	13765	15291	24.24639581	21.9515072	0.90535
Porphobilinogen synthase (EC 4.2.1.24)	262	15317	16303	136.9168357	235.927992	1.72315
Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen-III synthase (EC 4.2.1.75)	261	16304	17884	132.9113924	153.709177	1.15648
Porphobilinogen deaminase (EC 2.5.1.61)	260	17881	18882	85.91408591	152.44955	1.77444
Siroheme synthase / Precorrin-2 oxidase (EC 1.3.1.76)	259	18879	19457	129.7577855	183.524221	1.41436
Mov34/MPN/PAD-1	258	19459	19863	257.4257426	343.179455	1.33312
ThiS, thiamine-biosynthesis	257	19857	20129	375	335.253676	0.89401
Threonine synthase (EC 4.2.3.1)	256	20160	21362	6.655574043	9.28951747	1.39575
Sulfate-binding protein sbp	255	21474	22541	8.434864105	8.72071228	1.03389
Sulfate transport system permease protein cysT	254	22551	23396	6.00240096	3.35114046	0.5583
Sulfate transport system permease protein cysW	253	23393	24238	1.183431953	1.10118343	0.9305
Sulfate and thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)	252	24250	25317	2.811621368	3.48828491	1.24067
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10)	251	25307	26017	30.98591549	30.1429577	0.9728
Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	250	26014	26910	58.1655481	58.2863535	1.00208
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25)	249	26910	28295	29.60288809	32.2483755	1.08937
Nitrogenase iron protein (EC 1.18.6.1)	248	28502	29380	15.9453303	21.1958998	1.32929
Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)	247	29477	30799	8.320726172	5.63086233	0.67673
Nitrogenase (EC 1.18.6.1)	246	30802	32160	16.93667158	15.7595729	0.9305
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	245	32180	33028	108.490566	158.009434	1.45643

hypothetical protein	244	33039	33293	149.6062992	157.525591	1.05293
Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits	243	33290	34156	91.22401848	104.224596	1.14251
tRNA nucleotidyltransferase (EC 2.7.7.25)	242	34257	35549	37.92569659	38.8908669	1.02545
Alpha amylase	241	35628	39512	171.9876416	182.07518	1.05865
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	240	39525	41555	149.1358025	135.554321	0.90893
Membrane spanning protein	239	41722	43269	22.62443439	23.4579832	1.03684
Nitrogen regulatory protein P-II	238	43256	43966	57.74647887	31.4535211	0.54468
nodulin 21-related protein	237	43968	44837	44.87917146	44.972382	1.00208
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	236	44906	45814	20.92511013	29.7186123	1.42024
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	235	45811	46911	15.45454545	16.9181818	1.09471
Predicted nucleoside ABC transporter, ATP-binding component	234	46904	48457	18.67353509	35.9497746	1.92517
Membrane lipoprotein TpN38(b) precursor	233	48491	49579	41.36029412	66.7086397	1.61287
hypothetical protein	232	49751	49864	35.39823009	24.7035398	0.69788
Cytochrome c-type biogenesis protein ResA	231	49877	50491	17.91530945	27.2785016	1.52264
Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)	230	50526	51497	15.44799176	27.7904222	1.79897
O-acetylhomoserine sulfhydrylase (EC 4.2.99.10) / O-succinylhomoserine sulfhydrylase (EC 4.2.99.9)	229	51714	53819	203.236554	236.500238	1.16367
hypothetical protein	228	54022	54408	2.590673575	0	0
Adenylosuccinate lyase (EC 4.3.2.2)	227	54448	55920	108.8435374	132.295578	1.21547
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	226	55944	57380	137.1866295	147.091574	1.0722
hypothetical protein	225	57401	58033	99.6835443	78.0324367	0.7828
Lactoylglutathione lyase (EC 4.4.1.5)	224	58035	58421	64.76683938	74.7292746	1.15382
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	223	58517	60043	150.0655308	164.636304	1.0971
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	222	60048	60902	179.1569087	201.572014	1.12511
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	221	60899	61741	197.1496437	163.555819	0.8296
Multiple sugar ABC transporter, substrate-binding protein	220	61820	63142	338.1240545	375.860061	1.1116
Adenylosuccinate synthetase (EC 6.3.4.4)	219	63334	64566	193.9935065	166.160714	0.85653
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	218	64646	66319	106.993425	101.782128	0.95129
hypothetical protein	217	66589	66819	286.9565217	258.921739	0.9023
hypothetical protein	216	66816	67217	122.1945137	64.9725686	0.53171
hypothetical protein	215	67265	68143	234.6241458	207.719818	0.88533
hypothetical protein	214	68140	68823	308.9311859	321.519766	1.04075
Virulence associated protein B	213	68933	69157	49.10714286	29.078125	0.59214
VapC toxin protein	212	69120	69557	34.32494279	19.1636156	0.5583
hypothetical protein	211	69569	69706	36.49635036	67.919708	1.861
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	210	69853	70815	336.7983368	287.274948	0.85296
Flippase	209	70859	72220	12.49081558	9.5716385	0.76629
SAM-dependent methyltransferase (EC 2.1.1.-)	207	72221	73042	35.3227771	6.80024361	0.19252

hypothetical protein		73023	73145	0	0	#DIV/0!
Conserved domain protein		73099	73509	9.756097561	2.2695122	0.23263
hypothetical protein		73490	73669	5.586592179	0	0
Conserved domain protein		73733	73990	35.01945525	21.7237354	0.62033
Glycosyl transferase, group 2 family protein	203	74016	75029	29.61500494	30.3124383	1.02355
dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	202	75026	75928	89.80044346	39.2006652	0.43653
capsular polysaccharide biosynthesis protein	201	75939	77114	8.510638298	3.95957447	0.46525
Glycosyltransferase	200	77215	78372	9.507346586	10.4550562	1.09968
hypothetical protein	199	78445	78570	64	74.44	1.16313
hypothetical protein		78581	78751	58.82352941	5.47352941	0.09305
hypothetical protein		78818	79132	130.5732484	53.3407643	0.40851
HlpA protein	196	79190	80074	62.21719457	44.209276	0.71056
Glycosyltransferase	195	80146	81249	23.57207616	11.8105168	0.50104
Beta-1,3-galactosyltransferase / Beta-1,4-galactosyltransferase	194	81253	82020	24.77183833	9.7053455	0.39179
Tyrosine-protein kinase wzc (EC 2.7.1.112)	193	82437	83168	80.71135431	81.4664843	1.00936
Capsule polysaccharide export protein	192	83165	84631	103.6834925	105.998295	1.02233
hypothetical protein	191	84721	85575	15.22248244	7.62704918	0.50104
Phosphoglycerol transferase I (EC 2.7.8.20)	190	85559	87334	27.6056338	13.1056338	0.47474
hypothetical protein	189	87419	87814	0	2.3556962	#DIV/0!
hypothetical protein	188	87811	88050	0	7.78661088	#DIV/0!
hypothetical protein	187	88147	88434	62.71777003	16.2108014	0.25847
hypothetical protein	186	88431	88814	7.832898172	4.85900783	0.62033
Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	185	89156	90346	137.8151261	186.1	1.35036
FOG: GGDEF domain	184	90446	91513	59.04404873	50.5801312	0.85665
sensory box histidine kinase/response regulator	183	91482	92903	81.63265306	56.9693878	0.69788
Molybdopterin-guanine dinucleotide biosynthesis protein B	182	92921	93436	100.9708738	106.600971	1.05576
4-hydroxybenzoyl-CoA thioesterase family active site	181	93435	93890	105.4945055	81.8021978	0.77542
Transglutaminase-like domain protein	180	93895	97914	42.54789749	67.3738492	1.58348
hypothetical protein	179	97892	99085	59.51383068	85.0163453	1.42851
methanol dehydrogenase regulatory protein	178	99054	100004	126.3157895	163.572105	1.29495
hypothetical protein	177	100170	101258	297.7941176	318.148897	1.06835
Diaphanous protein homolog 2	176	101409	102164	294.0397351	415.335762	1.41252
Intergenic (EXPRESSED)		102165	102563	3028.350515	2774.71263	0.91625
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	175	102564	104477	66.38787245	80.257449	1.20892
hypothetical protein	174	104531	105418	60.87936866	115.394589	1.89546
Tripeptide aminopeptidase (EC 3.4.11.4)	173	105418	106680	150.5546751	156.312203	1.03824
hypothetical protein		106760	106957	0	0	#DIV/0!
Taurine transport ATP-binding protein tauB	171	106946	107845	2.224694105	0	0
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	170	107847	108683	1.196172249	0	0
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	169	108749	109810	5.655042413	1.75400566	0.31017
hypothetical protein	168	109825	111102	7.830853563	1.45732185	0.1861
hypothetical protein	167	111117	111602	10.30927835	9.59278351	0.9305
transcriptional regulator, PemK family	166	111712	112056	14.53488372	2.70494186	0.1861

Endopeptidase essential in most Bacteria (E. coli YgjD/B. subtilis YdiE)	165	112092	113150	157.8449905	156.549149	0.99179
Putative periplasmic protein	164	113131	114240	313.7962128	216.473399	0.68985
RNA polymerase sigma factor RpoS	163	114534	115388	296.2529274	318.156909	1.07394
Type 4 fimbriae expression regulatory protein pilR	162	115568	116983	10.60070671	11.1791519	1.05457
Sensor protein of zinc sigma-54-dependent two-component system	161	116980	118329	20.0148258	18.6237954	0.9305
hypothetical protein	160	118328	118543	18.60465116	8.65581395	0.46525
hypothetical protein	159	118677	119177	32	37.22	1.16313
Transcriptional regulator, Hth-3 family	158	119308	119856	111.3138686	113.765511	1.02202
Acetyl-coenzyme A synthetase (EC 6.2.1.1)	157	119858	121570	223.1308411	220.124124	0.98652
PHP, C-terminal	156	121577	122371	182.6196474	151.176952	0.82782
Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	155	122394	123269	262.8571429	264.793714	1.00737
Probable AAA family ATPase	154	123347	125155	114.4911504	116.3125	1.01591
hypothetical protein		125179	125328	0	6.24496644	#DIV/0!
hypothetical protein		125777	125959	10.98901099	0	0
hypothetical protein	151	126054	126215	6.211180124	0	0
hypothetical protein	150	126277	126486	143.5406699	102.399522	0.71338
Glutamate 5-kinase (EC 2.7.2.11)	149	126513	127304	187.5792142	273.607098	1.45862
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	148	127322	128581	179.5075457	276.415409	1.53985
hypothetical protein	147	128593	128802	28.70813397	22.2607656	0.77542
Acetyltransferase	146	128822	129499	51.69867061	17.8677991	0.34561
Ribonuclease D (EC 3.1.26.3)	145	129514	130362	12.97169811	8.77830189	0.67673
ENDO-TYPE 6-AMINOHEXANOATE OLIGOMER HYDROLASE	144	130355	131380	52.68292683	63.5463415	1.2062
Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)	143	131377	131928	90.74410163	116.523593	1.28409
Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)	142	131925	132731	111.662531	129.300248	1.15796
Polysaccharide deacetylase	141	132794	133870	19.51672862	13.8364312	0.70895
Histone acetyltransferase HPA2 and related acetyltransferases	140	134066	134575	33.39882122	32.9056974	0.98524
lipoprotein, putative	139	134585	135640	103.3175355	156.994313	1.51953
hypothetical protein	138	135735	136463	64.56043956	65.1861264	1.00969
hypothetical protein		136805	136951	143.8356164	178.452055	1.24067
Threonyl-tRNA synthetase (EC 6.1.1.3)	136	136970	138787	168.4094662	162.338195	0.96395
Nitroreductase	135	138802	139335	356.4727955	469.614447	1.31739
Xylitol dehydrogenase (EC 1.1.1.9)	134	139422	140456	102.5145068	72.8921663	0.71104
Oxidoreductase, short chain dehydrogenase/reductase family	133	140469	141236	181.2255541	180.76206	0.99744
Transcriptional regulator, DeoR family	132	141259	142056	77.79171895	133.095358	1.71092
Transcriptional regulator, DeoR family	131	142246	143037	2.528445006	7.05815424	2.7915
Trypsin domain/PDZ domain protein	130	143288	144526	273.8287561	233.752423	0.85364
Cobalt-zinc-cadmium resistance protein	129	144529	145500	67.97116375	69.9552008	1.02919
hypothetical protein	128	145544	145657	0	0	#DIV/0!
hypothetical protein	126	145656	147533	46.88332445	43.1291955	0.91993
hypothetical protein		147530	147646	0	0	#DIV/0!
Single-stranded DNA-binding protein	125	147662	148132	44.68085106	45.5351064	1.01912
hypothetical protein	124	148515	148664	6.711409396	0	0

Peptidase, U32 family	123	148846	151005	93.09865679	81.4564613	0.87495
Von Willebrand factor type A domain protein	122	151136	153097	223.8653748	281.380163	1.25692
GldJ	121	153099	153929	373.9445115	397.342581	1.06257
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	120	154043	157774	124.8994908	129.686411	1.03833
Na+ driven multidrug efflux pump	119	157791	159149	55.22827688	59.6122975	1.07938
Sugar ABC transporter, sugar-binding protein	118	159162	160430	71.76656151	77.7862776	1.08388
Shikimate kinase (EC 2.7.1.71)	117	160608	161240	64.87341772	60.3647152	0.9305
Protease prsW (EC 3.4.-.-) (Protease responsible for activating sigma-W)	116	161270	161932	54.38066465	42.1676737	0.77542
Mll3043 protein	114	162124	163485	20.57310801	16.4085231	0.79757
hypothetical protein	113	163717	164178	71.5835141	88.8112798	1.24067
hypothetical protein	112	164175	165371	37.62541806	26.4523411	0.70304
Uncharacterized protein conserved in bacteria	111	165389	166105	79.60893855	72.7765363	0.91418
hypothetical protein	110	166107	166760	101.0719755	96.8973966	0.9587
Chromosome partition protein smc	109	166771	169764	163.7153358	182.493652	1.1147
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Multiple sugar ABC transporter, ATP-binding protein	108	170093	171211	982.1109123	853.929338	0.86948
hypothetical protein	107	171687	171941	456.6929134	278.417323	0.60964
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	106	172070	172660	188.1355932	176.637288	0.93888
hypothetical protein	105	172702	172893	130.8900524	170.510471	1.3027
hypothetical protein	104	172896	173030	238.8059701	333.313433	1.39575
hypothetical protein	103	173083	173208	0	0	#DIV/0!
hypothetical protein	102	173378	173512	1925.373134	3458.12687	1.79608
RTX toxin, putative	101	173472	176051	3235.362544	3273.88794	1.01191
Transposase IS66	100	176257	176649	10.20408163	9.49489796	0.9305
hypothetical protein	99	176719	177555	180.6220096	253.772727	1.40499
putative transposase	98	177762	178364	14.95016611	12.3654485	0.82711
hypothetical protein		178400	178660	253.8461538	182.521154	0.71902
hypothetical protein		178749	178934	91.89189189	45.2675676	0.49262
unique zas2 16S rRNA 2		179568	179578	794500	708017.45	0.89115
unique zas2 16S rRNA 1		179986	179996	1726300	2322155.8	1.34516
unique zas2 23S rRNA 1		181329	181339	256100	225739.3	0.88145
hypothetical protein		184218	184370	0	0	#DIV/0!
hypothetical protein	90	184673	184849	22.72727273	5.28693182	0.23263
hypothetical protein	89	185040	185921	19.29625426	12.6742338	0.65682
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	88	185930	186817	13.52874859	16.7846674	1.24067
Putative ABC transporter of substrate X, permease subunit II	87	186842	187702	10.46511628	3.24593023	0.31017
Putative ABC transporter of substrate X, permease subunit I	86	187714	188568	4.683840749	5.44789227	1.16313
Putative ABC transporter of substrate X, ATP-binding subunit	85	188568	189635	14.05810684	6.97656982	0.49627
Possible ABC transporter, periplasmic substrate X binding protein precursor	84	189691	190860	24.8075278	41.3909324	1.66848
hypothetical protein		190901	191029	31.25	7.26953125	0.23263
hypothetical protein		191008	191130	0	0	#DIV/0!
Novel Xylose regulator from LacI family	81	191145	192176	4.849660524	3.61008729	0.7444
Iron-sulfur cluster-binding protein	79	192242	193405	37.83319003	28.8030954	0.76132

Glycoprotein gp2	80	193356	195098	63.14580941	72.1110792	1.14198
sensory box histidine kinase/response regulator	78	195135	198515	63.90532544	75.7063609	1.18466
hypothetical protein	77	198628	199386	72.55936675	106.798813	1.47188
hypothetical protein	76	199361	199507	0	6.37328767	#DIV/0!
Flagellar hook-length control protein fliK	75	199550	203389	56.26465225	62.2918729	1.10712
conserved hypothetical integral membrane protein	73	203711	204361	718.4615385	632.74	0.88069
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	72	204420	205700	131.25	108.316016	0.82526
Neutral metalloprotease precursor (EC 3.4.24.-)	71	205707	207101	55.95408895	38.715208	0.69191
hypothetical protein		207055	207216	12.42236025	40.4565217	3.25675
hypothetical protein	70	207176	208996	53.84615385	62.8854396	1.16787
hypothetical protein	68	208993	209985	62.5	49.7142137	0.79543
hypothetical protein		210015	210176	12.42236025	5.77950311	0.46525
Phage shock protein A	66	210340	211038	290.8309456	347.937679	1.19636
hypothetical protein	65	211072	211449	352.7851459	426.993369	1.21035
anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	64	211484	212053	413.0052724	412.101933	0.99781
tRNA:Cm32/Um32 methyltransferase	62	212279	213085	45.9057072	62.3411911	1.35803
N-acetylmannosaminyltransferase (EC 2.4.1.187)	63	213066	213884	94.13202934	72.801956	0.7734
Small ribosomal subunit 16S rRNA methyltransferase ## U1498-specific in E.coli	61	213857	214738	107.8320091	109.84336	1.01865
Carboxyl-terminal protease (EC 3.4.21.102)	60	214743	216260	279.4990112	331.226104	1.18507
hypothetical protein	59	216359	216958	11.68614357	17.0876461	1.46221
Diadenosine tetraphosphatase	58	217015	217833	31.78484108	38.6760391	1.21681
Chloramphenicol acetyltransferase (EC 2.3.1.28)	57	217865	218536	11.92250373	8.32041729	0.69788
Conserved domain protein		218541	220751	196.3800905	259.782127	1.32285
Uncharacterized protein MJ1020	55	220759	221529	458.4415584	640.474026	1.39707
Expressed protein	54	221645	222757	32.37410072	51.0436151	1.57668
hypothetical protein		222833	223498	64.66165414	48.9736842	0.75738
Methyl-accepting chemotaxis protein	52	223548	225371	191.4426769	209.273176	1.09314
T. pallidum predicted coding region TP0592	51	225501	226424	132.1776815	164.324485	1.24321
DNA-binding protein	50	226519	226872	186.9688385	234.601983	1.25477
Cell division protein ftsH (EC 3.4.24.-)	49	226881	228842	66.63249616	108.264223	1.6248
hypothetical protein	48	228903	229043	0	0	#DIV/0!
type 4 fimbrial biogenesis protein PilY1	47	229042	231918	33.03198887	33.3245828	1.00886
putative autotransporter protein	46	231989	234967	51.71255876	34.9952989	0.67673
Outer membrane autotransporter barrel	45	234969	238925	73.30637007	55.2748989	0.75403
hypothetical protein	44	238938	239774	41.86602871	27.8259569	0.66464
Cell surface protein	43	239774	241756	16.64984864	19.7179617	1.18427
Calcium-binding acidic-repeat protein precursor	42	241759	243375	21.03960396	19.001547	0.90313
VgrG protein	41	243511	244494	174.9745677	209.196846	1.19558
Galactokinase (EC 2.7.1.6)	40	244555	245904	115.6412157	117.260934	1.01401
DNA polymerase IV (EC 2.7.7.7)	39	245958	247148	44.53781513	46.9159664	1.0534
hypothetical protein	38	247266	248966	447.6470588	357.421471	0.79844
hypothetical protein	37	248979	250403	405.8988764	357.432233	0.88059

Methylthioribose-1-phosphate isomerase (EC 5.3.1.23)	35	250805	251935	168.1415929	242.09469	1.43983
Conserved domain protein	34	251928	252545	58.34683955	76.9132901	1.31821
5'-methylthioadenosine phosphorylase (EC 2.4.2.28)	33	252588	253334	144.772118	135.957775	0.93912
hypothetical protein	32	253546	253743	101.5228426	89.7436548	0.88398
hypothetical protein	31	253910	254401	22.40325866	36.0071283	1.60723
hypothetical protein	30	254525	255451	7.559395248	7.03401728	0.9305
hypothetical protein		255438	255599	0	0	#DIV/0!
hypothetical protein		255731	255898	0	0	#DIV/0!
hypothetical protein		256006	256146	0	0	#DIV/0!
hypothetical protein		256307	256543	8.474576271	11.8283898	1.39575
hypothetical protein	25	256579	256734	0	0	#DIV/0!
hypothetical protein	24	256792	258108	2.279635258	0	0
hypothetical protein		258205	258354	0	0	#DIV/0!
Mll0579 protein	22	258381	259094	4.207573633	0	0
Putative mannosyltransferase involved in polysaccharide biosynthesis	21	259142	259918	1.288659794	0	0
Glycosyltransferase	20	259942	260937	1.005025126	0	0
Conserved membrane protein, possible 4-hydroxybenzoate octaprenyltranferase	19	260934	261893	2.085505735	0	0
Transporter	18	261890	262258	0	0	#DIV/0!
putative hydrolase	17	262264	262938	1.483679525	0	0
hypothetical protein	16	262987	263124	0	0	#DIV/0!
hypothetical protein	15	263087	263563	0	0	#DIV/0!
hypothetical protein	14	263560	264981	5.629838142	1.3096411	0.23263
DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase	13	264981	266288	0	0.71193573	#DIV/0!
capsular polysaccharide biosynthesis protein	12	266358	267467	4.508566276	0.83904418	0.1861
Methyltransferase	11	267581	268276	2.877697842	0	0
Glycosyltransferase	10	268298	269365	3.748828491	0.87207123	0.23263
Alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	9	269679	270644	3.10880829	0	0
UDP-glucose 4-epimerase (EC 5.1.3.2)	8	270687	271607	9.782608696	1.01141304	0.10339
Glycosyltransferase	7	271604	272269	4.511278195	1.39924812	0.31017
Putative capsular polysaccharide biosynthesis protein D	6	272286	273476	5.042016807	2.34579832	0.46525
Tyrosine-protein kinase wzc (EC 2.7.1.112)	5	273488	274492	6.972111554	11.1215139	1.59514
Capsular polysaccharide export system periplasmic protein KpsD	4	274489	275949	9.589041096	13.3839041	1.39575
Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	3	275985	277424	4.169562196	3.87977762	0.9305
hypothetical protein	2	277433	278572	0.877963126	0.81694469	0.9305
Acyltransferase (EC 2.3.1.-)	1	278654	279783	0.885739593	1.64836138	1.861
hypothetical protein	3895	279937	280194	35.01945525	25.344358	0.72372
hypothetical protein		280232	280345	8.849557522	0	0
hypothetical protein	3893	280335	280466	15.26717557	0	0
Integrase domain protein	3892	280502	281740	8.077544426	7.51615509	0.9305
hypothetical protein	3891	281354	281806	6.637168142	0	0
Integrase domain protein	3890	281910	283160	5.6	3.722	0.66464
Acetyltransferase	3889	283286	284350	0	0	#DIV/0!

Transposase IS4 family protein		284522	285469	9.503695882	3.93030623	0.41356
Transposase IS4 family		285433	286065	14.24050633	27.9738924	1.96439
Transposase	3886	286261	287352	1.863932898	0	0
INTERGENIC		287353	287591	5.434782609	0	0
hypothetical protein	3885	287603	287728	0	0	#DIV/0!
hypothetical protein	3884	287708	287842	0	0	#DIV/0!
O-methyltransferase (EC 2.1.1.-)	3883	288040	288423	0	2.42950392	#DIV/0!
Permease of the drug/metabolite transporter (DMT) superfamily	3882	288893	289786	11.19820829	4.16797312	0.3722
Fe-S oxidoreductase	3881	289857	291578	36.60662406	43.2539221	1.18159
hypothetical protein	3880	291840	292043	349.7536946	132.928571	0.38006
hypothetical protein	3879	292040	292213	161.849711	102.193642	0.63141
Voltage-gated chloride channel	3878	292452	293852	44.28571429	43.8664286	0.99053
DNA polymerase II (EC 2.7.7.7)	3877	293827	296409	40.12465914	46.0356447	1.14732
Cardiolipin synthetase (EC 2.7.8.-)	3876	296534	298072	65.66970091	61.1056567	0.9305
GCN5-related N-acetyltransferase, fig|164756.6.peg.1929 homolog	3875	298128	298985	25.67094516	30.4014002	1.18427
Beta-hexosaminidase (EC 3.2.1.52)	3874	298989	300680	61.50206978	51.7250148	0.84103
hypothetical protein	3873	300696	300818	0	15.2540984	#DIV/0!
Transcriptional regulator, DeoR family	3872	300859	301884	17.56097561	23.6029268	1.34406
Nucleotidyltransferase domain protein	3871	301963	302286	160.9907121	83.5433437	0.51893
hypothetical protein	3870	302279	302677	22.61306533	28.0552764	1.24067
hypothetical protein		303050	303172	0	0	#DIV/0!
DNA polymerase III alpha subunit (EC 2.7.7.7)	3868	303217	303810	42.15851602	70.6112985	1.6749
hypothetical protein	3867	303857	304531	17.8041543	2.7611276	0.15508
Flagellar biosynthesis protein flhA	3866	304723	306756	0.983767831	0.91539597	0.9305
hypothetical protein	3865	306802	307545	0	0	#DIV/0!
hypothetical protein	3864	307631	308413	20.46035806	10.7090793	0.52341
TPR repeat	3863	308572	309924	4.437869822	2.06471893	0.46525
TPR repeat		309934	310896	3.118503119	4.83627859	1.55083
TPR domain protein, putative component of TonB system	3861	311107	312696	4.405286344	5.8558842	1.32929
hypothetical protein	3860	312812	313357	3.669724771	3.4146789	0.9305
TPR repeat	3859	313490	314581	7.332722273	3.41154904	0.46525
Thioredoxin reductase (EC 1.8.1.9)	3858	314625	315551	96.11231102	127.617171	1.32779
hypothetical protein	3857	315642	317126	51.21293801	66.4642857	1.2978
hypothetical protein	3856	317376	318287	9.879253568	7.14983535	0.72372
hypothetical protein	3855	318432	318941	7.858546169	7.31237721	0.9305
Cell surface protein	3854	319024	321189	36.02771363	38.6812933	1.07365
Transcriptional regulator, MerR family	3853	321299	321640	8.797653959	51.8460411	5.89317
hypothetical protein	3852	321649	321822	202.3121387	166.736994	0.82416
hypothetical protein	3851	321819	322010	146.5968586	92.5628272	0.63141
hypothetical protein		322043	322156	8.849557522	0	0
Thymidylate synthase thyX (EC 2.1.1.-)	3849	322141	322983	489.3111639	353.634204	0.72272
Conserved domain protein	3848	323005	323916	342.4807903	337.063666	0.98418
N-acetylhexosamine 1-kinase	3846	323916	325046	135.3982301	133.399115	0.98524
hypothetical protein	3847	325023	325166	104.8951049	13.013986	0.12407
Multiple sugar ABC transporter, substrate-binding protein	3845	325129	326397	679.8107256	886.470032	1.304
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	3844	326470	327381	118.5510428	93.9692645	0.79265

Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	3843	327391	328242	57.57931845	51.3907168	0.89252
Uncharacterized protein YphG, TPR-domain containing	3842	328245	330521	78.20738137	67.0483304	0.85731
Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	3841	330595	331656	131.0084826	164.876532	1.25852
Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	3840	332132	333217	50.69124424	90.9059908	1.79333
Glycine cleavage system H protein	3839	333242	333613	123.9892183	168.041779	1.35529
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2)	3838	333624	334973	67.45737583	96.567828	1.43154
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2)	3837	334970	336403	86.53175157	94.80321	1.09559
Lipoate-protein ligase A	3836	336414	337442	41.82879377	57.0248054	1.36329
Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	3835	337465	338970	63.12292359	80.3754153	1.27332
hypothetical protein	3834	339034	339756	94.18282548	87.6371191	0.9305
hypothetical protein	3833	339771	340451	91.17647059	106.733824	1.17063
Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit B	3832	340448	341800	64.34911243	119.065459	1.8503
hypothetical protein		341829	342008	0	0	#DIV/0!
Iron-sulfur cluster-binding protein	3830	341995	342807	0	0	#DIV/0!
Flagellar synthesis regulator fleN	3829	342943	344082	135.2063213	230.378402	1.7039
hypothetical protein	3828	344073	344624	226.8602541	197.583485	0.87095
hypothetical protein	3827	344739	344897	12.65822785	17.6677215	1.39575
hypothetical protein		345083	345220	284.6715328	135.839416	0.47718
hypothetical protein	3825	345201	345380	156.424581	119.561453	0.76434
hypothetical protein	3824	345616	346023	31.94103194	34.2936118	1.07365
hypothetical protein		346013	346261	342.7419355	356.441532	1.03997
hypothetical protein		346371	346757	103.626943	173.564767	1.6749
DNA polymerase III alpha subunit (EC 2.7.7.7)	3821	346906	350898	104.5226131	112.221106	1.07365
conserved hypothetical membrane protein	3820	350909	351496	66.439523	98.2810903	1.47926
ATP-dependent DNA helicase RecG (EC 3.6.1.-)	3819	351521	353806	54.70459519	59.454267	1.08682
RNA polymerase sigma factor RpoD	3818	354130	355032	29.93348115	93.8752772	3.13613
CbbY family protein	3817	355050	355742	85.26011561	91.4364162	1.07244
hypothetical membrane protein	3816	356003	357115	374.1007194	583.236061	1.55903
transcriptional regulator, Crp/Fnr family	3815	357308	357964	64.02439024	85.1067073	1.32929
transcriptional regulator, Crp/Fnr family	3814	357966	358967	215.7842158	214.730769	0.99512
COG0613, Predicted metal-dependent phosphoesterases (PHP family)	3813	359114	360001	140.9244645	113.296505	0.80395
hypothetical protein	3812	360039	360458	582.3389021	661.787589	1.13643
conserved hypothetical protein-putative a phopsphoesterase or an exonuclease, fig|138119.3.peg.2719 homolog	3811	360530	361507	131.013306	169.528147	1.29398
hypothetical protein	3810	361585	362448	1.158748552	4.31286211	3.722
Protein involved in catabolism of external DNA	3809	362540	363424	28.28054299	35.7884615	1.26548
Outer membrane autotransporter barrel domain precursor	3808	363707	366472	1010.126582	977.950452	0.96815

COG1272: Predicted membrane protein hemolysin III homolog	3807	366574	367230	9.146341463	5.67378049	0.62033
COG0488: ATPase components of ABC transporters with duplicated ATPase domains	3805	367284	368981	342.1985816	353.611998	1.03335
hypothetical protein	3806	368978	369736	207.1240106	185.363456	0.89494
Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	3804	369824	370555	47.87961696	48.370725	1.01026
Phosphoserine aminotransferase (EC 2.6.1.52)	3803	370591	371697	116.636528	137.976492	1.18296
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	3802	371718	372893	97.87234043	101.365106	1.03569
hypothetical protein	3801	372958	373077	42.01680672	39.0966387	0.9305
Flavodoxin	3800	373078	373506	7.009345794	21.7406542	3.10167
hypothetical protein	3799	373677	375989	33.30449827	50.7106401	1.52264
hypothetical protein	3798	376120	376851	43.77564979	47.0978112	1.07589
Uncharacterized protein TP_0900	3797	376851	379853	22.98467688	24.7968021	1.07884
ATP-dependent nuclease, subunit A	3796	379846	383655	14.70202153	19.2988973	1.31267
Transcription accessory protein (S1 RNA-binding domain)	3795	383668	386190	169.7065821	196.283109	1.1566
Methyltransferase gidB (EC 2.1.-.-)	3794	386262	386993	41.03967168	59.8269494	1.45778
hypothetical protein	3793	386978	388363	20.2166065	17.46787	0.86404
HTH transcriptional regulator TetR family	3792	388509	389099	5.084745763	7.88559322	1.55083
Metallo-beta-lactamase superfamily hydrolase	3791	389096	389743	29.36630603	5.75270479	0.19589
Phage infection protein	3790	389740	390915	16.17021277	21.3817021	1.32229
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	3789	390919	392307	10.1010101	6.04220779	0.59818
Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	3788	392401	392895	216.5991903	192.12753	0.88702
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	3787	392892	393611	189.1515994	218.712796	1.15628
Amidophosphoribosyltransferase (EC 2.4.2.14)	3786	393586	395058	113.451087	180.790082	1.59355
Mannose-6-phosphate isomerase (EC 5.3.1.8)	3785	395158	395508	97.14285714	124.952857	1.28628
Autoinducer 2 (AI-2) kinase LsrK (EC 2.7.1.-)	3784	395539	397161	68.43403206	68.2672626	0.99756
Autoinducer 2 (AI-2) aldolase LsrF (EC 4.2.1.-)	3783	397323	398201	222.095672	221.497153	0.99731
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	3782	398243	399343	199.8175182	176.591241	0.88376
hypothetical protein	3781	399336	399491	167.7419355	138.074194	0.82313
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	3780	399488	400099	80.19639935	82.2373159	1.02545
Fe-S oxidoreductase	3779	400130	401299	312.2326775	264.265184	0.84637
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	3778	401317	402978	251.6556291	282.903371	1.12417
Biotin synthase (EC 2.8.1.6)	3777	403002	403979	143.2958035	137.146366	0.95709
hypothetical protein	3776	404093	405622	111.1837802	102.84794	0.92503
hypothetical protein		405639	405773	0	0	#DIV/0!
Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	3774	405772	407103	58.60255447	69.2107438	1.18102
N-acetylglutamate synthase (EC 2.3.1.1)	3773	407198	408550	88.01775148	86.7181953	0.98524
Hemerythrin family protein	3772	408679	409149	700	528.603191	0.75515
ATP-dependent protease La (EC 3.4.21.53) Type I	3771	409606	412047	160.8247423	237.51732	1.47687

Uncharacterized protein BB_0097	3770	412053	412454	69.82543641	113.701995	1.62838
Peptidase, M48 family	3769	412548	413408	113.9534884	130.919186	1.14888
TPR domain protein, putative component of TonB system	3768	413415	414713	238.0585516	222.947227	0.93652
hypothetical protein	3767	414715	415659	205.5084746	177.425847	0.86335
hypothetical protein		415717	415902	5.405405405	0	0
Energy conserving hydrogenase Ehb polyferredoxin (protein K)	3765	415901	416329	761.682243	1010.94042	1.32725
Histone acetyltransferase HPA2 and related acetyltransferases	3764	416512	416994	20.74688797	17.3744813	0.83745
Integration host factor beta subunit	3763	417098	417595	1229.376258	1495.91449	1.21681
Core component MtsA of methionine-regulated ECF transporter	3762	417964	418515	45.37205082	62.4836661	1.37714
ATPase component MtsB of energizing module of methionine-regulated ECF transporter	3761	418610	420310	21.76470588	32.8411765	1.50892
Transmembrane component MtsC of energizing module of methionine-regulated ECF transporter	3760	420307	421137	10.84337349	15.6951807	1.44744
Putative cytoplasmic protein	3759	421472	422986	267.5033025	395.185931	1.47731
radical activating enzyme	3758	423018	423869	207.9905993	224.150999	1.0777
Hypothetical sugar kinase in cluster with indigoidine synthase indA , PfkB family of kinases	3757	423866	424819	77.64952781	92.7570829	1.19456
Indigoidine synthase A-like protein, uncharacterized enzyme involved in pigment biosynthesis	3756	424829	425752	193.9328277	258.080173	1.33077
alternate gene name: ipa-30d	3755	425778	426275	408.4507042	602.859155	1.47597
hypothetical protein	3754	426344	426493	288.590604	518.332215	1.79608
Cysteine synthase (EC 2.5.1.47)	3753	426527	427447	79.34782609	80.9130435	1.01973
hypothetical protein		427534	427674	0	0	#DIV/0!
hypothetical protein	3751	428089	428580	18.3299389	26.5315682	1.44744
hypothetical protein		428685	428846	6.211180124	0	0
hypothetical protein		428952	429539	6.814310051	9.51107325	1.39575
hypothetical protein	3748	429503	429712	33.49282297	17.8086124	0.53171
Glycosyl transferase, group 2 family protein	3747	430147	430980	1.200480192	1.11704682	0.9305
hypothetical protein	3746	431010	432404	0.717360115	0	0
Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52)	3745	432424	433467	0.958772771	0	0
Glycosyl transferase, group 2 family protein	3744	433512	434348	0	2.22607656	#DIV/0!
hypothetical protein		434604	434732	0	0	#DIV/0!
Phospholipid-lipopolysaccharide ABC transporter	3742	434745	436454	1.755412522	0.54447045	0.31017
hypothetical protein	3741	436464	437312	0	0	#DIV/0!
Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)	3740	437315	438382	0.937207123	0	0
UDP-glucose 4-epimerase (EC 5.1.3.2)	3739	438397	439407	0.99009901	0.92128713	0.9305
hypothetical protein	3738	439499	440356	2.333722287	0	0
hypothetical protein		440532	440726	0	0	#DIV/0!

putative protein family member (5Q829)	3736	440746	441336	0	0	#DIV/0!
Alpha-1,2-fucosyltransferase	3735	441373	442269	0	0	#DIV/0!
HlpA protein	3734	442269	443189	1.086956522	0	0
Maltose O-acetyltransferase (EC 2.3.1.79)	3733	443190	443801	0	0	#DIV/0!
Mannosyltransferase (EC 2.4.1.-)	3732	443899	445071	0	1.58788396	#DIV/0!
Tyrosine-protein kinase wzc (EC 2.7.1.112)	3731	445107	446114	6.951340616	5.54419067	0.79757
hypothetical protein	3730	446178	447797	6.79431748	2.87368746	0.42295
hypothetical protein	3729	447830	448009	27.93296089	15.5949721	0.5583
Nodulation protein noeA	3728	448021	449400	7.976794779	20.2429297	2.53773
hypothetical protein		449427	449543	0	0	#DIV/0!
Capsular polysaccharide export system periplasmic protein KpsD	3726	449540	451003	14.35406699	17.1725906	1.19636
Exopolysaccharide production protein exoZ	3725	451065	452120	0	0.88199052	#DIV/0!
hypothetical protein	3724	452701	452991	24.13793103	0	0
hypothetical protein	3723	452991	453428	11.4416476	2.12929062	0.1861
Glutamine ABC transporter, periplasmic glutamine-binding protein (TC 3.A.1.3.2)	3722	453578	454624	186.4244742	206.382409	1.10706
amino acid ABC transporter, permease protein	3721	454643	455302	160.8497724	179.322458	1.11484
Glutamine transport ATP-binding protein glnQ (TC 3.A.1.3.2)	3720	455316	456092	81.18556701	85.1359536	1.04866
Serine acetyltransferase (EC 2.3.1.30)	3719	456114	457073	20.85505735	28.1381648	1.34923
Cysteine desulfurase (EC 2.8.1.7)	3718	457085	458962	45.81779435	54.0354289	1.17935
Major membrane protein I	3717	458949	459893	29.66101695	47.3135593	1.59514
Sulfur carrier protein adenylyltransferase ThiF	3716	460055	461227	44.36860068	40.491041	0.91261
Asr3294 protein	3715	461230	461514	28.16901408	26.2112676	0.9305
Mov34/MPN/PAD-1	3714	461538	461966	60.74766355	34.7850467	0.57262
Cysteine synthase (EC 2.5.1.47)	3713	461963	462865	24.3902439	34.0426829	1.39575
Xaa-Pro aminopeptidase (EC 3.4.11.9)	3712	462994	464214	78.68852459	107.541393	1.36667
hypothetical protein	3711	464351	465718	21.94586686	9.52962692	0.43423
hypothetical protein		465706	465858	0	0	#DIV/0!
no significant homology.	3708	465814	466071	206.2256809	264.305447	1.28163
Iron-sulfur flavoprotein	3709	466068	466625	118.491921	197.125673	1.66362
hypothetical protein	3707	466703	467272	7.029876977	6.54130053	0.9305
Transcriptional regulator, TetR family	3706	467379	467957	27.6816609	17.7084775	0.63972
Neopullulanase (EC 3.2.1.135)	3704	467970	469439	2.722940776	4.43396869	1.62838
hypothetical protein		469431	469544	0	8.23451327	#DIV/0!
hypothetical protein		469531	469746	0	0	#DIV/0!
hypothetical protein	3702	469750	470676	14.03887689	16.0777538	1.14523
hypothetical protein		470675	470989	6.369426752	0	0
hypothetical protein		471126	471245	0	0	#DIV/0!
Deoxyribonuclease TatD	3700	471235	472050	30.67484663	52.5190184	1.71212
hypothetical protein	3698	472199	473974	0.563380282	0	0
Subtilisin-like serine protease		474155	474688	1.876172608	1.74577861	0.9305
Cell division protein ftsH (EC 3.4.24.-)		474690	475037	5.763688761	13.407781	2.32625
Cell division protein ftsH (EC 3.4.24.-)		475047	475652	14.87603306	27.6842975	1.861
hypothetical protein	3694	475654	475788	74.62686567	83.3283582	1.1166
Type I restriction modification DNA specificity domain, putative	3693	475781	477193	26.20396601	10.5439093	0.40238
type I restriction-modification system, M subunit, putative	3692	477190	479208	44.59861249	35.5047076	0.79609
putative transcriptional regulator	3691	479269	479895	47.92332268	47.5654952	0.99253
hypothetical protein	3690	479895	480053	6.329113924	17.6677215	2.7915

Transposase, mutator type		480115	480483	119.5652174	65.7418478	0.54984
hypothetical protein		480541	480672	53.4351145	42.6183206	0.79757
Transposase for insertion sequence element ISRM5		480676	481296	53.22580645	63.033871	1.18427
hypothetical protein	3686	481547	482122	0	0	#DIV/0!
hypothetical protein	3685	482215	482745	1.886792453	1.75566038	0.9305
hypothetical protein	3684	482870	483079	4.784688995	0	0
hypothetical protein		483206	483358	26.31578947	18.3651316	0.69788
PIN domain protein	3682	483575	483973	16.33986928	9.12254902	0.5583
hypothetical protein		484029	484235	47.61904762	0	0
hypothetical protein	3680	484486	485352	17.32101617	13.9682448	0.80643
serine/threonine-protein kinase	3679	485688	486023	5.970149254	2.77761194	0.46525
4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	3678	486086	486475	7.712082262	0	0
Transcriptional regulator, MerR family		486748	486936	5.319148936	0	0
Isochorismatase (EC 3.3.2.1)	3676	486945	487496	9.074410163	3.37749546	0.3722
hypothetical protein	3675	487699	488451	0	0	#DIV/0!
Putative GTP-binding protien TM0445	3674	488769	489998	75.67127746	103.725386	1.37074
Aspartate ammonia-lyase (EC 4.3.1.1)	3673	489995	491398	53.45687812	41.1197434	0.76921
Magnesium transporter	3672	491679	493022	32.76247208	38.7997022	1.18427
hypothetical protein		493188	493313	56	81.884	1.46221
hypothetical protein	3670	493346	493609	285.1711027	392.720532	1.37714
Thiazole biosynthesis protein ThiH	3669	493703	495142	301.5983322	397.030577	1.31642
Biotin synthase and related enzymes	3668	495257	496297	173.0769231	220.099038	1.27168
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	3667	496355	498007	459.4430993	563.819915	1.22718
hypothetical protein	3666	498068	498187	0	0	#DIV/0!
hypothetical protein	3665	498675	500180	9.302325581	4.32790698	0.46525
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	3664	500287	501246	23.98331595	37.8409802	1.5778
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3663	501243	502355	30.57553957	60.2482014	1.97047
Oligopeptide transport system permease protein oppC (TC 3.A.1.5.1)	3662	502365	503390	14.63414634	13.6170732	0.9305
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	3661	503390	504331	30.81827843	39.5536663	1.28345
hypothetical protein		504518	504655	36.49635036	47.5437956	1.3027
hypothetical protein	3658	504668	504820	0	0	#DIV/0!
hypothetical protein	3657	505204	506205	4.995004995	1.85914086	0.3722
hypothetical protein	3656	506312	507787	25.76271186	29.0189831	1.12639
Outer membrane protein tpn50 precursor (Antigen tpp57)		508029	509249	68.85245902	73.2196721	1.06343
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	3654	509277	510509	154.2207792	118.578328	0.76889
Xylulose kinase (EC 2.7.1.17)	3653	510514	511989	78.6440678	87.6877966	1.115
Phosphoglycolate phosphatase (EC 3.1.3.18)	3652	511976	512653	73.85524372	50.8545052	0.68857
Transcription regulator [contains diacylglycerol kinase catalytic domain]	3651	512685	513809	100.5338078	125.83274	1.25165
hypothetical protein		513855	514091	4.237288136	7.88559322	1.861
hypothetical protein	3649	514091	514582	2.036659878	1.89511202	0.9305
FOG: TPR repeat	3648	514703	516055	1.479289941	2.06471893	1.39575

hypothetical protein	3647	516099	516812	0	0	#DIV/0!
hypothetical protein	3646	516799	517347	0	0	#DIV/0!
hypothetical protein	3645	517388	517780	0	0	#DIV/0!
hypothetical protein	3644	517853	518134	3.558718861	3.3113879	0.9305
Transcriptional regulator, Cro/CI family	3643	518282	518674	20.40816327	7.12117347	0.34894
Uncharacterized protein TP_0851	3642	518751	520967	50.09025271	83.140343	1.65981
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	3641	520964	522340	39.35860058	40.6924198	1.03389
putative membrane protein	3640	522474	523463	44.48938322	66.8003033	1.50149
Aspartyl-tRNA synthetase (EC 6.1.1.12); Aspartyl-tRNA(Asn) synthetase	3639	523552	524862	117.5572519	137.799237	1.17219
Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-)	3638	524970	526481	124.4209133	216.151886	1.73726
Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-)	3637	526484	528001	88.33223467	128.810152	1.45825
hypothetical protein	3636	528051	528431	102.6315789	156.715789	1.52697
ATP-dependent DNA helicase RecG-related protein	3635	528791	530404	13.63918165	9.2300062	0.67673
hypothetical protein	3634	530430	530678	12.09677419	26.2641129	2.17117
putative ORF-2	3633	530690	530941	7.96812749	3.70717131	0.46525
hypothetical protein	3632	531029	531781	1.329787234	4.94946809	3.722
hypothetical protein	3631	531804	531962	0	0	#DIV/0!
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	3630	531969	534398	46.9328942	38.3079457	0.81623
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	3629	534411	536969	50.03909304	52.0177873	1.03954
hypothetical protein	3628	536985	537122	0	0	#DIV/0!
hypothetical protein		537570	537692	15.87301587	59.0793651	3.722
DNA polymerase III alpha subunit (EC 2.7.7.7)	3623	538143	539135	3.024193548	0	0
transposase, mutator family	3621	539337	539549	10.47120419	9.7434555	0.9305
hypothetical protein	3622	539522	539641	37.97468354	23.556962	0.62033
4-carboxymuconolactone decarboxylase (EC 4.1.1.44)	3620	539625	539942	192.4290221	416.817035	2.16608
hypothetical protein	3619	539986	540360	184.4919786	99.5187166	0.53942
iron ABC transporter, solute-binding protein	3618	540786	541907	1.78412132	4.98037467	2.7915
Iron ABC transporter, ATP-binding protein	3617	541973	542749	0	2.39819588	#DIV/0!
Vitamin B12 ABC transporter, permease component BtuC	3616	542751	543791	1.923076923	0.89471154	0.46525
Outer membrane protein of RND family multidrug efflux pump	3615	544265	545602	15.75393848	19.5453863	1.24067
Probable Co/Zn/Cd efflux system membrane fusion protein	3614	545599	546717	13.47708895	19.2286613	1.42677
RND multidrug efflux transporter; Acriflavin resistance protein	3613	546727	549894	12.74093434	28.5746488	2.24274
RNA polymerase sigma factor RpoD	3612	549930	551678	94.39359268	91.5594966	0.96998
hypothetical protein	3611	551786	551935	13.42281879	6.24496644	0.46525
hypothetical protein	3610	551940	553481	22.06359507	13.284231	0.60209
Ferredoxin	3607	554021	554575	45.12635379	41.9900722	0.9305
Rubrerythrin	3606	554783	555328	1838.589981	1608.95362	0.8751

Peroxide stress regulator PerR, FUR family	3605	555528	555956	210.2803738	123.921729	0.58932
Activator of 2-hydroxyglutaryl-CoA dehydratase	3604	556233	560792	266.798419	339.589592	1.27283
Cobyrinic acid A,C-diamide synthase	3603	560901	562280	203.7708484	201.754532	0.9901
2,3-butanediol dehydrogenase, R-alcohol forming, (R)- and (S)-acetoin-specific (EC 1.1.1.4)	3602	562351	563400	181.1248808	196.92183	1.08722
Outer membrane protein	3601	563530	564450	128.2608696	111.255435	0.86742
Serine acetyltransferase (EC 2.3.1.30)	3600	564464	565348	238.6877828	228.414593	0.95696
Fructokinase (EC 2.7.1.4)	3599	565364	566344	65.30612245	78.8076531	1.20674
Uncharacterized protein TP_0836	3598	566389	567135	50.9383378	58.6239946	1.15088
TPR domain protein, putative component of TonB system	3597	567462	568142	169.1176471	142.311765	0.8415
NAD-reducing hydrogenase subunit HoxE (EC 1.12.1.2)	3596	568364	568867	608.3499006	321.882704	0.52911
NAD-reducing hydrogenase subunit HoxF (EC 1.12.1.2)	3595	568876	570750	762.185324	555.209963	0.72844
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	3594	570760	572505	1132.951289	821.186246	0.72482
FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8)	3593	572622	573152	1160.377358	1760.92736	1.51755
hypothetical protein		573275	573685	285.3658537	272.341463	0.95436
Adenylate cyclase (EC 4.6.1.1)	3591	573698	576460	38.01593049	51.544714	1.35587
hypothetical protein		576489	576620	0	0	#DIV/0!
Two-component response regulator	3589	576725	577396	5.961251863	4.16020864	0.69788
hypothetical protein	3588	577679	577792	0	8.23451327	#DIV/0!
putative autotransporter protein	3587	577812	581858	4.201680672	3.67968364	0.87576
hypothetical protein		581904	582074	0	0	#DIV/0!
Regulators of stationary/sporulation gene expression	3585	582247	582501	31.49606299	25.6437008	0.81419
hypothetical protein	3584	582514	582909	2.53164557	0	0
hypothetical protein		582911	583033	8.196721311	0	0
hypothetical protein	3582	583048	583494	31.39013453	27.1221973	0.86404
ABC transporter integral membrane protein	3581	583498	584646	62.71777003	85.1067073	1.35698
ABC transporter integral membrane protein	3580	584643	585725	72.08872458	63.6386322	0.88278
ABC-type sugar transport system, ATP-binding protein (EC 3.6.3.17)	3579	585722	587314	117.4623116	135.016018	1.14944
Hypothetical lipoprotein	3578	587382	588611	1406.834825	1651.27787	1.17375
Hypothetical lipoprotein	3577	588727	589947	620.1486375	759.92114	1.22539
Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	3576	590018	591016	244.6700508	312.685787	1.27799
hypothetical protein	3575	591126	592427	7.686395081	12.8739431	1.6749
ATPase	3574	592619	593836	7.395234182	6.88126541	0.9305
Nitroreductase	3573	593916	594116	5	0	0
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	3572	594124	595506	2.170767004	0	0
Uroporphyrinogen-III decarboxylase-like	3571	595680	596672	15.12096774	1.87600806	0.12407
Melibiose carrier protein, Na+/melibiose symporter	3570	596696	598060	8.797653959	3.41092375	0.38771
Virulence-associated cell-wall-anchored protein SasH (LPXTG motif); 5'-nucleotidase (EC 3.1.3.5)	3569	598155	599636	14.85482782	9.42437542	0.63443

Uroporphyrinogen-III decarboxylase	3568	599770	600852	27.72643253	13.7597043	0.49627
LysR family regulatory protein CidR	3567	600966	601844	25.05694761	21.1958998	0.84591
transcriptional regulator (Lrp/AsnC family)	3566	601871	602344	202.9598309	114.099366	0.56218
Alanine dehydrogenase (EC 1.4.1.1)	3565	602581	603696	2462.780269	1433.72108	0.58216
Amino acid transporter	3564	603721	605130	1449.254791	674.926189	0.46571
Sodium-dependent phosphate transporter	3563	605230	606906	102.6252983	83.8338305	0.81689
Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	3562	606945	607592	126.7387944	136.626739	1.07802
hypothetical protein	3561	607682	608851	46.19332763	55.7185629	1.2062
Putative cytoplasmic protein	3560	609199	609567	187.3278237	161.491736	0.86208
hypothetical protein	3559	609564	609770	325.2427184	239.400485	0.73607
hypothetical protein	3558	609833	610060	52.86343612	8.19823789	0.15508
hypothetical protein		610015	610158	41.95804196	58.5629371	1.39575
hypothetical protein	3556	610195	610395	120	69.7875	0.58156
hypothetical protein		610662	611093	18.56148492	17.2714617	0.9305
Cold-shock DEAD-box protein A	3554	611674	612444	164.9350649	250.147403	1.51664
hypothetical protein	3553	612428	612544	17.24137931	8.02155172	0.46525
hypothetical protein	3552	612507	613373	35.79676674	47.2771363	1.32071
6-phosphofructokinase (EC 2.7.1.11)	3551	613376	614479	120.5802357	139.195376	1.15438
hypothetical protein	3550	614586	615413	56.83192261	43.8808948	0.77212
hypothetical protein	3549	615404	615691	66.20209059	94.0226481	1.42024
Putative DNA-binding protein	3548	615756	616307	5.444646098	3.37749546	0.62033
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	3547	616399	617298	1.112347052	0	0
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	3546	617322	618968	0	2.82654921	#DIV/0!
CO dehydrogenase accessory protein CooC (nickel insertion)	3545	619014	619784	0	1.20844156	#DIV/0!
Inner membrane protein	3544	619801	621621	1.098901099	0.51126374	0.46525
Putative glutathione transporter, ATP-binding component	3543	621618	624248	0	0.35380228	#DIV/0!
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	3542	624245	625225	0	0	#DIV/0!
Nitrogenase iron protein (EC 1.18.6.1)	3541	625411	626178	5.215123859	4.85267275	0.9305
Nitrogenase molybdenum-iron protein alpha and beta chains-like protein	3540	626175	627572	5.726556908	7.9928418	1.39575
Nitrogenase vanadium-cofactor synthesis protein VnfN	3538	627672	628895	4.088307441	3.80417007	0.9305
hypothetical protein	3539	628867	629118	0	0	#DIV/0!
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	3537	629131	631215	5.75815739	10.2694338	1.78346
hypothetical protein	3536	631219	631452	17.16738197	87.8583691	5.11775
conserved hypothetical protein; possible membrane protein	3535	631642	632055	4.842615012	0	0
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	3534	632074	633018	31.77966102	50.2706568	1.58185
Sugar ABC transporter, permease protein	3533	633015	634151	34.33098592	50.784331	1.47926
sugar ABC transporter, ATP-binding protein	3532	634138	635718	61.39240506	81.860443	1.3334
putative lipoprotein	3531	635847	636929	1147.874307	1228.0536	1.06985
2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	3530	637013	638968	440.9207161	505.944501	1.14747
hypothetical protein	3529	639012	639641	52.46422893	44.3799682	0.84591

hypothetical protein	3528	639716	639943	4.405286344	0	0
Putative deoxyribonuclease YcfH	3527	640086	640946	103.4883721	126.591279	1.22324
Glutamine synthetase type III, GlnN (EC 6.3.1.2)	3525	641148	643292	316.9245195	455.434599	1.43704
hypothetical protein		643405	643536	7.633587786	0	0
Probable two-component sensor, near polyamine transporter	3523	643589	644818	10.57770545	14.3852726	1.35996
hypothetical protein	3522	644883	645503	17.74193548	16.508871	0.9305
hypothetical protein	3521	645607	645801	30.92783505	9.59278351	0.31017
BNR repeat domain protein	3520	645813	648089	13.18101933	18.806239	1.42677
hypothetical protein	3519	648086	648466	2.631578947	2.44868421	0.9305
Two-component response regulator yvqC	3518	648537	649157	19.35483871	51.0274194	2.63642
HicB	3517	649443	649613	29.41176471	71.1558824	2.4193
hypothetical protein	3516	649678	649911	218.8841202	95.8454936	0.43788
hypothetical protein	3515	649904	650362	30.56768559	16.2532751	0.53171
hypothetical protein	3514	650425	650658	12.87553648	0	0
Nitrogen regulatory protein P-II	3513	650761	651102	96.77419355	79.1334311	0.81771
Ammonium transporter precursor	3512	651114	652475	117.5606172	92.2979427	0.78511
Mo/Fe-nitrogenase-specific transcriptional regulator NifA	3511	652707	654314	103.2980709	105.962352	1.02579
hypothetical protein	3510	654649	655356	188.1188119	206.631542	1.09841
Uncharacterized protein TP_1001	3509	655418	656443	20.48780488	30.8653659	1.50652
Thioredoxin	3508	656499	656822	235.2941176	152.682663	0.6489
Methionine ABC transporter permease protein	3507	656917	657585	23.95209581	26.4663174	1.10497
Methionine ABC transporter ATP-binding protein	3506	657572	658312	63.51351351	71.6736486	1.12848
Response regulator	3505	658473	659561	53.30882353	71.8400735	1.34762
Sensory box histidine kinase/response regulator	3504	659551	662514	44.3616661	48.8410091	1.10097
hypothetical protein	3503	662654	662770	181.0344828	64.1724138	0.35448
Aspartate carbamoyltransferase (EC 2.1.3.2)	3502	662828	663751	46.5872156	40.3250271	0.86558
Aspartate carbamoyltransferase regulatory chain (pyrI)	3501	663753	664187	18.43317972	34.3041475	1.861
Dihydroorotase (EC 3.5.2.3)	3500	664230	665525	38.61003861	40.2378378	1.04216
Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1)	3499	665529	666371	21.37767221	22.1021378	1.03389
Dihydroorotate dehydrogenase, catalytic subunit (EC 1.3.3.1)	3498	666368	667273	40.8839779	55.521547	1.35803
hypothetical protein	3497	667350	667940	171.1864407	233.413559	1.3635
hypothetical protein	3496	667972	668526	814.0794224	739.025271	0.9078
hypothetical protein		668548	668670	90.16393443	7.62704918	0.08459
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	3494	668754	669677	198.2665222	232.877031	1.17457
Integral membrane protein	3493	669717	670625	158.5903084	120.924009	0.76249
Nicotinamidase (EC 3.5.1.19)	3492	670612	671352	154.0540541	119.456081	0.77542
Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	3491	671349	672797	103.5911602	95.1063536	0.91809
Uridine kinase (EC 2.7.1.48)	3490	672799	674508	105.9098888	98.0046811	0.92536
archaeal ATPase, fused to C-terminal DUF234 domain	3489	674575	675885	16.03053435	15.6267176	0.97481
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	3488	675953	676912	19.81230448	27.1678832	1.37126

hypothetical protein	3487	676912	677442	156.6037736	112.362264	0.71749
FIG018583: protein of unknown function	3486	677439	678134	87.76978417	65.6035971	0.74745
Dimethyladenosine transferase (EC 2.1.1.-)	3485	678112	679050	93.81663113	81.3443497	0.86706
ComEC/Rec2-related protein	3484	679034	680590	44.34447301	53.2226864	1.20021
hypothetical protein	3483	680639	681685	187.3804971	160.124283	0.85454
hypothetical protein	3482	681817	682491	51.92878338	37.2752226	0.71781
Flagellar protein flgJ [peptidoglycan hydrolase] (EC 3.2.1.-)	3481	682543	683055	238.28125	327.128906	1.37287
Flagellar basal-body rod protein flgG	3480	683068	683865	410.7142857	554.264668	1.34951
Flagellar basal-body rod protein flgF	3479	683881	684732	766.1574618	792.729142	1.03468
hypothetical protein		684733	684939	14.5631068	9.03398058	0.62033
hypothetical protein	3477	684899	685195	253.3783784	223.194257	0.88087
hypothetical protein	3476	685197	685454	202.3346304	152.066148	0.75156
Helix-turn-helix domain protein	3475	685480	685842	52.48618785	46.2679558	0.88153
hypothetical protein	3474	685937	686149	231.1320755	263.349057	1.13939
Predicted cell-wall-anchored protein SasA (LPXTG motif)	3473	686215	687849	368.4210526	403.748164	1.09589
Von Willebrand factor, type A	3472	687869	690157	249.1258741	203.750219	0.81786
hypothetical protein	3471	690256	690429	115.6069364	53.7861272	0.46525
hypothetical protein	3470	690426	690602	125	58.15625	0.46525
Tyrosyl-tRNA synthetase (EC 6.1.1.1)	3469	690794	692044	193.6	297.76	1.53802
Virulence factor mviN homolog	3468	692149	693768	79.06114886	97.7053737	1.23582
Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	3467	693867	695330	91.59261791	154.553315	1.6874
Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	3466	695471	700210	78.24427481	137.128393	1.75257
Hydroxylamine reductase (EC 1.7.-.-)	3465	700784	702349	8.945686901	14.8642173	1.66161
hypothetical protein		702367	702498	7.633587786	7.10305344	0.9305
Methyl-directed repair DNA adenine methylase (EC 2.1.1.72)	3463	702582	703439	9.334889148	7.60035006	0.81419
hypothetical protein	3462	703411	703854	6.772009029	0	0
Nucleotidyltransferase domain protein	3461	703844	704167	18.57585139	2.88080495	0.15508
Aldo/keto reductase	3460	704193	705353	103.4482759	94.6543103	0.91499
hypothetical protein	3459	705393	706082	206.095791	186.370102	0.90429
Proline/sodium symporter PutP (TC 2.A.21.2.1) @ Propionate/sodium symporter	3458	706161	707738	127.4571972	148.691186	1.1666
hypothetical protein	3455	708812	709105	2979.522184	1600.58703	0.5372
COG0799: Uncharacterized homolog of plant Iojap protein	3454	709137	709496	373.2590529	295.479109	0.79162
Transcriptional regulator	3453	709471	710691	91.80327869	106.778689	1.16313
Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18) / Hydrolase (HAD superfamily), yqeK # fusion with NadD	3452	710688	711857	101.7964072	124.968777	1.22763
COG0536: GTP-binding protein Obg	3451	711861	712910	153.4795043	230.629171	1.50267
LSU ribosomal protein L27p	3450	713011	713295	1031.690141	1349.88028	1.30842
hypothetical protein	3449	713297	713638	1079.178886	1547.19501	1.43368
LSU ribosomal protein L21p	3448	713644	713976	1518.072289	1855.39458	1.2222
hypothetical protein		714083	714247	18.29268293	28.3689024	1.55083
Phytoene synthase (EC 2.5.1.32)	3446	714305	715453	140.2439024	151.570993	1.08077
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	3445	715477	716232	103.3112583	117.082781	1.1333
Na+ driven multidrug efflux pump	3444	716229	717587	34.60972018	42.482327	1.22747

Arginyl-tRNA synthetase (EC 6.1.1.19)	3443	717595	719424	162.2807018	172.42818	1.06253
COG1496: Uncharacterized conserved protein	3442	719436	720206	115.5844156	125.677922	1.08733
Uncharacterized protein TP_0110	3441	720203	721933	60.11560694	51.0968208	0.84998
hypothetical protein	3439	722504	722917	108.9588378	92.374092	0.84779
hypothetical protein	3438	722917	723480	145.6483126	100.81794	0.6922
hypothetical protein		723582	723695	0	0	#DIV/0!
hypothetical protein	3436	723789	723938	0	0	#DIV/0!
Putative secreted protein	3434	724640	725137	56.33802817	43.0613682	0.76434
Pirin	3433	725162	725893	71.03064067	79.0536212	1.11295
Adenine phosphoribosyltransferase (EC 2.4.2.7)	3432	726072	726605	105.065666	122.204503	1.16313
hypothetical protein	3431	726730	727269	5.565862709	10.3580705	1.861
Response regulator containing a CheY-like receiver domain and a GGDEF domain	3430	727450	728355	89.50276243	123.381215	1.37852
hypothetical protein	3429	728520	729053	120.0750469	87.2889306	0.72695
hypothetical protein	3428	729607	729867	180.7692308	118.101923	0.65333
PIN domain protein	3427	729873	730307	78.34101382	77.1843318	0.98524
radical activating enzyme	3426	730323	731312	51.56723964	67.7411527	1.31365
hypothetical protein	3425	731422	731757	325.3731343	194.432836	0.59757
RNA polymerase sigma-H factor AlgT	3424	731754	732314	92.85714286	58.15625	0.6263
hypothetical protein	3423	732311	732784	105.7082452	66.8858351	0.63274
Ketoisovalerate oxidoreductase subunit vorC (EC 1.2.7.7)	3422	732798	733028	1052.173913	473.341304	0.44987
2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3)	3421	733025	734155	211.5044248	230.566372	1.09013
2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3)	3420	734152	734931	215.661104	314.148267	1.45668
2-oxoglutarate oxidoreductase, gamma subunit (EC 1.2.7.3)	3419	734931	735464	185.7410882	195.527205	1.05269
hypothetical protein	3418	735517	735852	50.74626866	63.8850746	1.25891
Cytotoxic translational repressor of toxin-antitoxin stability system	3417	735849	736199	85.71428571	53.1714286	0.62033
Deoxyribose-phosphate aldolase (EC 4.1.2.4)	3416	736398	737135	75.98371777	59.3398915	0.78096
B. burgdorferi predicted coding region BB0418	3415	737246	738193	48.57444562	40.2856389	0.82936
hypothetical protein	3414	738321	739589	132.4921136	112.27642	0.84742
Flagellar hook-length control protein fliK		739603	743517	65.66172713	67.7548544	1.03188
putative autotransporter protein	3412	743514	746525	227.1670541	195.618233	0.86112
Adenylate cyclase (EC 4.6.1.1)	3411	746631	748520	61.40815246	59.1106406	0.96259
hypothetical protein	3410	748513	751584	69.03288831	71.2040052	1.03145
hypothetical protein	3408	751574	752755	32.17612193	23.6367485	0.73461
Methylated-DNA--protein-cysteine methyltransferase	3409	752752	753087	98.50746269	105.549254	1.07148
hypothetical protein		753308	753433	8	0	0
Transcriptional activator of maltose regulon, MalT	3406	753509	756088	4.265219077	3.60798759	0.84591
Transcriptional activator of maltose regulon, MalT	3405	756145	758619	2.425222312	1.8805578	0.77542
Transcriptional regulator, AraC family	3404	758820	760298	8.119079838	11.9617727	1.47329
Two-component response regulator yesN	3403	760303	761916	5.57966522	5.19187849	0.9305
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	3402	761943	762581	20.37617555	23.3354232	1.14523
FOG: WD40 repeat	3401	762653	765697	22.99605782	29.3455979	1.27611

Translation elongation factor LepA	3399	765756	767576	178.3333333	170.591667	0.95659
hypothetical protein		767563	767700	14.59854015	0	0
hypothetical protein	3398	767738	771766	16.38530288	9.47132572	0.57804
hypothetical protein	3397	771777	772859	44.36229205	40.4191312	0.91111
Apoptotic chromatin condensation inducer in the nucleus	3396	772934	773953	180.5691855	154.322375	0.85464
hypothetical protein		773983	774198	0	4.32790698	#DIV/0!
hypothetical protein	3394	774327	775523	775.9197324	502.594482	0.64774
hypothetical protein	3393	775548	775973	465.8823529	258.350588	0.55454
hypothetical protein	3391	775987	776970	138.3519837	85.1932859	0.61577
Uncharacterized protein TP_0930	3392	776967	778637	32.33532934	54.6041916	1.68869
Uncharacterized protein TP_0928	3390	778641	780185	483.1606218	552.032383	1.14254
Branched-chain amino acid aminotransferase (EC 2.6.1.42)	3389	780483	781568	348.3870968	518.85023	1.48929
Outer membrane protein/protective antigen OMA87-like precursor	3388	781590	782885	111.969112	147.299228	1.31553
Glycosyltransferase	3387	782891	784114	130.0081766	149.123467	1.14703
hypothetical protein		784264	784377	0	0	#DIV/0!
Histone H1-like protein	3384	784361	784609	6681.451613	7166.35081	1.07257
Chromate transport protein	3383	784695	785246	14.51905626	32.0862069	2.20994
Chromate transport protein	3382	785243	785812	43.93673111	58.8717047	1.33992
Aspartyl-tRNA synthetase (EC 6.1.1.12)	3381	785892	787748	115.8405172	128.344828	1.10794
hypothetical protein	3380	787773	787889	0	0	#DIV/0!
hypothetical protein	3379	788087	788392	6.557377049	3.05081967	0.46525
Outer membrane lipoprotein omp16 precursor	3378	788439	789641	46.5890183	40.2545757	0.86404
hypothetical protein	3377	789676	789819	6.993006993	6.50699301	0.9305
hypothetical protein	3376	789876	790367	40.73319756	34.1120163	0.83745
Cold-shock DNA-binding domain protein	3375	790529	791476	79.19746568	62.8848997	0.79403
Oxidoreductase (EC 1.1.1.-)	3374	791491	792660	125.748503	140.092387	1.11407
Ferric siderophore transport system, periplasmic binding protein TonB	3373	792713	793384	90.90909091	117.872578	1.2966
Biopolymer transport protein ExbD/TolR	3372	793377	793775	206.0301508	151.96608	0.73759
Biopolymer transport protein	3371	793772	794185	133.1719128	92.374092	0.69365
MotA/TolQ/ExbB proton channel family protein	3370	794182	794826	212.7329193	192.168478	0.90333
hypothetical protein	3369	794835	795686	162.1621622	148.705053	0.91701
hypothetical protein	3368	795689	795931	152.892562	119.196281	0.77961
hypothetical protein		795891	796034	27.97202797	0	0
DNA repair protein RadC	3367	796031	796813	1.278772379	2.3797954	1.861
Oxidoreductase, aldo/keto reductase family	3365	796942	798102	104.3103448	123.531897	1.18427
hypothetical protein	3364	798202	798447	1506.122449	2677.56122	1.77778
Inner membrane protein CreD	3363	798569	799219	72.30769231	65.8507692	0.9107
tRNA dihydrouridine synthase B (EC 1.-.-.-)	3362	799227	800264	28.92960463	31.4054966	1.08558
Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	3361	800436	800873	773.4553776	832.552632	1.07641
Flavoprotein	3360	801042	802259	427.2801972	509.21364	1.19176
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	3359	802980	804116	191.9014085	154.810299	0.80672
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	3358	804131	804922	145.3855879	144.692162	0.99523
Argininosuccinate lyase (EC 4.3.2.1)	3357	805025	806431	151.4935989	162.142603	1.07029
motif=sugar transport proteins signatures	3356	806521	806907	69.94818653	40.9805699	0.58587

hypothetical protein	3355	806886	807143	89.49416342	54.3093385	0.60685
DNA-binding protein	3354	807268	807606	2.958579882	2.75295858	0.9305
hypothetical protein	3353	807766	808074	25.97402597	6.04220779	0.23263
hypothetical protein	3352	808071	809087	2.952755906	2.74753937	0.9305
hypothetical protein	3351	809245	809451	58.25242718	49.6868932	0.85296
Argininosuccinate synthase (EC 6.3.4.5)	3350	809647	810948	470.3618168	660.447267	1.40413
N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)	3349	811039	812247	21.52317881	38.5140728	1.78942
Sensor histidine protein kinase UhpB, glucose-6-phosphate specific (EC 2.7.13.3)	3348	812234	813520	73.09486781	61.5027216	0.84141
Transcriptional regulatory protein UhpA	3347	813513	814133	19.35483871	33.0177419	1.70592
amino acid ABC transporter, permease protein	3346	814269	814967	0	0	#DIV/0!
amino acid ABC transporter, amino acid-binding protein	3345	815016	815834	2.444987775	1.13753056	0.46525
Probable amino-acid ABC transporter permease protein ytmM	3344	815869	816606	0	1.26255088	#DIV/0!
amino acid ABC transporter, ATP-binding protein	3343	816603	817361	0	1.22757256	#DIV/0!
Lantibiotic modifying enzyme	3342	817374	818738	2.93255132	0.68218475	0.23263
hypothetical protein	3341	818869	819186	15.77287066	11.7413249	0.7444
amino acid ABC transporter, permease protein	3340	819345	820043	1.432664756	0	0
amino acid ABC transporter, amino acid-binding protein	3339	820078	820887	2.472187886	1.15018541	0.46525
Probable amino-acid ABC transporter permease protein ytmM	3338	820916	821626	0	2.62112676	#DIV/0!
amino acid ABC transporter, ATP-binding protein	3337	821623	822381	0	0	#DIV/0!
Lantibiotic modifying enzyme	3336	822392	823783	5.751258088	4.01365924	0.69788
iron-sulfur flavoprotein	3335	823802	824359	25.13464991	18.3761221	0.73111
Acetylornithine aminotransferase (EC 2.6.1.11)	3334	824372	825736	93.84164223	68.9006598	0.73422
Acetylglutamate kinase (EC 2.7.2.8)	3333	825729	826619	102.1814007	108.967853	1.06642
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	3332	826638	827780	120.3866432	102.207821	0.849
hypothetical protein	3331	828050	828421	179.8365123	139.448229	0.77542
Glycerol kinase (EC 2.7.1.30)	3330	828470	829954	94.55782313	118.369728	1.25182
Putative malate dehydrogenase (EC 1.1.1.37), similar to archaeal MJ1425	3329	829974	831083	291.2533814	335.617674	1.15232
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	3328	831158	832477	1278.999242	1537.19447	1.20187
SN-glycerol-3-phosphate transport system permease protein ugpE (TC 3.A.1.1.3)	3327	832555	833379	115.2912621	118.570995	1.02845
SN-glycerol-3-phosphate transport system permease protein ugpA (TC 3.A.1.1.3)	3326	833376	834251	106.2857143	141.436	1.33072
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	3325	834320	835138	106.3569682	136.503667	1.28345
Conserved domain protein	3323	835275	835835	12.5	16.6160714	1.32929
hypothetical protein		835816	835992	5.681818182	10.5738636	1.861
Plasmid maintenance system killer	3322	836035	836316	110.3202847	43.0480427	0.39021
Virulence associated protein	3321	836374	836676	119.205298	73.9470199	0.62033
Conserved domain protein	3320	837199	838164	121.2435233	107.995855	0.89074
Uncharacterized protein y4uA	3319	838478	839986	1.98938992	4.31929708	2.17117

Possible membrane transport protein	3318	840011	841285	0.784929356	2.1911303	2.7915
Putative enzyme	3317	841426	843720	2.615518745	2.43374019	0.9305
Citrate lyase alpha chain (EC 4.1.3.6)	3316	843723	845261	1.300390117	1.210013	0.9305
Citrate lyase beta chain (EC 4.1.3.6)	3315	845258	846166	1.101321586	2.04955947	1.861
Citrate lyase gamma chain, acyl carrier protein (EC 4.1.3.6)	3314	846145	846441	6.756756757	0	0
PrpF protein involved in 2-methylcitrate cycle	3313	846465	847625	3.448275862	2.40646552	0.69788
Transcriptional regulator, LysR family	3312	847700	848608	12.11453744	10.2477974	0.84591
hypothetical protein		848628	848762	0	6.94402985	#DIV/0!
Conserved domain protein	3310	849023	849433	17.07317073	61.2768293	3.58907
hypothetical protein	3309	849443	850282	11.91895113	23.2902265	1.95405
Chaperone protein DnaJ	3308	850287	850991	11.36363636	19.8259943	1.74469
Chaperone protein DnaK	3307	851014	852744	10.40462428	20.4387283	1.96439
hypothetical protein	3306	852781	853245	4.310344828	4.01077586	0.9305
hypothetical protein	3305	853259	853930	5.961251863	2.77347243	0.46525
membrane protein	3304	853933	854688	6.622516556	16.0218543	2.4193
Glutathione peroxidase (EC 1.11.1.9)	3303	854751	855281	37.73584906	54.4254717	1.44228
NAD-reducing hydrogenase subunit HoxE (EC 1.12.1.2)	3302	855510	856001	1234.215886	941.870672	0.76313
NAD-reducing hydrogenase subunit HoxF (EC 1.12.1.2)	3301	856014	857918	835.6092437	652.425158	0.78078
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	3300	857921	859663	1268.656716	1147.90155	0.90482
hypothetical protein	3299	859847	860881	325.9187621	269.071083	0.82558
hypothetical protein	3298	861130	861879	861.1481976	1034.85514	1.20172
Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)	3297	861876	864512	1020.485584	1132.06127	1.10934
Uncharacterized protein TP_0625	3296	864664	865044	205.2631579	208.138158	1.01401
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3295	865132	865710	17.30103806	9.65916955	0.5583
ATPase component NikO of energizing module of nickel ECF transporter	3294	865751	866524	102.1992238	81.85511	0.80094
Transmembrane component NikQ of energizing module of nickel ECF transporter	3293	866512	867330	141.809291	100.102689	0.7059
Core component NikM of nickel ECF transporter / Additional core component NikN of nickel ECF transporter	3292	867358	868365	283.0188679	132.136544	0.46688
hypothetical protein	3291	868594	868797	4.926108374	4.58374384	0.9305
hypothetical protein	3290	868868	869035	269.4610778	16.7155689	0.06203
DNA polymerase III alpha subunit (EC 2.7.7.7)	3289	869227	869886	95.59939302	5.64795144	0.05908
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	3288	870374	872107	80.7847663	864.457588	10.7008
NAD-reducing hydrogenase subunit HoxF (EC 1.12.1.2)	3287	872126	874009	97.18534254	1030.81413	10.6067
NAD-reducing hydrogenase subunit HoxE (EC 1.12.1.2)	3286	874002	874493	183.299389	2230.54684	12.1689
hypothetical protein		874542	874673	0	0	#DIV/0!
Methionine biosynthesis and transport regulator MtaR, LysR family	3284	874786	875715	26.91065662	161.259957	5.99242
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	3283	875727	877490	39.13783324	194.755814	4.97615
hypothetical protein	3282	877487	878695	47.18543046	229.543874	4.86472
predicted protein	3281	879668	880534	83.1408776	33.3088915	0.40063

Methyltransferase (EC 2.1.1.-)	3280	880524	881393	56.38665132	36.406214	0.64565
hypothetical protein		881534	881680	226.0273973	31.8664384	0.14098
Ubiquinone biosynthesis SAM-dependent O-methyltransferase (EC 2.1.1.-)	3278	881732	882385	1356.814701	183.820061	0.13548
Periplasmic binding protein precursor	3277	882407	883468	1388.312912	256.961828	0.18509
Iron(III) dicitrate transport system permease protein fecD (TC 3.A.1.14.1)	3276	883461	884558	506.8368277	127.233364	0.25103
Vitamin B12 ABC transporter, ATPase component BtuD	3275	884552	885319	447.1968709	116.464146	0.26043
Formylmethanofuran dehydrogenase subunit E	3274	885421	885945	692.7480916	111.873092	0.16149
Periplasmic binding protein precursor	3273	885955	887037	697.7818854	77.3983364	0.11092
Transport system permease protein precursor	3272	887030	888097	359.8875351	47.9639175	0.13327
ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components	3271	888094	888861	232.0730117	69.1505867	0.29797
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	3270	888911	890509	1202.753442	406.438673	0.33792
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	3269	890514	891500	775.862069	265.183063	0.34179
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	3268	891497	892330	429.7719088	122.87515	0.28591
Dipeptide transport ATP-binding protein dppD (TC 3.A.1.5.2)	3267	892335	893267	531.1158798	214.65397	0.40416
Dipeptide transport ATP-binding protein dppF (TC 3.A.1.5.2)	3266	893251	893922	697.466468	242.678838	0.34794
Aspartate aminotransferase (EC 2.6.1.1)	3265	894043	895332	194.7245927	160.978666	0.8267
MoxR-like ATPase in aerotolerance operon	3264	895416	896549	120.3208556	97.8600713	0.81333
hypothetical protein	3263	896559	897467	83.70044053	100.428414	1.19986
hypothetical protein	3262	897464	898480	43.30708661	43.0447835	0.99394
BatA (Bacteroides aerotolerance operon)	3261	898477	899478	37.96203796	48.3376623	1.27332
BatB	3260	899475	900554	38.92493049	41.3938832	1.06343
lipoprotein, putative	3258	900547	901191	35.71428571	40.4565217	1.13278
hypothetical protein		901188	901325	51.09489051	88.2956204	1.72807
hypothetical protein	3257	901380	902813	34.1939986	45.4535939	1.32929
Uncharacterized protein TP_0674	3256	902827	903447	66.12903226	73.5395161	1.11206
Translation initiation factor 1	3255	903456	903680	553.5714286	440.325893	0.79543
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	3254	903908	905278	151.0948905	164.365693	1.08783
hypothetical protein		905348	905629	103.202847	69.5391459	0.67381
hypothetical protein		905619	905765	47.94520548	82.8527397	1.72807
Flagellar hook-length control protein fliK		906182	909742	22.19101124	21.955618	0.98939
hypothetical protein	3250	910298	910453	19.35483871	6.00322581	0.31017
transcriptional regulator, PemK family	3249	910440	910787	11.52737752	8.04466859	0.69788
Transposase IS4 family protein	3248	910853	911206	16.99716714	5.27195467	0.31017
Nucleotidyltransferase family protein	3247	911452	911805	14.16430595	5.27195467	0.3722
hypothetical protein	3246	911792	912013	0	0	#DIV/0!
hypothetical protein		912101	912235	0	0	#DIV/0!
hypothetical protein	3243	912537	913157	188.3116883	126.886364	0.67381
hypothetical protein	3244	913147	913278	7.633587786	7.10305344	0.9305
Trk system potassium uptake protein trkA	3242	913250	914695	64.40443213	77.9712604	1.21065
Potassium uptake protein TrkH	3241	914692	916137	42.21453287	63.750519	1.51016
IrgA-associated membrane protein LrgB	3240	916175	916852	73.85524372	126.44904	1.71212
Antiholin-like protein LrgA	3239	916855	917211	39.3258427	44.4339888	1.12989

Cell surface protein	3238	917425	919803	150.9671993	94.3021447	0.62465
Conserved protein	3237	919814	920455	280.8112324	264.198128	0.94084
Molecular chaperone (small heat shock protein)	3236	920627	921082	13.18681319	18.4054945	1.39575
hypothetical protein		921188	921370	0	0	#DIV/0!
DNA-damage-inducible protein J	3234	921482	921763	131.6725979	155.635231	1.18199
AviX3	3233	921756	922019	72.24334601	60.1463878	0.83255
hypothetical protein	3232	922031	922465	62.21198157	102.912442	1.65422
hypothetical protein	3231	922468	922587	0	0	#DIV/0!
Cell surface protein IsdA, transfers heme from hemoglobin to apo-IsdC	3230	922612	923670	5.671077505	7.03591682	1.24067
Leucyl-tRNA synthetase (EC 6.1.1.4)	3229	923827	926316	191.7973462	214.011259	1.11582
Permeases of the major facilitator superfamily	3228	926340	927530	99.15966387	114.162185	1.1513
Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) # NAD-specific	3227	927783	928649	117.7829099	495.33545	4.2055
2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	3226	928662	929687	155.1219512	486.583415	3.13678
hypothetical protein		929680	929856	159.0909091	174.46875	1.09666
hypothetical protein		929981	930226	0	0	#DIV/0!
hypothetical protein	3223	930386	933067	252.1447221	142.993659	0.56711
hypothetical protein	3222	933153	933275	8.196721311	0	0
Thiamin ABC transporter, ATPase component	3221	933420	934490	36.44859813	26.9584112	0.73963
Thiamin ABC transporter, transmembrane component	3220	934480	936267	6.155567991	5.20705092	0.84591
Thiamin ABC transporter, substrate-binding component	3219	936237	937283	19.12045889	13.3436902	0.69788
hypothetical protein	3218	937348	937512	225.6097561	107.801829	0.47782
Circadian phase modifier	3217	937612	938325	133.2398317	182.706872	1.37126
UPF0272 protein CA_C0774	3216	938306	939712	246.0881935	219.057966	0.89016
ATP-utilizing enzyme of the PP-loop superfamily	3215	939722	940552	157.8313253	158.072892	1.00153
Permease of the major facilitator superfamily	3214	941127	942332	82.15767635	115.057676	1.40045
hypothetical protein	3213	942332	942793	75.92190889	98.9034707	1.3027
NADPH nitroreductase	3212	942795	943319	175.5725191	156.267176	0.89004
hypothetical protein	3211	943408	943560	118.4210526	116.3125	0.98219
ATP phosphoribosyltransferase (EC 2.4.2.17)	3210	943582	944436	228.3372365	228.811475	1.00208
Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	3209	944474	945100	261.9808307	181.34345	0.6922
Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-)	3208	945114	945743	127.1860095	112.429253	0.88398
Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)	3207	945771	946571	231.25	210.525625	0.91038
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	3206	946565	947881	186.1702128	161.211246	0.86593
Histidinol-phosphate aminotransferase (EC 2.6.1.9)	3205	947878	948939	111.2158341	86.8232799	0.78067
Histidinol dehydrogenase (EC 1.1.1.23)	3204	948981	951149	72.87822878	90.9898524	1.24852
Transcriptional regulator	3203	951152	951652	22	14.888	0.67673
hypothetical protein		951703	951843	0	0	#DIV/0!
hypothetical protein	3201	951974	953170	4236.622074	3636.4189	0.85833

DNA repair protein RadA	3200	953243	954646	104.2857143	105.678214	1.01335
hypothetical protein	3199	954695	954895	0	0	#DIV/0!
hypothetical protein	3198	955239	956414	114.0425532	140.168936	1.22909
Kynurenine formamidase, bacterial (EC 3.5.1.9)	3197	956537	957205	32.93413174	72.4341317	2.19936
Chaperone protein HtpG	3196	957207	959114	142.6324069	315.696644	2.21336
hypothetical protein	3195	959256	959384	0	0	#DIV/0!
Sensory box histidine kinase/response regulator	3194	959390	961825	86.02150538	80.0430108	0.9305
Putative cytochrome C-type biogenesis protein	3193	961828	962538	5.633802817	5.24225352	0.9305
Cytochrome c-type biogenesis protein CcsA/ResC	3192	962543	963328	7.643312102	4.74140127	0.62033
hypothetical protein	3191	963374	965803	32.52367229	29.1140387	0.89516
Uracil-DNA glycosylase (EC 3.2.2.-)	3190	965800	966006	106.7961165	130.992718	1.22657
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	3189	966138	967877	148.9361702	185.13686	1.24306
GTP-binding protein EngA	3188	967886	969463	128.725428	171.112873	1.32929
Transcriptional regulator, MerR family	3187	969465	969806	41.05571848	43.659824	1.06343
Methyltransferase (EC 2.1.1.-)	3186	969806	971065	42.89118348	81.2986497	1.89546
Zinc ABC transporter, inner membrane permease protein ZnuB	3185	971269	972114	40.23668639	36.3390533	0.90313
Zinc ABC transporter, ATP-binding protein ZnuC	3184	972111	972980	50.63291139	54.6093211	1.07853
Zinc ABC transporter, periplasmic-binding protein ZnuA	3183	972977	973954	29.68270215	40.0010235	1.34762
hypothetical protein	3182	973956	975326	53.28467153	29.8846715	0.56085
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)		975378	976331	16.78908709	21.4805876	1.27944
hypothetical protein	3180	976328	977761	65.59665038	53.8949756	0.82161
hypothetical protein	3179	977925	978812	104.8478016	75.5310034	0.72039
Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)	3178	978989	982519	73.25383305	98.8094832	1.34886
Probable glycolate oxidase	3177	982628	983527	57.84204672	57.9621802	1.00208
S-ribosylhomocysteine lyase (EC 4.4.1.21) / Autoinducer-2 production protein LuxS	3176	983547	984023	302.5210084	351.869748	1.16313
Flagellar hook-length control protein fliK	3175	984247	986280	36.39940974	31.1234629	0.85505
putative autotransporter protein	3174	986255	989479	66.99751861	44.4469603	0.66341
hypothetical protein	3173	989493	990779	35.76982893	28.9424572	0.80913
Geobacter sulfurreducens, CxxxxCH...CXXCH motif	3172	990978	992747	55.39853024	56.2823629	1.01595
putative autotransporter protein	3171	992760	996047	44.11317311	38.2164588	0.86633
hypothetical protein	3170	996041	997330	24.82544608	26.7094647	1.07589
Cell surface protein	3169	997339	999288	29.24576706	34.8519754	1.19169
Calcium-binding acidic-repeat protein precursor	3168	999290	1000927	26.87843616	27.852474	1.03624
hypothetical protein	3167	1000976	1001629	24.50229709	32.7741194	1.33759
5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	3166	1001629	1002339	97.18309859	94.3605634	0.97096
Sensor histidine kinase (EC 2.7.3.-)	3165	1002451	1003638	13.47935973	13.3264532	0.98866
Transcriptional regulatory protein UhpA	3164	1003661	1004272	22.91325696	22.8436989	0.99696
GGDEF domain protein	3163	1004309	1005436	303.4605146	269.159716	0.88697

hypothetical protein	3162	1005436	1005903	280.5139186	326.770878	1.1649
Predicted endonuclease distantly related to archaeal Holliday junction resolvase	3161	1006081	1006437	174.1573034	141.143258	0.81044
HD domain protein	3160	1006427	1007758	186.696901	162.468254	0.87022
Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB	3159	1007755	1008000	351.0204082	300.038776	0.85476
hypothetical protein		1008005	1009033	123.540856	164.738327	1.33347
LSU ribosomal protein L19p	3157	1009061	1009480	553.699284	595.164678	1.07489
tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)	3156	1009458	1010282	319.1747573	281.182646	0.88097
16S rRNA processing protein RimM	3155	1010291	1010797	664.0316206	555.357708	0.83634
hypothetical protein	3154	1010854	1011087	1557.939914	1673.30258	1.07405
SSU ribosomal protein S16p	3153	1011112	1011360	1262.096774	1384.49395	1.09698
T. pallidum predicted coding region TP0123	3152	1011586	1014447	38.44809507	35.7759525	0.9305
sensory box histidine kinase/response regulator	3151	1014467	1017499	14.84168865	13.8101913	0.9305
hypothetical protein	3150	1017536	1017745	19.13875598	44.5215311	2.32625
PIN domain protein	3149	1017738	1018166	35.04672897	28.2628505	0.80643
hypothetical protein	3148	1018169	1018426	23.3463035	18.1031128	0.77542
Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)	3147	1018648	1019817	57.4912892	125.633711	2.18527
Transcriptional regulator	3146	1020000	1020572	3.496503497	1.62674825	0.46525
hypothetical protein	3145	1020741	1021403	3.021148036	2.81117825	0.9305
hypothetical protein	3144	1021425	1021751	3.067484663	5.70858896	1.861
hypothetical protein	3143	1021805	1023097	68.11145511	59.7767028	0.87763
hypothetical protein	3142	1023194	1023988	2.518891688	8.2034005	3.25675
Uncharacterized protein TP_0584	3141	1024030	1025469	97.28978457	128.032662	1.31599
hypothetical protein	3140	1025668	1025805	109.4890511	135.839416	1.24067
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	3139	1025892	1027451	142.3989737	216.062219	1.5173
Cell division protein	3138	1027529	1028272	410.4979812	862.872813	2.10201
Dephospho-CoA kinase (EC 2.7.1.24)	3137	1028278	1028919	308.8923557	124.840874	0.40416
Macrolide-efflux protein	3136	1028895	1030271	7.994186047	9.46729651	1.18427
N-acetyltransferase	3135	1030347	1031228	36.32236095	35.9103292	0.98866
Flagellar motor switch protein fliM	3134	1031239	1032267	224.609375	245.34668	1.09233
Dihydrofolate synthase (EC 6.3.2.12) / Folylpolyglutamate synthase (EC 6.3.2.17)	3133	1032458	1033861	363.5067712	287.174982	0.79001
CO dehydrogenase accessory protein CooC (nickel insertion)	3132	1034497	1035270	344.1138422	329.827943	0.95848
Core component Fbp of predicted folate ECF transporter	3131	1035431	1035985	277.9783394	241.862816	0.87008
ATPase component of general energizing module of ECF transporters	3130	1035988	1036815	263.6033857	252.033857	0.95611
Transmembrane component of general energizing module of ECF transporters	3129	1036812	1037375	74.60035524	42.9715808	0.57602
hypothetical protein	3128	1037378	1037512	0	0	#DIV/0!
5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	3127	1037563	1038507	2266.949153	2625.90254	1.15834
Formate--tetrahydrofolate ligase (EC 6.3.4.3)	3126	1038588	1040321	1463.358338	1599.515	1.09304
Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	3125	1040390	1041019	424.4833068	593.212242	1.39749

Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	3124	1041088	1041939	708.5781434	884.576381	1.24838
hypothetical protein	3123	1041979	1043199	36.06557377	38.1352459	1.05739
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	3122	1043196	1044947	114.2204455	92.9968589	0.81419
hypothetical protein		1045419	1045787	13.58695652	12.642663	0.9305
hypothetical protein		1046234	1046398	18.29268293	17.0213415	0.9305
hypothetical protein	3119	1046437	1046784	5.763688761	5.36311239	0.9305
Putative cytoplasmic protein	3118	1046844	1047842	21.04208417	8.39128257	0.39879
hypothetical protein		1047876	1048004	7.8125	7.26953125	0.9305
ATPase involved in DNA repair	3116	1048068	1050731	4.881712354	2.44592565	0.50104
Helicase domain protein	3115	1050775	1055754	17.07170114	17.5671822	1.02902
hypothetical protein	3114	1055751	1056779	3.891050584	0.90515564	0.23263
hypothetical protein	3113	1056792	1057016	102.6785714	108.004464	1.05187
probable transcription regulator NMA0738	3112	1057047	1057670	15.10067114	23.4186242	1.55083
hypothetical protein	3111	1057807	1058655	7.075471698	5.48643868	0.77542
protein T24A6.7	3110	1058664	1059272	1.644736842	1.53042763	0.9305
hypothetical protein	3109	1059415	1060005	8.474576271	1.57711864	0.1861
hypothetical protein	3108	1060040	1060219	11.17318436	10.396648	0.9305
hypothetical protein	3107	1060200	1060973	0	1.20375162	#DIV/0!
hypothetical protein	3106	1061036	1061209	0	0	#DIV/0!
hypothetical protein	3105	1061274	1061597	3.095975232	0	0
hypothetical protein	3104	1061625	1062425	15	9.305	0.62033
hypothetical protein	3103	1062643	1062906	114.0684411	77.8365019	0.68237
Molybdopterin biosynthesis protein A	3102	1062984	1064204	136.0655738	128.897131	0.94732
hypothetical protein	3101	1064278	1064919	110.7644306	84.1950078	0.76013
hypothetical protein		1064976	1065104	31.25	0	0
Formate dehydrogenase H (EC 1.2.1.2); selenocysteine-containing	3099	1065082	1067280	601.455869	33.4438126	0.0556
Electron transport protein hydN	3098	1067277	1067795	1100.3861	59.2789575	0.05387
Formate dehydrogenase chain D (EC 1.2.1.2)	3097	1067822	1068559	398.9145183	21.463365	0.0538
hypothetical protein	3096	1068556	1068936	286.8421053	7.34605263	0.02561
Fe-S-cluster-containing hydrogenase components 2	3095	1068951	1069496	552.293578	39.2688073	0.0711
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	3094	1069499	1070863	494.8680352	31.3804985	0.06341
Formate dehydrogenase chain D (EC 1.2.1.2)	3093	1070856	1071467	62.19312602	1.52291326	0.02449
hypothetical protein	3092	1071468	1071587	16.80672269	7.81932773	0.46525
Benzoyl-CoA reductase subunit BadG (EC 1.3.99.15)	3091	1071559	1072356	10.03764115	12.8425345	1.27944
hypothetical protein	3090	1072357	1073511	25.9965338	31.4467071	1.20965
ABC-type polar amino acid transport system, ATPase component	3089	1073537	1074343	18.61042184	19.6259305	1.05457
Amino acid ABC transporter, periplasmic amino acid-binding portion	3088	1074423	1075232	65.51297899	108.117429	1.65032
Probable amino-acid ABC transporter, permease protein precursor	3087	1075306	1075971	1.503759398	6.9962406	4.6525
hypothetical protein	3086	1075961	1076152	20.94240838	29.2303665	1.39575
hypothetical protein	3085	1076276	1076404	0	0	#DIV/0!
L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)	3084	1076415	1077893	54.12719892	95.0646143	1.75632

Selenocysteine-specific translation elongation factor	3083	1077895	1079853	66.90500511	84.5909091	1.26434
Cysteine desulfurase (EC 2.8.1.7)	3082	1079907	1081100	79.63118189	107.635373	1.35167
Hypothetical protein Cj1505c	3081	1081108	1081731	181.3804173	165.787319	0.91403
Selenide,water dikinase (EC 2.7.9.3); selenocysteine-containing	3080	1081754	1082806	116.9201521	99.0646388	0.84728
hypothetical protein	3079	1082790	1083086	104.7297297	106.881757	1.02055
hypothetical protein	3077	1083258	1083428	5.882352941	5.47352941	0.9305
Predicted hydroxymethylpyrimidine transporter CytX	3076	1083473	1084651	2.546689304	2.3696944	0.9305
incorrect stop		1084851	1085285	1087.557604	1072.00461	0.9857
Formate dehydrogenase H (EC 1.2.1.2); selenocysteine-containing		1085334	1087043	167.9344646	331.038034	1.97123
MoxR-like ATPases	3073	1087167	1088594	118.4302733	134.325858	1.13422
hypothetical protein	3072	1088597	1090063	23.8744884	31.101296	1.3027
probable electron transfer protein	3071	1090109	1092052	509.5213587	450.164694	0.88351
hypothetical protein	3070	1092045	1092740	323.7410072	249.025899	0.76921
Carbon monoxide dehydrogenase CooS subunit (EC 1.2.99.2)	3069	1092873	1094768	2697.62533	2523.88918	0.9356
CO dehydrogenase accessory protein CooC (nickel insertion)	3068	1094768	1095541	1878.39586	1479.41074	0.78759
CO dehydrogenase/acetyl-CoA synthase, acetyl-CoA synthase subunit (EC 2.3.1.169)	3067	1095614	1097758	1811.567164	1908.3062	1.0534
Acetyl-CoA synthase corrinoid iron-sulfur protein, small subunit	3066	1097840	1098784	1330.508475	1265.63771	0.95124
Acetyl-CoA synthase corrinoid iron-sulfur protein, large subunit	3065	1098797	1100128	1616.078137	1982.64313	1.22682
5-methyltetrahydrofolate:corrinoid iron-sulfur protein methyltransferase	3064	1100195	1100980	2183.43949	2269.94586	1.03962
hypothetical protein	3063	1100987	1101289	5605.960265	6479.60762	1.15584
hypothetical protein	3062	1101356	1101526	3876.470588	4313.14118	1.11265
hypothetical protein	3061	1101526	1101981	3305.494505	3315.03407	1.00289
DNA polymerase I (EC 2.7.7.7)	3060	1102079	1105090	113.2514115	147.099967	1.29888
Methyl-accepting chemotaxis sensory transducer precursor	3059	1105178	1106998	351.0989011	382.425275	1.08922
HD_GYP hydrolase domain fused to HD hydrolase domain	3058	1107002	1108237	109.3117409	133.359109	1.21999
Sensory box histidine kinase/response regulator	3057	1108290	1110563	104.7535211	123.684419	1.18072
Response regulator	3056	1110645	1111250	171.9008264	141.497521	0.82313
Na+/H+ antiporter NhaD type	3055	1111311	1112606	74.9034749	86.942471	1.16073
8-amino-7-oxononanoate synthase (EC 2.3.1.47)	3054	1112637	1113812	36.59574468	43.5553191	1.19017
Pimeloyl-CoA synthase (EC 6.2.1.14)	3053	1113817	1114575	26.38522427	22.0963061	0.83745
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62)	3052	1114611	1115960	80.05930319	61.3895478	0.7668
Dethiobiotin synthetase (EC 6.3.3.3)	3051	1115970	1116668	83.09455587	87.9842407	1.05884
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)	3050	1116736	1118556	867.9141442	1131.24629	1.30341
hypothetical protein	3048	1118717	1119067	151.4285714	135.587143	0.89539
Uncharacterized protein TP_0700	3049	1119064	1119453	236.503856	394.68509	1.66883
hypothetical protein		1119705	1119839	29.85074627	20.8320896	0.69788

Large exoproteins involved in heme utilization or adhesion	3046	1119838	1121661	29.62150302	16.8439386	0.56864
lipoprotein, putative	3045	1121715	1122986	40.12588513	47.586546	1.18593
hypothetical protein	3044	1123007	1123486	93.94572025	110.727557	1.17863
GTP-binding protein Era	3043	1123528	1124454	62.6349892	89.4325054	1.42784
Homoserine kinase (EC 2.7.1.39)	3042	1124467	1125084	189.6272285	190.02107	1.00208
Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor	3041	1125652	1126407	22.51655629	23.4165563	1.03997
hypothetical protein	3040	1126444	1127265	114.4945189	133.738124	1.16807
Phosphoesterase family protein	3039	1127269	1128135	94.68822171	138.607968	1.46384
Cellobiose phosphotransferase system YdjC-like protein	3038	1128278	1129039	55.19053876	52.5775296	0.95265
Ferric iron ABC transporter, permease protein	3037	1129052	1130677	153.2307692	173.502462	1.1323
Ferric iron ABC transporter, ATP-binding protein # pitD	3036	1130700	1131797	290.793072	268.038286	0.92175
Ferric iron ABC transporter, iron-binding protein	3035	1131825	1132892	672.9147142	457.837395	0.68038
B. burgdorferi predicted coding region BB0351	3034	1132993	1134429	38.99721448	40.1747911	1.0302
hypothetical protein	3033	1134458	1134580	98.36065574	22.8811475	0.23263
Hydrolase (HAD superfamily)	3032	1134598	1136127	903.7037037	973.735354	1.07749
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	3031	1136241	1137221	17.34693878	14.2423469	0.82103
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3030	1137214	1138248	4.835589942	4.49951644	0.9305
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	3029	1138258	1139169	3.293084523	2.0428101	0.62033
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	3028	1139162	1140133	5.149330587	4.79145211	0.9305
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	3027	1140245	1141867	12.33045623	13.7681874	1.1166
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	3026	1142182	1143798	3.712871287	8.63706683	2.32625
hypothetical protein	3025	1143947	1144315	2.717391304	7.58559783	2.7915
hypothetical protein	3024	1144343	1144708	16.43835616	7.64794521	0.46525
Hypothetical oxidoreductase ydjG (EC 1.-.-.-)	3023	1144721	1145719	11.02204409	15.8502004	1.43805
aminopeptidase	3021	1145745	1146857	4.496402878	10.8781475	2.4193
Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	3022	1146850	1148304	6.877579092	7.67950481	1.1166
Uroporphyrinogen III decarboxylase (EC 4.1.1.37)	3020	1148398	1149444	19.12045889	24.9082218	1.3027
hypothetical protein	3019	1149448	1149540	0	0	#DIV/0!
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	3018	1149482	1150870	42.50720461	52.2903458	1.23015
Lipopolysaccharide ABC transporter, ATP-binding protein LptB	3017	1150878	1151633	160.2649007	157.753642	0.98433
hypothetical protein	3016	1151637	1152305	92.81437126	83.5778443	0.90048
hypothetical protein	3015	1152296	1153033	206.2415197	162.869064	0.7897
CTP synthase (EC 6.3.4.2)	3014	1153057	1154685	402.4767802	339.358824	0.84318
Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	3013	1154856	1155677	308.1607795	228.941535	0.74293

Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	3012	1155709	1156863	396.0138648	404.775563	1.02212
Ubiquinone/menaquinone biosynthesis methyltransferase UbiE/COQ5 (EC 2.1.1.-)	3011	1156939	1157682	145.3566622	122.730821	0.84434
Signal peptidase-like protein	3010	1157725	1158669	139.0658174	143.22983	1.02994
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	3009	1158734	1159288	83.03249097	119.251805	1.43621
hypothetical protein	3008	1159281	1159739	362.4454148	316.938865	0.87445
Membrane proteins related to metalloendopeptidases	3007	1159770	1160810	328.8461538	380.252404	1.15632
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	3006	1161064	1162014	129.4736842	74.44	0.57494
two-component sensor histidine kinase	3005	1162011	1163552	36.34003894	26.568462	0.73111
DNA-binding response regulator	3004	1163545	1165044	48.69913276	33.5203469	0.68832
Xylose ABC transporter, periplasmic xylose-binding protein xylF	3003	1165025	1166143	56.35062612	54.0988372	0.96004
hypothetical protein	3002	1166109	1166252	6.993006993	0	0
L-arabinose-binding periplasmic protein precursor araF (TC 3.A.1.2.2)	3001	1166292	1167440	669.452182	4007.11142	5.98566
L-arabinose transport ATP-binding protein araG (TC 3.A.1.2.2)	3000	1167547	1169073	105.3704963	333.360639	3.1637
L-arabinose transport system permease protein (TC 3.A.1.2.2)	2999	1169115	1170308	52.40549828	199.050258	3.79827
Methylcobalamin:coenzyme M methyltransferase, methylamine-specific	2998	1170460	1171461	37.96203796	183.125375	4.82391
Translation elongation factor G, mitochondrial	2997	1171653	1173746	507.0014486	1003.28658	1.97886
hypothetical protein	2996	1173752	1174453	333.8088445	473.878031	1.41961
High-affnity carbon uptake protein Hat/HatR	2995	1174476	1177706	44.58204334	67.4108359	1.51206
Nitroreductase family protein	2994	1177721	1178242	67.17850288	114.303263	1.70149
putative oxidoreductase	2993	1178303	1179277	54.41478439	49.6776181	0.91294
2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	2992	1179312	1180415	15.41251133	11.8105168	0.76629
4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	2991	1180412	1181077	6.015037594	15.3917293	2.55888
Transcriptional regulator KdgR, KDG operon repressor	2990	1181197	1182015	39.1198044	30.7133252	0.78511
alpha-arabinosides ABC transport system, substrate-binding protein araN	2989	1182140	1183444	52.14723926	50.663727	0.97155
sugar ABC transporter, permease protein	2988	1183467	1184345	15.9453303	13.7773349	0.86404
ABC transporter sugar permease	2987	1184348	1185193	7.100591716	5.50591716	0.77542
Beta-galactosidase (EC 3.2.1.23)	2986	1185213	1187570	15.27365295	5.92172253	0.38771
Gluconate dehydratase (EC 4.2.1.39)	2985	1187608	1188756	11.32404181	16.2108014	1.43154
Cold-shock DEAD-box protein A	2984	1188760	1190628	177.7301927	183.310493	1.0314
Regulatory protein recX	2983	1190913	1191554	138.8455538	227.907176	1.64144
SSU ribosomal protein S9p (S16e)	2982	1191596	1191988	471.9387755	434.391582	0.92044
LSU ribosomal protein L13p (L13Ae)	2981	1192060	1192488	640.1869159	850.059579	1.32783
hypothetical protein	2980	1192572	1192793	149.321267	168.41629	1.12788
hypothetical protein	2979	1192809	1193108	56.85618729	71.5769231	1.25891
Methyl-accepting chemotaxis protein	2978	1193430	1195610	46.78899083	67.8667431	1.45049

Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	2977	1195629	1196744	425.1121076	549.954709	1.29367
Dihydrodipicolinate synthase (EC 4.2.1.52)	2976	1196826	1197758	245.7081545	282.544528	1.14992
Dihydrodipicolinate reductase (EC 1.3.1.26)	2975	1197837	1198646	88.99876391	92.0148331	1.03389
Aspartokinase (EC 2.7.2.4)	2974	1198643	1199998	175.1662971	245.519956	1.40164
Ribonuclease R (EC 3.1.-.-)	2973	1200139	1202064	96.62337662	110.20987	1.14061
Chemotaxis protein CheA (EC 2.7.3.-)	2972	1202140	1204503	927.1495129	794.137018	0.85654
Positive regulator of CheA protein activity (CheW)	2971	1204529	1205875	945.7652303	819.890788	0.86691
Chemotaxis protein CheX	2970	1205900	1206370	1184.444444	1139.34556	0.96192
PTS system, mannitol-specific IIC component (EC 2.7.1.69) / PTS system, mannitol-specific IIB component (EC 2.7.1.69) / PTS system, mannitol-specific IIA component (EC 2.7.1.69)	2968	1206725	1208146	16.88951443	12.4415904	0.73665
Phosphocarrier protein of PTS system	2967	1208161	1208418	27.23735409	21.7237354	0.79757
Mannitol operon activator, BglG family	2966	1208433	1210466	12.29709788	3.20388588	0.26054
PTS system, mannitol-specific IIA component (EC 2.7.1.69)	2965	1210476	1210916	18.18181818	16.9181818	0.9305
1-phosphofructokinase (EC 2.7.1.56)	2964	1210913	1211887	16.42710472	7.64271047	0.46525
Putative oxidoreductase	2963	1212013	1213284	14.94885917	11.7136113	0.78358
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	2962	1213286	1214905	6.79431748	6.32211242	0.9305
Endoribonuclease L-PSP	2961	1215000	1215377	47.74535809	108.599469	2.27456
Putative lipoprotein	2960	1215492	1216304	35.71428571	36.6699507	1.02676
Hcp transcriptional regulator HcpR (Crp/Fnr family)	2959	1216373	1217041	17.96407186	36.2170659	2.01608
Ferredoxin 3 fused to uncharacterized domain	2958	1217045	1217839	21.41057935	26.9540302	1.25891
Beta-glucoside bgl operon antiterminator, BglG family	2957	1218049	1218891	4.750593824	7.73574822	1.62838
Cof-like hydrolase	2956	1218888	1219772	6.787330317	5.26300905	0.77542
Phosphoglycerate mutase family	2955	1219843	1220697	26.93208431	71.912178	2.67013
PTS system, beta-glucoside-specific IIB component (EC 2.7.1.69) / PTS system, beta-glucoside-specific IIC component (EC 2.7.1.69) / PTS system, beta-glucoside-specific IIA component (EC 2.7.1.69)	2954	1220773	1222725	17.93032787	35.751793	1.99393
5'-nucleotidase (EC 3.1.3.5)	2953	1222740	1224215	12.20338983	23.9722034	1.96439
6-phospho-beta-glucosidase (EC 3.2.1.86)	2952	1224228	1225658	18.18181818	27.3293706	1.50312
Phosphocarrier protein of PTS system	2951	1225655	1225912	0	7.24124514	#DIV/0!
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	2950	1225921	1227543	16.64611591	26.3890259	1.5853
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	2948	1227678	1229864	42.08600183	37.0327081	0.87993
Transcriptional regulator, ArsR family	2947	1229867	1230238	26.9541779	40.1293801	1.4888
Sulfate permease	2946	1230413	1232161	57.78032037	55.8938787	0.96735
DNA repair helicase	2945	1232258	1234057	174.5414119	205.858255	1.17942
Uncharacterized protein TP_0021	2944	1234054	1236183	102.8651949	125.87318	1.22367
Maebl	2943	1236229	1237008	127.0860077	175.588575	1.38165
hypothetical protein		1237088	1237201	0	0	#DIV/0!

methyl-accepting chemotaxis protein	2941	1237122	1239356	2.697841727	1.67356115	0.62033
Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	2940	1239494	1241134	1142.682927	1252.20335	1.09584
hypothetical protein		1241152	1241340	21.27659574	9.89893617	0.46525
hypothetical protein	2938	1241339	1242079	1029.72973	1124.14459	1.09169
Crossover junction endodeoxyribonuclease ruvC (EC 3.1.22.4)	2937	1242066	1242746	116.1764706	142.311765	1.22496
Positive regulator of CheA protein activity (CheW)	2936	1242819	1243292	473.5729387	322.625793	0.68126
4-keto-6-deoxy-N-Acetyl-D-hexosaminyl-(Lipid carrier) aminotransferase	2935	1243426	1244535	388.638413	367.501353	0.94561
NAD kinase (EC 2.7.1.23)	2934	1244559	1245452	281.075028	269.87626	0.96016
DNA repair protein RecN	2933	1245445	1247265	257.1428571	234.670055	0.91261
hypothetical protein	2932	1247278	1248129	126.9095182	84.193302	0.66341
Multidrug resistance ABC transporter ATP-binding and permease protein	2931	1248095	1249918	66.92265496	49.5109709	0.73982
Multidrug resistance ABC transporter ATP-binding and permease protein	2930	1249911	1252067	32.93135436	35.8216605	1.08777
hypothetical protein	2929	1252113	1252400	247.3867596	252.888502	1.02224
Methyl-accepting chemotaxis protein	2928	1252588	1254489	299.3161494	366.619937	1.22486
Ankyrin repeat protein	2927	1254555	1257371	269.1761364	325.47674	1.20916
TPR domain protein, putative component of TonB system	2926	1257438	1258904	65.48431105	57.1248295	0.87234
hypothetical protein	2925	1259063	1259989	132.8293737	75.3644708	0.56738
putative autotransporter protein	2924	1260212	1262860	692.2205438	772.371224	1.11579
hypothetical protein	2923	1263020	1263169	13.42281879	0	0
Twin-arginine translocation protein TatB	2921	1263257	1264312	132.7014218	140.236493	1.05678
hypothetical protein		1264290	1264442	177.6315789	183.651316	1.03389
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	2920	1264449	1266638	84.05664687	67.5877113	0.80407
Cell division protein ftsK	2919	1266702	1268999	91.85894645	111.805834	1.21715
hypothetical protein		1269041	1269172	30.53435115	0	0
transposase	2917	1269204	1270328	4.448398577	2.48354093	0.5583
sensory box histidine kinase/response regulator	2916	1270712	1273642	9.215017065	7.30426621	0.79265
Oxidoreductase, aldo/keto reductase family		1273692	1273829	51.09489051	54.3357664	1.06343
hypothetical protein		1273826	1273963	51.09489051	54.3357664	1.06343
Pantothenate kinase type II, eukaryotic (EC 2.7.1.33)	2913	1274121	1274939	145.0189155	83.3108449	0.57448
Phosphinothricin N-acetyltransferase	2912	1274940	1275449	82.51473477	40.2180747	0.4874
spore peptidoglycan hydrolase (N-acetylglucosaminidase)	2911	1275949	1277013	40.41353383	31.4830827	0.77902
Molybdenum ABC transporter, periplasmic molybdenum-binding protein modA (TC 3.A.1.8.1)	2910	1277113	1277934	92.57003654	104.270402	1.12639
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1) / Molybdenum transport system permease protein modB (TC 3.A.1.8.1)		1277931	1278632	25.67760342	46.4586305	1.80931
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1) / Molybdenum transport system permease protein modB (TC 3.A.1.8.1)		1278629	1279705	44.60966543	25.9433086	0.58156
Molybdate-binding domain of ModE	2906	1279737	1279949	400.9433962	320.408019	0.79914

unknown	2907	1279946	1280503	113.1059246	150.35009	1.32929
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	2905	1280623	1281249	31.94888179	13.3777955	0.41873
hypothetical protein	2904	1281601	1282521	110.8695652	81.9244565	0.73893
sensory box histidine kinase/response regulator	2903	1282588	1285014	114.0967342	127.708144	1.1193
hypothetical protein	2902	1285251	1285487	300.8474576	287.824153	0.95671
hypothetical protein	2901	1285513	1285755	148.7603306	84.5909091	0.56864
Corrinoid methyltransferase protein	2900	1285918	1286541	9.63081862	2.98715891	0.31017
Uroporphyrinogen-III decarboxylase	2899	1286538	1287659	5.352363961	4.15031222	0.77542
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	2898	1287679	1288482	9.9626401	5.79389788	0.58156
Major facilitator superfamily transporter-permease	2897	1288572	1289750	6.791171477	3.15959253	0.46525
COG0523: Putative GTPases (G3E family)	2896	1289840	1290850	13.86138614	6.4490099	0.46525
hypothetical protein	2895	1290863	1291525	7.552870091	1.40558912	0.1861
hypothetical protein	2894	1291594	1292154	80.35714286	61.4794643	0.76508
Mo/Fe-nitrogenase-specific transcriptional regulator NifA	2893	1292159	1293784	5.538461538	4.00830769	0.72372
hypothetical protein	2892	1293760	1293888	0	0	#DIV/0!
hypothetical protein		1293903	1294022	0	0	#DIV/0!
Nitrogenase iron protein (EC 1.18.6.1)	2890	1294089	1294931	8.423586041	12.3170878	1.46221
Nitrogen regulatory protein P-II	2889	1295027	1295389	8.287292818	10.281768	1.24067
Nitrogen regulatory protein P-II	2888	1295386	1295763	0	14.8090186	#DIV/0!
Nitrogenase (molybdenum-iron) alpha chain (EC 1.18.6.1)	2887	1295773	1297413	6.097560976	13.0496951	2.14015
Nitrogenase (molybdenum-iron) beta chain (EC 1.18.6.1)	2886	1297426	1298802	8.810572687	8.19823789	0.9305
Nitrogenase molybdenum-cofactor synthesis protein NifE	2885	1298818	1300368	5.177993528	3.61359223	0.69788
Nitrogenase molybdenum-cofactor synthesis protein NifN	2884	1300365	1301753	1.44092219	6.03350144	4.18725
FeMo cofactor biosynthesis protein NifB	2883	1301750	1303036	1.555209953	3.61780715	2.32625
Ferredoxin, 2Fe-2S	2882	1303103	1303411	0	3.0211039	#DIV/0!
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	2881	1303498	1304226	4.120879121	2.55631868	0.62033
2-isopropylmalate synthase (EC 2.3.3.13)	2880	1304272	1305936	22.83653846	40.8212139	1.78754
hypothetical protein		1305926	1306321	101.2658228	138.986076	1.37249
Molybdopterin biosynthesis protein A	2878	1306471	1307508	286.4030858	245.860174	0.85844
Putative carboxymethylenebutenolidase (EC 3.1.1.45)	2877	1307569	1308336	555.410691	544.712516	0.98074
Putative arylsulfatase regulatory protein	2876	1308342	1309607	181.027668	179.479842	0.99145
hypothetical protein	2875	1309939	1311318	31.90717912	20.2429297	0.63443
hypothetical protein		1311493	1311648	0	0	#DIV/0!
Cytotoxic translational repressor of toxin-antitoxin stability system	2872	1311699	1312040	105.5718475	57.3035191	0.54279
putative DNA-binding protein	2871	1312024	1312362	73.96449704	66.0710059	0.89328
INTERGENIC		1312363	1312651	79.13669065	100.413669	1.26886
hypothetical protein	2870	1312668	1312838	5.882352941	5.47352941	0.9305
hypothetical protein	2869	1312852	1313283	4.64037123	10.7946636	2.32625
hypothetical protein	2868	1313276	1313479	29.55665025	22.9187192	0.77542
Flagellar protein flbB	2866	1313841	1314458	769.8541329	461.479741	0.59944

Flagellar hook-length control protein fliK	2865	1314521	1315912	353.7023724	312.396477	0.88322
Flagellar basal-body rod modification protein flgD	2864	1315937	1316374	386.7276888	432.245995	1.1177
Flagellar hook protein flgE	2863	1316388	1317818	518.1818182	671.521678	1.29592
Flagellar protein flbD	2862	1317950	1318147	263.9593909	155.870558	0.59051
Flagellar motor rotation protein motA	2861	1318153	1318935	214.8337596	228.460358	1.06343
Flagellar motor rotation protein motB	2860	1319014	1319745	148.1481481	242.517147	1.63699
hypothetical protein	2859	1319714	1319827	8.849557522	24.7035398	2.7915
Flagellar biosynthesis protein fliL	2858	1319831	1320394	293.0728242	388.39698	1.32526
hypothetical protein	2857	1320429	1320551	32.78688525	15.2540984	0.46525
Flagellar motor switch protein fliM	2856	1320548	1321579	173.6178468	179.601843	1.03447
Flagellar motor switch protein fliN	2855	1321576	1322661	275.5760369	320.743779	1.1639
Flagellar biosynthesis protein fliZ	2854	1322717	1323382	82.70676692	106.342857	1.28578
Flagellar biosynthesis protein fliP	2853	1323379	1324206	103.406326	78.1076642	0.75535
Flagellar biosynthesis protein fliQ	2852	1324220	1324489	29.73977695	58.8048327	1.97731
Flagellar biosynthesis protein fliR	2851	1324592	1325407	28.2208589	46.8104294	1.65872
Flagellar biosynthesis protein flhB	2850	1325404	1326546	45.53415061	75.7762697	1.66416
Flagellar biosynthesis protein flhA	2849	1326586	1328685	81.94378275	111.713197	1.36329
Flagellar biosynthesis protein flhF	2848	1328714	1330054	101.4925373	129.853358	1.27944
Flagellar synthesis regulator fleN	2847	1330054	1330941	114.994363	148.963923	1.2954
hypothetical protein	2846	1330952	1331638	126.8221574	90.8797376	0.71659
RNA polymerase sigma factor for flagellar operon	2845	1331648	1332460	497.5369458	410.245074	0.82455
hypothetical protein	2844	1332489	1334459	150.2538071	115.722081	0.77018
hypothetical protein	2843	1334440	1334778	245.5621302	258.778107	1.05382
Uncharacterized protein BB_0265	2842	1334785	1335558	120.3104787	98.7076326	0.82044
hypothetical protein		1335569	1335694	56	7.444	0.13293
UDP-sugar hydrolase (EC 3.6.1.45); 5'-nucleotidase (EC 3.1.3.5)	2839	1335889	1337439	413.7483787	458.008755	1.10697
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	2838	1337622	1338059	66.36155606	40.4565217	0.60964
hypothetical protein		1338051	1338245	10.30927835	0	0
Cell surface protein	2836	1338258	1339172	66.73960613	38.6859956	0.57966
N-acetylmuramoyl-L-alanine amidase/putative S-layer protein	2835	1339192	1340091	8.898776418	3.1051168	0.34894
hypothetical protein	2834	1340248	1340436	15.95744681	4.94946809	0.31017
hypothetical protein		1340588	1340743	45.16129032	18.0096774	0.39879
hypothetical protein	2832	1340776	1341087	221.8649518	179.517685	0.80913
hypothetical protein	2831	1341138	1341689	143.3756806	113.146098	0.78916
PIN domain protein	2830	1342437	1342733	37.16216216	47.1537162	1.26886
hypothetical protein		1342730	1343041	54.66237942	68.8151125	1.25891
hypothetical protein	2828	1343242	1344570	4.518072289	1.40135542	0.31017
Uncharacterized protein TP_0789 precursor	2827	1344567	1345361	2.518891688	2.34382872	0.9305
membrane protein, putative	2826	1345369	1348011	0	0.70439061	#DIV/0!
Transcriptional regulator	2825	1348189	1348743	10.83032491	11.7572202	1.08558
hypothetical protein	2824	1348882	1350000	443.6493739	438.616726	0.98866
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	2823	1350037	1351401	102.6392962	66.8541056	0.65135
Sigma factor RpoE regulatory protein RseC	2822	1351508	1351918	34.14634146	18.1560976	0.53171
hypothetical protein	2821	1351969	1352085	0	16.0431034	#DIV/0!

Putative ankyrin repeat-containing protein TP_0502	2820	1352063	1352980	190.8396947	135.972737	0.7125
NAD-dependent protein deacetylase of SIR2 family	2819	1352990	1353805	98.1595092	61.6527607	0.62809
hypothetical protein	2818	1353823	1354731	47.35682819	25.6194934	0.54099
Glutamyl-tRNA synthetase (EC 6.1.1.17); Glutamyl-tRNA(Gln) synthetase	2819	1354742	1356244	127.8295606	128.857523	1.00804
Peptidase M18, aminopeptidase I:Peptidase M20	2816	1356304	1357761	397.3919012	365.941318	0.92086
hypothetical protein	2815	1357803	1357988	556.7567568	382.259459	0.68658
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	2814	1358048	1358809	39.4218134	53.8002628	1.36473
ATP-dependent Clp protease ATP-binding subunit clpA	2813	1358874	1361420	361.2421384	359.544615	0.9953
ATP-dependent Clp protease adaptor protein clpS	2812	1361491	1361802	144.6945338	110.702572	0.76508
Exodeoxyribonuclease III (EC 3.1.11.2)	2811	1361949	1362731	62.65984655	88.0524297	1.40524
GlpG protein (membrane protein of glp regulon)	2810	1362741	1363310	56.23901582	42.5184534	0.75603
hypothetical protein	2809	1363303	1363995	40.46242775	32.2716763	0.79757
hypothetical protein	2808	1363989	1364831	39.19239905	43.0991686	1.09968
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	2807	1364904	1365518	275.2442997	239.444625	0.86993
Ribonuclease HII (EC 3.1.26.4)	2806	1365528	1366139	52.37315876	82.2373159	1.57022
hypothetical protein	2805	1366237	1366476	405.8577406	194.665272	0.47964
hypothetical protein		1366466	1366714	145.1612903	116.3125	0.80126
hypothetical protein	2803	1367030	1367662	45.88607595	26.5015823	0.57755
hypothetical protein	2802	1367736	1367996	0	0	#DIV/0!
Galactokinase (EC 2.7.1.6)	2801	1368072	1369238	268.4391081	201.900943	0.75213
5'-nucleotidase surE (EC 3.1.3.5)	2800	1369235	1370017	60.10230179	83.2928389	1.38585
TPR domain protein, putative component of TonB system	2799	1370021	1370719	174.7851003	159.971347	0.91525
hypothetical protein		1370716	1372809	91.7343526	109.365982	1.1922
hypothetical protein	2797	1372883	1373158	10.90909091	3.38363636	0.31017
Conserved domain protein	2796	1373155	1373445	141.3793103	77.0068966	0.54468
Thiamine biosynthesis protein thiI	2795	1373529	1374710	65.19898391	55.1524132	0.84591
Cysteine desulfurase (EC 2.8.1.7)	2794	1374710	1375864	96.18717504	119.336222	1.24067
Transcriptional regulator, ArsR family	2793	1376031	1376321	134.4827586	51.337931	0.38174
Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	2792	1376326	1377411	101.3824885	89.1907834	0.87975
Aspartokinase (EC 2.7.2.4) / Homoserine dehydrogenase (EC 1.1.1.3)	2791	1377597	1380140	169.4848604	218.812033	1.29104
hypothetical protein	2790	1380165	1380290	16	7.444	0.46525
hypothetical protein	2789	1380425	1380676	63.74501992	33.3645418	0.52341
hypothetical protein	2788	1380686	1380934	108.8709677	135.072581	1.24067
Flagellar hook-length control protein fliK	2787	1381369	1384683	9.656004828	10.3888051	1.07589
putative autotransporter protein	2786	1384698	1389701	10.99340396	12.4612233	1.13352
Large repetitive protein	2785	1389914	1393204	4.863221884	7.35349544	1.51206
putative autotransporter protein	2784	1393220	1396744	12.76958002	12.9382804	1.01321
hypothetical protein		1396746	1396886	0	0	#DIV/0!
hypothetical protein	2782	1396874	1397287	9.685230024	9.01210654	0.9305
Cell surface protein		1397340	1399262	6.25	5.33098958	0.85296

Treponemal membrane protein B precursor (Antigen tmpB)	2780	1399267	1401744	4.844570044	7.13746468	1.47329
Iron-sulfur cluster-binding protein	2779	1401778	1402638	46.51162791	55.180814	1.18639
hypothetical protein	2778	1402807	1403109	99.33774834	40.0546358	0.40322
hypothetical protein	2777	1403063	1403377	95.54140127	88.9012739	0.9305
Iron-sulfur cluster-binding protein	2776	1403451	1404542	87.99266728	81.0242896	0.92081
Glycogen phosphorylase (EC 2.4.1.1)	2775	1404662	1407202	1169.230769	1358.86036	1.16218
hypothetical protein		1407341	1407556	60.46511628	17.3116279	0.28631
iron-sulfur flavoprotein	2773	1407621	1408364	14.80484522	5.00942127	0.33836
hypothetical protein	2772	1408431	1408856	16.47058824	4.37882353	0.26586
hypothetical protein	2771	1408828	1409061	42.91845494	63.8969957	1.4888
Sugar (Glycoside-Pentoside-Hexuronide) transporter	2770	1409092	1410474	45.58610709	59.2503618	1.29975
FKBP-type peptidyl-prolyl cis-trans isomerase fklB (EC 5.2.1.8)	2769	1410632	1411342	349.2957746	448.212676	1.28319
C4-type zinc finger protein, DksA/TraR family	2768	1411834	1412166	280.1204819	355.944277	1.27068
Histidinol-phosphatase (EC 3.1.3.15)	2767	1412191	1413069	109.3394077	113.398064	1.03712
response regulator in two-component regulatory system with PhoQ	2766	1413078	1414445	75.34747623	76.917703	1.02084
ThiJ/PfpI family protein	2765	1415124	1415693	65.25573192	77.1313933	1.18199
hypothetical protein	2764	1415733	1416134	127.1820449	141.547382	1.11295
Phosphoesterase family protein	2763	1416131	1416967	162.6794258	171.407895	1.05365
TPR domain protein, putative component of TonB system	2762	1416982	1417533	337.5680581	227.980944	0.67536
GAF domain/HD domain protein	2761	1417743	1419650	137.9129523	117.59334	0.85266
hypothetical protein	2760	1419743	1421194	125.4307374	135.951757	1.08388
Heat shock protein 60 family co-chaperone GroES	2759	1421315	1421581	1360.902256	1934.46053	1.42145
hypothetical protein		1421582	1421695	646.0176991	543.477876	0.84127
RlpA-like lipoprotein precursor	2757	1421751	1422710	397.2888425	640.385819	1.61189
hydrolase, haloacid dehalogenase-like family	2756	1422777	1423619	283.847981	335.952494	1.18356
Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein soj	2755	1423742	1424500	141.1609499	168.177441	1.19139
Chromosome (plasmid) partitioning protein ParB / Stage 0 sporulation protein J	2754	1424490	1425485	95.47738693	149.628141	1.56716
Transcriptional regulator, XRE family	2753	1425526	1425864	29.58579882	24.7766272	0.83745
hypothetical protein	2752	1426040	1426207	0	0	#DIV/0!
Zn-dependent hydrolases, including glyoxylases	2751	1426270	1427121	126.9095182	126.836663	0.99943
Lysyl-tRNA synthetase (class I) (EC 6.1.1.6)	2750	1427134	1428786	313.4872418	329.575638	1.05132
Nucleoside diphosphate kinase (EC 2.7.4.6)	2749	1428795	1429973	521.2224109	689.58107	1.32301
hypothetical protein	2748	1429972	1430109	0	0	#DIV/0!
Activator of (R)-2-hydroxyglutaryl-CoA dehydratase	2747	1430112	1434536	51.53707052	59.1027351	1.1468
membrane protein	2746	1434538	1435113	31.30434783	35.6017391	1.13728
HD family hydrolase, diverged	2745	1435110	1435568	28.38427948	28.4432314	1.00208
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	2744	1435667	1437127	29.45205479	57.359589	1.94756
hypothetical protein	2743	1437275	1437919	246.8944099	255.743012	1.03584
membrane protein	2742	1437960	1438553	145.0252951	128.669477	0.88722

ATPase	2740	1439028	1440257	18.71440195	13.628153	0.72822
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	2739	1440645	1443866	37.5659733	32.6440546	0.86898
DNA-binding protein	2738	1444014	1445165	59.94787142	33.1455256	0.55291
hypothetical protein	2737	1445162	1445638	56.72268908	31.2773109	0.55141
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	2736	1445653	1446870	8.216926869	6.88126541	0.83745
ATP-dependent DNA helicase	2735	1446867	1447295	16.35514019	26.088785	1.59514
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	2734	1447292	1448992	19.41176471	20.2520588	1.04329
Methyl-accepting chemotaxis protein	2733	1449014	1451110	26.30320421	38.715208	1.47188
hypothetical protein	2732	1451251	1452597	87.66716196	124.435364	1.41941
RNA polymerase sigma-54 factor rpoN	2731	1452788	1454146	192.9307806	165.132916	0.85592
Ribosome hibernation protein YhbH	2729	1454173	1454514	76.24633431	51.8460411	0.67998
23S rRNA (guanine-N-2-) -methyltransferase rlmL EC 2.1.1.-)	2730	1454501	1455571	62.61682243	40.8724299	0.65274
Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	2728	1455552	1456283	154.5827633	110.743502	0.7164
Methionine ABC transporter substrate-binding protein	2727	1456332	1457141	64.27688504	102.366502	1.59259
hypothetical protein	2726	1457235	1457798	51.50976909	84.2904085	1.6364
Phosphomannomutase (EC 5.4.2.8) / Phosphoglucosamine mutase (EC 5.4.2.10)	2725	1457800	1459713	115.0026137	132.789597	1.15467
Cysteine desulfurase (EC 2.8.1.7)	2724	1459938	1461128	140.5723906	155.866582	1.1088
Iron-sulfur cluster assembly scaffold protein NifU	2723	1461166	1461768	539.8671096	618.272425	1.14523
hypothetical protein	2721	1462503	1462898	2.53164557	7.06708861	2.7915
hypothetical protein	2720	1462944	1463141	71.06598985	23.6167513	0.33232
hypothetical protein	2719	1463171	1463614	66.8202765	47.1682028	0.7059
hypothetical protein	2718	1463619	1463867	173.3870968	120.064516	0.69247
hypothetical protein	2717	1464321	1464761	34.09090909	19.0329545	0.5583
hypothetical protein	2716	1464884	1465348	4.310344828	10.0269397	2.32625
hypothetical protein	2715	1465404	1465637	4.291845494	0	0
hypothetical protein	2714	1465851	1466276	0	2.18941176	#DIV/0!
hypothetical protein	2713	1466276	1466614	0	0	#DIV/0!
Outer membrane protein	2712	1466649	1467920	1.573564123	1.46420142	0.9305
RND multidrug efflux transporter; Acriflavin resistance protein	2711	1467955	1471065	4.823151125	4.48794212	0.9305
Membrane fusion protein of RND family multidrug efflux pump	2710	1471062	1472174	2.697841727	2.51034173	0.9305
hypothetical protein	2709	1472511	1472912	0	2.32044888	#DIV/0!
Rrf2 family transcriptional regulator, group III	2708	1472966	1473400	6.912442396	2.14400922	0.31017
transcriptional regulator, MarR family	2707	1473408	1473860	0	6.40252294	#DIV/0!
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	2706	1473850	1475205	5.559968229	6.6517077	1.19636
sensor histidine kinase	2705	1475297	1476388	3.666361137	5.11732356	1.39575
DNA-binding response regulator, OmpR family	2704	1476385	1477056	4.470938897	11.0938897	2.48133
hypothetical protein	2703	1477034	1477240	0	0	#DIV/0!
hypothetical protein	2702	1477250	1477897	38.63987635	27.3253478	0.70718
MoxR-like ATPases	2701	1477888	1478955	27.17900656	23.5459231	0.86633
hypothetical protein	2700	1479006	1480064	10.39697543	6.15642722	0.59214

Ferredoxin	2699	1480173	1481195	116.4383562	138.391389	1.18854
hypothetical protein	2698	1481188	1482087	47.83092325	63.1373749	1.32001
Aspartate aminotransferase (EC 2.6.1.1)	2697	1482240	1483457	140.5094495	170.502465	1.21346
Histidyl-tRNA synthetase (EC 6.1.1.21)	2696	1483489	1484811	91.5279879	111.209531	1.21503
hypothetical protein	2695	1484858	1485652	73.04785894	86.7216625	1.18719
hypothetical protein	2694	1485669	1486901	247.5649351	226.582792	0.91525
Uncharacterized protein TP_0608	2693	1486935	1487654	869.2628651	793.319193	0.91263
Uncharacterized lipoprotein TP_0503 precursor	2692	1487773	1488357	229.4520548	229.438356	0.99994
Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	2691	1488410	1488886	86.13445378	54.7352941	0.63546
Acyl carrier protein / HmrB protein involved in methicillin resistance	2690	1489908	1490144	1529.661017	934.442797	0.61088
Ribonuclease III (EC 3.1.26.3)	2689	1490110	1490961	247.9435958	262.420682	1.05839
hypothetical protein	2688	1491041	1491556	95.14563107	99.3737864	1.04444
tRNA nucleotidyltransferase (EC 2.7.7.25)	2687	1491566	1492927	69.0668626	88.1958119	1.27696
Thiamin pyrophosphokinase (EC 2.7.6.2)	2686	1493031	1493678	64.91499227	67.5942813	1.04127
SSU ribosomal protein S6p	2685	1493774	1494055	1740.213523	1861	1.06941
Single-stranded DNA-binding protein	2684	1494061	1494528	732.3340471	896.627409	1.22434
SSU ribosomal protein S18p	2683	1494552	1494872	1831.25	2012.20625	1.09882
hypothetical protein	2682	1494970	1495947	168.8843398	206.671955	1.22375
LSU ribosomal protein L9p	2681	1496093	1496686	318.7183811	376.593592	1.18159
Replicative DNA helicase (EC 3.6.1.-) [SA14-24]	2680	1496687	1498066	148.6584482	226.046048	1.52057
hypothetical protein	2678	1498342	1498638	104.7297297	110.025338	1.05056
Uncharacterized protein TP_0598	2679	1498635	1500605	138.071066	174.763959	1.26575
hypothetical protein		1500570	1500749	324.0223464	155.949721	0.48129
Membrane-associated zinc metalloprotease	2677	1500735	1502090	129.8892989	129.789299	0.99923
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	2675	1502091	1503239	95.81881533	114.28615	1.19273
Phosphatidate cytidylyltransferase (EC 2.7.7.41)	2674	1503254	1504108	149.882904	155.809719	1.03954
Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	2673	1504101	1504844	422.6110363	274.265814	0.64898
Ribosome recycling factor	2672	1504899	1505453	435.0180505	475.327617	1.09266
Translation elongation factor Ts	2671	1505471	1506319	639.1509434	706.653302	1.10561
SSU ribosomal protein S2p (SAe)	2670	1506408	1507328	911.2627986	1336.99829	1.46719
Septum formation protein Maf	2669	1507492	1508079	52.8109029	61.8219761	1.17063
hypothetical protein	2668	1508169	1508645	126.0504202	111.42542	0.88398
Multidrug resistance ABC transporter ATP-binding and permease protein	2667	1508648	1510480	27.29257642	23.8719978	0.87467
Multidrug resistance ABC transporter ATP-binding and permease protein	2666	1510482	1512224	32.14695752	23.5028703	0.73111
hypothetical protein	2664	1512784	1513290	0	0	#DIV/0!
Cell surface protein	2663	1513303	1514667	2.19941349	2.04655425	0.9305
Conserved domain protein	2662	1514680	1516935	5.798394291	9.13068689	1.57469
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	2661	1516945	1518144	111.946533	153.917293	1.37492
L-arabinose-specific 1-epimerase (mutarotase)	2660	1518268	1519320	107.4144487	107.909696	1.00461
hypothetical protein		1519314	1519430	25.86206897	0	0
V-type ATP synthase subunit E (EC 3.6.3.14) (V-type ATPase subunit E)	2658	1519442	1520056	793.1596091	656.199511	0.82732
hypothetical protein	2657	1520060	1520662	602.9900332	588.904485	0.97664

V-type ATP synthase subunit A (EC 3.6.3.14)	2656	1520659	1522419	656.8627451	847.860438	1.29077
V-type ATP synthase beta chain 1 (EC 3.6.3.14) (V-type ATPase subunit B 1)	2655	1522489	1523787	504.3137255	553.921176	1.09837
V-type ATP synthase subunit D 1 (EC 3.6.3.14) (V type ATPase subunit D 1)	2654	1523799	1524401	1224.252492	1013.96678	0.82823
V-type ATP synthase subunit I (EC 3.6.3.14)	2653	1524427	1526364	331.7805383	352.068064	1.06115
V-type ATP synthase subunit K (EC 3.6.3.14)	2652	1526649	1527089	820.4545455	1137.74773	1.38673
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.4.3)	2651	1527168	1528247	117.7015755	144.878591	1.2309
hypothetical protein	2650	1528564	1529124	532.1428571	378.846429	0.71193
Uncharacterized protein BB_0089	2649	1529288	1530457	125.748503	107.457228	0.85454
hypothetical protein	2648	1530518	1531096	316.6089965	196.403114	0.62033
Uracil phosphoribosyltransferase (EC 2.4.2.9)	2647	1531121	1532191	412.1495327	435.68271	1.0571
TPR domain protein, putative component of TonB system	2646	1532188	1533213	200.9756098	215.149756	1.07053
YlxP-like protein	2645	1533228	1533515	127.6595745	191.379433	1.49914
hypothetical protein	2643	1533525	1534217	174.8554913	213.799855	1.22272
membrane protein, putative	2644	1534209	1536257	21.97265625	22.2629395	1.01321
lipoprotein, putative	2642	1536378	1537058	61.76470588	47.8933824	0.77542
tRNA (guanine46-N7-)-methyltransferase (EC 2.1.1.33)	2641	1537060	1537734	114.2433234	75.9310089	0.66464
DNA ligase (EC 6.5.1.2)	2640	1537752	1539722	110.6598985	107.220051	0.96892
ATP-dependent helicase HrpB	2639	1539719	1542496	14.76413396	25.8006842	1.74752
hypothetical protein	2638	1542721	1542864	6.993006993	0	0
hypothetical protein		1542884	1543300	144.2307692	154.33774	1.07008
hypothetical protein	2636	1543306	1543503	172.5888325	136.977157	0.79366
hypothetical protein	2635	1543543	1544169	75.0798722	144.182907	1.92039
Thymidylate kinase (EC 2.7.4.9)	2634	1544144	1544809	51.12781955	47.5744361	0.9305
hypothetical protein	2633	1544960	1549561	51.51054119	34.9872854	0.67923
Outer membrane protein assembly factor YaeT precursor	2632	1549561	1552071	214.7410359	159.779084	0.74405
Outer membrane protein H precursor	2631	1552087	1552617	471.6981132	308.996226	0.65507
DNA mismatch repair protein MutS	2630	1552704	1555424	113.6029412	103.312868	0.90942
hypothetical protein	2629	1555528	1556385	2.333722287	5.42882147	2.32625
Competence protein F	2628	1556399	1557154	9.271523179	12.3245033	1.32929
Pyridoxal kinase (EC 2.7.1.35)	2627	1557168	1558025	66.51108518	74.9177363	1.12639
Transcriptional regulator	2626	1558038	1558985	64.61864407	71.9560381	1.11355
hypothetical protein	2625	1558972	1559640	53.89221557	84.9708084	1.57668
TPR domain protein, putative component of TonB system	2624	1559763	1560470	66.47807638	97.3932107	1.46504
TPR domain protein, putative component of TonB system	2623	1560488	1562473	70.02518892	84.8465995	1.21166
ACT domain protein	2622	1562546	1562815	66.91449814	72.6412639	1.08558
Glycerol-3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94)	2621	1562948	1564309	133.8757396	172.748151	1.29036
hypothetical protein	2620	1564379	1564618	205.0209205	116.799163	0.56969
hypothetical protein	2619	1564611	1564874	98.85931559	127.368821	1.28838
Internalin-like protein (LPXTG motif) Lin1204 homolog	2618	1565153	1566250	34.63992707	52.5897903	1.51818
putative autotransporter protein		1566265	1568820	23.48336595	38.239726	1.62838
putative DNA-binding protein	2616	1568928	1569215	48.7804878	25.9372822	0.53171
hypothetical protein	2615	1569215	1569355	107.1428571	6.64642857	0.06203

hypothetical protein	2614	1569484	1569663	33.51955307	25.9916201	0.77542
hypothetical protein	2613	1569660	1570088	35.04672897	26.088785	0.7444
hypothetical protein	2612	1570110	1570604	10.12145749	7.53441296	0.7444
hypothetical protein, putative phage associated protein	2611	1570626	1571309	43.9238653	46.3206442	1.05457
TolA protein	2610	1571356	1573320	40.22403259	58.2746945	1.44875
hypothetical protein		1573311	1573433	8.196721311	0	0
DinG family ATP-dependent helicase YoaA	2608	1573433	1575946	83.96339037	92.1983685	1.09808
hypothetical protein	2607	1575963	1577465	95.87217044	87.3505326	0.91111
Iron-sulfur cluster regulator IscR	2606	1577529	1577948	71.59904535	97.7136038	1.36473
Helicase PriA essential for oriC/DnaA-independent DNA replication	2605	1578138	1580123	90.68010076	103.128463	1.13728
DNA polymerase, bacteriophage-type	2604	1580126	1580998	180.0458716	165.398509	0.91865
Ribonucleotide reductase transcriptional regulator NrdR	2603	1581042	1581509	164.882227	139.475375	0.84591
Glycosyltransferase	2602	1581690	1582823	146.5136805	153.57767	1.04821
ATP-dependent protease La (EC 3.4.21.53) Type I	2601	1582827	1585316	55.04218562	69.1613098	1.25651
ATP-dependent Clp protease ATP-binding subunit clpX	2600	1585324	1586577	313.7570394	345.100965	1.0999
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	2599	1586561	1587175	211.7263844	233.382736	1.10228
Cell division trigger factor (EC 5.2.1.8)	2598	1587188	1588549	211.6091109	201.004409	0.94989
hypothetical protein		1588514	1588726	56.60377358	92.1721698	1.62838
hypothetical protein		1589540	1590019	0	0	#DIV/0!
Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	2594	1590344	1592476	0.469043152	0	0
hypothetical protein	2593	1592674	1592817	0	0	#DIV/0!
hypothetical protein	2592	1592932	1593168	0	0	#DIV/0!
hypothetical protein	2591	1593161	1593586	0	0	#DIV/0!
Exonuclease SbcC	2590	1593849	1594610	0	0	#DIV/0!
Site-specific recombinase, phage integrase family	2589	1594624	1596099	1.355932203	1.26169492	0.9305
hypothetical protein	2584	1597814	1598227	133.1719128	110.398305	0.82899
hypothetical protein	2583	1598202	1598336	22.3880597	20.8320896	0.9305
Excinuclease ABC subunit A	2582	1598551	1601478	188.2473522	184.383328	0.97947
hypothetical protein		1601475	1604993	67.65207504	81.465037	1.20418
Transcription termination factor Rho	2580	1605225	1607132	514.8462354	603.394221	1.17199
LSU ribosomal protein L31p	2579	1607189	1607392	866.9950739	1026.75862	1.18427
T. pallidum predicted coding region TP0665		1607423	1608097	195.8456973	201.562315	1.02919
hypothetical protein	2577	1608181	1608327	0	0	#DIV/0!
Cell division protein mraZ	2576	1608284	1608748	211.2068966	254.684267	1.20585
S-adenosyl-methyltransferase mraW (EC 2.1.1.-)	2575	1608756	1609706	134.7368421	150.838947	1.11951
cell division protein FtsL, putative	2574	1609703	1609996	122.8668942	142.909556	1.16313
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	2573	1610142	1611221	84.3373494	49.1552363	0.58284
Cell division protein ftsW	2572	1611221	1612354	78.55251545	72.2718447	0.92004
Cell division protein ftsQ	2571	1612347	1613168	108.4043849	85.0030451	0.78413
Cell division protein ftsA	2570	1613161	1614429	149.0536278	165.846215	1.11266
Cell division protein ftsZ (EC 3.4.24.-)	2569	1614530	1615741	241.1230388	264.320396	1.09621
Site-specific tyrosine recombinase	2568	1615757	1616656	78.97664071	96.2586207	1.21882

TPR domain protein	2567	1616664	1617410	150.1340483	129.72118	0.86404
Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake	2566	1617403	1618383	88.7755102	63.6158163	0.71659
DNA topoisomerase I (EC 5.99.1.2)	2565	1618390	1620558	136.1957525	100.095337	0.73494
Site-specific tyrosine recombinase	2564	1620548	1621516	111.5702479	128.808884	1.15451
ATP-dependent protease hslV (EC 3.4.25.-)	2563	1621513	1622085	166.0839161	146.407343	0.88153
ATP-dependent hsl protease ATP-binding subunit hslU	2562	1622085	1623665	200.1274697	152.414595	0.76159
Flagellar basal-body rod protein flgB	2561	1623718	1624134	305.2884615	290.78125	0.95248
Flagellar basal-body rod protein flgC	2560	1624146	1624604	388.6462882	514.009825	1.32256
Flagellar hook-basal body complex protein fliE	2559	1624624	1625022	241.2060302	175.345477	0.72695
Flagellar M-ring protein fliF	2558	1625121	1626827	176.366843	167.391534	0.94911
Flagellar motor switch protein fliG	2557	1626831	1627889	180.5293006	170.620983	0.94512
Flagellar assembly protein fliH	2556	1627886	1628923	172.6133076	128.313886	0.74336
Flagellum-specific ATP synthase fliI	2555	1628932	1630281	167.5315048	222.106004	1.32576
Flagellar protein fliJ	2554	1630278	1630736	76.41921397	105.646288	1.38246
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	2553	1630769	1631791	122.3091977	132.928571	1.08682
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	2552	1631781	1632533	73.13829787	111.363032	1.52264
Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB	2551	1632530	1633249	51.46036161	100.944367	1.96159
hypothetical protein	2550	1633393	1634715	40.09077156	33.0813162	0.82516
hypothetical protein	2549	1634715	1635488	53.04010349	57.7800776	1.08937
Lipoprotein releasing system transmembrane protein LolC	2548	1635488	1636792	26.07361963	19.9800613	0.76629
Macrolide export ATP-binding/permease protein macB (EC 3.6.3.-)		1636795	1638243	37.98342541	35.3435773	0.9305
Cell division transporter, ATP-binding protein ftsE (TC 3.A.5.1.1)	2546	1638240	1638923	79.06295754	47.6830161	0.6031
Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)	2545	1638936	1640303	24.87198244	20.4206291	0.82103
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	2544	1640313	1642316	52.42136795	28.3377434	0.54058
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	2543	1642333	1644342	74.16625187	54.653559	0.73691
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	2542	1644359	1646401	90.59745348	56.0487267	0.61866
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	2541	1646418	1648454	85.95284872	47.9874754	0.5583
2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (EC 2.5.1.64) / 2-oxoglutarate decarboxylase (EC 4.1.1.71)	2540	1648485	1651403	49.34886909	35.0771076	0.7108
putative glycosyltransferase	2539	1651396	1653180	60.53811659	38.5969731	0.63756
Polysaccharide ABC transporter, ATP-binding protein	2538	1653177	1653947	189.6103896	108.75974	0.5736
O-antigen export system permease protein RfbD	2537	1653948	1654724	54.12371134	35.9729381	0.66464
putative glycosyltransferase	2536	1654731	1656320	68.59660164	45.6758968	0.66586
Putative N-acetylgalactosaminyl-diphosphoundecaprenol glucuronosyltransferase	2535	1656327	1657085	17.15039578	12.2757256	0.71577
Glycosyltransferase	2534	1657096	1658076	60.20408163	53.1714286	0.88319
UDP-galactopyranose mutase (EC 5.4.99.9)	2533	1658073	1659188	99.55156951	103.481614	1.03948

DNA-directed RNA polymerase omega chain (EC 2.7.7.6) (RNAP omega subunit) (Transcriptase omega chain) (RNA polymerase omega subunit)	2532	1659624	1659818	164.9484536	191.85567	1.16313
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	2531	1659852	1660850	58.11623246	61.5360721	1.05884
hypothetical protein		1661319	1661483	6.097560976	5.67378049	0.9305
hypothetical protein	2529	1661743	1662159	122.5961538	98.4182692	0.80278
Isoleucyl-tRNA synthetase (EC 6.1.1.5)	2528	1662259	1665489	153.7025513	198.607032	1.29215
hypothetical protein	2527	1665492	1666439	76.02956705	78.6061246	1.03389
hypothetical protein	2526	1666457	1666747	341.3793103	320.862069	0.9399
hypothetical protein	2525	1666757	1667065	81.16883117	108.75974	1.33992
hypothetical protein	2524	1667129	1672678	38.9259326	29.1776897	0.74957
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	2523	1672687	1675242	34.83365949	31.6843444	0.90959
hypothetical protein	2522	1675389	1677158	195.0254381	167.795082	0.86038
COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like	2521	1677244	1678263	33.36604514	42.0049068	1.25891
hypothetical protein	2520	1678260	1678637	90.18567639	69.1087533	0.76629
NADH pyrophosphatase (EC 3.6.1.22)	2518	1678667	1679566	84.53837597	110.749166	1.31005
hypothetical protein	2519	1679563	1679913	625.7142857	475.884286	0.76055
TPR repeat	2517	1679964	1681013	219.2564347	234.177312	1.06805
HflC protein	2516	1681043	1682023	223.4693878	195.594898	0.87526
HflK protein	2515	1682023	1682994	148.3007209	181.11689	1.22128
Antigen, p83/100	2514	1683181	1684755	218.5514612	218.14136	0.99812
glycosyl hydrolase, family 9	2513	1684868	1687237	23.6386661	24.7452512	1.04681
Putative translation initiation inhibitor, yjgF family	2512	1687247	1687708	21.69197397	16.1475054	0.7444
NdaD D-aminoacylase	2511	1687745	1689349	31.17206983	22.6243766	0.72579
low-specificity D-threonine aldolase	2510	1689354	1690469	25.11210762	21.6977578	0.86404
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	2509	1690473	1691330	18.6697783	17.3722287	0.9305
Sugar ABC transporter permease	2508	1691332	1692267	22.45989305	15.9229947	0.70895
Sugar ABC transporter, sugar-binding protein	2507	1692348	1693622	153.0612245	170.908163	1.1166
putative DNA-binding protein	2506	1693851	1694534	111.2737921	126.700586	1.13864
Ribonuclease Z (EC 3.1.26.11)	2505	1694647	1695573	260.2591793	281.360691	1.08108
ABC-type multidrug transport system, ATPase component	2504	1695592	1696623	318.1377304	351.080989	1.10355
gliding motility protein GldF	2503	1696620	1697354	130.7901907	188.888965	1.44421
gliding motility protein GldG	2502	1697358	1698983	300.3076923	356.166769	1.18601
hypothetical protein	2501	1698973	1699953	190.8163265	251.614796	1.31862
GGDEF domain protein	2500	1699955	1701130	143.8297872	148.088085	1.02961
COG1355, Predicted dioxygenase	2499	1701186	1702097	135.0164654	114.397366	0.84728
Xylulose kinase (EC 2.7.1.17)	2498	1702108	1703598	118.7919463	84.9315436	0.71496
Xylose isomerase (EC 5.3.1.5)	2497	1703641	1704981	212.6865672	197.210448	0.92724
hypothetical protein	2496	1705031	1706710	28.5884455	26.6015485	0.9305
Uncharacterized protein TP_0177	2495	1706703	1708271	16.58163265	30.8584184	1.861
hypothetical protein	2494	1708273	1709193	36.95652174	79.9016304	2.16204
Conserved domain protein	2493	1709193	1711295	143.6726927	129.703378	0.90277
Uncharacterized protein TP_0181	2492	1711462	1711917	200	126.793407	0.63397
Uncharacterized protein TP_0183 precursor	2491	1711933	1712754	81.60779537	75.9360536	0.9305
SsrA-binding protein	2490	1712849	1713310	52.06073753	78.7190889	1.51206

Serine/threonine kinase	2489	1713307	1714875	144.7704082	172.095026	1.18874
Signal peptidase I (EC 3.4.21.89)	2488	1714881	1715930	158.2459485	125.071973	0.79036
Signal peptidase I (EC 3.4.21.89)	2487	1715952	1716680	39.83516484	66.4642857	1.66848
Similar to coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)	2485	1716687	1717979	11.60990712	17.2848297	1.4888
hypothetical protein	2486	1717950	1718135	5.405405405	0	0
adsorption protein	2484	1718390	1720558	7.380073801	7.29635609	0.98866
Two component transcriptional regulator, LuxR family	2483	1720655	1721323	28.44311377	27.8592814	0.97947
Sensor histidine kinase	2482	1721287	1722033	41.55495979	29.9356568	0.72039
hypothetical protein	2481	1722095	1722823	9.615384615	5.11263736	0.53171
hypothetical protein		1722807	1722929	0	0	#DIV/0!
hypothetical protein	2479	1722933	1723937	12.94820717	11.1215139	0.85892
Uncharacterized protein TP_0813	2478	1724613	1725620	142.999007	127.516385	0.89173
dCMP deaminase (EC 3.5.4.12); late competence protein comEB	2477	1725704	1726195	199.592668	225.51833	1.12989
Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	2476	1726593	1727387	17.63224181	9.37531486	0.53171
hypothetical protein	2475	1727849	1728280	113.6890951	90.675174	0.79757
hypothetical protein	2474	1728326	1728898	145.1048951	95.9781469	0.66144
hypothetical protein	2473	1728895	1729044	67.11409396	37.4697987	0.5583
hypothetical protein	2472	1729111	1729413	16.55629139	9.24337748	0.5583
Adenylate cyclase (EC 4.6.1.1)	2471	1729727	1730470	13.4589502	21.2900404	1.58185
LysM domain/M23/M37 peptidase domain protein	2470	1730572	1731486	149.8905908	166.960613	1.11388
RNA polymerase sigma factor RpoD	2469	1731553	1732626	188.1467545	161.940263	0.86071
DNA mismatch repair protein MutL	2468	1732628	1734586	79.67313585	125.460674	1.57469
Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	2467	1734586	1734819	304.72103	227.633047	0.74702
Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	2466	1734831	1736198	98.02487198	88.4893928	0.90272
Uncharacterized protein TP_0285	2465	1736257	1737822	54.95207668	56.4840256	1.02788
hypothetical protein	2464	1737797	1738933	64.26056338	65.528169	1.01973
N-Acetylneuraminate cytidylyltransferase (EC 2.7.7.43)	2463	1738930	1739691	81.4717477	83.1458607	1.02055
Ubiquinone biosynthesis SAM-dependent O-methyltransferase (EC 2.1.1.-)		1739688	1741652	45.82484725	40.7449084	0.88914
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	2461	1741622	1743259	56.20036652	60.2522908	1.0721
N-acetylmuramoyl-L-alanine amidase	2460	1743256	1744485	70.78925956	81.7689178	1.1551
hypothetical protein	2459	1744482	1745054	412.5874126	281.427448	0.6821
Flagellar filament outer layer protein precursor (Sheath protein)	2458	1745135	1746157	3733.855186	3945.06507	1.05657
GTP pyrophosphokinase	2457	1746254	1747513	107.2279587	95.3411438	0.88914
Intergenic (Expressed, possible tmRNA)		1747514	1748178	29521.08434	28409.6785	0.96235
Response regulator	2456	1748179	1749240	672.3809524	611.471429	0.90941
Multi-sensor hybrid histidine kinase precursor	2455	1749230	1749601	517.5202156	574.351752	1.10982
NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	2454	1749805	1750863	1463.298379	1844.14633	1.26027
Phosphoglycerate kinase (EC 2.7.2.3)	2453	1750940	1752202	298.7951807	341.557028	1.14311
Triosephosphate isomerase (EC 5.3.1.1)	2452	1752320	1753072	344.4148936	418.230053	1.21432

Sensory box histidine kinase/response regulator	2451	1753128	1755923	105.5456172	95.8797853	0.90842
Citrate synthase (si) (EC 2.3.3.1)	2450	1756102	1757445	61.05733433	80.3708116	1.31632
DinB family protein	2449	1757540	1758055	1.941747573	0	0
hypothetical protein		1758106	1758231	128	74.44	0.58156
Translation elongation factor G-related protein	2447	1758246	1760333	138.4762817	89.6169142	0.64716
SJCHGC01885 protein	2446	1760402	1761556	183.7088388	108.04766	0.58815
Topoisomerase IV subunit B (EC 5.99.1.-)	2445	1761618	1763690	283.0917874	169.018357	0.59704
Pyrophosphate-energized proton pump (EC 3.6.1.1)	2444	1763765	1765882	195.0873878	141.970477	0.72773
D-glycerate transporter (predicted)	2443	1765962	1767353	148.0948958	152.519051	1.02987
Topoisomerase IV subunit A (EC 5.99.1.-)	2442	1767503	1769419	125.2609603	114.127088	0.91111
Glycine N-methyltransferase (EC 2.1.1.20)	2441	1769420	1770199	44.92939666	44.1957638	0.98367
hypothetical protein	2440	1770337	1770753	74.51923077	31.3149038	0.42023
hypothetical protein	2439	1770750	1771997	37.6904571	25.3704892	0.67313
hypothetical protein	2438	1772025	1772750	111.7241379	64.1724138	0.57438
Large repetitive protein	2437	1772725	1773690	84.97409326	60.7476684	0.7149
Outer membrane autotransporter barrel	2436	1773710	1777471	82.424887	56.903749	0.69037
Adenylate cyclase (EC 4.6.1.1)	2435	1777638	1780277	60.25009473	41.2536946	0.68471
2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	2434	1780316	1781971	439.8064126	392.915306	0.89338
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	2433	1782155	1783702	471.2346477	562.991597	1.19472
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	2432	1783746	1785296	196.1290323	209.512581	1.06824
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	2431	1785388	1786329	39.31987248	49.4420829	1.25743
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	2430	1786340	1787212	43.57798165	43.7505734	1.00396
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	2429	1787214	1788230	62.00787402	50.3715551	0.81234
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	2428	1788227	1789246	58.88125613	73.9651619	1.25618
Deblocking aminopeptidase (EC 3.4.11.-)	2427	1789236	1790291	33.17535545	50.2734597	1.51539
Endoglucanase M (EC 3.2.1.4)	2426	1790293	1791318	34.14634146	32.6809756	0.95709
hypothetical protein	2425	1791446	1792606	134.4827586	144.387931	1.07365
Sensory box histidine kinase/response regulator		1792616	1794826	180.9954751	199.152262	1.10032
ATPase, AAA family	2423	1794834	1797158	84.3373494	96.8937177	1.14888
hypothetical protein	2422	1797189	1798400	169.2815855	132.928571	0.78525
Uncharacterized protein TP_0126	2421	1798415	1799047	180.3797468	136.924842	0.75909
Uncharacterized protein TP_0788	2420	1799148	1799939	70.79646018	59.994311	0.84742
hypothetical protein	2419	1800027	1800380	84.98583569	47.4475921	0.5583
Chorismate mutase II (EC 5.4.99.5)	2418	1800377	1800748	24.25876011	27.5889488	1.13728
hypothetical protein	2416	1801053	1801901	201.6509434	126.18809	0.62577
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	2415	1801909	1802742	44.41776711	73.72509	1.65981
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	2414	1802780	1804234	110.7290234	131.191541	1.1848
Protein yicC	2413	1804231	1805097	189.3764434	110.671478	0.5844
Cytidylate kinase (EC 2.7.4.14)	2412	1805094	1805627	99.43714822	109.984053	1.10607
A/G-specific adenine glycosylase (EC 3.2.2.-)	2411	1805629	1806438	56.86032138	63.2601978	1.11255

hypothetical protein	2409	1806648	1807424	81.18556701	61.1539948	0.75326
Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)	2408	1807428	1808969	61.64828034	47.0986372	0.76399
hypothetical protein	2407	1808960	1810663	59.30710511	50.8141515	0.8568
hypothetical protein	2406	1810687	1812552	141.5549598	122.736193	0.86706
Glycosyltransferase	2405	1812554	1813651	54.6946217	45.8040109	0.83745
OxaI/YidC membrane insertion protein	2404	1813661	1816354	5.941329372	2.76420349	0.46525
OxaI/YidC membrane insertion protein	2403	1816366	1819089	5.508630187	4.442343	0.80643
OxaI/YidC membrane insertion protein	2402	1819105	1821828	8.446566287	6.15093647	0.72822
Glycosyltransferase	2401	1821825	1822793	19.62809917	17.302686	0.88153
putative bifunctional polymerase	2400	1822889	1824115	69.33115824	44.0203915	0.63493
OxaI/YidC membrane insertion protein	2399	1824112	1826802	24.16356877	10.3773234	0.42946
Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) / Phosphomannomutase (EC 5.4.2.8)	2398	1826796	1828103	52.02754399	35.5967865	0.68419
Phosphoheptose isomerase (EC 5.-.-.-)	2397	1828100	1828732	128.164557	101.589399	0.79265
D,D-heptose 7-phosphate kinase	2396	1828711	1829745	51.25725338	19.7978723	0.38625
Glycosyltransferase	2395	1829781	1830842	24.50518379	21.9250707	0.89471
hypothetical protein	2394	1830842	1831828	26.36916836	23.5927992	0.89471
Glycosyltransferase	2393	1831825	1833033	22.35099338	21.5678808	0.96496
transposase, mutator family	2392	1833068	1834282	55.50660793	43.4506608	0.7828
Beta-1,3-galactosyltransferase / Beta-1,4-galactosyltransferase	2391	1834294	1835361	14.05810684	10.4648547	0.7444
Conserved domain protein	2390	1835374	1836393	5.888125613	3.65260059	0.62033
Glycosyl transferase, family 2	2389	1836405	1837325	54.34782609	14.1597826	0.26054
GDP-L-fucose synthetase (EC 1.1.1.271)	2388	1837331	1838317	122.7180527	83.0466531	0.67673
GDP-mannose 4,6 dehydratase (EC 4.2.1.47)	2387	1838283	1839368	238.7096774	180.096774	0.75446
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	2386	1839385	1840347	182.952183	137.350312	0.75074
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	2385	1840375	1841496	90.99018733	80.5160571	0.88489
dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	2384	1841451	1842338	90.19165727	91.2666291	1.01192
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	2383	1842335	1842868	46.9043152	31.424015	0.66996
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	2382	1842868	1843743	40	36.1565714	0.90391
HlpA protein	2381	1843751	1845331	13.29113924	8.83386076	0.66464
Glycosyl transferase, group 2 family protein	2380	1845376	1846272	14.50892857	5.19252232	0.35788
hypothetical protein	2379	1846281	1847135	0	1.08957845	#DIV/0!
Acetyltransferase, CYSE/LACA/LPXA/NODL family	2378	1847449	1849179	4.046242775	4.30289017	1.06343
UDP-glucose 4-epimerase (EC 5.1.3.2)	2377	1849274	1850128	5.854800937	0	0
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	2376	1850131	1850670	16.69758813	12.0844156	0.72372
CDP-4-dehydro-6-deoxy-D-glucose 3-dehydratase (EC 4.2.1.-)	2375	1850748	1852085	62.82722513	60.5486163	0.96373
Similar to CDP-glucose 4,6-dehydratase (EC 4.2.1.45)	2374	1852078	1853151	91.33271202	106.664958	1.16787
Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	2373	1853127	1853909	34.52685422	24.9878517	0.72372
Alpha-1,2-fucosyltransferase	2372	1853911	1854726	9.81595092	9.13374233	0.9305
Polysaccharide ABC transporter, ATP-binding protein	2371	1854739	1856019	130.46875	97.4117188	0.74663

hypothetical protein	2370	1856133	1857794	71.6435882	57.140879	0.79757
O-antigen export system, permease protein	2369	1857784	1858629	56.80473373	78.1840237	1.37636
UDP-glucuronate 5'-epimerase (EC 5.1.3.12)	2368	1858622	1859689	129.3345829	117.729616	0.91027
UDP-glucose dehydrogenase (EC 1.1.1.22)	2367	1859697	1861028	185.5747558	148.208866	0.79865
2-aminoethylphosphonate:pyruvate aminotransferase (EC 2.6.1.37)	2366	1861032	1862846	243.660419	219.031698	0.89892
Phosphonopyruvate decarboxylase (EC 4.1.1.82)	2365	1862860	1863981	113.2917038	104.587868	0.92317
Phosphoenolpyruvate phosphomutase (EC 5.4.2.9)	2364	1863986	1865284	293.5285054	251.622111	0.85723
hypothetical protein	2363	1865294	1866925	82.77130595	94.1339669	1.13728
3-dehydroquinate synthase (EC 4.2.3.4)	2362	1866922	1868055	222.4183583	284.981024	1.28128
Transcriptional regulator, marR family	2361	1868067	1868645	164.3598616	149.717128	0.91091
Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4)		1868857	1869696	65.55423123	95.3790226	1.45496
Xanthine dehydrogenase iron-sulfur subunit (EC 1.17.1.4)	2359	1869680	1870165	171.1340206	143.891753	0.84081
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	2358	1870162	1872252	181.8181818	207.91555	1.14354
UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (EC 2.6.1.-)	2357	1872272	1873522	240.8	272.4504	1.13144
UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-)	2356	1873512	1875050	271.7815345	278.907997	1.02622
Transcription antitermination protein NusG	2355	1875071	1875613	302.5830258	135.626384	0.44823
hypothetical protein	2354	1875713	1876216	230.6163022	149.841948	0.64975
extensin-like protein	2353	1876231	1877463	228.8961039	236.40138	1.03279
Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1)	2352	1877578	1880358	242.0289855	253.190399	1.04612
lipoprotein, putative	2351	1880479	1881681	216.3061564	174.178453	0.80524
hypothetical protein	2350	1881706	1882284	200.6920415	173.865052	0.86633
Uncharacterized protein TP_0070	2349	1882578	1882988	273.1707317	260.993902	0.95542
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	2347	1883010	1883387	137.9310345	64.1724138	0.46525
Outer membrane protease E precursor (EC 3.4.23.-)	2348	1883380	1884417	54.96624879	49.3514947	0.89785
hypothetical protein	2346	1884469	1884810	155.4252199	106.420821	0.68471
Cell surface protein	2345	1884921	1886639	8.731082654	5.41618161	0.62033
RecA protein	2344	1886725	1888125	238.5714286	279.814643	1.17288
N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)	2343	1888139	1889362	236.3041701	215.316026	0.91118
Segregation and condensation protein A	2342	1889450	1890253	196.762142	219.00934	1.11307
Segregation and condensation protein B	2341	1890253	1890798	155.9633028	143.416514	0.91955
Ribosomal large subunit pseudouridine synthase B (EC 5.4.99.-)	2340	1890782	1891624	175.7719715	171.291568	0.97451
SSU ribosomal protein S1p	2339	1891608	1894004	910.041841	726.490795	0.7983
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	2338	1894030	1895544	316.9107856	234.793276	0.74088
TPR repeat-containing protein TP_0282	2337	1895547	1896236	156.7489115	152.607402	0.97358
hypothetical protein	2336	1896239	1897030	53.09734513	63.5233881	1.19636
hypothetical protein	2335	1897020	1897175	6.451612903	0	0
Methionine ABC transporter ATP-binding protein	2334	1897221	1898291	15.88785047	9.56588785	0.60209
Methionine ABC transporter permease protein	2333	1898288	1898968	13.23529412	23.2625	1.75761

Methionine ABC transporter substrate-binding protein	2332	1898985	1899845	53.48837209	73.5744186	1.37552
N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)	2331	1899858	1901012	32.06239168	22.5771231	0.70416
Fe-S oxidoreductase (EC 1.8.-.-)	2330	1901017	1903467	42.85714286	39.1189796	0.91278
Rod shape-determining protein rodA	2329	1903469	1904779	41.98473282	23.4400763	0.5583
Cell division protein ftsI [Peptidoglycan synthetase] (EC 2.4.1.129)	2328	1904776	1906653	91.73333333	74.9362667	0.81689
Rod shape-determining protein mreD	2327	1906653	1907156	57.65407555	36.9980119	0.64172
Rod shape-determining protein mreC	2326	1907149	1908039	82.02247191	60.6393258	0.7393
Rod shape-determining protein mreB	2325	1908058	1909083	365.6862745	280.062255	0.76585
TPR domain protein	2324	1909093	1910043	196.8421053	175.325789	0.89069
INTERGENIC (Expressed possible RNaseP)		1910044	1910503	847.4945534	539.244009	0.63628
hypothetical protein	2322	1910504	1910851	3787.234043	2327.66413	0.61461
Zn-ribbon protein, possibly nucleic acid-binding	2323	1910839	1911681	758.9073634	443.147862	0.58393
RNA polymerase sigma factor RpoD	2321	1911803	1913572	182.5890334	134.656868	0.73749
DNA primase (EC 2.7.7.-)	2320	1913569	1915473	162.289916	125.597952	0.77391
COG1559 protein yceG like	2319	1915473	1916573	170.9090909	158.185	0.92555
Metal-dependent hydrolases of the beta-lactamase superfamily I	2318	1916576	1917517	91.78228388	81.4311633	0.88722
hypothetical protein	2317	1917517	1917984	137.0449679	109.587794	0.79965
Membrane spanning protein	2316	1918157	1919716	132.7774214	124.743105	0.93949
Nitrogen regulatory protein P-II	2315	1919709	1920482	197.9301423	140.838939	0.71156
hypothetical protein		1920566	1920739	34.68208092	16.1358382	0.46525
DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	2313	1920728	1921378	47.69230769	27.1992308	0.57031
ADA regulatory protein	2312	1921375	1921941	21.20141343	14.7959364	0.69788
Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)	2311	1921919	1922434	40.77669903	21.6815534	0.53171
putative lipoprotein	2310	1922427	1923326	73.41490545	50.7169077	0.69083
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	2309	1923383	1924819	53.62116992	47.3025766	0.88216
DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	2308	1924923	1925342	4.77326969	22.2076372	4.6525
ABC-type multidrug transport system, permease component	2307	1925490	1926290	8.75	18.61	2.12686
Daunorubicin resistance ATP-binding protein	2306	1926287	1927057	16.88311688	16.9181818	1.00208
hypothetical protein	2305	1927054	1927443	17.99485861	28.7043702	1.59514
hypothetical protein	2304	1927527	1927649	0	0	#DIV/0!
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	2303	1927791	1929104	16.75552171	21.2604722	1.26886
Transcriptional regulator, LuxR family	2302	1929117	1930469	6.656804734	4.12943787	0.62033
sensory box histidine kinase/response regulator	2301	1930624	1933788	6.977481763	5.60719949	0.80361
Two-component response regulator	2300	1933867	1934538	2.980625931	6.93368107	2.32625
probable adhesin	2299	1934703	1936628	22.85714286	25.1355844	1.09968
hypothetical protein	2298	1936666	1937145	20.87682672	33.0240084	1.58185
hypothetical protein	2297	1937142	1938341	24.18682235	33.3707256	1.37971
hypothetical protein	2296	1938354	1939061	19.8019802	34.2192362	1.72807
hypothetical protein	2295	1939151	1940137	4.056795132	1.88742394	0.46525

Halomucin precursor		1940097	1942580	2.013693113	1.49899315	0.7444
hypothetical protein	2293	1942558	1942677	0	0	#DIV/0!
Cell surface protein	2292	1942852	1944453	3.123048095	2.324797	0.7444
Calcium-binding acidic-repeat protein precursor	2291	1944450	1946159	1.170275015	2.1778818	1.861
ATP-dependent DNA helicase recG (EC 3.6.1.-)	2290	1946382	1946690	9.74025974	0	0
hypothetical protein	2289	1946660	1946830	0	5.47352941	#DIV/0!
hypothetical protein	2288	1947229	1947405	0	7.56504065	#DIV/0!
hypothetical protein		1947425	1947625	35	18.61	0.53171
hypothetical protein	2286	1947809	1948873	7.518796992	7.87077068	1.04681
some similarities to hypothetical proteins	2285	1948866	1950875	22.89696366	7.87381782	0.34388
hypothetical protein	2284	1950800	1951021	0	0	#DIV/0!
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	2283	1951205	1952773	50.38265306	35.6058673	0.70671
type I restriction-modification system, M subunit (EC 2.1.1.72)	2282	1952760	1953902	16.63747811	7.33318739	0.44076
Putative DNA-binding protein	2281	1953899	1954774	19.42857143	12.7611429	0.65682
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	2280	1954771	1958007	13.90605686	10.0641224	0.72372
ATPase involved in DNA repair	2279	1958000	1960852	2.805049088	0.97878682	0.34894
hypothetical protein	2278	1960885	1962576	11.82732111	5.50266115	0.46525
hypothetical protein		1962581	1962709	31.25	14.5390625	0.46525
ATP-dependent DNA helicase		1962714	1962950	19.60784314	13.6838235	0.69788
ATP-dependent DNA helicase		1962951	1964027	12.78409091	7.93039773	0.62033
hypothetical protein	2275	1964019	1964252	13.21585903	0	0
putative cytoplasmic protein	2273	1964275	1965606	2.253944403	0	0
ATPase	2271	1965740	1965997	0	0	#DIV/0!
hypothetical protein	2272	1965994	1966125	0	0	#DIV/0!
hypothetical protein		1966524	1967507	1.017293998	1.89318413	1.861
hypothetical protein		1967526	1971092	0.280426248	0	0
transposase, mutator family	2268	1971114	1972328	42.17926186	44.1537786	1.04681
hypothetical protein	2267	1972618	1972737	25.21008403	0	0
hypothetical protein	2266	1973172	1973393	0	0	#DIV/0!
hypothetical protein		1973490	1974191	7.235890014	4.0397974	0.5583
hypothetical protein	2264	1974955	1975176	9.049773756	0	0
putative DNA primase/helicase	2263	1975443	1976879	0.69637883	1.9439415	2.7915
hypothetical protein	2262	1976879	1977214	0	0	#DIV/0!
hypothetical protein	2261	1977204	1977425	0	0	#DIV/0!
hypothetical protein	2260	1977404	1977607	0	4.58374384	#DIV/0!
hypothetical protein	2259	1977682	1978347	1.503759398	1.39924812	0.9305
site-specific recombinase, phage integrase family	2258	1978806	1980161	19.92619926	22.6616236	1.13728
Pyruvate,phosphate dikinase (EC 2.7.9.1)	2255	1980571	1983579	602.7306027	689.431402	1.14385
hypothetical protein		1983527	1983667	0	0	#DIV/0!
ATP-dependent helicase	2253	1983685	1986411	78.64755605	82.4147372	1.0479
hypothetical protein	2252	1986437	1987321	93.89140271	95.7867647	1.02019
hypothetical protein	2251	1987378	1987521	139.8601399	52.0559441	0.3722
hypothetical protein	2250	1987546	1988097	250.4537205	227.980944	0.91027
Glucose-6-phosphate isomerase (EC 5.3.1.9)	2249	1988127	1989701	168.5750636	169.881361	1.00775
Arginine pathway regulatory protein ArgR, repressor of arg regulon	2248	1989782	1990255	114.1649049	64.9186047	0.56864

hypothetical protein	2247	1990481	1991872	26.59956866	28.0956147	1.05624
hypothetical protein	2246	1991844	1991969	0	0	#DIV/0!
TM2 domain protein	2245	1992013	1992519	106.8548387	90.0483871	0.84272
Recombination inhibitory protein MutS2	2244	1992523	1995207	50.67064083	63.4431818	1.25207
Ribosome small subunit-stimulated GTPase EngC	2243	1995200	1996135	75.93582888	104.494652	1.37609
Glutamate racemase (EC 5.1.1.3)	2242	1996132	1997025	76.14781635	70.8555431	0.9305
hypothetical protein	2241	1997031	1997423	30.6122449	47.4744898	1.55083
Pentapeptide repeat family protein	2240	1997444	1998037	52.27655987	21.9679595	0.42023
Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	2238	1998038	1998757	73.71349096	67.2962448	0.91294
hypothetical protein	2239	1998754	2000472	116.9965076	88.8253783	0.75921
hypothetical protein	2237	2000484	2001263	152.7599487	106.308729	0.69592
hypothetical protein	2236	2001335	2001994	47.04097117	40.947648	0.87047
hypothetical protein	2235	2001994	2002293	16.72240803	9.3361204	0.5583
hypothetical protein	2234	2002419	2002595	39.77272727	42.2954545	1.06343
putative protein family member (5Q829)	2233	2003059	2003910	28.20211516	25.1486486	0.89173
DnaJ-like protein DjlA	2232	2004164	2004745	91.22203098	75.2728055	0.82516
putative lipoprotein	2231	2004750	2006117	171.1777615	106.867959	0.62431
Putative lipoprotein	2230	2006169	2006792	520.0642055	534.701445	1.02815
Response regulator of zinc sigma-54-dependent two-component system	2229	2006893	2008251	67.99704361	58.4571323	0.8597
Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	2228	2008251	2009471	82.78688525	51.8639344	0.62648
Drug resistance transporter EmrB/QacA subfamily	2227	2009704	2011104	28.57142857	21.2685714	0.7444
Serine phosphatase RsbU, regulator of sigma subunit	2226	2011343	2011795	92.92035398	45.289823	0.4874
anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	2225	2011862	2012434	94.40559441	56.9361888	0.6031
Serine phosphatase RsbU, regulator of sigma subunit	2224	2012460	2014028	37.62755102	25.5175383	0.67816
DNA polymerase III delta prime subunit (EC 2.7.7.7)	2223	2014041	2015408	88.51499634	113.674835	1.28424
Colicin V production protein	2222	2015401	2015901	32	33.498	1.04681
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	2221	2015898	2017055	120.1382887	112.592913	0.93719
NADPH:quinone oxidoreductase	2220	2017126	2017689	65.71936057	36.3605684	0.55327
hypothetical protein	2219	2017878	2018852	268.9938398	231.191992	0.85947
Uncharacterized protein TP_0454	2218	2018849	2019586	107.1913161	126.255088	1.17785
Putative deoxyribonuclease YjjV	2217	2019633	2020481	29.48113208	25.2376179	0.85606
Strepotococcal cysteine protease (Streptopain) (EC 3.4.22.10) / Streptococcal pyrogenic exotoxin B (SpeB)	2216	2020559	2021995	2.78551532	1.295961	0.46525
Asparaginyl-tRNA synthetase (EC 6.1.1.22)	2215	2022197	2023624	180.8585503	216.745602	1.19843
D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	2214	2023630	2024949	109.9317665	162.255497	1.47597
hypothetical protein	2213	2024954	2025148	293.814433	239.819588	0.81623
hypothetical protein	2212	2025198	2025323	144	111.66	0.77542
Membrane proteins related to metalloendopeptidases	2211	2025407	2026687	121.875	152.660156	1.2526

Signal peptidase I (EC 3.4.21.89)	2210	2026741	2027154	46.00484262	24.783293	0.53871
Cell division protein ftsI [Peptidoglycan synthetase] (EC 2.4.1.129)	2209	2027151	2029043	104.6511628	138.689746	1.32526
Conserved domain protein	2208	2029030	2030928	23.18229715	40.6909905	1.75526
hypothetical protein		2031008	2031145	0	6.7919708	#DIV/0!
Integrase	2206	2031219	2032406	27.82462057	18.8296796	0.67673
hypothetical protein		2032504	2032671	0	0	#DIV/0!
hypothetical protein	2204	2032661	2033203	1.84501845	0	0
hypothetical protein	2203	2033446	2034636	2.521008403	1.56386555	0.62033
Iron-sulfur cluster-binding protein		2034900	2035307	2.457002457	2.28624079	0.9305
Iron-sulfur cluster-binding protein		2035460	2035759	13.37792642	9.3361204	0.69788
Phage-related protein	2200	2036195	2037775	5.696202532	0.58892405	0.10339
hypothetical protein		2038758	2038895	0	0	#DIV/0!
putative DNA primase/helicase	2198	2039179	2040573	2.896451846	4.71650978	1.62838
hypothetical protein	2197	2040638	2040976	0	0	#DIV/0!
hypothetical protein	2196	2040976	2041269	10.92896175	5.08469945	0.46525
hypothetical protein	2195	2041280	2043082	1.408450704	0.65528169	0.46525
hypothetical protein	2194	2043079	2043630	0	0	#DIV/0!
hypothetical protein	2193	2043631	2043912	0	0	#DIV/0!
hypothetical protein	2192	2043872	2044159	0	0	#DIV/0!
hypothetical protein	2191	2044152	2044418	4.975124378	4.62935323	0.9305
hypothetical protein	2190	2044429	2044596	0	0	#DIV/0!
hypothetical protein	2189	2044599	2045153	0	0	#DIV/0!
hypothetical protein	2188	2045275	2045541	0	0	#DIV/0!
hypothetical protein	2187	2045551	2047047	1.740644038	0.80983464	0.46525
hypothetical protein	2186	2047044	2047907	3.424657534	0	0
hypothetical protein	2185	2047904	2048341	0	2.19976359	#DIV/0!
hypothetical protein	2184	2048338	2048946	0	0	#DIV/0!
hypothetical protein	2183	2049061	2049213	125	159.164474	1.27332
GCN5-related N-acetyltransferase; Histone acetyltransferase HPA2 and related acetyltransferases	2182	2049217	2049771	32.49097473	50.3880866	1.55083
hypothetical protein	2181	2050038	2050190	59.21052632	61.2171053	1.03389
Transcription regulator of multidrug efflux pump operon, TetR (AcrR) family	2180	2050242	2050808	33.56890459	11.5079505	0.34282
Ferredoxin	2179	2050893	2051714	3.65408039	1.13337393	0.31017
hypothetical protein	2178	2051711	2052364	6.125574273	1.42496172	0.23263
Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	2177	2052383	2053180	2.509410289	3.50250941	1.39575
transposase, mutator family	2176	2053336	2054565	9.298393914	3.93279797	0.42295
hypothetical protein		2054605	2054760	0	0	#DIV/0!
hypothetical protein		2054991	2055116	0	0	#DIV/0!
hypothetical protein	2173	2055137	2056057	7.608695652	0	0
hypothetical protein	2172	2056341	2056568	4.405286344	0	0
hypothetical protein	2171	2056565	2056894	18.23708207	0	0
hypothetical protein	2170	2057000	2057131	0	0	#DIV/0!
hypothetical protein	2169	2057179	2057415	4.237288136	7.88559322	1.861
Fic-1 cell filamentation-like protein	2168	2057418	2058023	3.305785124	0	0
hypothetical protein	2167	2058030	2058143	0	0	#DIV/0!
hypothetical protein		2058322	2059512	5.042016807	0	0
hypothetical protein		2059682	2059807	0	0	#DIV/0!

probable methyltransferase	2164	2059780	2060406	0	0	#DIV/0!
hypothetical protein	2163	2060695	2060835	0	6.64642857	#DIV/0!
hypothetical protein		2060799	2061248	2.638522427	2.45514512	0.9305
hypothetical protein	2161	2061251	2061517	5.681818182	5.28693182	0.9305
Antitoxin of toxin-antitoxin stability system	2160	2061714	2061992	17.98561151	10.0413669	0.5583
Plasmid stabilization system protein	2159	2061994	2062329	0	0	#DIV/0!
transposase, mutator family	2158	2062418	2062540	0	10.0053763	#DIV/0!
transposase, mutator family	2157	2062643	2063857	58.25242718	53.3826125	0.9164
Putative transposase		2063886	2064119	13.15789474	8.1622807	0.62033
transposase, mutator family		2064134	2064817	8.8365243	4.11119293	0.46525
hypothetical protein	2154	2064988	2065221	0	7.98712446	#DIV/0!
HD domain protein	2153	2065544	2066710	66.03773585	64.640223	0.97884
Hemolysins and related proteins containing CBS domains	2152	2066715	2068064	28.2108389	23.4870082	0.83255
ATP-dependent RNA helicase YfmL	2151	2068075	2069247	126.2798635	105.594283	0.83619
Glycosyltransferase		2069258	2069551	300.3412969	203.249147	0.67673
Glycosyltransferase		2069508	2070413	175.6906077	153.198343	0.87198
Proline/sodium symporter PutP (TC 2.A.21.2.1) @ Propionate/sodium symporter	2148	2070559	2072022	91.28345916	109.207618	1.19636
Indolepyruvate oxidoreductase, subunit A	2147	2072103	2073776	123.501199	121.054257	0.98019
Indolepyruvate oxidoreductase, subunit B	2146	2073773	2074360	136.286201	215.584327	1.58185
Phenylacetate-coenzyme A ligase (EC 6.2.1.30)	2145	2074357	2075703	174.7211896	206.162825	1.17995
hypothetical protein		2075840	2075953	0	0	#DIV/0!
Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein	2143	2076037	2077044	1.986097319	1.84806356	0.9305
Radical SAM domain protein	2142	2077096	2078307	0	2.30511974	#DIV/0!
Taurine transporter substrate-binding protein	2141	2078351	2079358	0.993048659	0.92403178	0.9305
Radical SAM domain protein	2140	2079389	2080600	3.303055326	0.76837325	0.23263
Radical SAM domain protein	2139	2080671	2081891	3.278688525	8.3897541	2.55888
L-proline Glycine Betaine ABC transport ATP-binding protein proV (TC 3.A.1.12.1)	2138	2081888	2082724	0	1.11303828	#DIV/0!
Choline ABC transporter permease protein	2137	2082740	2083507	1.303780965	0	0
Alkanesulfonates-binding protein	2136	2083545	2084576	3.879728419	3.61008729	0.9305
Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein	2135	2084623	2085621	3.006012024	5.59418838	1.861
putative PQQ enzyme repeat	2134	2085635	2087131	4.679144385	2.48796791	0.53171
putative PQQ enzyme repeat	2133	2087143	2088540	6.442376521	8.65891195	1.34406
hypothetical protein	2132	2088512	2088625	0	0	#DIV/0!
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	2131	2088643	2090208	176.3578275	151.615016	0.8597
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	2130	2090230	2091183	23.08499475	39.0556139	1.69182
Oligopeptide transport system permease protein oppC (TC 3.A.1.5.1)	2129	2091193	2092047	15.22248244	20.7019906	1.35996
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	2128	2092044	2093024	22.44897959	23.7372449	1.05739
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	2127	2093021	2093992	12.35839341	20.1240989	1.62838
Phenylacetate-coenzyme A ligase (EC 6.2.1.30)	2126	2094088	2095389	188.5625966	225.793663	1.19745

Amino acid-binding ACT	2125	2095399	2095815	173.0769231	116.3125	0.67203
Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)	2124	2095892	2097373	187.0357866	227.441594	1.21603
Nucleotidyltransferase substrate binding protein, HI0074	2123	2097429	2097848	119.3317422	108.817422	0.91189
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	2122	2097839	2098141	76.1589404	43.1357616	0.56639
hypothetical protein	2121	2098163	2099140	79.83623337	138.098772	1.72978
hypothetical protein	2120	2099451	2099777	3.067484663	2.85429448	0.9305
hypothetical protein	2119	2099859	2100074	0	0	#DIV/0!
hypothetical protein	2118	2100543	2100677	0	0	#DIV/0!
hypothetical protein	2117	2100720	2100836	0	0	#DIV/0!
hypothetical protein		2100860	2101660	0	0	#DIV/0!
hypothetical protein	2115	2101846	2102700	74.94145199	78.4496487	1.04681
Surface proteins containing Ig-like domains-like precursor	2114	2102793	2105747	67.02775897	61.4243399	0.9164
Large exoproteins involved in heme utilization or adhesion	2113	2105926	2108499	51.6906335	46.651574	0.90252
Autotransporter adhesin		2108509	2110230	36.02556653	24.3303312	0.67536
hypothetical protein	2111	2110234	2111244	34.65346535	46.0643564	1.32929
COG1565: Uncharacterized conserved protein		2110879	2111649	5.194805195	9.66753247	1.861
hypothetical protein		2111964	2112083	0	0	#DIV/0!
hypothetical protein	2108	2112106	2112621	3.883495146	1.80679612	0.46525
hypothetical protein	2107	2112721	2113329	0	0	#DIV/0!
hypothetical protein	2106	2113361	2113807	0	0	#DIV/0!
hypothetical protein	2105	2113814	2114665	0	2.18683901	#DIV/0!
hypothetical protein	2104	2114669	2116156	0	0.62575656	#DIV/0!
hypothetical protein	2103	2116166	2116393	0	0	#DIV/0!
hypothetical protein	2102	2116393	2116914	0	1.78598848	#DIV/0!
hypothetical protein	2101	2117188	2117475	0	3.24216028	#DIV/0!
hypothetical protein	2100	2117432	2117737	6.557377049	0	0
hypothetical protein	2099	2117761	2118285	1.908396947	1.77576336	0.9305
hypothetical protein		2118258	2118389	0	0	#DIV/0!
hypothetical protein	2097	2118393	2120354	1.019887812	0	0
hypothetical protein	2096	2120365	2120655	0	6.81684982	#DIV/0!
hypothetical protein	2095	2120658	2121011	2.83286119	0	0
Putative DNA primase/helicase	2094	2120996	2122384	1.46627566	0	0
hypothetical protein	2093	2122946	2123059	0	0	#DIV/0!
hypothetical protein		2123260	2123388	0	0	#DIV/0!
hypothetical protein	2091	2123776	2123919	0	6.50699301	#DIV/0!
hypothetical protein	2090	2123916	2124044	0	0	#DIV/0!
hypothetical protein		2124115	2124366	0	3.70717131	#DIV/0!
hypothetical protein	2088	2124457	2124657	0	0	#DIV/0!
hypothetical protein	2087	2124746	2125018	0	0	#DIV/0!
hypothetical protein	2086	2125018	2125560	1.84501845	0	0
ORF009	2085	2125575	2126795	0	0	#DIV/0!
Phage portal protein, HK97	2084	2126792	2128021	0	0	#DIV/0!
Two component transcriptional regulator, LuxR family	2083	2128025	2128726	1.426533524	0	0
Probable prohead protease	2082	2128720	2129388	0	0	#DIV/0!
Major capsid protein, HK97 family	2081	2129457	2130758	0	0	#DIV/0!
Phage integrase	2080	2130883	2132121	0	0	#DIV/0!

hypothetical protein	2079	2132376	2150243	2.406671517	1.82277383	0.75738
hypothetical protein	2078	2150352	2152667	223.7580994	219.461339	0.9808
hypothetical protein	2076	2152649	2152849	5	0	0
hypothetical protein	2077	2152839	2153969	60.17699115	79.0513274	1.31365
Large repetitive protein	2075	2154054	2169251	156.4124498	136.234948	0.871
hypothetical protein		2169233	2169409	11.36363636	0	0
Hemolysins and related proteins containing CBS domains	2073	2169492	2170757	29.24901186	34.5719368	1.18199
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	2072	2170754	2171158	4.95049505	9.21287129	1.861
hypothetical protein	2071	2171348	2171605	42.80155642	7.24124514	0.16918
hypothetical protein	2070	2171613	2171888	7.272727273	10.1509091	1.39575
FOG: CheY-like receiver	2069	2171966	2176516	33.2306338	25.18739	0.75796
Sensory box histidine kinase/response regulator	2068	2176506	2179028	36.08247423	22.5061459	0.62374
Adenylate cyclase (EC 4.6.1.1)	2067	2179032	2180321	26.37703646	24.5438324	0.9305
hypothetical protein		2180471	2181121	0	1.44487578	#DIV/0!
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	2065	2181067	2181528	4.338394794	4.03687636	0.9305
transposase, mutator family	2064	2181654	2182868	41.30052724	55.6010545	1.34626
hypothetical protein	2063	2182963	2183175	18.86792453	4.38915094	0.23263
hypothetical protein	2062	2183168	2183509	17.59530792	19.101173	1.08558
hypothetical protein	2061	2183502	2184095	8.431703204	9.4148398	1.1166
hypothetical protein	2060	2184428	2184646	9.174311927	4.26834862	0.46525
hypothetical protein	2059	2184732	2184926	5.154639175	4.79639175	0.9305
hypothetical protein	2058	2184901	2185020	0	0	#DIV/0!
hypothetical protein	2057	2185042	2185191	7.575757576	0	0
hypothetical protein		2185371	2185769	0	7.10305344	#DIV/0!
hypothetical protein	2055	2185960	2186085	0	0	#DIV/0!
hypothetical protein		2186124	2186282	0	0	#DIV/0!
hypothetical protein	2053	2186366	2186509	0	6.50699301	#DIV/0!
putative DNA primase/helicase	2052	2186638	2188032	1.43472023	0.66750359	0.46525
hypothetical protein	2051	2188032	2188367	0	0	#DIV/0!
hypothetical protein	2050	2188649	2188939	3.448275862	0	0
hypothetical protein	2049	2188948	2190990	2.448579824	0.91136141	0.3722
hypothetical protein	2048	2191033	2191557	3.816793893	1.77576336	0.46525
hypothetical protein	2047	2191584	2191967	0	0	#DIV/0!
hypothetical protein	2046	2192006	2192386	0	2.52168022	#DIV/0!
NLP/P60 family secreted protein	2045	2192383	2192904	0	1.78598848	#DIV/0!
hypothetical protein	2044	2192904	2193131	4.405286344	0	0
hypothetical protein	2043	2193151	2194662	0	1.23163468	#DIV/0!
hypothetical protein	2042	2194659	2195537	0	1.05979499	#DIV/0!
hypothetical protein	2041	2195534	2195968	0	0	#DIV/0!
hypothetical protein	2040	2195992	2196588	0	0	#DIV/0!
hypothetical protein		2196673	2196831	0	0	#DIV/0!
putative DNA helicase	2038	2197009	2197848	14.30274136	1.1090584	0.07754
hypothetical protein	2037	2197910	2198575	3.007518797	2.79849624	0.9305
hypothetical protein	2036	2198728	2199282	0	0	#DIV/0!
hypothetical protein	2035	2199304	2199582	0	0	#DIV/0!
hypothetical protein	2034	2199809	2200576	0	0	#DIV/0!
hypothetical protein		2200786	2200938	0	0	#DIV/0!
hypothetical protein	2032	2201133	2201549	0	0	#DIV/0!

hypothetical protein		2201565	2202080	5.825242718	0	0
hypothetical protein		2202080	2202214	0	0	#DIV/0!
DNA polymerase III alpha subunit (EC 2.7.7.7)	2029	2202498	2205446	39.41055517	38.5848184	0.97905
DNA polymerase IV (EC 2.7.7.7)	2028	2205439	2206656	27.5	28.6904167	1.04329
COG1801: Uncharacterized conserved protein	2027	2206659	2207462	30.53435115	31.9637405	1.04681
transcriptional regulator, putative	2026	2207575	2208198	20.70393375	32.7505176	1.58185
hypothetical protein	2025	2208226	2208588	11.04972376	2.57044199	0.23263
putative helicase	2024	2208590	2213590	39.4	38.1505	0.96829
Exonuclease SbcC	2023	2213635	2214786	3.475238923	0	0
hypothetical protein	2022	2215253	2215789	7.462686567	3.47201493	0.46525
hypothetical protein	2021	2215828	2215953	0	0	#DIV/0!
hypothetical protein		2216482	2216640	0	0	#DIV/0!
hypothetical protein	2019	2216641	2216970	0	0	#DIV/0!
hypothetical protein	2018	2217029	2217448	0	0	#DIV/0!
Major capsid protein, HK97 family	2017	2217487	2218791	3.900156006	0	0
hypothetical protein	2016	2218860	2219555	1.438848921	2.67769784	1.861
BarA-associated response regulator UvrY (= GacA = SirA)	2015	2219536	2220258	2.770083102	2.57756233	0.9305
Portal protein	2014	2220248	2221438	3.439380911	9.60103181	2.7915
ORF009	2013	2221495	2222730	0	0	#DIV/0!
hypothetical protein	2012	2222733	2223269	3.731343284	0	0
hypothetical protein	2011	2223253	2223579	3.184713376	0	0
site-specific recombinase, phage integrase family	2010	2223709	2225178	31.56384505	17.3550933	0.54984
hypothetical protein		2225626	2225766	0	0	#DIV/0!
hypothetical protein	2007	2225887	2244411	18.03066292	24.6639765	1.36789
hypothetical protein	2006	2244493	2245524	146.4597478	170.576625	1.16467
BNR domain protein	2005	2245502	2249899	210.1432795	180.301569	0.85799
Cytoplasmic filament protein A	2004	2249918	2251879	143.2942376	135.233299	0.94375
Predicted beta-xyloside ABC transporter, substrate-binding component	2003	2251876	2253201	113.9622642	80.7603774	0.70866
hypothetical protein	2002	2253207	2253875	32.93413174	22.2874251	0.67673
hypothetical protein	2001	2253877	2255142	20.55335968	27.9517787	1.35996
Esterase/lipase	2000	2255152	2256057	35.35911602	26.7325967	0.75603
exported protein	1999	2256410	2256886	94.53781513	107.515756	1.13728
hypothetical protein	1998	2256888	2257595	182.4611033	167.147808	0.91607
transcriptional regulator, Crp/Fnr family	1997	2257730	2258905	166.8085106	123.538723	0.7406
hypothetical protein		2258891	2259022	213.740458	63.9274809	0.29909
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	1995	2259058	2260038	67.34693878	58.8683673	0.87411
putative adenylate/guanylate cyclase	1994	2260025	2262103	37.5360924	41.644129	1.10944
hypothetical protein	1993	2262155	2262367	28.30188679	17.5566038	0.62033
hypothetical protein	1992	2262385	2262966	848.5370052	1092.25645	1.28722
hypothetical protein	1991	2263161	2263310	416.1073826	224.818792	0.54029
Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	1990	2263640	2267203	1034.913426	1284.42279	1.24109
B. burgdorferi predicted coding region BB0351	1989	2267515	2269047	201.6971279	225.336488	1.1172
hypothetical protein	1988	2269057	2270355	254.2372881	256.640216	1.00945
HAD superfamily hydrolase	1987	2270389	2271033	57.45341615	41.9013975	0.72931
Sensory box histidine kinase/response regulator	1986	2271058	2273616	72.04385278	58.2928739	0.80913
FOG: CheY-like receiver	1985	2273636	2277232	62.56952169	54.5983037	0.8726

hypothetical protein	1983	2277254	2277958	53.97727273	47.5823864	0.88153
hypothetical protein		2277938	2278078	0	0	#DIV/0!
Ferric iron ABC transporter, iron-binding protein	1982	2278310	2279359	951.3822688	656.406101	0.68995
Ferric iron ABC transporter, permease protein	1981	2279453	2281234	204.379562	136.884335	0.66976
Putrescine transport ATP-binding protein potG (TC 3.A.1.11.2)	1980	2281227	2282366	86.0403863	69.4402985	0.80707
hypothetical protein	1979	2282653	2283735	60.07393715	32.6792976	0.54398
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	1978	2283732	2284499	62.58148631	32.7555411	0.52341
L-2-haloalkanoic acid dehalogenase	1977	2284492	2285262	77.92207792	31.4194805	0.40322
Ferric iron ABC transporter, permease protein	1976	2285309	2287174	39.14209115	19.9571046	0.50986
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Multiple sugar ABC transporter, ATP-binding protein	1975	2287239	2288360	84.74576271	51.4638715	0.60727
CELL PROCESSES	1974	2288382	2289578	92.80936455	78.5790134	0.84667
hypothetical protein	1973	2289688	2290116	32.71028037	15.2184579	0.46525
Ribose operon repressor	1972	2290211	2291275	90.22556391	49.8482143	0.55248
Ribokinase (EC 2.7.1.15)	1971	2291259	2292152	129.8992161	128.165174	0.98665
Mg(2+) transport ATPase/permease	1970	2292180	2292881	91.29814551	74.3338088	0.81419
tetrapyrrole methylase family protein/MazG family protein	1969	2292907	2293788	262.2020431	255.597049	0.97481
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	1968	2293811	2294785	155.0308008	133.747433	0.86272
Peptidyl-tRNA hydrolase (EC 3.1.1.29)	1967	2294801	2295424	32.10272873	34.3523274	1.07008
Alpha-galactosidase (EC 3.2.1.22)	1966	2295496	2297352	53.34051724	57.654903	1.08088
Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	1965	2297353	2299005	112.590799	116.030872	1.03055
Cu(I)-responsive transcriptional regulator	1964	2299264	2300076	45.56650246	30.9402709	0.67901
Transposase	1963	2300239	2301294	25.59241706	16.7578199	0.6548
Uroporphyrinogen-III decarboxylase	1962	2301377	2302345	21.69421488	12.4963843	0.57602
COG0523: Putative GTPases (G3E family)	1961	2302410	2303021	11.45662848	16.7520458	1.46221
hypothetical protein	1960	2303022	2303438	24.03846154	20.1310096	0.83745
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	1959	2303531	2304589	72.77882798	91.4669187	1.25678
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	1958	2304599	2305600	160.8391608	208.223776	1.29461
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	1957	2305612	2306499	171.3641488	199.317926	1.16313
Binding-protein-dependent transport systems inner membrane component	1956	2306506	2307453	214.3611404	219.114572	1.02217
ABC transporter, substrate binding protein	1955	2307511	2309124	549.2870428	734.362368	1.33694
Iron-sulfur flavoprotein	1954	2309297	2309866	297.0123023	345.053603	1.16175
NimC/NimA family protein	1952	2309998	2310390	464.2857143	382.169643	0.82313
hypothetical protein	1953	2310380	2311498	117.1735242	152.309034	1.29986
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	1951	2311517	2312152	809.4488189	577.349606	0.71326
Similar to C-terminal domain of competence/damage-inducible protein CinA	1950	2312188	2312718	135.8490566	131.674528	0.96927
hypothetical protein	1949	2312711	2313127	966.3461538	881.290865	0.91198
Two-component system response regulator	1948	2313111	2313848	245.5902307	253.772727	1.03332
Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE	1947	2313848	2315476	124.6928747	112.597359	0.903

Integration host factor alpha subunit	1946	2315473	2315883	924.3902439	848.797561	0.91822
SSU ribosomal protein S20p	1945	2315944	2316219	730.9090909	433.105455	0.59256
hypothetical protein	1944	2316384	2316521	1897.810219	1623.28102	0.85534
D-allose-6-phosphate isomerase (EC 5.3.1.-)	1943	2316584	2317039	54.94505495	59.3065934	1.07938
Iron-dependent repressor IdeR/DtxR	1942	2317109	2317489	300	335.469737	1.11823
NOL1/NOP2/sun family protein	1941	2317452	2318273	32.88672351	61.2021924	1.861
tRNA pseudouridine synthase A (EC 4.2.1.70)	1940	2318279	2319121	36.81710214	41.9940618	1.14061
hypothetical protein	1939	2319114	2319980	84.29561201	97.7777136	1.15994
Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	1938	2319988	2320362	133.6898396	154.254011	1.15382
uncharacterized secreted protein, YBBR Bacillus subtilis homolog	1937	2320424	2321392	170.4545455	144.18905	0.84591
ABC transporter, permease protein ybbP / Tlr1762 protein	1936	2321382	2322239	186.697783	172.636523	0.92468
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	1935	2322314	2324239	102.8571429	118.910649	1.15608
hypothetical protein	1934	2324428	2324568	3821.428571	2545.58214	0.66613
hypothetical protein	1933	2324934	2325068	216.4179104	402.753731	1.861
Flagellin protein flaA	1932	2325141	2326001	1486.873508	2304.04236	1.54959
Flagellin protein flaA	1931	2326331	2327185	3943.793911	3679.50644	0.93299
Flagellin protein flaG	1930	2327342	2327725	629.2428198	483.471279	0.76834
Flagellar hook-associated protein fliD	1929	2327787	2329817	183.2512315	186.1	1.01555
hypothetical protein	1928	2329829	2330788	67.77893639	86.3550574	1.27407
hypothetical protein	1927	2330805	2331899	131.6270567	134.386654	1.02097
hypothetical protein	1926	2331956	2332219	60.8365019	67.2224335	1.10497
ATPase YjeE, predicted to have essential role in cell wall biosynthesis	1925	2332248	2332652	160.8910891	140.496287	0.87324
Inactive homolog of metal-dependent proteases, putative molecular chaperone	1924	2332649	2333344	51.79856115	52.2151079	1.00804
Response regulator	1923	2333381	2334538	72.60155575	67.5557476	0.9305
Carbon storage regulator homolog	1922	2334544	2334777	167.3819742	99.8390558	0.59647
Transmembrane protein	1921	2334771	2335220	229.3986637	142.994432	0.62334
Flagellar hook-associated protein flgL	1920	2335249	2336496	268.0577849	240.466292	0.89707
Flagellar hook-associated protein flgK	1919	2336555	2338435	230.3191489	220.746277	0.95844
Uncharacterized protein TP_0661	1918	2338447	2338938	181.2627291	144.028513	0.79458
Iron-sulfur flavoprotein	1916	2339271	2339921	66.15384615	71.5769231	1.08198
hypothetical protein		2339932	2340054	24.59016393	7.62704918	0.31017
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	1913	2340265	2340993	43.95604396	25.5631868	0.58156
Acyl-CoA dehydrogenase (EC 1.3.99.3)	1912	2341026	2341655	55.64387917	39.9419714	0.71781
Transcription-repair coupling factor	1911	2341678	2345115	51.23726346	44.1547307	0.86177
hypothetical protein		2345269	2346066	30.69053708	24.9878517	0.81419
hypothetical protein		2346059	2346190	7.633587786	0	0
hypothetical protein	1908	2346228	2346422	46.39175258	43.1675258	0.9305
hypothetical protein	1907	2346499	2347791	7.73993808	2.88080495	0.3722
hypothetical protein	1906	2347818	2348216	5.025125628	0	0
hypothetical protein	1905	2348217	2348582	21.91780822	2.54931507	0.11631
hypothetical protein	1904	2348598	2349218	25.80645161	9.00483871	0.34894
Transposase	1903	2349263	2350318	26.54028436	22.049763	0.8308
hypothetical protein		2350372	2350545	23.12138728	10.7572254	0.46525
Lea protein - soybean	1901	2350601	2353684	16.21796951	10.261758	0.63274
hypothetical protein		2353763	2353894	0	0	#DIV/0!

hypothetical protein	1899	2353882	2354517	0	0	#DIV/0!
hypothetical protein	1898	2354582	2355064	0	1.93049793	#DIV/0!
Lea protein - soybean	1897	2355045	2358128	0.973078171	0.60363283	0.62033
hypothetical protein	1896	2358212	2358688	0	0	#DIV/0!
Leucine-rich repeat containing protein	1895	2358771	2361188	2.068680182	3.46483244	1.6749
hypothetical protein	1894	2361429	2361629	265	176.795	0.66715
hypothetical protein	1892	2361669	2362583	67.83369803	37.6679431	0.5553
hypothetical protein		2362580	2362714	7.462686567	6.94402985	0.9305
hypothetical protein	1891	2362687	2364162	19.3637621	12.8699862	0.66464
hypothetical protein	1890	2364199	2365062	8.955223881	0	0
hypothetical protein		2365134	2365304	0	0	#DIV/0!
hypothetical protein	1888	2365308	2365517	0	0	#DIV/0!
hypothetical protein	1887	2365565	2365750	0	0	#DIV/0!
hypothetical protein	1886	2365803	2366042	0	0	#DIV/0!
Flagellar motor switch protein fliM	1885	2366044	2366628	0	0	#DIV/0!
Lea protein - soybean	1884	2366628	2369609	0	0.31214358	#DIV/0!
hypothetical protein	1883	2369624	2370436	0	0	#DIV/0!
hypothetical protein	1882	2370460	2371053	0	1.56913997	#DIV/0!
hypothetical protein	1881	2371044	2371898	2.341920375	0	0
hypothetical protein		2371901	2372035	0	0	#DIV/0!
sensory box histidine kinase/response regulator	1879	2372140	2374617	7.317073171	9.45630081	1.29236
Probable AAA family ATPase	1878	2374859	2376535	2.983293556	8.32786396	2.7915
hypothetical protein	1877	2376614	2377168	16.24548736	8.39801444	0.51694
hypothetical protein	1876	2377170	2377439	7.434944238	0	0
hypothetical protein	1875	2377522	2377722	105	125.6175	1.19636
hypothetical protein	1874	2377801	2377938	0	0	#DIV/0!
Transcriptional regulator, DeoR family	1873	2377935	2378966	7.759456838	6.31765276	0.81419
hypothetical protein		2379059	2379190	0	0	#DIV/0!
hypothetical protein	1871	2379201	2379716	1.941747573	1.80679612	0.9305
hypothetical protein	1870	2379788	2379907	0	0	#DIV/0!
hypothetical protein	1869	2380202	2380645	0	0	#DIV/0!
hypothetical protein		2380700	2380822	0	0	#DIV/0!
Cell surface protein	1867	2380970	2382556	16.39344262	17.0141866	1.03787
hypothetical protein	1866	2382596	2383660	2.819548872	0	0
hypothetical protein	1865	2384012	2384203	10.47120419	9.7434555	0.9305
hypothetical protein		2384580	2384699	0	0	#DIV/0!
transcriptional regulator, PemK family	1863	2385490	2385831	93.84164223	81.8621701	0.87234
hypothetical protein	1862	2385884	2386585	64.19400856	38.4942939	0.59966
Probable two-component sensor, near polyamine transporter	1861	2386659	2387867	14.07284768	23.8787252	1.69679
Two component transcriptional regulator, LuxR family	1860	2387864	2388469	13.2231405	30.7603306	2.32625
hypothetical protein	1859	2388501	2389160	25.79666161	14.1198786	0.54735
hypothetical protein	1858	2389210	2390109	23.3592881	7.24527253	0.31017
hypothetical protein		2390102	2390344	33.05785124	53.8305785	1.62838
Lea protein - soybean	1856	2390554	2391981	18.22004205	11.0851437	0.6084
Transcriptional regulator	1855	2392044	2393177	0.882612533	0	0
Serine/threonine protein kinase	1854	2393167	2394330	0.859845228	0.80008598	0.9305
Probable transcriptional regulatory protein sgaR	1853	2394374	2395033	1.517450683	2.82397572	1.861
Putative kinase protein	1852	2395047	2396366	3.032600455	3.5272934	1.16313

Chaperone protein DnaK	1851	2396380	2397186	7.444168734	2.308933	0.31017
hypothetical protein	1850	2397257	2398123	6.928406467	4.29792148	0.62033
hypothetical protein	1849	2398134	2398739	6.611570248	6.15206612	0.9305
hypothetical protein	1848	2398751	2399452	5.706134094	6.63694722	1.16313
hypothetical protein	1847	2399456	2401438	6.559031282	4.2252775	0.64419
Formate efflux transporter (TC 2.A.44 family)	1846	2401560	2402393	84.03361345	73.72509	0.87733
MiaB family protein, possibly involved in tRNA or rRNA modification	1844	2403296	2404906	61.49068323	79.7571429	1.29706
TPR domain protein	1843	2404911	2405543	101.2658228	85.3939873	0.84327
hypothetical protein	1842	2405550	2405924	96.25668449	69.6631016	0.72372
Phosphate acetyltransferase (EC 2.3.1.8)	1841	2406113	2407111	1028.056112	1070.35471	1.04114
Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	1840	2407225	2407581	148.8764045	109.77809	0.73738
Pyruvate,phosphate dikinase (EC 2.7.9.1)	1839	2407593	2409350	48.3779169	57.1963574	1.18228
Uncharacterized protein TP_0747	1838	2409350	2410426	37.17472119	40.6445167	1.09334
hypothetical protein		2410420	2410527	0	0	#DIV/0!
DHH family/DHHA1 domain protein	1836	2410519	2411517	87.1743487	139.854709	1.60431
hypothetical protein	1835	2411514	2413019	144.5702865	164.898734	1.14061
ATP-dependent Clp protease ATP-binding subunit clpA	1834	2413474	2416089	130.0191205	116.712811	0.89766
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	1833	2416114	2417388	315.3724247	342.854596	1.08714
ATP-dependent RNA helicase	1832	2417500	2419953	64.81858948	72.8316347	1.12362
unknown	1831	2419943	2421256	22.08682407	32.5993907	1.47597
Predicted amino-acid acetyltransferase (EC 2.3.1.1) complementing ArgA function in Arginine Biosynthesis pathway	1830	2421231	2421662	169.3735499	118.741299	0.70106
Holliday junction DNA helicase RuvA	1829	2421697	2422290	111.2984823	67.4730185	0.60623
Transcriptional regulator, DeoR family	1828	2422354	2423382	85.60311284	62.4557393	0.7296
RNA polymerase sigma factor RpoD	1827	2423727	2424614	72.15332582	76.5800451	1.06135
Probable AAA family ATPase	1826	2424698	2426923	11.23595506	9.61865169	0.85606
hypothetical protein	1825	2426925	2427068	48.95104895	52.0559441	1.06343
hypothetical protein	1824	2427236	2427619	20.88772846	4.85900783	0.23263
Ribosomal protein S12	1823	2427678	2428442	18.32460733	18.2689791	0.99696
hypothetical protein	1822	2428503	2428907	17.32673267	50.6707921	2.92443
hypothetical protein	1821	2428904	2429317	4.842615012	2.25302663	0.46525
hydrolase, putative	1820	2429364	2430167	57.28518057	68.367995	1.19347
hypothetical protein	1819	2430176	2432812	34.14264036	26.1217754	0.76508
ATP-dependent nuclease, subunit A	1818	2432809	2435967	22.1659278	21.8039899	0.98367
hypothetical protein		2435951	2436064	17.69911504	0	0
hypothetical protein	1816	2436052	2436645	5.059021922	3.13827993	0.62033
Protein of unknown function DUF262 family	1815	2436716	2438041	6.037735849	5.61811321	0.9305
hypothetical protein	1814	2438038	2440005	11.6929334	4.25749873	0.36411
GldJ	1813	2440214	2441764	15.48387097	4.80258065	0.31017
hypothetical protein	1812	2441761	2442384	3.210272873	1.49357945	0.46525
hypothetical protein	1811	2442437	2442772	20.89552239	16.6656716	0.79757
hypothetical protein	1810	2442772	2443077	81.96721311	45.7622951	0.5583
Holliday junction DNA helicase RuvB	1809	2443206	2444285	115.8480074	114.695551	0.99005
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)	1808	2444260	2445282	59.68688845	50.0758317	0.83898
Uncharacterized protein TP_0927	1807	2445343	2445558	120.9302326	99.5418605	0.82313
Neopullulanase (EC 3.2.1.135)		2445551	2447377	37.78751369	53.5062979	1.41598

D-glycerate 2-kinase (EC 2.7.1.-)	1805	2447403	2448650	80.19246191	74.6190858	0.9305
Putative sucrose phosphorylase (EC 2.4.1.7)	1803	2449080	2450915	39.23705722	51.2155313	1.30528
Cytidine deaminase (EC 3.5.4.5)	1802	2450915	2451313	25.12562814	65.4623116	2.6054
hypothetical protein	1801	2451403	2453517	81.83538316	101.677152	1.24246
Acetyl-coenzyme A synthetase (EC 6.2.1.1)	1800	2453645	2455387	205.510907	214.196613	1.04226
Transcriptional regulator, Hth-3 family	1799	2455415	2455969	119.133574	157.882671	1.32526
3-dehydroquinate dehydratase (EC 4.2.1.10) / Shikimate 5-dehydrogenase (EC 1.1.1.25)	1798	2455981	2457501	110.5263158	114.475987	1.03574
hypothetical protein	1797	2457538	2458053	60.19417476	45.1699029	0.7504
FemA protein	1796	2458050	2459168	100.1788909	103.203936	1.0302
Methionyl-tRNA synthetase (EC 6.1.1.10)	1795	2459168	2461651	227.5473218	199.740838	0.8778
ATPase	1794	2461769	2463067	6.163328197	2.15061633	0.34894
hypothetical protein		2463074	2463256	43.95604396	20.4505495	0.46525
Flagellar hook-length control protein fliK	1793	2463247	2464617	143.7956204	137.19781	0.95412
hypothetical protein		2464614	2464748	156.7164179	131.936567	0.84188
DNA-binding protein	1790	2464869	2465198	21.27659574	8.48480243	0.39879
Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	1789	2465206	2465916	23.94366197	24.9007042	1.03997
hypothetical protein	1788	2465968	2467137	110.3507271	93.1295979	0.84394
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	1787	2467215	2468195	162.244898	193.695918	1.19385
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	1786	2468192	2469154	64.44906445	60.9371102	0.94551
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	1785	2469177	2470133	77.40585774	84.6793933	1.09397
Oligopeptide transport system permease protein oppC (TC 3.A.1.5.1)	1784	2470145	2471083	38.37953092	55.5522388	1.44744
Proline dipeptidase	1783	2471108	2472241	37.06972639	34.4933804	0.9305
D-aminoacylase (EC 3.5.1.81)	1782	2472280	2473893	68.19590825	73.8400496	1.08276
Microsomal dipeptidase (EC 3.4.13.19)	1781	2473924	2475138	377.2652389	410.830313	1.08897
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	1780	2475192	2476832	356.097561	392.058232	1.10099
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	1779	2476988	2477641	162.3277182	240.81853	1.48353
Hemerythrin-like, metal-binding protein	1778	2478206	2478655	318.4855234	230.034521	0.72228
hypothetical protein		2478720	2478875	0	0	#DIV/0!
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)		2478890	2480008	74.51701932	125.835787	1.68869
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	1775	2480005	2483274	63.03813038	84.9810886	1.34809
hypothetical protein		2483349	2484116	357.2359844	326.342243	0.91352
Putative enzyme	1773	2484189	2486504	78.18574514	83.2023758	1.06416
Lipoprotein releasing system transmembrane protein LolC	1772	2486593	2487852	69.10246227	55.4308975	0.80216
Lipoprotein releasing system ATP-binding protein lolD	1771	2487849	2488592	80.75370121	95.179004	1.17863
Lipoprotein releasing system transmembrane protein LolC	1770	2488585	2489934	88.95478132	84.8417346	0.95376
hypothetical protein	1769	2489934	2491400	100.6160164	76.4271047	0.75959

Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	1768	2491393	2492274	87.40068104	69.708286	0.79757
hypothetical protein	1767	2492286	2493794	86.87002653	69.7257958	0.80265
incorrect start	1766	2493781	2494725	190.1181525	238.871643	1.25644
hypothetical protein	1765	2494985	2495857	33.25688073	27.7442661	0.83424
putative membrane protein	1764	2495892	2496956	21.61654135	35.8557331	1.65872
membrane protein, putative	1763	2496953	2498236	91.19251754	158.105222	1.73375
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	1762	2498238	2498687	126.9487751	138.849666	1.09375
Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)	1761	2498709	2500898	416.0951075	622.035208	1.49494
SSU ribosomal protein S15p (S13e)	1760	2501047	2501316	516.7286245	425.47026	0.82339
Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)	1759	2501341	2502129	219.5431472	231.444162	1.05421
tRNA pseudouridine synthase B (EC 4.2.1.70)	1758	2502116	2503087	78.26982492	130.327497	1.66511
Ribosome-binding factor A	1757	2503062	2503436	184.4919786	136.838235	0.7417
Translation initiation factor 2	1756	2503442	2506342	437.9310345	482.25569	1.10121
Transcription termination protein NusA	1755	2506323	2507870	354.8597521	450.985975	1.27089
COG0779: clustered with transcription termination protein NusA	1754	2507875	2508384	269.1552063	323.572692	1.20218
hypothetical protein	1753	2508615	2509103	157.7868852	156.354508	0.99092
hypothetical protein		2509091	2509591	50	70.718	1.41436
Alpha-amylase (EC 3.2.1.1)	1751	2509785	2511677	85.62367865	97.377907	1.13728
Electron transport complex protein rnfA	1750	2511792	2512421	22.25755167	39.9419714	1.79454
hypothetical protein	1749	2512418	2513044	73.48242812	87.6988818	1.19347
hypothetical protein	1748	2513034	2513534	136	152.602	1.12207
Electron transport complex protein rnfD	1747	2513531	2514682	92.96264118	70.3331885	0.75657
Electron transport complex protein rnfC	1746	2514682	2516178	211.8983957	222.051136	1.04791
hypothetical protein	1745	2516175	2517644	70.11572498	57.0081688	0.81306
Integral membrane protein	1744	2517777	2518265	293.0327869	270.760246	0.92399
Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	1743	2518499	2519656	40.62229905	40.2117545	0.98989
2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	1742	2519682	2521652	517.2588832	595.142132	1.15057
Xaa-Pro dipeptidase (EC 3.4.13.9)	1741	2521774	2522874	115.4545455	95.5877273	0.82793
hypothetical protein	1740	2522962	2523825	60.25492468	51.7543453	0.85892
VgrG protein	1739	2523842	2525602	77.84090909	85.6482955	1.1003
hypothetical protein	1738	2525717	2525851	14.92537313	6.94402985	0.46525
Poly(A) polymerase (EC 2.7.7.19)	1737	2525932	2527155	190.5151267	167.383483	0.87858
Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23); putative	1736	2527169	2528134	304.6632124	302.774093	0.9938
23S rRNA (Uracil-5-) -methyltransferase rumA (EC 2.1.1.-)	1735	2528199	2529446	31.27506014	55.2181235	1.76556
hypothetical protein	1734	2529443	2530813	18.24817518	17.6591241	0.96772
hypothetical protein	1733	2530887	2531399	349.609375	308.955078	0.88372
Cell division protein	1732	2531422	2532510	202.2058824	236.045956	1.16735
Uncharacterized protein TP_0753	1731	2532485	2532817	75.30120482	30.8298193	0.40942
tRNA-i(6)A37 methylthiotransferase	1730	2532827	2534170	78.92777364	109.470588	1.38697
hypothetical protein	1729	2534192	2534563	229.1105121	248.300539	1.08376
hypothetical protein		2534710	2535153	94.80812641	81.9176072	0.86404
Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-)	1727	2535163	2535693	24.52830189	31.6018868	1.28838

Uncharacterized protein TP_0066	1726	2535757	2536104	216.1383285	166.256484	0.76921
TPR domain protein	1725	2536097	2537254	243.7337943	198.646067	0.81501
23S rRNA methyltransferase and Florfenicol/chloramphenicol resistance protein / Radical SAM family enzyme, UPF0063 family	1723	2537254	2538339	178.2086796	189.021237	1.06067
hypothetical protein	1724	2538305	2538421	68.96551724	72.1939655	1.04681
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	1722	2538471	2539571	167.2727273	161.568636	0.9659
hypothetical protein	1721	2539582	2540712	69.91150442	72.4637168	1.03651
hypothetical protein		2540718	2541740	89.04109589	66.4642857	0.74645
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	1719	2541826	2542575	61.41522029	108.082109	1.75986
TPR domain protein	1718	2542558	2543544	362.0689655	227.434584	0.62815
Transcription elongation factor GreA	1717	2543578	2546271	246.1938359	219.063127	0.8898
PBS lyase HEAT-like repeat domain protein	1716	2546302	2547939	119.1203421	131.872938	1.10706
tRNA-guanine transglycosylase (EC 2.4.2.29)	1715	2547936	2549078	154.2506573	101.939089	0.66087
Transcriptional regulator, TetR family	1714	2549303	2549923	116.1290323	75.0403226	0.64618
hypothetical protein	1713	2549953	2550090	167.8832117	95.0875912	0.56639
Protein tyrosine phosphatase (EC 3.1.3.48)	1712	2550246	2551961	1665.889213	1390.05306	0.83442
hypothetical protein	1711	2551986	2552780	816.1209068	526.189547	0.64474
FOG: CheY-like receiver	1710	2552970	2556059	27.19326643	21.6885724	0.79757
Transcriptional regulator, luxR family, associated with agmatine catabolism	1709	2556079	2557518	25.71230021	14.8724809	0.57842
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	1708	2557522	2558832	22.13740458	14.2061069	0.64172
hypothetical protein		2559089	2559232	0	0	#DIV/0!
hypothetical protein	1706	2559235	2559414	0	0	#DIV/0!
Methyl-accepting chemotaxis protein	1705	2559411	2561594	2.290426019	0.85249656	0.3722
Response regulator	1704	2561634	2562731	0	3.3928897	#DIV/0!
Anaerobic sulfite reductase subunit C (EC 1.8.1.-)	1703	2562789	2563751	3.118503119	1.93451143	0.62033
Anaerobic sulfite reductase subunit B	1702	2563762	2564556	1.259445844	3.51574307	2.7915
Anaerobic sulfite reductase subunit A	1701	2564543	2565571	0.972762646	0	0
transcriptional regulator, Crp/Fnr family	1700	2565628	2566314	10.20408163	4.06924198	0.39879
hypothetical protein	1699	2566494	2566727	141.6309013	187.697425	1.32526
hypothetical protein	1698	2566720	2566863	76.92307692	45.548951	0.59214
hypothetical protein	1697	2566847	2566966	0	0	#DIV/0!
Methionine ABC transporter ATP-binding protein	1696	2566966	2567775	102.5957973	156.425216	1.52467
ABC transporter permease protein	1695	2567772	2568704	121.5053763	110.05914	0.9058
ABC transporter substrate-binding protein	1694	2568717	2569712	222.1105528	280.552764	1.26312
hypothetical protein	1693	2569738	2569902	12.19512195	11.347561	0.9305
hypothetical protein	1692	2569923	2570234	41.80064309	50.8633441	1.21681
Plasmid stabilization system antitoxin protein	1691	2570224	2570529	81.96721311	45.7622951	0.5583
Adenylate cyclase (EC 4.6.1.1)	1690	2570627	2572654	137.1484953	154.241737	1.12463
Magnesium and cobalt efflux protein corC	1689	2572706	2573506	306.25	236.114375	0.77099
predicted metal-dependent hydrolase	1688	2573507	2573977	195.7446809	85.1308511	0.43491
Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog	1687	2573978	2576392	117.6470588	124.888981	1.06156
Phosphate starvation-inducible protein PhoH, predicted ATPase	1686	2576367	2577425	194.7069943	223.390359	1.14732

Alanine racemase (EC 5.1.1.1)	1685	2577954	2579075	95.45049063	148.581178	1.55663
TRAP-type C4-dicarboxylate transport system, large permease component	1684	2579075	2580985	62.30366492	65.7683246	1.05561
TRAP-type transport system, periplasmic component, predicted N-acetylneuraminate-binding protein	1683	2580991	2581974	342.8280773	334.146999	0.97468
Uncharacterized protein TP_0956	1682	2582117	2583049	317.5965665	325.475322	1.02481
Phosphoglucomutase (EC 5.4.2.2)	1681	2583058	2584836	340.509915	356.911331	1.04817
hypothetical protein	1680	2584932	2585348	151.4423077	143.153846	0.94527
hypothetical protein	1679	2585645	2585812	11.9760479	11.1437126	0.9305
hypothetical protein		2585884	2586003	25.21008403	23.4579832	0.9305
hypothetical protein	1677	2586103	2586363	326.9230769	640.613462	1.95952
Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	1676	2586380	2588437	463.7822071	647.324016	1.39575
Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	1675	2588508	2589911	369.7359029	593.102427	1.60412
hypothetical protein	1674	2590171	2590293	0	0	#DIV/0!
Iron(III) ABC transporter, solute-binding protein	1672	2590408	2591502	11.88299817	13.6087751	1.14523
hypothetical protein	1673	2591487	2591603	17.24137931	16.0431034	0.9305
Vitamin B12 ABC transporter, permease component BtuC	1671	2591554	2592558	5.976095618	7.41434263	1.24067
Iron(III) ABC transporter, ATP-binding protein	1670	2592555	2593370	4.90797546	4.56687117	0.9305
Iron(III) ABC transporter, solute-binding protein	1669	2593392	2594465	16.77539609	27.750233	1.65422
Molybdopterin biosynthesis protein A	1668	2594482	2595693	101.5689513	76.8373245	0.7565
ABC transporter, permease protein	1667	2595789	2599031	45.95928439	47.070327	1.02417
ABC transporter, ATP-binding protein	1666	2599031	2599732	87.01854494	84.9529244	0.97626
hypothetical protein	1665	2599867	2601156	54.3056633	75.7971296	1.39575
Methyl-accepting chemotaxis protein	1664	2601244	2603319	65.72295248	82.3243175	1.2526
hypothetical protein	1663	2603502	2604737	96.3562753	112.262753	1.16508
hypothetical protein	1662	2604739	2605119	86.84210526	107.742105	1.24067
Positive regulator of CheA protein activity (CheW)	1661	2605839	2606306	70.66381156	67.745182	0.9587
hypothetical protein	1660	2606321	2606881	50	46.525	0.9305
Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	1659	2606874	2607884	97.02970297	68.1752475	0.70262
Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	1658	2607881	2609521	49.3902439	54.4682927	1.10281
Methyl-accepting chemotaxis protein	1657	2609534	2611612	86.62175168	83.2882579	0.96152
Methyl-accepting chemotaxis protein	1656	2611609	2613174	83.70607029	105.238658	1.25724
Chemotaxis protein CheA (EC 2.7.3.-)	1655	2613183	2615531	60.90289608	85.5996593	1.40551
Adenylate cyclase (EC 4.6.1.1)	1654	2615524	2617413	62.46691371	58.6180519	0.93839
Foldase protein prsA precursor (EC 5.2.1.8)	1653	2617483	2617761	273.381295	153.967626	0.5632
Response regulator	1652	2617784	2619037	229.8483639	227.241022	0.98866
UPF0178 protein TP_0845	1651	2619044	2619514	48.93617021	83.1510638	1.69917
Mannose-6-phosphate isomerase (EC 5.3.1.8)	1650	2619511	2620758	97.03287891	79.8424218	0.82284
Uncharacterized protein TP_0846	1649	2620776	2621075	133.7792642	152.489967	1.13986
Uncharacterized protein TP_0847	1648	2621086	2621586	516	481.999	0.93411
LSU ribosomal protein L20p	1647	2621598	2621966	673.0769231	981.626374	1.45842
LSU ribosomal protein L35p	1646	2622051	2622251	760.4166667	877.190104	1.15357
Translation initiation factor 3	1645	2622269	2622784	1506.796117	1472.53883	0.97726
hypothetical protein		2622852	2623049	25.38071066	18.893401	0.7444
hypothetical protein	1643	2623029	2623661	33.2278481	64.7816456	1.94962

Large repetitive protein	1642	2623730	2627794	326.5255906	337.489419	1.03358
hypothetical protein	1641	2627837	2628055	36.69724771	12.8050459	0.34894
Cell surface protein	1640	2628012	2628833	87.69792935	80.4695493	0.91758
Conserved domain protein	1639	2628860	2629717	169.1948658	109.662194	0.64814
Large repetitive protein	1638	2629908	2647037	172.8647323	171.226341	0.99052
3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	1637	2647275	2648567	481.4241486	515.664087	1.07112
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	1635	2648610	2649134	213.740458	221.97042	1.0385
hypothetical protein	1636	2649131	2650039	31.93832599	15.371696	0.48129
hypothetical protein	1634	2650036	2650668	17.40506329	20.6123418	1.18427
sensory box histidine kinase/response regulator	1633	2650725	2652728	11.96670135	15.9763267	1.33507
Conserved protein	1631	2652768	2653199	134.5707657	114.423434	0.85028
Serine phosphatase RsbU, regulator of sigma subunit	1632	2653171	2654346	146.3829787	124.330638	0.84935
Serine phosphatase RsbU, regulator of sigma subunit	1630	2654359	2655531	98.97610922	65.8971843	0.66579
hypothetical protein	1629	2655556	2656890	67.46626687	77.4254123	1.14762
Glycosyltransferases involved in cell wall biogenesis	1628	2656883	2657866	62.05493388	61.5284842	0.99152
Cysteinyl-tRNA synthetase (EC 6.1.1.16)	1627	2657921	2659354	301.6997167	293.252479	0.972
RNA polymerase sigma-54 factor rpoN	1626	2659392	2659946	151.6245487	105.814982	0.69788
hypothetical protein	1625	2659936	2660514	185.1211073	167.425606	0.90441
hypothetical protein	1624	2660511	2661059	156.9343066	142.631387	0.90886
Transglutaminase-like enzymes, putative cysteine proteases	1623	2661062	2662690	129.6068796	142.318489	1.09808
Uridylate kinase (EC 2.7.4.-)	1622	2662714	2663397	117.1303075	122.61347	1.04681
Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, beta subunit (EC 2.7.1.90)	1621	2663475	2665130	303.3232628	244.010272	0.80446
ATP-dependent DNA helicase RecQ	1620	2665215	2667167	47.64344262	58.6329406	1.23066
Xanthosine/inosine triphosphate pyrophosphatase ; HAM1 protein homolog	1619	2667182	2667775	148.3979764	161.621417	1.08911
hypothetical protein	1618	2667846	2668328	43.56846473	52.123444	1.19636
ATP-dependent DNA helicase Rep	1617	2668334	2670382	90.46454768	91.9124694	1.01601
hypothetical protein	1616	2670489	2671607	29.51699463	19.9749553	0.67673
tRNA nucleotidyltransferase, A-adding (EC 2.7.7.-)	1615	2671607	2672923	53.19148936	69.9996201	1.31599
Transcriptional regulator, GntR family	1614	2673100	2673795	34.5323741	45.5208633	1.31821
hypothetical protein		2673814	2673930	0	0	#DIV/0!
hypothetical protein	1612	2674000	2675001	2.997002997	4.64785215	1.55083
Beta-glucosidase (EC 3.2.1.21)	1611	2675038	2676420	3.617945007	4.71309696	1.3027
Multiple sugar ABC transporter, substrate-binding protein	1610	2676443	2677741	6.933744222	9.31933744	1.34406
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	1609	2677815	2678699	0	1.05260181	#DIV/0!
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	1608	2678702	2679550	1.179245283	2.19457547	1.861
Oxidoreductase, aldo/keto reductase family	1607	2679554	2680471	5.452562704	0	0
Dihydroxy-acid dehydratase (EC 4.2.1.9)	1606	2680491	2682209	8.149010477	5.95779977	0.73111
Beta-glucosidase (EC 3.2.1.21)	1605	2682282	2683631	103.7805782	142.782431	1.37581

Beta-mannosidase (EC 3.2.1.25)	1604	2683649	2686153	141.3738019	128.203874	0.90684
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	1603	2686157	2686996	94.15971395	83.1793802	0.88339
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	1602	2687000	2687899	156.8409344	169.746385	1.08228
Predicted beta-xyloside ABC transporter, substrate-binding component	1601	2687996	2689345	1714.712472	2070.1714	1.2073
Chitobiose phosphorylase (EC 2.4.1.-)	1600	2689480	2692044	59.6723869	83.4691888	1.39879
Carboxylesterase, type B precursor	1599	2692216	2693931	362.0991254	1452.99067	4.01269
hypothetical protein	1598	2693907	2694065	0	11.778481	#DIV/0!
hypothetical protein		2694453	2694605	0	0	#DIV/0!
hypothetical protein	1592	2700048	2700179	22.90076336	0	0
hypothetical protein	1591	2700154	2700537	86.1618799	104.468668	1.21247
hypothetical protein	1590	2700641	2700802	267.0807453	225.400621	0.84394
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	1589	2700764	2702755	99.94977398	120.109744	1.2017
Translation elongation factor G	1588	2702896	2704938	241.4299706	193.208619	0.80027
Carboxylesterase, type B precursor	1587	2705005	2709777	67.47694887	35.2934828	0.52305
hypothetical protein	1585	2709765	2709944	22.34636872	0	0
sensory box histidine kinase/response regulator	1586	2709934	2713692	100.615467	82.6668451	0.82161
Chromosome partitioning protein parB / Stage 0 sporulation protein J	1584	2713706	2714098	104.5918367	102.070153	0.97589
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	1583	2714193	2716913	173.1617647	223.388419	1.29006
Iron-sulfur flavoprotein	1582	2716925	2717548	12.84109149	11.9486356	0.9305
hypothetical protein		2718081	2718194	17.69911504	0	0
hypothetical protein	1580	2718403	2719404	117.8821179	131.999001	1.11975
Membrane proteins related to metalloendopeptidases	1579	2719401	2720381	179.5918367	172.807143	0.96222
Ferredoxin	1578	2720418	2720588	7100	7427.57941	1.04614
Glycogen branching enzyme, archaeal type (EC 2.4.1.18)	1577	2720701	2722281	81.64556962	113.662342	1.39214
Outer membrane protein	1576	2722282	2722974	104.0462428	94.1257225	0.90465
Multimeric flavodoxin WrbA family protein	1575	2723073	2723690	79.4165316	131.205024	1.65211
Serine phosphatase RsbU, regulator of sigma subunit	1574	2723824	2726391	75.84050039	67.2957389	0.88733
Probable 3-phenylpropionic acid transporter	1573	2726477	2727634	72.60155575	77.2065687	1.06343
D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	1572	2727684	2728529	73.37278107	50.6544379	0.69037
GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II / Guanosine-3',5'-bis(diphosphate) 3' pyrophosphohydrolase (EC 3.1.7.2)	1571	2728556	2729125	179.2618629	148.814587	0.83015
Valyl-tRNA synthetase (EC 6.1.1.9)	1570	2729135	2731825	208.1784387	185.408178	0.89062
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1569	2731914	2733287	56.80990532	23.0422433	0.4056
hypothetical protein		2733303	2733530	8.810572687	28.6938326	3.25675
hypothetical protein	1567	2733502	2733618	68.96551724	56.1508621	0.81419
hypothetical protein		2733696	2733824	429.6875	312.589844	0.72748
hypothetical protein		2733846	2733977	22.90076336	14.2061069	0.62033
Proline-specific permease proY	1564	2734319	2735692	23.30662782	26.4308084	1.13405

COG0523: Putative GTPases (G3E family)		2735711	2736307	78.8590604	39.0310403	0.49495
hypothetical protein	1562	2736463	2736750	27.87456446	12.9686411	0.46525
LysR family regulatory protein CidR	1561	2736893	2737801	7.709251101	9.22301762	1.19636
Uroporphyrinogen-III decarboxylase	1560	2737930	2738973	35.47459252	41.930489	1.18199
Permeases of the major facilitator superfamily	1559	2739043	2740224	52.49788315	60.6676545	1.15562
Uroporphyrinogen-III decarboxylase-like	1558	2740341	2741351	7.920792079	5.52772277	0.69788
hypothetical protein		2741398	2741547	0	0	#DIV/0!
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	1556	2741601	2742401	782.5	781.62	0.99888
Corrinoid methyltransferase protein	1555	2742463	2743092	1647.058824	2423.14626	1.4712
Conserved protein	1554	2743168	2743710	223.2472325	231.766605	1.03816
probable electron transfer protein	1553	2743714	2745528	117.9713341	122.596196	1.0392
Uroporphyrinogen-III decarboxylase	1552	2745634	2746638	106.5737052	58.3879482	0.54786
hypothetical protein		2746604	2746729	24	0	0
Regulator of polyketide synthase expression	1550	2746835	2748352	22.41265656	11.6542518	0.51999
Regulator of polyketide synthase expression	1549	2748374	2749945	37.55569701	34.3532782	0.91473
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	1548	2749942	2750817	61.71428571	109.533143	1.77484
Protein-export membrane protein secF (TC 3.A.5.1.1)	1547	2750848	2752068	276.2295082	408.809836	1.47996
Protein-export membrane protein secD (TC 3.A.5.1.1)	1546	2752068	2753723	364.9546828	574.604834	1.57446
Preprotein translocase subunit YajC (TC 3.A.5.1.1)	1545	2753892	2754317	447.0588235	361.252941	0.80807
hypothetical protein	1544	2754415	2754705	220.6896552	154.013793	0.69788
Rubredoxin	1543	2754801	2754962	403.7267081	716.658385	1.77511
Rubrerythrin	1542	2754972	2755547	485.2173913	365.726957	0.75374
hypothetical protein		2755606	2755740	67.1641791	62.4962687	0.9305
Endoglucanase D precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase D) (Cellulase D)	1540	2756085	2757875	200.5586592	267.713687	1.33484
TPR domain protein, putative component of TonB system	1539	2758274	2760046	54.17607223	74.0409142	1.36667
hypothetical protein	1538	2760043	2760681	65.830721	91.8832288	1.39575
ortholog to Borrelia burgdorferi BB0398	1537	2760746	2761846	84.54545455	114.197727	1.35073
hypothetical protein	1536	2761830	2761958	0	0	#DIV/0!
Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-)	1535	2761909	2763309	50.71428571	73.1107143	1.44162
OmpA family protein	1534	2763324	2764211	104.8478016	154.209132	1.47079
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	1533	2764275	2766077	109.1922006	129.5961	1.18686
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	1532	2766085	2767185	40.90909091	73.5940909	1.79897
Peptide/opine/nickel uptake family ABC transporter, permease/ATP- binding protein	1531	2767193	2769508	105.8315335	124.602592	1.17737
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	1530	2769509	2770492	91.55645982	110.751272	1.20965
Hypothetical ATP-binding protein UPF0042, contains P-loop	1529	2770572	2771360	83.75634518	105.094543	1.25477
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Multiple sugar ABC transporter, ATP-binding protein	1528	2771388	2772500	195.1438849	211.705486	1.08487

Ferric iron ABC transporter, permease protein	1527	2772502	2774295	143.8929169	133.373397	0.92689
hypothetical protein	1526	2774393	2775523	275.2212389	301.383186	1.09506
hypothetical protein	1525	2775712	2775825	8.849557522	0	0
ATP-dependent RNA helicase RhlB		2775799	2777685	384.9016481	527.332802	1.37005
ABC transporter, ATP-binding protein	1523	2777740	2779437	240.5437352	316.216017	1.31459
hypothetical protein	1522	2779451	2780704	19.15403033	14.1097366	0.73665
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	1521	2780724	2781710	3.042596349	9.43711968	3.10167
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	1520	2781769	2782731	0	0.96725572	#DIV/0!
ABC-type sugar transport system, ATP-binding protein (EC 3.6.3.17)	1519	2782709	2784217	0.663129973	1.23408488	1.861
Transcriptional regulator of rhamnose utilization, AraC family	1518	2784355	2785272	40.34896401	24.3533261	0.60357
Uncharacterized protein TP_0369 precursor	1517	2785318	2786865	53.65223012	57.7427279	1.07624
hypothetical protein	1516	2786862	2787296	357.1428571	132.928571	0.3722
hypothetical protein		2787281	2787394	0	0	#DIV/0!
Ribokinase (EC 2.7.1.15)	1514	2787445	2788359	25.16411379	35.6318381	1.41598
Catabolite control protein A	1513	2788356	2789339	35.60528993	39.7568667	1.1166
6-phospho-beta-glucosidase (EC 3.2.1.86)	1512	2789377	2790741	49.85337243	45.7063783	0.91682
Ferric iron ABC transporter, iron-binding protein # pitA	1511	2790768	2791778	239.6039604	229.400495	0.95742
Ferric iron ABC transporter, permease protein	1510	2791806	2793485	63.72840977	66.5038714	1.04355
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Multiple sugar ABC transporter, ATP-binding protein	1509	2793498	2794553	54.02843602	29.9876777	0.55504
Phosphoesterase PHP domain protein precursor	1508	2794550	2795443	26.87569989	18.7558791	0.69788
hypothetical protein	1507	2795506	2795676	347.0588235	191.573529	0.55199
Peptide chain release factor 1	1506	2795678	2796763	386.0465116	401.629767	1.04037
Methylase of polypeptide chain release factors	1505	2796775	2797755	116.3265306	165.211224	1.42024
GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I	1504	2797760	2800027	137.6268196	124.778121	0.90664
Uncharacterized protein TP_0214	1503	2800111	2800311	1715	2014.5325	1.17465
LSU ribosomal protein L17p	1502	2800324	2800863	1536.178108	1491.56215	0.97096
DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)	1501	2800853	2801908	1078.822412	1030.35423	0.95507
SSU ribosomal protein S4p (S9e)	1500	2801918	2802553	1184.713376	1380.93312	1.16563
SSU ribosomal protein S11p (S14e)	1499	2802613	2802996	1840.73107	1355.66319	0.73648
SSU ribosomal protein S13p (S18e)	1498	2803024	2803389	2961.643836	2605.4	0.87971
Preprotein translocase secY subunit (TC 3.A.5.1.1)	1497	2803614	2804942	586.4946889	563.383156	0.96059
LSU ribosomal protein L15p (L27Ae)	1496	2804942	2805394	500	524.950221	1.0499
LSU ribosomal protein L30p (L7e)	1495	2805394	2805579	843.2432432	1076.36216	1.27646
SSU ribosomal protein S5p (S2e)	1494	2805582	2806109	1607.210626	1885.71917	1.17329
LSU ribosomal protein L18p (L5e)	1493	2806118	2806480	1569.060773	1244.09392	0.79289
LSU ribosomal protein L6p (L9e)	1492	2806537	2807076	474.9536178	564.514842	1.18857
SSU ribosomal protein S8p (S15Ae)	1491	2807087	2807485	615.7760814	449.860051	0.73056
SSU ribosomal protein S14p (S29e)	1490	2807495	2807680	1316.939891	1591.51093	1.20849
LSU ribosomal protein L5p (L11e)		2807688	2808191	948.3101392	1017.44533	1.0729
LSU ribosomal protein L24p (L26e)	1488	2808237	2808599	1607.734807	1711.91436	1.0648
LSU ribosomal protein L14p (L23e)	1487	2808623	2808991	1896.73913	1400.80707	0.73853

SSU ribosomal protein S17p (S11e)	1486	2809006	2809314	1074.675325	664.642857	0.61846
LSU ribosomal protein L29p (L35e)	1485	2809325	2809546	1049.773756	1048.3914	0.99868
LSU ribosomal protein L16p (L10e)	1484	2809560	2809985	1014.117647	1486.61059	1.46592
SSU ribosomal protein S3p (S3e)	1483	2810053	2810760	907.6704545	947.682528	1.04408
LSU ribosomal protein L22p (L17e)	1482	2810761	2811132	1466.307278	1326.77763	0.90484
SSU ribosomal protein S19p (S15e)	1481	2811141	2811422	736.6548043	784.798932	1.06536
LSU ribosomal protein L2p (L8e)	1480	2811432	2812262	1043.373494	1097.54157	1.05192
LSU ribosomal protein L23p (L23Ae)	1479	2812286	2812573	1554.006969	1137.99826	0.7323
LSU ribosomal protein L4p (L1e)	1478	2812570	2813241	676.6020864	757.157973	1.11906
LSU ribosomal protein L3p (L3e)	1477	2813252	2813872	1358.064516	1484.29758	1.09295
SSU ribosomal protein S10p (S20e)	1476	2813910	2814218	1498.349835	1907.06436	1.27278
Translation elongation factor Tu	1475	2814291	2815481	2670.588235	4008.18739	1.50086
hypothetical protein		2815446	2815541	3336.842105	1381.05789	0.41388
hypothetical protein		2815811	2816008	2081.218274	2177.46447	1.04625
SSU ribosomal protein S7p (S5e)	1472	2816095	2816565	1091.489362	1221.52872	1.11914
SSU ribosomal protein S12p (S23e)	1471	2816576	2816950	2040.106952	3065.17647	1.50246
hypothetical protein	1470	2817173	2817484	19.2926045	20.9437299	1.08558
Prevent-host-death family protein	1469	2817477	2817731	47.24409449	25.6437008	0.54279
Spermidine Putrescine transport ATP-binding protein potA (TC_3.A.1.11.1)	1468	2817913	2819154	100.7252216	85.4770346	0.84862
Spermidine Putrescine ABC transporter permease component potB (TC_3.A.1.11.1)	1467	2819151	2820056	22.09944751	30.8453039	1.39575
Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	1466	2820053	2820946	19.03695409	15.6298992	0.82103
ABC transporter, periplasmic spermidine putrescine-binding protein potD (TC_3.A.1.11.1)	1465	2820943	2822010	133.0834114	103.776476	0.77979
hypothetical protein	1464	2822036	2822179	1330.985915	2378.67254	1.78715
putative autotransporter protein	1463	2822436	2823368	151.2875536	182.705472	1.20767
putative autotransporter protein	1462	2823743	2825947	137.9310345	156.631352	1.13558
hypothetical protein		2826323	2826475	6.578947368	0	0
Hemerythrin	1460	2826517	2826924	130.2211302	128.029484	0.98317
Oligoendopeptidase F (EC 3.4.24.-)	1459	2826969	2828774	122.982749	148.092933	1.20418
hypothetical protein	1458	2828846	2829706	32.55813953	41.1151163	1.26282
Translation elongation factor P; Translation initiation factor 5A	1457	2830138	2830701	522.2024867	433.021314	0.82922
Methyltransferase small	1456	2830844	2832103	47.65687053	104.949166	2.20218
Putative pheromone precursor lipoprotein	1455	2832295	2832711	9.615384615	8.94711538	0.9305
Putative ABC transport system ATP-binding protein	1454	2832708	2833403	0	6.6942446	#DIV/0!
Putative membrane protein	1453	2833443	2834585	3.50262697	4.07399299	1.16313
ABC transporter permease protein	1452	2834575	2835858	6.235385814	7.25253313	1.16313
Putative high-affinity iron permease	1451	2835860	2837110	0.8	2.9776	3.722
Periplasmic protein p19 involved in high-affinity Fe2+ transport	1450	2837228	2837809	13.76936317	12.8123924	0.9305
Putative high-affinity iron permease	1449	2837879	2839033	0.866551127	2.41897747	2.7915
hypothetical protein	1448	2839032	2839295	0	3.53802281	#DIV/0!
hypothetical protein	1447	2839575	2839766	52.94117647	27.3676471	0.51694
PIN domain protein	1446	2839778	2840146	27.11864407	9.46271186	0.34894
hypothetical protein	1445	2840181	2841665	40.43126685	71.4804582	1.76795
Predicted beta-xyloside ABC transporter, ATP-binding component	1444	2841675	2842520	62.72189349	31.9343195	0.50914

Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	1443	2842530	2843411	51.07832009	53.8654938	1.05457
Multiple sugar ABC transporter, substrate-binding protein	1442	2843514	2844821	658.7605203	931.923871	1.41466
hypothetical protein	1441	2844968	2845783	67.48466258	69.6447853	1.03201
DNA-damage-inducible protein J	1440	2845993	2846259	82.70676692	27.9849624	0.33836
AviX3	1439	2846252	2846518	52.63157895	69.962406	1.32929
hypothetical protein	1438	2846771	2852821	2.148760331	1.69181818	0.78735
hypothetical protein	1437	2852832	2854058	1.63132137	0.75897227	0.46525
hypothetical protein	1436	2854711	2854950	0	0	#DIV/0!
Putative transposase		2854958	2855353	5.83090379	2.71282799	0.46525
transposase, mutator family		2855368	2856048	7.385524372	8.24667651	1.1166
hypothetical protein	1433	2856340	2856606	0	0	#DIV/0!
hypothetical protein	1432	2856966	2857139	0	0	#DIV/0!
hypothetical protein		2857119	2857247	0	0	#DIV/0!
Helix-turn-helix domain protein	1430	2857398	2857748	62.85714286	21.2685714	0.33836
hypothetical protein	1429	2857787	2858029	0	0	#DIV/0!
hypothetical protein		2858084	2858206	8.196721311	0	0
Conserved domain protein	1427	2858314	2858664	128.5714286	93.05	0.72372
Uncharacterized protein TP_0969 precursor	1426	2858818	2860254	29.94428969	25.2712396	0.84394
Probable Co/Zn/Cd efflux system membrane fusion protein	1425	2860241	2861251	88.11881188	63.5688119	0.7214
Cell division transporter, ATP-binding protein ftsE (TC 3.A.5.1.1)		2861251	2861931	27.94117647	62.9455882	2.25279
ABC transporter, ATP-binding protein		2861900	2863117	41.90632703	64.9897288	1.55083
glutamate transporter, putative	1422	2863129	2864361	73.05194805	73.2617695	1.00287
Orotate phosphoribosyltransferase (EC 2.4.2.10)	1421	2864418	2865020	86.37873754	95.8322259	1.10944
Phosphoglycolate phosphatase (EC 3.1.3.18)	1420	2865028	2865732	71.02272727	87.234375	1.22826
conserved hypothetical protein; putative cell growth regulatory protein	1419	2865796	2866065	78.0669145	69.1821561	0.88619
Programmed cell death toxin MazF	1418	2866071	2866415	229.6511628	143.361919	0.62426
Treponemal membrane protein B precursor (Antigen tmpB)		2866507	2868945	12.71534044	13.3582855	1.05056
Cell surface protein	1416	2868950	2870872	5.202913632	5.32544225	1.02355
hypothetical protein		2870871	2870984	35.39823009	0	0
hypothetical protein		2871015	2871185	5.882352941	0	0
hypothetical protein		2871176	2871475	10.03344482	15.5602007	1.55083
PilT protein, N-terminal	1412	2871593	2871991	40.16064257	37.3694779	0.9305
hypothetical protein	1411	2871988	2872233	61.45251397	25.9916201	0.42295
hypothetical protein	1410	2872249	2872416	0	6.12171053	#DIV/0!
hypothetical protein	1409	2872435	2872662	26.43171806	40.9911894	1.55083
hypothetical protein	1408	2872672	2872947	55.35055351	61.804428	1.1166
hypothetical protein	1407	2872987	2873133	0	6.37328767	#DIV/0!
HigA protein (antitoxin to HigB)	1406	2873541	2873840	73.57859532	90.2491639	1.22657
hypothetical protein	1405	2873920	2874096	22.72727273	37.0085227	1.62838
Outer membrane autotransporter barrel	1404	2874261	2876795	86.81925809	96.2079716	1.10814
Large repetitive protein		2876811	2880701	48.32904884	35.4020566	0.73252
hypothetical protein	1402	2880879	2881025	27.39726027	0	0
Hydrolase (HAD superfamily)	1401	2881173	2881952	50.06418485	50.1681643	1.00208
hypothetical protein	1400	2882009	2896942	0.602692024	0.37386995	0.62033
hypothetical protein	1399	2896946	2898487	0	0.60382868	#DIV/0!

Leader peptidase (Prepilin peptidase) (EC 3.4.23.43)	1398	2898642	2899076	0	0	#DIV/0!
General secretion pathway protein D / Type II secretion outermembrane pore forming protein (PulD)	1397	2899201	2901258	0	0.90471561	#DIV/0!
General secretion pathway protein E	1396	2901255	2902757	0	0	#DIV/0!
Type 4 fimbrial assembly protein pilC	1395	2902757	2903812	0	0	#DIV/0!
General secretion pathway protein G	1394	2903827	2904306	4.175365344	0	0
hypothetical protein	1393	2904278	2904505	0	0	#DIV/0!
hypothetical protein	1392	2904495	2905004	0	1.8280943	#DIV/0!
hypothetical protein	1391	2905016	2906020	0	0	#DIV/0!
hypothetical protein	1390	2905998	2907152	0	0	#DIV/0!
hypothetical protein	1389	2907172	2907660	0	0	#DIV/0!
hypothetical protein	1388	2907650	2908222	0	1.62674825	#DIV/0!
hypothetical protein	1387	2908225	2908890	0	0	#DIV/0!
hypothetical protein	1386	2909286	2909903	21.06969206	18.0972447	0.85892
ortholog to Borrelia burgdorferi BB0139	1385	2910082	2910456	294.1176471	318.459893	1.08276
RND multidrug efflux transporter; Acriflavin resistance protein	1384	2910453	2913731	286.1500915	402.232611	1.40567
Probable Co/Zn/Cd efflux system membrane fusion protein	1383	2913743	2914702	144.9426486	262.946298	1.81414
Outer membrane protein	1382	2914699	2916159	223.9726027	327.586986	1.46262
hypothetical protein	1381	2916161	2916307	212.3287671	286.797945	1.35073
hypothetical protein	1380	2916314	2917519	78.00829876	98.8414938	1.26706
Multidrug resistance ABC transporter ATP-binding and permease protein	1379	2918380	2920212	21.28820961	15.7453603	0.73963
Multidrug resistance ABC transporter ATP-binding and permease protein	1378	2920248	2921987	33.92754457	25.1486486	0.74125
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	1377	2922163	2923764	641.4740787	893.884447	1.39348
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	1376	2923880	2924812	68.6695279	67.8905579	0.98866
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	1375	2924814	2925713	62.29143493	72.4527253	1.16313
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	1374	2925718	2926713	78.3919598	82.2954774	1.04979
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	1373	2926710	2927717	35.74975174	55.4419067	1.55083
Muconate cycloisomerase (EC 5.5.1.1)	1372	2927767	2928831	86.46616541	120.68515	1.39575
Transglutaminase-like enzymes, putative cysteine proteases	1371	2928844	2930211	107.5347476	106.187271	0.98747
Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)	1370	2930287	2930823	74.62686567	102.42444	1.37249
Alanyl-tRNA synthetase family protein	1369	2930832	2932097	73.51778656	72.8217391	0.99053
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	1368	2932156	2932869	28.05049088	37.8464236	1.34923
hypothetical protein	1367	2932876	2934120	40.99678457	39.6434887	0.96699
Ornithine carbamoyltransferase (EC 2.1.3.3)	1366	2934269	2935216	108.7645195	124.787223	1.14732
Putative cytoplasmic protein	1365	2935246	2936379	7.060900265	9.85525154	1.39575
COG family: dihydrodipicolinate reductase	1364	2936631	2937689	24.57466919	17.5897921	0.71577
hypothetical protein	1363	2937698	2937997	33.44481605	24.8963211	0.7444
Threonine synthase (EC 4.2.3.1)	1362	2938048	2939403	23.61623616	23.3483395	0.98866

D-ornithine aminomutase S component	1361	2939413	2939769	22.47191011	20.9101124	0.9305
L-beta-lysine 5,6-aminomutase alpha subunit (EC 5.4.3.3)	1360	2939782	2942001	27.94051374	39.8366381	1.42577
Methylaspartate mutase (EC 5.4.99.1)	1359	2942015	2943409	53.08464849	44.0552367	0.82991
Na+/H+ antiporter NhaC	1358	2943591	2945042	78.56650586	111.583046	1.42024
UDP-sugar hydrolase (EC 3.6.1.45); 5'-nucleotidase (EC 3.1.3.5)	1357	2945208	2946779	115.21324	123.790261	1.07444
Hydrolase (HAD superfamily)	1356	2946789	2947562	69.85769728	52.9650712	0.75819
putative periplasmic binding transport protein	1355	2947694	2948527	15.6062425	22.3409364	1.43154
Amino acid ABC transporter, permease protein	1354	2948546	2949262	9.776536313	18.1941341	1.861
ABC-type polar amino acid transport system, ATPase component	1353	2949259	2950029	3.896103896	2.41688312	0.62033
L-serine dehydratase, alpha subunit (EC 4.3.1.17)	1352	2950075	2951688	15.51831161	23.1036623	1.4888
LacI-family regulatory protein	1351	2951817	2952869	48.47908745	88.4505703	1.82451
NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase	1350	2952925	2954661	333.5253456	364.481567	1.09282
hypothetical protein		2954819	2955007	10.63829787	0	0
hypothetical protein	1348	2954958	2956145	69.08171862	58.0092671	0.83972
mucin 2	1347	2956149	2957771	53.63748459	76.8723798	1.43318
putative autotransporter protein	1346	2957781	2960996	73.09486781	61.0685848	0.83547
NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase	1345	2961047	2961274	22.02643172	28.6938326	1.3027
hypothetical protein		2961376	2961531	6.451612903	6.00322581	0.9305
Predicted cell-wall-anchored protein SasA (LPXTG motif)	1343	2961721	2963562	88.53883759	78.3419337	0.88483
Large repetitive protein	1342	2963577	2965778	56.33802817	42.2762381	0.7504
hypothetical protein		2965790	2965930	21.42857143	19.9392857	0.9305
Metal-dependent hydrolases of the beta-lactamase superfamily I; PhnP protein	1340	2965895	2966719	71.60194175	93.7275485	1.30901
Hexokinase	1339	2966776	2968131	168.2656827	190.220295	1.13048
carboxylesterase type B	1338	2968291	2969916	263.3846154	1929.71385	7.3266
para-nitrobenzyl esterase (intracellular esterase B)	1337	2970016	2971620	337.2817955	1963.67986	5.82207
Dipeptide transport ATP-binding protein dppF (TC 3.A.1.5.2)		2971693	2972463	6.510416667	19.3854167	2.9776
ABC transporter, ATP-binding protein		2972466	2973332	4.618937644	1.07448037	0.23263
Binding-protein-dependent transport systems inner membrane component	1334	2973329	2974159	3.614457831	0	0
ABC transporter, permease protein	1333	2974169	2975131	3.118503119	1.93451143	0.62033
ABC transporter, periplasmic substrate-binding protein	1332	2975192	2976712	9.210526316	8.57039474	0.9305
Integral membrane protein	1331	2976873	2978054	7.620660457	7.87891617	1.03389
Alkaline phosphatase (EC 3.1.3.1)	1330	2978061	2979677	77.35148515	48.9433787	0.63274
Beta-glucosidase (EC 3.2.1.21)	1329	2979773	2981995	12.60126013	5.02520252	0.39879
Beta-xylosidase (EC 3.2.1.37)	1328	2982094	2984595	9.996001599	8.92922831	0.89328
hypothetical protein	1327	2984646	2984771	0	0	#DIV/0!
Catechol 2,3-dioxygenase (EC 1.13.11.2)	1326	2984784	2985710	219.2224622	169.821274	0.77465
2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	1325	2985738	2986022	52.81690141	13.1056338	0.24813
4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.-)	1324	2986040	2987047	60.57596822	36.0372393	0.59491
Acetaldehyde dehydrogenase (acetylating)	1323	2987049	2987915	58.89145497	62.3198614	1.05822

4-oxalocrotonate decarboxylase (EC 4.1.1.77)	1322	2987986	2988768	60.10230179	42.8363171	0.71272
2-hydroxymuconic semialdehyde hydrolase (EC 3.7.1.9)	1321	2988772	2989596	42.47572816	59.8501214	1.40904
hypothetical protein		2989612	2989734	24.59016393	30.5081967	1.24067
hypothetical protein		2989738	2989935	0	4.72335025	#DIV/0!
hypothetical protein	1318	2990002	2990499	420.5231388	372.574447	0.88598
Lactate-responsive regulator LldR in Firmicutes, GntR family	1317	2990588	2991319	30.09575923	26.7311902	0.8882
hypothetical protein	1316	2991478	2992296	11.00244499	13.6503667	1.24067
TRAP-type C4-dicarboxylate transport system, periplasmic component	1315	2992327	2993397	16.82242991	26.9584112	1.60253
Predicted rhamnogalacturonide-specific TRAP-type transporter, small transmembrane component RhiB	1314	2993426	2994028	11.62790698	1.54568106	0.13293
TRAP-type C4-dicarboxylate transport system, large permease component	1313	2994041	2995342	6.149116065	3.57609531	0.58156
hypothetical protein	1312	2995369	2996586	4.930156122	6.88126541	1.39575
Transketolase, N-terminal section (EC 2.2.1.1)	1311	2996637	2997473	10.76555024	5.56519139	0.51694
Transketolase, C-terminal section (EC 2.2.1.1)	1310	2997476	2998411	11.76470588	6.96631016	0.59214
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	1309	2998425	2999306	12.48581158	19.0113507	1.52264
2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC 2.7.8.25)	1308	2999469	3000914	22.83737024	23.1820069	1.01509
Fumarate hydratase class I, aerobic (EC 4.2.1.2); L(+)-tartrate dehydratase beta subunit (EC 4.2.1.32)	1307	3000952	3001524	48.95104895	39.041958	0.79757
Fumarate hydratase class I, aerobic (EC 4.2.1.2); L(+)-tartrate dehydratase alpha subunit (EC 4.2.1.32)	1306	3001524	3002363	39.33253874	42.1442193	1.07148
hypothetical protein	1305	3002418	3003353	72.72727273	54.7352941	0.75261
Methylaspartate ammonia-lyase (EC 4.3.1.2)	1304	3003412	3004662	141.6	105.7048	0.7465
Putative glutamate mutase subumit E	1303	3004672	3006120	109.8066298	102.175069	0.9305
METHYLASPARTATE MUTASE (EC 5.4.99.1)	1302	3006104	3007498	44.47632712	53.4002869	1.20065
Methylaspartate mutase S chain (EC 5.4.99.1)	1301	3007504	3007920	67.30769231	53.6826923	0.79757
hypothetical protein		3007994	3008113	0	0	#DIV/0!
Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit B	1299	3008198	3009643	93.42560554	65.6823529	0.70304
Regulatory protein GntR, HTH	1298	3009647	3010636	77.85642063	109.138524	1.40179
Flagellar hook-length control protein fliK	1297	3011133	3012992	57.55782679	61.0656267	1.06094
Flagellar hook-length control protein fliK	1296	3013004	3015493	43.39092005	38.5060265	0.88742
hypothetical protein	1295	3015505	3017775	88.10572687	62.7165198	0.71183
hypothetical protein		3017845	3017988	0	0	#DIV/0!
hypothetical protein	1293	3018215	3018919	2.840909091	2.64346591	0.9305
hypothetical protein	1292	3018879	3019232	175.6373938	144.978754	0.82544
Superfamily II DNA/RNA helicases, SNF2 family	1291	3019425	3022697	8.251833741	4.83450489	0.58587
hypothetical protein	1290	3022690	3024843	5.109150023	1.29656294	0.25377
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	1289	3024882	3025970	42.27941176	46.1829044	1.09233
Citrate lyase alpha chain (EC 4.1.3.6)	1288	3025967	3027376	34.77643719	40.2842441	1.15838
Citrate lyase beta chain (EC 4.1.3.6)	1287	3027369	3028244	22.85714286	24.4588571	1.07008

Citrate lyase acyl carrier protein	1286	3028245	3028511	67.66917293	48.9736842	0.72372
hypothetical protein	1285	3028610	3028804	30.92783505	14.3891753	0.46525
Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate, subunit B	1284	3029211	3030647	217.270195	209.297702	0.96331
hypothetical protein	1283	3030649	3031413	129.5811518	86.4731675	0.66733
hypothetical protein	1282	3031424	3032149	78.62068966	69.3062069	0.88153
Anthranilate synthase, amidotransferase component (EC 4.1.3.27)	1281	3032197	3032973	73.45360825	63.5521907	0.8652
3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)	1280	3033334	3034398	241.5413534	258.860902	1.0717
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	1279	3034392	3035366	130.3901437	192.023101	1.47268
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	1278	3035390	3036124	433.1034483	428.671724	0.98977
3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41)	1277	3036138	3037403	531.2252964	609.054545	1.14651
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-)	1276	3037422	3037841	687.3508353	370.867542	0.53956
hypothetical protein		3037976	3038356	39.47368421	31.8328947	0.80643
DNA modification methylase (Adenine-specific methyltransferase) (EC 2.1.1.72)	1274	3038438	3039790	32.5443787	28.9060651	0.8882
Short-chain alcohol dehydrogenase family		3039791	3040318	89.18406072	82.9857685	0.9305
Short-chain alcohol dehydrogenase family		3040348	3041268	214.1304348	205.316848	0.95884
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	1271	3041308	3041901	227.6559865	233.801855	1.027
Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)	1270	3041922	3043253	87.90383171	92.2809917	1.04979
Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	1269	3043243	3044067	92.23300971	99.3737864	1.07742
Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)	1268	3044064	3044993	200.2152853	226.364909	1.13061
Acyl-CoA dehydrogenase (EC 1.3.99.3)	1267	3045001	3046737	391.1290323	553.154378	1.41425
Electron transfer flavoprotein, alpha subunit	1266	3046750	3047757	327.7060576	373.308838	1.13916
Electron transfer flavoprotein, beta subunit	1265	3047845	3048675	263.8554217	442.828313	1.6783
hypothetical protein		3048769	3048906	0	0	#DIV/0!
transcriptional regulator, putative	1263	3048839	3049186	20.17291066	32.1786744	1.59514
HIPA PROTEIN	1262	3049186	3050436	13.6	18.61	1.36838
Adenylate cyclase (EC 4.6.1.1)	1261	3050506	3051837	54.84598047	30.0612322	0.5481
Sensory box histidine kinase/response regulator	1260	3051827	3054091	35.33568905	33.7018551	0.95376
Transcription regulator [contains diacylglycerol kinase catalytic domain]	1259	3054084	3055103	13.73895976	28.3076546	2.06039
FOG: CheY-like receiver	1258	3055100	3057892	31.51862464	30.9944484	0.98337
Adenylate cyclase (EC 4.6.1.1)	1257	3057971	3059302	10.51840721	8.38918107	0.79757
Sensory box histidine kinase/response regulator	1256	3059292	3063527	3.541912633	9.44781582	2.66743
FOG: CheY-like receiver	1255	3063553	3066357	7.132667618	3.98216833	0.5583
Sensory box histidine kinase/response regulator	1254	3066354	3069575	9.313877678	3.75551071	0.40322
Bmp family protein	1253	3069572	3070711	14.04741001	8.98639157	0.63972
Bmp family protein	1252	3070723	3071868	6.986899563	7.3139738	1.04681

Sensory box histidine kinase/response regulator	1251	3071865	3074768	10.67860834	5.12848777	0.48026
FOG: CheY-like receiver	1250	3074765	3078013	10.1663586	4.87322859	0.47935
Sensory box histidine kinase/response regulator	1249	3078087	3080771	6.706408346	5.54694486	0.82711
hypothetical protein	1248	3080832	3080972	7.142857143	6.64642857	0.9305
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1247	3081335	3082711	5.813953488	4.73364826	0.81419
Nitroreductase	1246	3082737	3083489	25.26595745	42.0704787	1.66511
aminoglycoside 6-adenylyltransferase	1245	3083514	3083774	0	0	#DIV/0!
hypothetical protein	1244	3083782	3084093	0	0	#DIV/0!
hypothetical protein	1243	3084153	3084473	3.125	0	0
hypothetical protein	1242	3084517	3085089	0	0	#DIV/0!
hypothetical protein		3085342	3085548	4.854368932	0	0
hypothetical protein	1240	3085851	3086096	57.14285714	72.1612245	1.26282
Plasmid stabilization system protein	1239	3086177	3086485	32.46753247	30.211039	0.9305
Prevent-host-death family protein	1238	3086482	3086766	45.77464789	45.8697183	1.00208
ATP synthase epsilon chain (EC 3.6.3.14)	1237	3087118	3087543	127.0588235	186.1	1.46468
ATP synthase beta chain (EC 3.6.3.14)	1236	3087552	3088934	440.6657019	588.463821	1.3354
ATP synthase gamma chain (EC 3.6.3.14)	1235	3088993	3089880	169.1093574	184.631342	1.09179
ATP synthase alpha chain (EC 3.6.3.14)	1234	3089889	3091391	264	307.685333	1.16547
ATP synthase delta chain (EC 3.6.3.14)	1233	3091385	3091951	217.3144876	207.14311	0.9532
ATP synthase B chain (EC 3.6.3.14)	1232	3091951	3092454	590.4572565	369.980119	0.6266
ATP synthase C chain (EC 3.6.3.14)	1231	3092466	3092696	343.4782609	206.328261	0.6007
ATP synthase A chain (EC 3.6.3.14)	1230	3092852	3093574	178.6703601	163.675208	0.91607
hypothetical protein	1229	3093636	3094151	489.3203883	543.845631	1.11143
Methionine gamma-lyase (EC 4.4.1.11)	1228	3094223	3095431	1.655629139	4.62168874	2.7915
Predicted nicotinate-regulated transporter BH3254	1227	3095568	3096635	99.34395501	119.473758	1.20263
Molybdopterin-guanine dinucleotide biosynthesis protein B	1226	3096638	3097135	108.6519115	131.056338	1.2062
FIG060329: hypothetical protein	1225	3097125	3097553	189.2523364	130.443925	0.68926
Molybdenum cofactor biosynthesis protein A	1224	3097556	3098560	176.2948207	139.945717	0.79382
Molybdenum cofactor biosynthesis protein C	1223	3098566	3099096	105.6603774	91.2943396	0.86404
Integration host factor beta subunit	1222	3099398	3099901	3952.286282	5333.26342	1.34941
N-acetylneuraminate synthase (EC 2.5.1.56)	1221	3100112	3101221	21.64111812	18.458972	0.85296
Outer membrane stress sensor protease DegQ	1220	3101502	3103013	232.9583058	180.43448	0.77454
Methionine aminopeptidase (EC 3.4.11.18)	1219	3103102	3103896	192.6952141	165.239924	0.85752
Chaperone protein DnaJ	1218	3103905	3104681	180.4123711	141.493557	0.78428
hypothetical protein	1217	3104674	3105075	182.0448878	153.149626	0.84127
Universal stress protein	1216	3105100	3105585	284.5360825	237.901031	0.8361
V-type ATP synthase subunit D (EC 3.6.3.14)	1215	3105582	3106232	329.2307692	271.992308	0.82614
hypothetical protein	1214	3106329	3107207	69.476082	72.0660592	1.03728
hypothetical protein	1213	3107280	3107846	1.766784452	4.9319788	2.7915
hypothetical protein	1212	3107983	3108819	51.4354067	35.6172249	0.69247
Probable N-glycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3.2.2.-); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP lyase)]	1211	3108816	3109466	27.69230769	22.9046154	0.82711
hypothetical protein	1210	3109463	3109606	6.993006993	6.50699301	0.9305

4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	1209	3109628	3110683	342.1800948	214.323697	0.62635
SpoVG family protein	1208	3110726	3111007	604.9822064	453.660142	0.74987
LSU ribosomal protein L25p	1206	3111277	3111921	773.2919255	878.484472	1.13603
ABC transporter, permease protein, putative	1205	3111990	3113249	30.97696585	14.042494	0.45332
hypothetical protein	1204	3113399	3113632	25.75107296	43.9291845	1.70592
Transcriptional regulator, MarR family	1203	3113816	3114274	17.46724891	28.4432314	1.62838
tRNA(Ile)-lysidine synthetase	1202	3114392	3115819	97.40714786	125.196917	1.28529
Cell division protein ftsH (EC 3.4.24.-)	1201	3115809	3117722	261.8923157	292.818087	1.11809
hypothetical protein	1200	3117722	3119455	117.1379111	149.80352	1.27886
Serine protease precursor MucD/AlgY associated with sigma factor RpoE	1199	3119461	3121299	145.2665941	164.53346	1.13263
Possible 5-nitroimidazole antibiotic resistance	1198	3121306	3121785	127.348643	110.727557	0.86948
transcriptional regulator, PemK family	1197	3121941	3122258	6.309148265	8.80599369	1.39575
Proteic killer gene system protein , suppressor of inhibitory function of MazF	1196	3122258	3122590	12.04819277	8.40813253	0.69788
hypothetical protein	1195	3122655	3123356	369.4721826	292.025678	0.79039
Transcriptional regulator	1194	3123428	3124552	149.4661922	153.979537	1.0302
2-methylthioadenine synthetase	1193	3124555	3126021	68.89495225	88.2261255	1.28059
ATP-dependent DNA helicase UvrD/PcrA	1192	3126092	3128560	38.89789303	51.6525527	1.3279
Uncharacterized protein TP_0678	1191	3128553	3129398	30.76923077	41.8449704	1.35996
hypothetical protein	1190	3129480	3129617	0	6.7919708	#DIV/0!
Putative biofilm-associated surface protein	1189	3129627	3132245	45.45454545	41.2291826	0.90704
hypothetical protein		3132304	3132420	8.620689655	8.02155172	0.9305
hypothetical protein	1187	3132410	3132550	0	0	#DIV/0!
Diaminopimelate decarboxylase (EC 4.1.1.20)	1186	3132554	3133825	177.0259638	188.149882	1.06284
LL-diaminopimelate aminotransferase	1185	3133839	3135044	180.0829876	151.351037	0.84045
hypothetical protein	1184	3135137	3135403	124.0601504	115.43797	0.9305
Plasmid stability protein	1183	3135400	3135813	53.26876513	65.3377724	1.22657
ATP-dependent DNA helicase RecQ	1182	3135904	3137610	2.344665885	4.36342321	1.861
hypothetical protein	1181	3137664	3137894	100	141.597826	1.41598
Serine/threonine protein kinase PrkC, regulation of stationary phase	1180	3137923	3139008	132.718894	137.21659	1.03389
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	1179	3139018	3140067	96.2821735	108.218303	1.12397
Peptide deformylase (EC 3.5.1.88)	1178	3140069	3140557	258.1967213	255.506148	0.98958
Mannose-6-phosphate isomerase (EC 5.3.1.8) / Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	1177	3140872	3142041	175.3635586	163.971771	0.93504
Acetate kinase (EC 2.7.2.1)	1176	3142145	3143482	913.7284321	1084.76894	1.18719
heat shock protein	1175	3143677	3144228	154.2649728	190.828494	1.23702
hypothetical protein	1174	3144327	3145097	97.4025974	84.5909091	0.86847
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	1173	3145184	3146890	83.82180539	58.3607855	0.69625
COG1355, Predicted dioxygenase	1172	3146937	3147794	93.34889148	81.4323221	0.87234
Fibronectin/fibrinogen-binding protein	1171	3147887	3149371	30.32345013	36.9942722	1.21999
Beta-hexosaminidase (EC 3.2.1.52)	1170	3149405	3150583	53.48047538	52.1332767	0.97481
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	1169	3150585	3151271	48.10495627	70.5335277	1.46624
hypothetical protein	1168	3151299	3152936	156.3836286	151.767563	0.97048
hypothetical protein	1167	3153043	3153927	46.3800905	59.9983032	1.29362
hypothetical protein	1166	3154027	3154710	43.9238653	49.045388	1.1166
Flagellar biosynthesis protein fliS	1165	3154821	3155282	579.175705	764.988069	1.32082
hypothetical protein	1164	3155514	3155762	28.22580645	41.2721774	1.46221

Gsl0633 protein	1163	3155818	3156054	25.42372881	23.6567797	0.9305
hypothetical protein	1162	3156051	3156464	36.31961259	31.5423729	0.86847
hypothetical protein	1161	3156555	3156701	13.69863014	12.7465753	0.9305
hypothetical protein		3156744	3156857	115.0442478	57.6415929	0.50104
hypothetical protein	1159	3156841	3157095	185.0393701	186.832677	1.00969
hypothetical protein	1158	3157113	3157250	167.8832117	142.631387	0.84959
hypothetical protein	1157	3157271	3157897	281.1501597	175.397764	0.62386
hypothetical protein	1156	3157925	3158053	70.3125	50.8867188	0.72372
hypothetical protein	1155	3158109	3158525	240.3846154	266.176683	1.1073
hypothetical protein	1154	3158712	3159626	129.1028446	77.3719912	0.59931
V-type ATP synthase subunit B (EC 3.6.3.14)	1153	3159743	3161200	143.7456807	167.194195	1.16313
V-type ATP synthase subunit A (EC 3.6.3.14)	1152	3161231	3163045	205.6384743	260.786899	1.26818
V-type ATPase, subunit E, putative [EC:3.6.3.14]	1151	3163042	3163743	169.7574893	199.108417	1.1729
V-type ATPase, subunit F, putative	1150	3163762	3164106	244.1860465	243.444767	0.99696
V-type ATP synthase subunit K (EC 3.6.3.14)	1149	3164106	3164417	160.7717042	209.437299	1.3027
V-type ATP synthase subunit I (EC 3.6.3.14)	1148	3164420	3166483	162.8696074	203.871062	1.25174
Uncharacterized protein TP_0534	1147	3166518	3167597	224.2817424	209.556534	0.93435
hypothetical protein	1146	3167597	3168010	305.0847458	261.35109	0.85665
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	1145	3168035	3168508	308.6680761	245.903805	0.79666
Preprotein translocase subunit SecG (TC 3.A.5.1.1)	1144	3168524	3168910	391.1917098	332.665803	0.85039
Predicted molybdate-responsive regulator YvgK in bacilli	1143	3169236	3170240	145.4183267	153.84761	1.05797
Spermidine/putrescine-binding protein	1142	3170262	3171314	64.63878327	107.02519	1.65574
ABC transporter, ATP-binding protein	1141	3171311	3172183	32.11009174	58.6897936	1.82777
Ni2+-binding GTPase involved in regulation of expression and maturation of hydrogenase	1140	3172176	3172889	36.46563815	30.016129	0.82313
methlytransferase, UbiE/COQ5 family	1139	3172886	3173587	44.22253923	69.0242511	1.56084
Flagellar hook-length control protein fliK	1138	3173864	3175609	1.719197708	1.59971347	0.9305
BNR repeat domain protein	1136	3175635	3177710	0.481927711	1.79373494	3.722
hypothetical protein	1137	3177664	3177795	0	0	#DIV/0!
Ig domain protein, group 2 domain protein	1135	3177839	3180271	0.822368421	0	0
5'-nucleotidase (EC 3.1.3.5)	1134	3180348	3182177	0	0	#DIV/0!
TonB-dependent receptor	1133	3182226	3184259	0	0.45769798	#DIV/0!
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1)	1132	3184276	3185040	0	2.43586387	#DIV/0!
Ferric siderophore transport system, periplasmic binding protein TonB	1131	3185309	3186022	5.610098177	2.61009818	0.46525
ABC transporter, solute-binding protein	1130	3186142	3187281	4.389815628	12.2541703	2.7915
Vitamin B12 ABC transporter, permease component BtuC	1129	3187289	3188323	2.901353965	3.59961315	1.24067
ABC transporter related	1128	3188317	3189162	10.65088757	24.2260355	2.27456
Acetoin utilization protein AcuB	1127	3189210	3189854	66.77018634	153.156832	2.29379
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)	1126	3189856	3190560	63.92045455	88.556108	1.38541
Branched-chain amino acid transport ATP-binding protein livG (TC 3.A.1.4.1)	1125	3190553	3191359	91.81141439	116.601117	1.27001

Branched-chain amino acid transport system permease protein livM (TC 3.A.1.4.1)	1124	3191349	3192344	51.25628141	88.8417085	1.73328
High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	1123	3192346	3193245	60.06674082	89.0133482	1.48191
Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	1122	3193266	3194456	348.7394958	480.106723	1.37669
Homolog of plant auxin-responsive GH3-like protein	1121	3194547	3196250	28.84049441	67.9117128	2.35473
Glycoprotein gp2	1120	3196603	3198747	121.2686567	135.408582	1.1166
Flagellar biosynthesis protein fliL	1119	3198879	3199442	26.64298401	41.3188277	1.55083
Potassium efflux system kefA / Small-conductance mechanosensitive channel	1118	3199445	3200464	59.8626104	44.7443572	0.74745
Mannose-6-phosphate isomerase	1117	3200552	3200896	279.0697674	238.034884	0.85296
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	1116	3200906	3202747	240.0436443	287.830606	1.19908
Conserved protein	1114	3202797	3203354	114.9012567	162.043986	1.41029
hypothetical protein		3203351	3203569	27.52293578	17.0733945	0.62033
hypothetical protein	1113	3203606	3203863	0	0	#DIV/0!
hypothetical protein	1112	3203836	3204054	13.76146789	0	0
plasmid stability protein, putative	1111	3204570	3204755	48.64864865	85.5054054	1.75761
hypothetical protein	1110	3204968	3205240	102.9411765	153.943015	1.49545
Fe-S oxidoreductase	1109	3205298	3206416	180.6797853	251.351521	1.39114
Low-specificity L-threonine aldolase (EC 4.1.2.5)	1108	3206617	3207663	157.7437859	161.013862	1.02073
Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP-specific)	1107	3207660	3208817	75.19446845	92.4870354	1.22997
hypothetical protein	1106	3208830	3209279	48.99777283	43.5200445	0.8882
Sll1036 protein	1105	3209325	3210128	105.8530511	92.7023661	0.87576
Metal-dependent phosphohydrolase, HD subdomain	1104	3210253	3211110	85.18086348	123.77713	1.45311
TPR domain protein, putative component of TonB system	1103	3211103	3212668	150.798722	153.398722	1.01724
Fibronectin type III domain protein	1102	3212665	3214467	93.22974473	79.004717	0.84742
Excinuclease ABC subunit C	1101	3214451	3216496	46.45476773	72.801956	1.56716
hypothetical protein	1100	3216617	3216823	0	18.0679612	#DIV/0!
hypothetical protein	1099	3216835	3217158	18.57585139	5.76160991	0.31017
possible M. jannaschii predicted coding region MJ1674	1098	3217182	3218513	28.54996243	24.4684448	0.85704
CRISPR-associated RAMP protein, Csm5 family	1097	3218510	3219670	45.68965517	36.8991379	0.8076
hypothetical protein	1096	3219687	3220565	83.14350797	55.1093394	0.66282
hypothetical protein	1095	3220575	3221249	56.37982196	53.8419881	0.95499
unknown	1094	3221279	3221770	67.20977597	75.8044807	1.12788
hypothetical protein	1093	3221776	3223977	52.24897774	48.1949114	0.92241
hypothetical protein	1092	3223987	3224934	62.30200634	56.0068638	0.89896
Mannose-6-phosphate isomerase (EC 5.3.1.8)	1091	3226012	3227220	211.9205298	281.923013	1.33032
hypothetical protein	1090	3227268	3227846	204.1522491	194.793253	0.95416
Flagellar filament outer layer protein	1089	3227980	3228702	1087.257618	1116.08449	1.02651
flagellar filament outer layer protein FlaA, putative	1088	3228715	3229446	894.6648427	784.114911	0.87643
hypothetical protein	1087	3229589	3230515	110.1511879	84.4082073	0.76629

hypothetical protein		3230515	3230640	0	14.888	#DIV/0!
Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	1085	3230677	3231675	702.811245	947.316265	1.3479
similar to ENSANGP00000029682	1084	3231799	3234069	125.1101322	103.707709	0.82893
hypothetical protein	1083	3234117	3234803	11.66180758	2.71282799	0.23263
hypothetical protein	1082	3234816	3234947	45.80152672	28.4122137	0.62033
Phosphatase	1081	3234980	3236032	23.76425856	34.4957224	1.45158
GTPase and tRNA-U34 5-formylation enzyme TrmE	1080	3236035	3237513	71.04194858	64.2158322	0.90391
tRNA uridine 5-carboxymethylaminomethyl modification enzyme gidA	1079	3237517	3239424	49.2920818	64.4079706	1.30666
Protein crcB homolog	1078	3239405	3239806	89.7755611	51.0498753	0.56864
hypothetical protein		3239799	3239933	97.01492537	83.3283582	0.85892
HIT family protein	1076	3239984	3240328	154.0697674	262.37936	1.70299
Seryl-tRNA synthetase (EC 6.1.1.11)	1075	3240328	3241611	246.2977397	256.739673	1.0424
hypothetical protein		3241610	3241732	0	0	#DIV/0!
hypothetical protein	1073	3241864	3242028	6.097560976	5.67378049	0.9305
Predicted cell-wall-anchored protein SasA (LPXTG motif)	1072	3242028	3244127	23.82086708	19.0621725	0.80023
Cell surface protein	1071	3244140	3246974	20.81863091	18.058398	0.86742
Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC 6.3.5.3) / Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (EC 6.3.5.3)	1070	3247034	3251158	101.1154219	109.430771	1.08224
GTP-binding and nucleic acid-binding protein YchF	1069	3251370	3252497	342.5022183	418.601154	1.22219
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	1068	3252510	3252956	163.67713	146.042601	0.89226
Lysyl-tRNA synthetase-related protein	1067	3252965	3254020	103.3175355	127.006635	1.22928
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	1066	3254033	3255478	89.96539792	101.099308	1.12376
hypothetical protein	1065	3255539	3256567	55.44747082	90.5155642	1.63246
Methyltransferase	1064	3256714	3257361	41.73106646	41.7071097	0.99943
UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	1063	3257419	3259002	157.2962729	156.356917	0.99403
MG(2+) CHELATASE FAMILY PROTEIN / ComM-related protein	1062	3259127	3260800	16.73640167	28.3655111	1.69484
Putative regulatory protein	1061	3260832	3261392	21.42857143	29.9089286	1.39575
hypothetical protein	1060	3261403	3261519	0	8.02155172	#DIV/0!
Permease of the drug/metabolite transporter (DMT) superfamily	1059	3261541	3262461	63.04347826	72.8217391	1.1551
Sugar/maltose fermentation stimulation protein homolog	1058	3262454	3263671	19.72062449	24.4667214	1.24067
BNR repeat domain protein	1057	3264103	3265707	1.246882793	0.58011222	0.46525
hypothetical protein		3265797	3265958	6.211180124	5.77950311	0.9305
Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)	1055	3266072	3266845	90.55627426	114.356404	1.26282
Sensory box histidine kinase/response regulator	1054	3266855	3270067	116.8224299	121.167913	1.0372
Putative pheromone precursor lipoprotein	1053	3270082	3270582	326	212.154	0.65078

Autoinducer 2 (AI-2) ABC transport system, periplasmic AI-2 binding protein LsrB	1052	3270572	3271651	215.9406858	203.519926	0.94248
Thiol peroxidase, Tpx-type (EC 1.11.1.15)	1050	3271809	3272324	153.3980583	99.3737864	0.64782
hypothetical protein		3272279	3272416	58.39416058	6.7919708	0.11631
hypothetical protein	1049	3272840	3272968	7.8125	0	0
hypothetical protein	1048	3273158	3273286	0	7.26953125	#DIV/0!
TetR family transcriptional regulator probably coupled to RND multidrug efflux transporter	1047	3273504	3274073	15.8172232	13.0826011	0.82711
Iron-sulfur cluster-binding protein	1046	3274122	3275171	2.85986654	4.43517636	1.55083
hypothetical protein	1045	3275215	3275850	0	0	#DIV/0!
Hypothetical SAV0801 homolog in superantigen-encoding pathogenicity islands SaPI	1044	3275871	3276821	6.315789474	13.7126316	2.17117
hypothetical protein	1043	3276934	3277092	6.329113924	5.88924051	0.9305
hypothetical protein	1042	3277673	3277840	0	0	#DIV/0!
Nitroreductase	1041	3277981	3278607	6.389776358	23.7827476	3.722
Transcriptional regulator, Cro/CI family	1040	3278645	3278992	17.75147929	8.25887574	0.46525
hypothetical protein	1039	3279000	3279233	0	3.99356223	#DIV/0!
hypothetical protein	1038	3279554	3281041	2.017484869	1.25151311	0.62033
hyopothetical protein	1037	3281038	3281829	1.264222503	2.35271808	1.861
membrane protein, putative	1036	3281834	3284452	1.145912911	1.06627196	0.9305
Transcriptional regulator, AcrR family	1035	3284561	3285229	2.994011976	1.39296407	0.46525
hypothetical protein		3285304	3285438	149.2537313	55.5522388	0.3722
S-adenosylmethionine synthetase (EC 2.5.1.6)	1033	3285454	3286623	291.7023097	345.45509	1.18427
putative outer membrane protein probably involved in nutrient binding	1032	3286720	3289389	34.84451105	36.6064069	1.05056
hypothetical protein	1031	3289425	3290579	77.98960139	91.9211438	1.17863
Hypothetical protein YaeJ with similarity to translation release factor	1030	3290592	3291017	44.70588235	98.5235294	2.20382
hypothetical protein	1029	3291103	3292419	88.90577508	119.494301	1.34406
Phosphoglycolate phosphatase (EC 3.1.3.18)	1028	3292432	3293097	63.15789474	64.3654135	1.01912
hypothetical protein	1027	3293103	3296222	161.849711	155.083333	0.95819
Endonuclease III (EC 4.2.99.18)	1026	3296227	3297018	115.0442478	119.988622	1.04298
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	1025	3297029	3297502	209.3023256	157.378436	0.75192
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)		3297495	3298247	117.0212766	112.600399	0.96222
Transcriptional regulator	1023	3298257	3298760	455.2683897	505.022863	1.10929
Surface protein	1022	3298890	3301736	738.2290935	693.134223	0.93891
Putative sugar transporter	1021	3301894	3303249	28.04428044	12.3608856	0.44076
hypothetical protein	1020	3303518	3303775	3.891050584	0	0
Helicase, SNF2/RAD54 family	1019	3303793	3307449	63.73085339	71.7727024	1.12618
putative outer membrane protein precursor	1018	3307594	3309042	582.1823204	783.342196	1.34553
hypothetical protein	1017	3309248	3309499	131.4741036	144.579681	1.09968
contains Pfam domain, PF05193: Peptidase M16 inactive domain; go_function: metalloendopeptidase activity [goid 0004222]; go_process: proteolysis and peptidolysis [goid 0006508] / peptidase M16 family protein / insulinase family protein	1016	3309531	3312632	70.9448565	87.0187036	1.22657

Flagellar motor switch protein fliG	1015	3312629	3314323	61.3931523	83.4923259	1.35996
Dihydroflavonol-4-reductase (EC 1.1.1.219)	1014	3314306	3315328	110.5675147	144.764677	1.30929
Ferredoxin	1013	3315328	3316092	81.15183246	112.049738	1.38074
hypothetical protein	1012	3316411	3317055	29.50310559	14.4487578	0.48974
transposase, mutator family	1011	3317258	3318472	49.13793103	49.7336207	1.01212
Transposase IS4 family		3318566	3319213	1.545595054	1.4381762	0.9305
hypothetical protein	1009	3319764	3319880	25.86206897	16.0431034	0.62033
hypothetical protein		3319904	3320152	0	0	#DIV/0!
hypothetical protein		3320163	3320324	0	0	#DIV/0!
hypothetical protein	1006	3320402	3320929	5.69259962	0	0
Regulator of polyketide synthase expression	1005	3321404	3322855	15.85113715	7.05410062	0.44502
Uroporphyrinogen-III decarboxylase	1004	3322984	3324237	19.15403033	5.94094174	0.31017
Recombination protein O	1003	3324338	3325015	47.26735598	35.7355982	0.75603
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	1002	3325043	3326347	118.0981595	112.744632	0.95467
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	1001	3326382	3328526	139.9253731	149.730644	1.07008
hypothetical protein	1000	3328559	3329203	62.11180124	44.7911491	0.72114
Peptidase M23B precursor	999	3329338	3330504	21.44082333	25.5368782	1.19104
SSU ribosomal protein S21p	998	3330600	3330812	1495.283019	1702.99057	1.13891
hypothetical protein	997	3330852	3330968	34.48275862	32.0862069	0.9305
2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	996	3331123	3331788	15.03759398	19.5894737	1.3027
hypothetical protein	994	3331785	3331976	10.47120419	38.973822	3.722
hypothetical protein	995	3331946	3332911	19.68911917	7.71398964	0.39179
Aspartate aminotransferase (EC 2.6.1.1)	993	3333307	3334653	49.03417533	67.7481426	1.38165
hypothetical protein	992	3334892	3335011	0	0	#DIV/0!
hypothetical protein	991	3335187	3335861	4.451038576	4.14169139	0.9305
hypothetical protein	990	3335858	3336019	80.74534161	23.1180124	0.28631
Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	989	3336020	3336838	353.3007335	404.96088	1.14622
Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)	988	3336838	3337638	232.5	330.3275	1.42076
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	987	3337645	3339387	73.47876005	85.4649828	1.16313
FOG: GGDEF domain	986	3339389	3340798	154.0099361	153.212207	0.99482
Uncharacterized protein TP_0273	985	3341292	3341681	46.27249357	38.2724936	0.82711
hypothetical protein	984	3341683	3342414	9.575923393	7.6374829	0.79757
Acetolactate synthase small subunit (EC 2.2.1.6)	983	3342622	3343137	357.2815534	375.813592	1.05187
Ketol-acid reductoisomerase (EC 1.1.1.86)	982	3343254	3344255	318.5035389	282.254803	0.88619
2-isopropylmalate synthase (EC 2.3.3.13)	981	3344414	3345985	341.1839593	344.12508	1.00862
2-isopropylmalate synthase (EC 2.3.3.13)	980	3345982	3347643	223.5150031	190.886405	0.85402
3-isopropylmalate dehydrogenase (EC 1.1.1.85)	979	3347658	3348791	174.7572816	184.785966	1.05739
hypothetical protein		3348811	3348990	50.27932961	31.1899441	0.62033
Dihydroxy-acid dehydratase (EC 4.2.1.9)	977	3348985	3350646	134.256472	133.888922	0.99726
Acetolactate synthase large subunit (EC 2.2.1.6)	976	3350650	3352449	168.4269038	144.824903	0.85987
Hypothetical similar to thiamin biosynthesis lipoprotein ApbE	974	3352433	3353461	77.82101167	58.8351167	0.75603
hypothetical protein	975	3353447	3353560	8.849557522	8.23451327	0.9305
Aryldialkylphosphatase related protein	973	3353535	3354383	15.33018868	15.3620283	1.00208

Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)	972	3354380	3355693	12.18583397	9.21287129	0.75603
Uncharacterized protein TP_1032	971	3355659	3356042	39.16449086	38.8720627	0.99253
Carbon starvation protein A	970	3356169	3357893	57.42459397	73.9434455	1.28766
sensory box histidine kinase/response regulator	969	3357896	3360127	121.4701927	138.886822	1.14338
Transcriptional regulator, Cro/CI family	968	3360135	3360488	144.4759207	134.434844	0.9305
hypothetical protein	967	3360472	3360594	8.196721311	7.62704918	0.9305
2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	966	3360614	3362572	102.145046	125.460674	1.22826
Putative ABC-type amino-acid transporter permease protein	965	3362677	3363369	2.89017341	1.34465318	0.46525
Putative ABC-type amino-acid transporter permease protein	964	3363366	3364178	3.694581281	4.58374384	1.24067
Major cell-binding factor precursor PebA	963	3364135	3364932	8.78293601	12.8425345	1.46221
Amino-acid ABC transporter ATP-binding protein PebC	962	3364950	3365672	5.540166205	6.44390582	1.16313
Cell surface protein	961	3366189	3367730	24.01038287	25.9646334	1.08139
hypothetical protein	960	3367806	3368381	153.0434783	121.369565	0.79304
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	959	3368579	3369064	84.53608247	80.5793814	0.9532
TnpR protein	958	3369061	3371127	134.0755082	138.268877	1.03128
Anaerobic dimethyl sulfoxide reductase chain A (EC 1.8.99.-)	957	3371171	3374083	41.8956044	45.0551168	1.07541
Diaminopimelate epimerase homolog	956	3374095	3374886	94.81668774	76.4633375	0.80643
Amino acid ABC transporter, amino acid-binding protein	955	3374948	3375775	263.6033857	389.302297	1.47685
ABC-type amino acid transport system, permease component	954	3375778	3376479	161.1982882	220.346648	1.36693
Glutamine transport ATP-binding protein glnQ (TC 3.A.1.3.2)	953	3376499	3377248	38.04347826	84.7058424	2.22655
hypothetical protein	952	3377311	3377634	6.191950464	5.76160991	0.9305
hypothetical protein	951	3377624	3377755	0	0	#DIV/0!
hypothetical protein		3377715	3377975	0	3.57884615	#DIV/0!
hypothetical protein	949	3378454	3379245	5.056890013	0	0
BpmI endonuclease-methyltransferase fusion protein type IIG	948	3379332	3382187	54.29071804	58.3395797	1.07458
hypothetical protein	947	3382231	3382392	0	0	#DIV/0!
Transcriptional regulator, DeoR family	946	3382467	3383468	14.01401401	14.9029029	1.06343
Probable DNA polymerase III polC-type (EC 2.7.7.7) (EC 6.5.1.2)	945	3383740	3384018	43.16546763	40.1654676	0.9305
hypothetical protein	944	3384036	3384368	63.25301205	72.8704819	1.15205
hypothetical protein	943	3384964	3386223	3.177124702	0.73907863	0.23263
hypothetical protein	942	3386237	3387358	0	0.83006244	#DIV/0!
MoxR-like ATPases	941	3387376	3388443	1.874414246	0	0
hypothetical protein		3388447	3389142	1.438848921	1.33884892	0.9305
Xaa-Pro dipeptidase (EC 3.4.13.9)	939	3389440	3390564	121.886121	103.480872	0.849
L-Aspartate dehydrogenase (EC 1.4.1.21)	938	3390581	3391402	107.1863581	91.8032887	0.85648

Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase)	937	3391402	3392007	90.90909091	133.807438	1.47188
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	936	3392086	3393639	206.052801	199.521249	0.9683
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	935	3393701	3394597	65.84821429	73.733817	1.11975
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	934	3394597	3395544	116.156283	156.229673	1.345
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	933	3395666	3396646	26.53061224	37.030102	1.39575
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	932	3396661	3397644	30.51881994	30.2909461	0.99253
DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	931	3397724	3402061	616.5743306	797.970337	1.2942
DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	930	3402091	3405624	502.8538813	536.418379	1.06675
LSU ribosomal protein L7/L12 (L23e)	929	3405765	3406151	577.7202073	520.694301	0.90129
LSU ribosomal protein L10p (P0)	928	3406296	3406847	911.0707804	868.016334	0.95274
LSU ribosomal protein L1p (L10Ae)	927	3406924	3407604	582.3529412	615.772059	1.05739
LSU ribosomal protein L11p (L12e)	926	3407601	3408032	1821.345708	1660.21926	0.91153
Transcription antitermination protein NusG	925	3408115	3408717	501.6611296	508.52907	1.01369
Preprotein translocase subunit SecE (TC 3.A.5.1.1)	924	3408698	3408877	212.2905028	166.346369	0.78358
hypothetical protein		3408860	3408997	700.729927	427.894161	0.61064
LSU ribosomal protein L33p	921	3409160	3409333	2780.346821	2587.11272	0.9305
hypothetical protein		3409480	3409626	54.79452055	19.119863	0.34894
Purine nucleoside phosphorylase (EC 2.4.2.1)	918	3409615	3410319	93.75	80.6257102	0.86001
sensory box histidine kinase/response regulator	917	3410367	3413306	64.30758761	85.7997618	1.33421
ABC transporter substrate-binding protein - sugar transport	916	3413321	3414715	93.25681492	73.4253945	0.78735
Tn916, transposase	914	3415105	3416313	12.41721854	6.16225166	0.49627
plasmid partition protein, putative	913	3416316	3417086	3.896103896	6.04220779	1.55083
Chromosome (plasmid) partitioning protein ParB / Stage 0 sporulation protein J	912	3417086	3417949	6.952491309	3.23464658	0.46525
hypothetical protein	911	3418736	3420652	12.52609603	7.77035491	0.62033
hypothetical protein		3420825	3420980	0	6.00322581	#DIV/0!
hypothetical protein	909	3421167	3422387	0	0	#DIV/0!
hypothetical protein	908	3422537	3422725	0	0	#DIV/0!
hypothetical protein	907	3423523	3423699	0	0	#DIV/0!
hypothetical protein	906	3423731	3424570	9.535160906	8.87246722	0.9305
hypothetical protein		3424581	3424718	0	0	#DIV/0!
DNA polymerase III alpha subunit (EC 2.7.7.7)	904	3424743	3427691	21.26917713	21.737622	1.02202
DNA polymerase IV (EC 2.7.7.7)	903	3427684	3428901	27.54590985	31.8451586	1.15608
COG1801: Uncharacterized conserved protein	902	3428904	3429707	36.75538657	25.9455006	0.7059
transcriptional regulator, putative	901	3429819	3430442	14.19878296	28.311359	1.99393
hypothetical protein	900	3430474	3432309	7.629427793	3.04250681	0.39879
hypothetical protein	899	3432400	3433143	1.34589502	0	0
DNA repair protein RadC	898	3433297	3433764	0	0	#DIV/0!
Threonyl-tRNA synthetase (EC 6.1.1.3)	897	3433910	3434833	5.417118093	10.0812568	1.861

hypothetical protein	896	3434933	3435469	0	1.73600746	#DIV/0!
hypothetical protein	895	3435542	3435766	0	0	#DIV/0!
hypothetical protein	894	3435756	3436004	0	0	#DIV/0!
hypothetical protein	893	3436006	3436485	2.087682672	3.88517745	1.861
hypothetical protein	892	3436485	3437363	1.138952164	2.11958998	1.861
hypothetical protein	891	3437378	3437587	0	0	#DIV/0!
hypothetical protein	890	3437587	3437784	10.15228426	0	0
Putative bacteriophage protein	889	3438064	3439125	4.712535344	5.26201697	1.1166
hypothetical protein	888	3439198	3439968	0	0	#DIV/0!
Single-stranded DNA-binding protein	887	3440033	3440428	0	0	#DIV/0!
hypothetical protein	886	3440496	3441326	0	1.12108434	#DIV/0!
hypothetical protein	885	3441316	3441705	0	0	#DIV/0!
hypothetical protein	884	3441809	3442150	5.865102639	5.45747801	0.9305
hypothetical protein	883	3442153	3442344	0	9.7434555	#DIV/0!
hypothetical protein	882	3442357	3442878	0	1.78598848	#DIV/0!
Cell wall-associated hydrolases (invasion-associated proteins)	881	3442866	3443420	0	1.67960289	#DIV/0!
hypothetical protein	880	3443465	3444061	0	0	#DIV/0!
hypothetical protein	879	3444064	3444984	1.086956522	1.01141304	0.9305
hypothetical protein	878	3445160	3445873	0	1.30504909	#DIV/0!
hypothetical protein	876	3445955	3446086	0	0	#DIV/0!
hypothetical protein	877	3446059	3446307	0	0	#DIV/0!
Flagellar hook-length control protein fliK	875	3446448	3448193	2.865329513	3.73266476	1.3027
hypothetical protein	874	3448200	3448658	4.366812227	0	0
hypothetical protein	873	3448655	3448768	0	8.23451327	#DIV/0!
hypothetical protein	872	3448785	3449036	282.8685259	170.52988	0.60286
hypothetical protein	871	3449046	3449276	747.826087	805.084783	1.07657
hypothetical protein	870	3449379	3449582	73.89162562	64.1724138	0.86847
hypothetical protein	869	3449569	3449694	72	37.22	0.51694
Surface proteins containing Ig-like domains-like precursor	868	3449771	3451861	99.5215311	98.3925837	0.98866
Flagellar hook-length control protein fliK		3452127	3455642	83.92603129	70.9456615	0.84534
hypothetical protein	866	3455639	3456160	15.35508637	10.7159309	0.69788
hypothetical protein	865	3456138	3456257	8.403361345	39.0966387	4.6525
Transposase and inactivated derivatives	864	3456361	3456963	3.322259136	0	0
hypothetical protein	863	3457088	3457390	0	0	#DIV/0!
hypothetical protein	862	3457552	3458037	2.06185567	0	0
hypothetical protein	861	3458194	3458379	10.81081081	15.0891892	1.39575
TRAP-type C4-dicarboxylate transport system, periplasmic component	860	3459180	3460193	177.0524233	181.314045	1.02407
TRAP-type transport system, large permease component, predicted N-acetylneuraminate transporter	859	3460190	3462076	80.44752264	78.8223229	0.9798
hypothetical protein	857	3462087	3462908	80.48780488	66.9506098	0.83181
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	858	3462887	3463252	49.31506849	63.7328767	1.29236
Homolog of plant auxin-responsive GH3-like protein	856	3463528	3465228	591.0757946	594.359719	1.00556
FOG: CheY-like receiver	855	3465339	3469112	54.02394876	65.0391256	1.20389
Adenylate kinase (EC 2.7.4.3)	854	3469206	3469841	256.6929134	249.110236	0.97046
Metal transporter, ZIP family	853	3469890	3470699	50.67985167	43.7070457	0.86241
Radical SAM domain protein	852	3470771	3471640	27.61795167	20.344649	0.73665
Capsule biosynthesis protein capA	851	3471819	3473474	74.32024169	87.7087613	1.18015

LSU ribosomal protein L28p	850	3473502	3473693	1397.905759	2153.30366	1.54038
serine protease inhibitor	849	3473802	3474389	359.4548552	380.44293	1.05839
5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	848	3474405	3475019	213.3550489	210.650651	0.98732
hypothetical protein	847	3475041	3475634	32.04047218	32.9519393	1.02845
Conserved domain protein	846	3475644	3475949	9.836065574	21.3557377	2.17117
hypothetical protein	845	3476052	3476207	6.451612903	0	0
Transcriptional regulator, HxlR family	843	3476161	3476523	74.58563536	84.8245856	1.13728
Acyl-ACP thioesterase	844	3476520	3477263	59.21938089	51.346568	0.86706
hypothetical protein	842	3477305	3478495	28.57142857	31.2773109	1.09471
hypothetical protein	841	3478495	3481254	35.15766582	22.5964117	0.64272
Mg-protoporphyrin IX monomethyl ester oxidative cyclase	840	3481408	3482922	37.64861295	49.1677675	1.30596
Putative 5'(3')-deoxyribonucleotidase (EC 3.1.3.-)	839	3482927	3483556	115.5698234	156.825843	1.35698
Glycogen debranching enzyme (EC 3.2.1.-)	838	3483572	3485725	123.5485369	131.385044	1.06343
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	837	3485735	3486571	31.10047847	32.27811	1.03787
Cystathionine beta-lyase (EC 4.4.1.8)	836	3486570	3487823	196.3288109	235.409816	1.19906
Methionine ABC transporter substrate-binding protein		3487923	3488324	92.26932668	139.226933	1.50892
Methionine ABC transporter substrate-binding protein		3488353	3488733	42.10526316	51.4223684	1.22128
Methionine ABC transporter ATP-binding protein	833	3488803	3489852	13.34604385	9.75738799	0.73111
Methionine ABC transporter permease protein	832	3489845	3490525	8.823529412	15.0522059	1.70592
N-acetyl-L,L-diaminopimelate deacetylase homolog (EC 3.5.1.18)	831	3490539	3491702	23.21582115	27.2029235	1.17174
putative peptide transport system secreted peptide-binding protein	830	3491838	3493442	278.6783042	361.990025	1.29895
Aspartyl aminopeptidase	829	3493607	3495016	50.39034776	46.8882186	0.9305
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	828	3495034	3496026	38.30645161	57.218246	1.4937
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	827	3496029	3497054	67.44868035	92.7771261	1.37552
Oligopeptide ABC transporter, permease	826	3497044	3497982	23.45415778	24.8001066	1.05739
Putative glutathione transporter, permease component	825	3497979	3499025	40.15296367	56.043499	1.39575
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	824	3499205	3500671	150.7503411	211.996589	1.40628
hypothetical protein	823	3500668	3500892	58.03571429	33.2321429	0.57262
Conserved protein	822	3500889	3501371	49.79253112	40.5404564	0.81419
hypothetical protein	821	3501368	3501619	43.8247012	33.3645418	0.76132
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	820	3501621	3502736	48.43049327	43.3955157	0.89604
Tyrosine recombinase xerC	819	3502796	3503788	26.20967742	20.6360887	0.78735
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	818	3503811	3504440	11.12877583	7.39666137	0.66464
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	817	3504553	3507948	13.25478645	18.637408	1.40609
hypothetical protein		3508101	3508295	56.70103093	43.1675258	0.76132
hypothetical protein	815	3508396	3508671	65.45454545	81.2072727	1.24067

hypothetical protein		3509185	3509301	0	0	#DIV/0!
hypothetical protein	813	3509482	3510456	105.7494867	59.2310062	0.56011
hypothetical protein	812	3510473	3511777	64.41717791	56.372316	0.87511
Leucine-rich repeat containing protein	811	3511948	3513660	7.009345794	3.26109813	0.46525
hypothetical protein	810	3513731	3514150	2.386634845	0	0
hypothetical protein	809	3514418	3516091	3.586371787	1.11237298	0.31017
Aerobic cobaltochelatase cobS subunit (EC 6.6.1.2)	808	3516109	3517284	1.70212766	7.91914894	4.6525
hypothetical protein		3517425	3517550	8	29.776	3.722
Uncharacterized protein TP_0783	805	3518008	3519222	112.0263591	124.168863	1.10839
T. pallidum predicted coding region TP0782	804	3519225	3520088	159.9073001	160.654114	1.00467
Methyltransferase/methylase	803	3520095	3520979	57.69230769	84.2081448	1.45961
Na+-driven multidrug efflux pump	802	3520995	3522365	24.08759124	30.5638686	1.26886
Phosphoglycolate phosphatase (EC 3.1.3.18)	801	3522364	3523098	100.8174387	102.684605	1.01852
hypothetical protein	800	3523106	3523417	38.585209	74.7990354	1.93854
COG2078: Uncharacterized ACR	799	3523456	3524031	85.2173913	129.46087	1.51918
Branched-chain amino acid transport protein	798	3524073	3524807	54.49591281	57.0470027	1.04681
branched-chain amino acid transport	797	3524800	3525159	41.78272981	57.0222841	1.36473
ABC transporter permease protein	796	3525217	3525987	46.75324675	45.9207792	0.98219
Putative ABC transporter ATP-binding protein	795	3525995	3526732	122.1166893	111.104478	0.90982
ABC transporter substrate binding protein (EC 2.5.1.47)	794	3526729	3527772	104.506232	72.2631831	0.69147
Tetratricopeptide TPR_2	793	3527800	3528732	101.9313305	97.8422747	0.95988
biphenyl-2,3-diol 1,2-dioxygenase III-related protein	791	3528734	3529123	43.70179949	45.4485861	1.03997
hypothetical protein	792	3529101	3529274	5.780346821	21.5144509	3.722
hypothetical protein	790	3529318	3530232	73.30415755	58.0289934	0.79162
hypothetical protein	789	3530261	3530425	170.7317073	107.801829	0.63141
hypothetical protein		3530451	3530573	65.57377049	160.168033	2.44256
hypothetical protein		3530755	3531003	92.74193548	161.336694	1.73963
cell surface protein	786	3531013	3531891	23.91799544	21.1958998	0.88619
hypothetical protein	785	3532306	3532704	7.537688442	4.6758794	0.62033
hypothetical protein	784	3532701	3532910	9.56937799	4.45215311	0.46525
hypothetical protein	783	3533243	3533470	8.810572687	4.09911894	0.46525
hypothetical protein	782	3533647	3534048	149.6259352	116.022444	0.77542
Alanyl-tRNA synthetase (EC 6.1.1.7)	781	3534187	3535977	312.886888	348.217501	1.11292
Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8)	780	3536041	3537399	381.443299	404.952504	1.06163
Transcription termination protein NusB	779	3537403	3537909	243.083004	163.66502	0.67329
hypothetical protein	778	3537906	3539639	61.74264282	90.7412002	1.46967
hypothetical protein	777	3539687	3540295	164.4736842	131.616776	0.80023
Enolase (EC 4.2.1.11)	776	3540528	3541829	850.5836576	966.706226	1.13652
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	775	3541911	3542084	5.780346821	0	0
Phage-related protein	774	3542127	3542432	72.13114754	15.2540984	0.21148
Cro repressor helix-turn-helix motif:Helix-turn-helix motif	773	3542419	3542706	125.4355401	64.8432056	0.51694
hypothetical protein		3542927	3543043	51.72413793	16.0431034	0.31017
hypothetical protein	770	3543423	3545093	144.5710858	108.846731	0.75289
hypothetical protein	769	3545109	3545381	80.88235294	68.4191176	0.84591
Lipoprotein signal peptidase (EC 3.4.23.36)	768	3545365	3545919	138.9891697	142.766245	1.02718

Hypothetical protein ybgI	767	3545931	3546692	128.7779238	106.377792	0.82606
hypothetical protein	766	3546689	3548152	24.60697198	50.245728	2.04193
Uncharacterized protein TP_0073	765	3548295	3549785	117.6075269	127.568548	1.0847
RNA-binding protein	764	3549927	3550196	2501.858736	2577.03532	1.03005
hypothetical protein		3550197	3550334	781.0218978	482.229927	0.61743
hypothetical protein	763	3550294	3550488	231.9587629	47.9639175	0.20678
RNA-binding protein		3550991	3551206	9730.232558	8937.12791	0.91849
hypothetical protein	760	3551312	3551680	187.5	209.868207	1.1193
hypothetical protein	759	3551682	3552263	86.05851979	120.116179	1.39575
unknown	758	3552264	3553262	190.3807615	178.081663	0.9354
unknown	757	3553326	3554957	69.28264868	94.1339669	1.35869
Methylcobalamin:coenzyme M methyltransferase, methanol-specific	756	3555023	3556060	20.25072324	32.3027965	1.59514
Dimethylamine corrinoid protein 2	755	3556057	3556752	97.84172662	73.6366906	0.75261
Conserved protein	754	3556786	3557361	38.26086957	29.1286957	0.76132
Methylcobalamin:coenzyme M methyltransferase, methanol-specific	753	3557362	3558390	39.88326848	31.6804475	0.79433
hypothetical protein	752	3558501	3558662	0	0	#DIV/0!
hypothetical protein	751	3558743	3558886	139.8601399	65.0699301	0.46525
Outer membrane autotransporter barrel	750	3558879	3561737	251.9244227	281.624388	1.11789
ATP-dependent DNA helicase pcrA (EC 3.6.1.-)	749	3561838	3565197	27.99285289	31.3122394	1.11858
Deoxyribonuclease-1 precursor (EC 3.1.21.1)	748	3565216	3566082	24.24942263	18.2661663	0.75326
hypothetical protein	747	3566095	3570063	17.64112903	8.6765373	0.49184
Nitroreductase	746	3570177	3570791	4.885993485	15.1547231	3.10167
Iron-sulfur cluster-binding protein	745	3570944	3571783	0	3.32717521	#DIV/0!
Rrf2 family transcriptional regulator, group III	744	3571979	3572464	37.11340206	42.2082474	1.13728
hypothetical protein	743	3572496	3572831	41.79104478	13.8880597	0.33232
Gsl2900 protein	742	3572877	3573077	0	0	#DIV/0!
hypothetical protein	741	3573165	3573452	48.7804878	32.4216028	0.66464
hypothetical protein	740	3573528	3574283	5.298013245	2.46490066	0.46525
hypothetical protein	739	3574349	3574747	2.512562814	2.3379397	0.9305
Transposase	738	3574869	3575924	26.54028436	22.049763	0.8308
hypothetical protein		3576080	3576268	0	0	#DIV/0!
hypothetical protein		3576358	3576567	63.7254902	77.5416667	1.21681
Glycyl-tRNA synthetase (EC 6.1.1.14)	735	3576708	3578096	335.0144092	351.954251	1.05056
Acylphosphate phosphohydrolase (EC 3.6.1.7), putative	734	3578109	3578405	91.21621622	100.594595	1.10281
Putative sugar transporter	733	3578415	3579758	47.65450484	47.1139241	0.98866
Exonuclease SbcC	731	3580249	3583431	21.68447517	30.7047454	1.41598
Exonuclease SbcD	730	3583428	3584693	12.64822134	11.0335968	0.87234
Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3)	729	3584819	3585832	6495.557749	7106.88894	1.09412
Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17)	728	3585909	3587423	308.4544254	290.089828	0.94046
Galactose/methyl galactoside ABC transport system, permease protein MglC (TC 3.A.1.2.3)	727	3587438	3588478	274.0384615	294.360096	1.07416
Multidrug resistance ABC transporter ATP-binding and permease protein	726	3588582	3590372	50.98039216	51.0862745	1.00208
Flavodoxin	725	3590474	3590953	121.085595	141.808977	1.17115

amino acid ABC transporter, ATP-binding protein	724	3591057	3591812	84.76821192	60.3900662	0.71241
Amino acid ABC transporter, amino acid-binding/permease protein	723	3591799	3592488	75.47169811	76.978955	1.01997
Amino acid ABC transporter, amino acid-binding/permease protein	722	3592509	3593330	322.7771011	369.479903	1.14469
S-adenosylhomocysteine deaminase (EC 3.5.4.28); Methylthioadenosine deaminase	721	3593374	3594570	56.02006689	76.2449833	1.36103
Ferredoxin	720	3594563	3595330	67.79661017	67.9374185	1.00208
creatininase (EC 3.5.2.10)	719	3595330	3596142	118.226601	121.469212	1.02743
Ig domain protein, group 2 domain protein		3596365	3598536	395.2095808	519.468448	1.31441
Cell division protein ftsJ / Ribosomal RNA large subunit methyltransferase J (EC 2.1.1.-)	717	3598610	3599254	97.82608696	130.03882	1.32929
Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltranstransferase (EC 2.5.1.10) / Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29)	716	3599307	3600359	119.7718631	112.332224	0.93788
hypothetical protein	715	3600370	3600966	379.1946309	346.595638	0.91403
Membrane proteins related to metalloendopeptidases	714	3601000	3602013	187.5616979	290.264561	1.54757
Cell division protein ftsK	713	3602036	3604147	82.89909995	55.539081	0.66996
hypothetical protein	712	3604228	3604353	0	0	#DIV/0!
NADH oxidase H2O-forming (EC 1.6.-.-)	711	3604403	3605737	1413.793103	1780.08696	1.25909
hypothetical protein	710	3605785	3606852	99.34395501	163.949391	1.65032
Deblocking aminopeptidase (EC 3.4.11.-)	709	3606861	3607937	223.9776952	370.989312	1.65637
creatininase (EC 3.5.2.10)	708	3607958	3608725	366.3624511	594.452412	1.62258
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	707	3608782	3610314	413.8381201	802.951044	1.94025
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	706	3610360	3611316	142.2594142	262.798117	1.84732
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	705	3611313	3612347	282.3984526	427.454062	1.51366
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	704	3612355	3613236	196.3677639	251.372304	1.28011
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	703	3613233	3614195	119.5426195	92.8565489	0.77677
Uracil-DNA glycosylase (EC 3.2.2.-)	702	3614584	3615585	28.97102897	28.8166833	0.99467
Putative DNA-binding protein	701	3615582	3616145	10.65719361	6.61101243	0.62033
Oxidoreductase	700	3616142	3617185	28.76318313	56.204698	1.95405
Methyl-accepting chemotaxis protein	699	3617238	3619388	68.93339544	69.7766651	1.01223
hypothetical protein	697	3619341	3619496	64.51612903	72.0387097	1.1166
Signal transduction histidine kinase	698	3619477	3621171	104.4864227	114.252656	1.09347
hypothetical protein	696	3621219	3622382	122.9578676	122.413156	0.99557
hypothetical protein	694	3622768	3622908	171.4285714	352.260714	2.05485
hypothetical protein	693	3622918	3623625	274.3988685	371.1471	1.35258
Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)	692	3623640	3624923	62.35385814	50.7677319	0.81419
hypothetical protein		3625001	3625606	176.8595041	141.497521	0.80006
hypothetical protein	690	3625618	3626850	160.7142857	200.903409	1.25007
hypothetical protein	689	3626856	3627440	246.5753425	181.638699	0.73665

anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	688	3627464	3627802	109.4674556	101.859467	0.9305
HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)	687	3627967	3628974	144.9851043	194.970705	1.34476
Catabolite repression HPr-like protein Crh	686	3628991	3629257	180.4511278	167.909774	0.9305
Nitrogen regulation protein ntrY (EC 2.7.3.-)	685	3629271	3631067	93.54120267	89.6305679	0.95819
Two component signal transduction response regulator	684	3631064	3632449	104.6931408	83.3083032	0.79574
SOS-response repressor and protease LexA (EC 3.4.21.88)	683	3632446	3633066	87.09677419	81.0435484	0.9305
DNA polymerase III delta subunit (EC 2.7.7.7)	682	3633074	3634042	83.67768595	119.196281	1.42447
Na+/H+ antiporter	681	3634062	3636128	8.712487899	23.4201355	2.68811
Purine nucleoside phosphorylase (EC 2.4.2.1)	680	3636375	3637187	8.620689655	3.43780788	0.39879
Biotin synthase-related enzyme	679	3637291	3638487	13.37792642	4.6680602	0.34894
hypothetical protein		3638532	3638645	8.849557522	0	0
Radical SAM domain protein	677	3638678	3639934	5.573248408	3.70421975	0.66464
Radical SAM domain protein	676	3640074	3641318	1.607717042	0.74799035	0.46525
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	675	3641340	3642317	2.047082907	1.90481064	0.9305
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	674	3642310	3643341	0	0	#DIV/0!
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	673	3643341	3644273	2.145922747	0.99839056	0.46525
Binding-protein-dependent transport systems inner membrane component	672	3644307	3645257	1.052631579	0.97947368	0.9305
ABC transporter peptide-binding protein	671	3645321	3646907	1.891551072	0	0
COG1092 family predicted tRNA methylase	670	3647261	3648622	102.1307862	86.1447465	0.84347
Polyphosphate kinase (EC 2.7.4.1)	669	3648628	3650829	139.7260274	96.4490868	0.69027
Exopolyphosphatase (EC 3.6.1.11)	668	3650860	3652398	96.22886866	54.4505852	0.56584
Trehalase (EC 3.2.1.28)	667	3652402	3653826	185.8657244	186.757597	1.0048
hypothetical protein		3653920	3654069	100.6711409	93.6744966	0.9305
Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-)	665	3654073	3656622	95.33150255	137.256964	1.43979
Uncharacterized protein TP_1003	664	3656676	3657524	70.75471698	109.728774	1.55083
Prolyl-tRNA synthetase (EC 6.1.1.15)	663	3657613	3659478	253.0831099	305.3437	1.2065
hypothetical protein	662	3659510	3659800	68.96551724	35.2948276	0.51178
hypothetical protein	661	3659824	3660540	32.12290503	27.2912011	0.84959
Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	660	3660546	3661373	24.18379686	18.0024184	0.7444
Spermidine Putrescine transport ATP-binding protein potA (TC_3.A.1.11.1)	659	3661382	3662446	16.91729323	3.4981203	0.20678
Ferric iron ABC transporter, permease protein	658	3662488	3664149	9.030704395	2.80102348	0.31017
Ferric iron ABC transporter, iron-binding protein	657	3664210	3665265	11.37440758	7.93791469	0.69788
Short chain dehydrogenase	656	3665304	3666080	37.37113402	4.79639175	0.12834
Xylulose kinase (EC 2.7.1.17)	655	3666099	3667622	22.98095863	11.6083388	0.50513
hypothetical protein	654	3667715	3667828	0	0	#DIV/0!
Modification methylase PstI (EC 2.1.1.72)	653	3667779	3668837	3.780718336	13.192344	3.48938
Type II restriction enzyme BsuBI (EC 3.1.21.4)	652	3668937	3669338	0	0	#DIV/0!
Ribose operon repressor	651	3669382	3670476	21.93784278	34.8724863	1.5896
Outer membrane protein A precursor	650	3670577	3671506	643.7029064	616.994618	0.95851

Pyruvate kinase (EC 2.7.1.40)	649	3671619	3673412	89.23591746	92.8943112	1.041
Excinuclease ABC subunit B	648	3673499	3675490	102.963335	118.240331	1.14837
hypothetical protein	647	3675671	3676234	948.4902309	1216.42629	1.28249
hypothetical protein	646	3676334	3677143	80.3461063	28.7546354	0.35788
hypothetical protein	645	3677187	3678344	36.30077787	32.1694036	0.88619
hypothetical protein	644	3678461	3679972	26.47253475	47.4179351	1.79121
TolA protein	643	3680035	3681294	40.50833995	37.6930103	0.9305
hypothetical protein		3681307	3681543	0	0	#DIV/0!
putative histidinol phosphatase and related hydrolases of the PHP family	641	3681698	3682432	28.61035422	39.2990463	1.3736
Chorismate synthase (EC 4.2.3.5)	640	3682513	3683697	69.25675676	88.8061655	1.28227
GTP-binding protein HflX	639	3683761	3685104	102.7550261	99.7706627	0.97096
ClpB protein	638	3685111	3687729	29.43425076	78.2530581	2.65857
Arsenical-resistance protein ACR3	637	3687811	3688800	12.13346815	15.9944388	1.31821
radical SAM domain protein	636	3688904	3690136	629.0584416	937.297484	1.49
UDP-glucose:sterol glucosyltransferase	635	3690133	3691356	285.3638594	493.781276	1.73036
UDP-glucose:sterol glucosyltransferase	633	3691369	3692631	288.4310618	482.208399	1.67183
Aspartate aminotransferase (EC 2.6.1.1)	634	3692603	3693778	62.12765957	65.7289362	1.05797
Iron-sulfur cluster regulator IscR	632	3693797	3694231	119.8156682	68.6082949	0.57262
Iron-sulfur cluster regulator IscR	631	3694228	3694662	71.42857143	72.8963134	1.02055
Cystathionine gamma-synthase (EC 2.5.1.48)	630	3694813	3696045	86.03896104	94.4094968	1.09729
Cystathionine beta-lyase (EC 4.4.1.8)	629	3696055	3697200	200	203.978603	1.01989
hypothetical protein		3697390	3697782	86.73469388	144.797194	1.66943
Ferrous iron transport protein B	627	3697769	3699934	76.35009311	110.464385	1.44681
hypothetical protein	626	3700288	3701397	9.017132552	5.87330929	0.65135
ADP-ribose pyrophosphatase (EC 3.6.1.13)	625	3701398	3701871	8.456659619	19.6723044	2.32625
hypothetical protein	624	3701959	3702798	35.7568534	18.8539928	0.52728
hypothetical protein	623	3702811	3703653	15.43942993	4.42042755	0.28631
phage tail assembly-like protein	622	3703664	3704242	6.920415225	3.21972318	0.46525
Transcriptional regulator, DeoR family	621	3704358	3705389	5.819592629	3.61008729	0.62033
hypothetical protein		3705357	3705491	0	0	#DIV/0!
hypothetical protein	618	3705845	3706693	0	0	#DIV/0!
putative lipoprotein	617	3706705	3708108	4.989308624	2.65288667	0.53171
sensory box histidine kinase/response regulator	616	3708286	3710994	40.25110783	51.5417282	1.2805
Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	615	3711025	3712401	122.0930233	111.578852	0.91388
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	614	3712405	3713472	151.8275539	167.437676	1.10281
Oligoendopeptidase F	613	3713564	3715447	152.4163569	147.753319	0.96941
Nucleoside diphosphate kinase (EC 2.7.4.6)	612	3715431	3715874	178.3295711	197.442438	1.10718
Fe-S OXIDOREDUCTASE (1.8.-.-)	611	3715934	3717775	41.281912	77.3310701	1.87324
Thioredoxin-like proteins and domains	610	3717765	3717989	549.1071429	942.962054	1.71726
Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, alpha subunit (EC 2.7.1.90)	608	3718180	3719538	231.9587629	267.227541	1.15205
hypothetical protein	609	3719535	3720398	63.73117034	69.0057937	1.08276
hypothetical tRNA/rRNA methyltransferase yfiF [EC:2.1.1.-]	607	3720400	3721176	104.3814433	122.30799	1.17174
VapC toxin protein	606	3721205	3721600	30.37974684	9.42278481	0.31017
Virulence associated protein B	605	3721600	3721875	105.4545455	37.22	0.35295

Endonuclease/exonuclease/phosphatase family protein	604	3722016	3723242	10.60358891	6.07177814	0.57262
Cytidylate kinase (EC 2.7.4.14)	603	3723335	3724156	388.5505481	372.880024	0.95967
ADP-ribose pyrophosphatase (EC 3.6.1.13)	601	3724282	3724866	97.60273973	146.585616	1.50186
Treponemal membrane protein B precursor (Antigen tmpB)	602	3724848	3725576	348.9010989	217.287088	0.62278
Treponemal membrane protein A precursor (Antigen tmpA) (Membrane protein A)	600	3725573	3726742	319.9315654	238.793841	0.74639
bacterial seryl-tRNA synthetase related	599	3726911	3727141	86.95652174	121.369565	1.39575
Ribonuclease HI (EC 3.1.26.4)	598	3727145	3727591	210.7623318	233.668161	1.10868
Oxidoreductase	597	3727635	3728633	143.2865731	160.366733	1.1192
Heat shock protein 60 family chaperone GroEL	596	3728822	3730468	1335.423197	3105.94483	2.32581
Transcriptional regulator, GntR family	595	3730643	3731392	42.72363151	42.2389853	0.98866
TRAP-type C4-dicarboxylate transport system, periplasmic component	594	3731498	3732508	76.84630739	103.079341	1.34137
TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter	593	3732591	3733097	19.76284585	25.7450593	1.3027
TRAP-type C4-dicarboxylate transport system, large permease component	592	3733108	3734403	37.83783784	33.7710425	0.89252
Mannonate dehydratase (EC 4.2.1.8)	591	3734424	3735491	27.17900656	51.4522024	1.89309
D-mannonate oxidoreductase (EC 1.1.1.57)	590	3735516	3737141	35.07692308	24.6224615	0.70196
Uronate isomerase (EC 5.3.1.12)	589	3737155	3738627	30.57065217	30.9745245	1.01321
4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	588	3738611	3739591	48.97959184	42.7270408	0.87234
2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	587	3739737	3740759	67.5146771	47.3444227	0.70125
Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like domain, possible membrane copper tolerance protein	586	3740836	3741630	20.1511335	10.5472292	0.52341
hypothetical protein	585	3741657	3742364	32.53182461	19.741867	0.60685
Copper-translocating P-type ATPase (EC 3.6.3.4)	584	3742384	3744840	48.45276873	54.5570033	1.12598
Copper chaperone	583	3744866	3745066	385	428.03	1.11177
Two-component response regulator SA14-24	582	3745063	3745791	170.3296703	177.664148	1.04306
two-component sensor histidine kinase	581	3745788	3747194	61.87766714	53.60633	0.86633
hypothetical protein	580	3747212	3747877	6.015037594	12.5932331	2.09363
hypothetical protein	579	3747897	3749174	0	1.45732185	#DIV/0!
hypothetical protein	578	3749177	3749725	0	3.3959854	#DIV/0!
Large exoproteins involved in heme utilization or adhesion	577	3749739	3751307	1.275510204	2.96715561	2.32625
Bacterial regulatory proteins, AsnC family	576	3751484	3751720	0	0	#DIV/0!
Putative preQ0 transporter	574	3751806	3752531	24.82758621	19.2517241	0.77542
hypothetical protein	575	3752528	3753235	45.26166902	36.8514851	0.81419
Dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis family 1	573	3753212	3754069	51.34189032	56.4597433	1.09968
tRNA(Cytosine32)-2-thiocytidine synthetase	572	3754062	3754808	21.44772118	26.1936997	1.22128
hypothetical protein	571	3754840	3755685	153.8461538	203.718935	1.32417

ABC transporter, periplasmic spermidine putrescine-binding protein potD (TC_3.A.1.11.1)	570	3755719	3756759	336.5384615	807.924519	2.40069
Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	569	3756829	3757695	20.7852194	49.426097	2.37794
Spermidine Putrescine ABC transporter permease component potB (TC_3.A.1.11.1)	568	3757692	3758525	26.41056423	78.1932773	2.96068
Spermidine Putrescine transport ATP-binding protein potA (TC_3.A.1.11.1)	567	3758573	3759751	176.3202726	268.687819	1.52386
Lysine 2,3-aminomutase (EC 5.4.3.2)	566	3759958	3761019	32.98774741	76.299246	2.31296
transcriptional regulator (AraC/XylS family)	565	3761177	3762130	15.73976915	15.6222455	0.99253
hypothetical protein		3762186	3762326	14.28571429	0	0
hypothetical protein	563	3762340	3762726	0	9.64248705	#DIV/0!
Galactoside O-acetyltransferase (EC 2.3.1.18)	562	3762728	3763336	6.578947368	6.12171053	0.9305
Acetylornithine deacetylase (EC 3.5.1.16)	561	3763474	3764733	149.324861	184.03058	1.23242
UDP-glucose 4-epimerase (EC 5.1.3.2)	560	3764770	3765741	128.7332647	154.284758	1.19848
internalin-like protein (LPXTG motif)	559	3765949	3767010	61.26295947	42.9731385	0.70145
N-Acetylneuraminate cytidylyltransferase (EC 2.7.7.43)	558	3767280	3768047	15.64537158	10.9185137	0.69788
hypothetical protein	557	3768338	3768670	57.22891566	72.8704819	1.27332
COG0488: ATPase components of ABC transporters with duplicated ATPase domains	556	3768778	3770886	145.1612903	139.928131	0.96395
Uncharacterized protein TP_0260		3770893	3772287	177.1879484	179.558465	1.01338
hypothetical protein		3772441	3773052	353.5188216	400.526187	1.13297
Glutaminyl-tRNA synthetase (EC 6.1.1.18)	553	3773232	3774950	185.3146853	182.738054	0.9861
Tributyrin esterase	552	3774960	3775745	192.3566879	148.16879	0.77028
Ferredoxin	551	3775814	3776944	494.6902655	551.712389	1.11527
Outer membrane protein	550	3776988	3778388	70.71428571	93.7146429	1.32526
Probable Co/Zn/Cd efflux system membrane fusion protein	549	3778435	3779532	71.1030082	96.6973564	1.35996
RND multidrug efflux transporter; Acriflavin resistance protein	547	3779529	3782648	42.32125681	52.5065726	1.24067
Outer membrane vitamin B12 receptor BtuB	548	3782645	3784615	24.36548223	13.6977157	0.56218
Cobalamin synthase	546	3784647	3785495	58.96226415	31.8213443	0.53969
Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)	545	3785492	3786538	326.0038241	225.953155	0.6931
hypothetical protein	544	3786540	3787355	77.3006135	42.2435583	0.54648
Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	543	3787352	3787882	126.4150943	61.4481132	0.48608
Nitrogenase vanadium-cofactor synthesis protein VnfN	542	3787896	3789197	98.38585703	58.6479631	0.5961
Nitrogenase iron protein (EC 1.18.6.1)	541	3789166	3791367	112.2217174	54.5363471	0.48597
Vitamin B12 ABC transporter, ATPase component BtuD	540	3791360	3792169	129.789864	93.1650185	0.71781
Vitamin B12 ABC transporter, permease component BtuC	539	3792179	3793192	110.5626851	63.3805528	0.57325
Vitamin B12 ABC transporter, B12-binding component BtuF	538	3793179	3794081	95.34368071	49.5166297	0.51935
Outer membrane vitamin B12 receptor BtuB	537	3794074	3796101	192.4025654	86.301924	0.44855
hypothetical protein	536	3796129	3796686	879.7127469	292.347397	0.33232
hypothetical protein		3796685	3796810	328	89.328	0.27234
Cobyric acid synthase	534	3797135	3798589	54.33287483	77.4350069	1.4252

Vitamin B12 ABC transporter, ATPase component BtuD	533	3798679	3799491	48.02955665	34.3780788	0.71577
Vitamin B12 ABC transporter, permease component BtuC	532	3799488	3800570	51.75600739	20.6395564	0.39879
Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	531	3800567	3801205	235.1097179	51.0462382	0.21712
Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	530	3801205	3801708	105.3677932	33.2982107	0.31602
Cobyric acid synthase	529	3801705	3803180	109.1525424	54.2528814	0.49704
L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	528	3803164	3804219	60.66350711	22.049763	0.36348
Adenosylcobinamide-phosphate synthase	527	3804180	3805169	45.50050556	11.2901921	0.24813
Cobyrinic acid A,C-diamide synthase	526	3805166	3806659	97.11989283	24.9296718	0.25669
Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-) / Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-)	525	3806656	3807915	76.25099285	25.8677522	0.33924
Cobalt-precorrin-6x reductase (EC 1.3.1.54)		3807912	3808658	95.17426273	24.9463807	0.26211
Cobalt-precorrin-3b C17-methyltransferase	523	3808651	3809382	80.71135431	26.7311902	0.33119
Cobalamin biosynthesis protein CbiG	522	3809375	3810166	99.87357775	15.2926675	0.15312
Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	521	3810163	3810915	98.40425532	19.7978723	0.20119
Cobalt-precorrin-6 synthase, anaerobic	520	3810912	3812117	131.120332	28.5713693	0.2179
Ferric siderophore transport system, periplasmic binding protein TonB	519	3812121	3812810	136.4296081	33.7626996	0.24747
TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins	518	3812807	3814774	82.86731063	22.2336045	0.2683
hypothetical protein		3814928	3815041	44.24778761	49.4070796	1.1166
Sirohydrochlorin cobaltochelatase CbiK (EC 4.99.1.3)	516	3815334	3816242	286.3436123	75.8337004	0.26483
Vitamin B12 ABC transporter, B12-binding component BtuF	515	3816239	3817198	46.92387904	14.5542231	0.31017
Uroporphyrinogen-III decarboxylase	514	3817849	3818976	106.4773736	51.1898846	0.48076
NAD-dependent protein deacetylase of SIR2 family	513	3819053	3819937	23.75565611	21.0520362	0.88619
DNA integration/recombination/invertion protein	512	3819927	3820472	55.04587156	34.146789	0.62033
Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)	511	3820568	3821197	55.64387917	69.5286169	1.24953
Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)	510	3821172	3823499	168.8869789	176.343146	1.04415
hypothetical protein	509	3823691	3824722	55.28612997	49.6387003	0.89785
hypothetical protein	508	3824729	3826816	206.9956876	207.768567	1.00373
LSU ribosomal protein L34p	506	3827190	3827345	464.516129	456.245161	0.98219
Ribonuclease P protein component (EC 3.1.26.5)	505	3827369	3827773	544.5544554	472.159653	0.86706
YidD	504	3827773	3827991	743.1192661	798.181193	1.0741
OxaI/YidC membrane insertion protein	503	3828031	3829833	265.2608213	285.036626	1.07455
Jag protein	502	3829894	3830634	260.8108108	267.833108	1.02692
hypothetical protein	501	3830809	3832380	77.65754297	78.7756206	1.0144
hypothetical protein		3832735	3832950	153.4883721	216.395349	1.40985
Putative RNA 2'-O-ribose methyltransferase mtfA (EC 2.1.1.-)	499	3832925	3833911	42.59634888	60.3975659	1.4179

Methyltransferase (EC 2.1.1.-); N6-adenine-specific DNA methylase	498	3833951	3835174	94.84873262	120.972608	1.27543
Fatty acid degradation regulator YsiA, TetR family	497	3835197	3835793	117.4496644	115.531879	0.98367
hypothetical protein	496	3835964	3836737	107.373868	131.208926	1.22198
methyl-accepting chemotaxis protein	495	3836808	3838976	5.073800738	3.43357934	0.67673
Methyl-accepting chemotaxis protein	494	3839225	3841393	747.2324723	730.494004	0.9776
Methyl-accepting chemotaxis protein	493	3841427	3843610	486.2258953	392.621442	0.80749
Putative transport protein	492	3843792	3844985	35.20536463	35.8784577	1.01912
Sua5 YciO YrdC YwlC family protein	491	3845071	3846159	51.47058824	88.089614	1.71146
Magnesium and cobalt transport protein CorA	490	3846170	3847243	130.4753029	115.336906	0.88398
PTS system, fructose-specific IIA component (EC 2.7.1.69)	489	3847339	3847791	836.2831858	494.070796	0.59079
hypothetical protein	488	3847892	3849109	798.6852917	872.391537	1.09228
hypothetical protein	487	3849138	3849962	1728.15534	1722.10255	0.9965
hypothetical protein	485	3850095	3851981	49.84093319	51.8040827	1.03939
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	486	3851945	3852673	57.69230769	85.6366758	1.48437
Sua5 YciO YrdC YwlC family protein	484	3852824	3853507	96.63250366	140.324305	1.45214
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	483	3853525	3855282	396.1297666	407.259249	1.0281
hypothetical protein	482	3855376	3855495	50.42016807	31.2773109	0.62033
hypothetical protein		3855453	3855569	17.24137931	8.02155172	0.46525
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	480	3855803	3857287	173.8544474	149.231132	0.85837
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	479	3857304	3858221	25.08178844	36.5299891	1.45643
Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	478	3858223	3859062	27.4135876	33.2717521	1.2137
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	477	3859074	3860072	30.06012024	20.512024	0.68237
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	476	3860069	3860899	30.12048193	31.3903614	1.04216
hypothetical protein	475	3860892	3861875	22.38046796	10.4125127	0.46525
Conserved domain protein	474	3861899	3862948	78.16968541	56.7702574	0.72624
Xaa-Pro dipeptidase (EC 3.4.13.9)	473	3862966	3864156	57.14285714	34.405042	0.60209
Anaerobic dimethyl sulfoxide reductase chain A (EC 1.8.99.-)	472	3864168	3867005	28.55128657	41.3264011	1.44744
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	471	3867157	3867873	19.55307263	5.19832402	0.26586
Beta-glucosidase (EC 3.2.1.21); 6-phospho-beta-glucosidase (EC 3.2.1.86)	470	3867885	3869324	11.81375956	8.40618485	0.71156
Protein tyrosine/serine phosphatase	469	3869350	3870189	10.72705602	12.1996424	1.13728
PTS system, cellobiose-specific IIC component (EC 2.7.1.69)	468	3870191	3871429	10.50080775	14.2806947	1.35996
PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	467	3871453	3871749	23.64864865	12.5743243	0.53171
PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	466	3871746	3872075	48.63221884	31.1109422	0.63972
NtrC family Transcriptional regulator, ATPase domain	465	3872251	3875004	20.3414457	23.3216491	1.14651

Catabolite repression HPr-like protein Crh	464	3875067	3875333	22.55639098	13.9924812	0.62033
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	463	3875335	3876948	26.6584005	25.9593924	0.97378
N-Acetylneuraminate cytidylyltransferase (EC 2.7.7.43)	462	3877077	3877883	11.1662531	8.08126551	0.72372
D-serine dehydratase (EC 4.3.1.18)	461	3878007	3879362	127.6752768	159.318081	1.24784
Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	460	3879405	3881126	185.3146853	215.815268	1.16459
Uncharacterized protein TP_0983 precursor	459	3881265	3881951	24.78134111	52.9001458	2.13468
hypothetical protein	458	3882029	3882406	0	0	#DIV/0!
hypothetical protein	457	3882409	3882678	0	0	#DIV/0!
Tryptophan synthase beta chain like (EC 4.2.1.20)	456	3882792	3884171	151.5591008	624.156998	4.11824
Rhomboid family protein	455	3884256	3884885	39.74562798	44.3799682	1.1166
diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	454	3884898	3885956	120.9829868	100.261815	0.82873
tRNA dihydrouridine synthase B (EC 1.-.-.-)	453	3886021	3886998	65.50665302	65.7159672	1.0032
Putative deoxyribonuclease YcfH	452	3886999	3887835	228.4688995	183.651316	0.80384
fructose response regulator of fruA and EII fructose/mannose	451	3888013	3888687	194.3620178	154.623145	0.79554
Probable peptidyl-prolyl cis-trans isomerase	450	3888700	3889770	594.3925234	692.22243	1.16459
Recombination protein RecR	449	3889824	3890435	96.56301146	109.649755	1.13553
conserved protein of unknown function likely to be involved in DNA repair	448	3890432	3890797	369.8630137	356.90411	0.96496
DNA polymerase III subunits gamma and tau (EC 2.7.7.7)	447	3890787	3892751	220.4439855	203.681982	0.92396
hypothetical protein	446	3893537	3895129	1380.653266	1160.20258	0.84033
carboxylesterase type B		3895004	3895147	468.5314685	188.702797	0.40275
Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	444	3895282	3896496	51.0708402	57.4855848	1.1256
Branched-chain amino acid transport system permease protein livM (TC 3.A.1.4.1)	443	3896493	3897401	23.1277533	14.3469163	0.62033
High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	442	3897410	3898339	24.75780409	35.0565124	1.41598
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)	441	3898341	3899060	34.7705146	16.8240612	0.48386
Branched-chain amino acid transport ATP-binding protein livG (TC 3.A.1.4.1)	440	3899044	3899769	51.03448276	97.542069	1.9113
PilT protein, N-terminal	439	3899878	3900276	12.56281407	11.6896985	0.9305
hypothetical protein	438	3900273	3900569	60.81081081	12.5743243	0.20678
Nitroreductase family protein	437	3900639	3901172	15.00938086	36.6613508	2.44256
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)	436	3901281	3902021	39.18918919	75.4459459	1.92517
Branched-chain amino acid transport ATP-binding protein livG (TC 3.A.1.4.1)	435	3902047	3902817	31.16883117	90.6331169	2.90781
Branched-chain amino acid transport system permease protein livM (TC 3.A.1.4.1)	434	3902795	3903868	56.95611578	96.4383754	1.6932
High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	433	3903878	3904789	31.3549832	62.5195969	1.99393

Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	432	3904910	3906109	236.030025	516.858215	2.1898
hypothetical protein		3906199	3906342	0	0	#DIV/0!
Pyrimidine ABC transporter, ATP-binding protein	430	3906393	3907196	4.98132005	12.7465753	2.55888
Hydroxymethylpyrimidine ABC transporter, transmembrane component	429	3907197	3908051	2.341920375	9.80620609	4.18725
Pyrimidine ABC transporter, transmembrane component 2	428	3908048	3908836	1.269035533	3.54251269	2.7915
Pyrimidine ABC transporter, substrate-binding component	427	3908904	3909986	26.80221811	69.6585028	2.59898
Dihydropyrimidinase (EC 3.5.2.2)	426	3910056	3911432	18.16860465	37.1929506	2.0471
Dihydropyrimidine dehydrogenase homolog	425	3911434	3912936	9.320905459	18.5852197	1.99393
Beta-ureidopropionase (EC 3.5.1.6)	424	3912947	3914170	92.39574816	116.407604	1.25988
Aminotransferase class-III	423	3914189	3915511	82.45083207	153.440998	1.861
Alcohol dehydrogenase (EC 1.1.1.1)	422	3915533	3916645	192.4460432	244.339928	1.26965
Threonine synthase (EC 4.2.3.1)	421	3916669	3918033	233.1378299	343.821114	1.47475
PAP2 family protein	419	3918046	3918837	68.26801517	27.0562579	0.39632
hypothetical protein		3918834	3918953	0	0	#DIV/0!
serine/threonine kinase	418	3918847	3919647	57.5	63.971875	1.11255
putative NADH-dependent flavin oxidoreductase	417	3919790	3920758	71.65109034	60.8738318	0.84959
putative membrane protein		3920807	3921250	38.37471783	16.8036117	0.43788
hypothetical protein	415	3921264	3921494	0	0	#DIV/0!
Conserved protein	414	3921484	3921963	10.43841336	17.4832985	1.6749
hypothetical protein	413	3921960	3922103	6.993006993	13.013986	1.861
hypothetical protein	412	3922225	3925368	3.818008272	3.25660197	0.85296
DNA or RNA helicase of superfamily II	411	3925412	3929110	33.80205516	25.4138724	0.75184
ATP-dependent helicase	410	3929114	3932410	40.65533981	39.523665	0.97216
SEC-C motif domain protein	409	3932529	3933041	261.71875	287.146484	1.09716
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	408	3933209	3934222	277.3938796	417.025666	1.50337
Transketolase, C-terminal section (EC 2.2.1.1)	407	3934326	3935276	130.5263158	144.962105	1.1106
Transketolase (EC 2.2.1.1)	406	3935280	3936107	112.4546554	189.025393	1.6809
Catabolite control protein A	405	3936262	3937290	31.12840467	34.3959144	1.10497
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	404	3937374	3938363	1079.878665	1551.46057	1.4367
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	403	3938400	3939401	42.95704296	54.8446553	1.27673
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	402	3939445	3940965	79.60526316	104.68125	1.315
Ribose operon repressor	401	3941116	3942111	16.08040201	23.379397	1.45391
IolI protein	400	3942120	3942986	17.32101617	12.8937644	0.7444
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	399	3943224	3944354	61.0619469	103.754867	1.69917
5-keto-2-deoxygluconokinase B (EC 2.7.1.92)	398	3944379	3945188	71.6934487	128.820766	1.79683
Epi-inositol hydrolase	397	3945215	3947092	85.77517315	112.036761	1.30617
Inosose dehydratase (EC 4.2.1.44)	396	3947102	3948577	196.6101695	227.735932	1.15831
Phosphoglycerate kinase (EC 2.7.2.3)	395	3948580	3949836	140.9235669	137.796975	0.97781
NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archaeal (EC 1.2.1.59)	394	3949900	3950928	228.5992218	303.22714	1.32646
NADP-dependent malic enzyme (EC 1.1.1.40)	393	3950983	3952437	196.698762	196.467331	0.99882
HIT family protein	392	3952556	3952969	104.1162228	108.145278	1.0387

Transcriptional regulator	391	3952982	3954304	96.06656581	135.844554	1.41407
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	390	3954377	3955813	135.097493	150.331476	1.11276
hypothetical protein		3955848	3955970	52.17391304	48.5478261	0.9305
Tryptophan synthase alpha chain (EC 4.2.1.20)	388	3956029	3956826	66.49937265	116.750314	1.75566
Tryptophan synthase beta chain (EC 4.2.1.20)	387	3956819	3958027	138.2450331	243.40894	1.76071
Phosphoribosylanthranilate isomerase (EC 5.3.1.24)		3958024	3958767	49.79811575	134.002019	2.69091
Indole-3-glycerol phosphate synthase (EC 4.1.1.48)	385	3958764	3959657	21.27659574	54.1836506	2.54663
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	384	3959654	3960709	23.69668246	69.6772512	2.94038
Anthranilate synthase, amidotransferase component (EC 4.1.3.27)	383	3960702	3961277	38.26086957	59.8756522	1.56493
Anthranilate synthase, aminase component (EC 4.1.3.27)	382	3961274	3962782	10.61007958	62.9383289	5.93194
Conserved domain protein	381	3963024	3963584	12.5	11.63125	0.9305
Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like domain, possible membrane copper tolerance protein	380	3963692	3965275	7.580543272	8.81711939	1.16313
Pheromone shutdown protein	379	3965337	3966515	116.2988115	109.005942	0.93729
Kef-type K+ transport systems (NAD-binding component fused to domain related to exopolyphosphatase)	378	3966512	3967570	77.5047259	94.1053875	1.21419
TPR repeat	377	3967572	3969032	187.6712329	170.166781	0.90673
hypothetical protein		3969119	3970966	86.62696264	71.0343801	0.82
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)	375	3970981	3972081	128.1818182	100.663182	0.78532
HDIG domain protein	374	3972078	3972680	121.2624585	143.748339	1.18543
Homoserine O-succinyltransferase (EC 2.3.1.46)	373	3972941	3973858	76.33587786	84.2219193	1.10331
DNA-3-methyladenine glycosylase (EC 3.2.2.20)	372	3973908	3974501	52.27655987	45.505059	0.87047
Probable zinc protease pqqL (EC 3.4.99.-)	371	3974573	3977449	103.2684284	110.327017	1.06835
Putative NADH dehydrogenase/NAD(P)H nitroreductase AF_2267 (EC 1.-.-.-)	370	3977524	3978102	247.4048443	283.33564	1.14523
2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	369	3978156	3978929	151.3583441	131.208926	0.86688
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D- alanyl ligase (EC 6.3.2.10)	368	3978926	3980482	113.1105398	103.455334	0.91464
D-alanine--D-alanine ligase (EC 6.3.2.4)	367	3980496	3981674	118.8455008	131.12309	1.10331
Polysialic acid transport protein kpsD precursor	366	3981729	3983252	29.54694682	42.1565988	1.42677
hypothetical protein	365	3983313	3983441	7.8125	0	0
hypothetical protein	363	3983611	3983802	20.94240838	43.8455497	2.09363
hypothetical protein		3983754	3983924	52.94117647	27.3676471	0.51694
hypothetical protein	362	3983896	3984105	90.90909091	71.2344498	0.78358
hypothetical protein	361	3984083	3984316	98.71244635	35.9420601	0.36411
ATPase		3984476	3984658	43.95604396	35.7884615	0.81419
hypothetical protein		3985014	3985160	6.849315068	0	0
hypothetical protein	358	3985646	3986557	15.36772777	20.428101	1.32929

Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	357	3986573	3988132	33.35471456	31.6334189	0.94839
Capsule polysaccharide export protein	356	3988224	3989690	113.9154161	130.117667	1.14223
Tyrosine-protein kinase wzc (EC 2.7.1.112)	355	3989687	3990694	44.68718967	49.897716	1.1166
Putative capsular polysaccharide biosynthesis protein D	354	3990706	3991896	44.53781513	21.1121849	0.47403
Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-)	353	3991908	3992573	24.06015038	22.3879699	0.9305
UDP-glucose 4-epimerase (EC 5.1.3.2)	352	3992570	3993331	11.82654402	6.11366623	0.51694
Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-) / Alpha-1,3-N-acetylgalactosamine transferase PglA (EC 2.4.1.-); Putative glycosyltransferase		3993487	3994239	26.59574468	17.3231383	0.65135
Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-) / Alpha-1,3-N-acetylgalactosamine transferase PglA (EC 2.4.1.-); Putative glycosyltransferase		3994232	3994606	8.021390374	2.48796791	0.31017
hypothetical protein	349	3994599	3995648	50.52430887	26.6110582	0.5267
hypothetical protein	348	3995669	3996955	22.55054432	6.51205288	0.28878
hypothetical protein	346	3997086	3997265	0	10.396648	#DIV/0!
hypothetical protein	347	3997223	3998230	42.70109235	17.5566038	0.41115
UDP-glucose dehydrogenase (EC 1.1.1.22)	345	3998217	3999482	36.36363636	19.1249012	0.52593
UDP-glucose 4-epimerase (EC 5.1.3.2)	344	3999489	4000460	42.22451081	16.2909372	0.38582
Alpha-1,4-N-acetylgalactosamine transferase PglH (EC 2.4.1.-)	343	4000476	4001561	19.35483871	4.28801843	0.22155
capsular polysaccharide biosynthesis protein	342	4001549	4002652	17.22574796	7.59247507	0.44076
hypothetical protein	341	4002649	4003821	3.412969283	0	0
Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)	340	4003891	4005780	50.29115934	35.958973	0.71502
hypothetical protein	339	4005806	4006873	22.49297095	8.72071228	0.38771
Lipopolysaccharide biosynthesis protein	338	4006967	4008277	14.50381679	3.55152672	0.24487
Aminotransferase	337	4008271	4009371	44.54545455	35.5281818	0.79757
Phosphoglycolate phosphatase (EC 3.1.3.18)	336	4009428	4010048	6.451612903	3.0016129	0.46525
Transketolase, C-terminal section (EC 2.2.1.1)	335	4010104	4011045	62.69925611	43.5090329	0.69393
Transketolase, N-terminal section (EC 2.2.1.1)	334	4011042	4011878	68.18181818	36.7302632	0.53871
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	333	4011924	4012799	3.428571429	1.06342857	0.31017
Xanthan biosynthesis acetyltransferase GumF	332	4012888	4013970	16.63585952	4.29990758	0.25847
Putative carbamoylphosphate synthase large subunit, short form	331	4013967	4015037	30.8411215	37.3939252	1.21247
Ubiquinone biosynthesis SAM-dependent O-methyltransferase (EC 2.1.1.-)		4015095	4015358	53.23193916	45.9942966	0.86404
Ubiquinone biosynthesis SAM-dependent O-methyltransferase (EC 2.1.1.-)		4015438	4015665	105.7268722	49.1894273	0.46525
hypothetical protein	328	4015961	4016398	70.9382151	31.9393593	0.45024
Tlr1343 protein	327	4016395	4016793	22.61306533	16.3655779	0.72372
hypothetical protein		4016903	4017076	5.780346821	0	0
hypothetical protein		4017052	4017225	121.3872832	59.1647399	0.4874
VapC toxin protein	324	4017216	4017653	27.45995423	25.5514874	0.9305
Virulence associated protein B	323	4017616	4017840	35.71428571	12.4620536	0.34894
hypothetical protein	322	4017950	4018633	234.2606149	245.22694	1.04681
hypothetical protein	321	4018630	4019508	236.9020501	162.148633	0.68445
hypothetical protein	320	4019556	4019957	97.25685786	62.6521197	0.64419

T. azotonutricium				**Normalized Avg. RNA-Seq**		
	TREAZ #	**Start**	**End**	**Single Culture**	**Co-Culture**	**Ratio**
hypothetical protein	319	4019954	4020184	173.9130435	145.643478	0.83745
ATPase	318	4020348	4021559	240.297275	264.320396	1.09997
hypothetical protein	317	4021636	4022088	278.7610619	275.856195	0.98958
hypothetical protein	316	4022081	4022368	696.8641115	654.916376	0.93981
hypothetical protein	315	4022365	4022778	692.4939467	675.90799	0.97605
Undecaprenyl-diphosphatase (EC 3.6.1.27)	314	4023121	4023918	76.5370138	64.2126725	0.83898
Heat shock protein GrpE	313	4024036	4024719	114.2020498	189.369693	1.6582
Chaperone protein DnaK	312	4024761	4026704	465.7963446	797.849086	1.71287
Chaperone protein DnaJ	311	4026762	4027886	115.658363	218.551601	1.88963
Electron transport complex protein rnfC	310	4028093	4029496	506.7712046	552.463649	1.09016
Electron transport complex protein rnfD	309	4029508	4030560	381.1787072	468.788023	1.22984
Electron transport complex protein rnfG	308	4030557	4031168	235.6792144	216.253682	0.91758
Na(+)-translocating NADH-quinone reductase subunit D (EC 1.6.5.-)	307	4031165	4031773	291.1184211	364.241776	1.25118
Electron transport complex protein rnfA	306	4031770	4032366	239.9328859	187.348993	0.78084
Electron transport complex protein rnfB	305	4032379	4033197	288.5085575	241.156479	0.83587
hypothetical protein	304	4033181	4034014	140.4561825	185.429772	1.3202
Metallo-beta-lactamase family protein, RNA-specific	303	4034047	4035480	139.5673412	144.152826	1.03286
Aldo/keto reductase	302	4035496	4036701	94.60580913	65.6369295	0.69379
TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	301	4036719	4037444	70.34482759	66.7393103	0.94875
hypothetical protein	300	4037527	4037997	191.4893617	211.837234	1.10626
Peptidase, M48 family	299	4038002	4038922	216.3043478	226.556522	1.0474
Adenylate cyclase (EC 4.6.1.1)	298	4039029	4041224	22.7998176	36.4901961	1.60046
hypothetical protein		4041243	4041416	260.1156069	91.4364162	0.35152
Flagellin protein flaA	296	4041436	4042458	2064.646465	2736.98586	1.32564
PUTATIVE ZINC PROTEASE PROTEIN	295	4042586	4043659	39.14259087	20.8126747	0.53171
hypothetical protein	294	4043699	4044130	58.00464037	45.337587	0.78162
Tetrapyrrole (Corrin-Porphyrin) methylase family protein UPF0011	293	4044147	4044893	128.6863271	99.7855228	0.77542
hypothetical protein	292	4044936	4045220	1179.577465	1140.19014	0.96661
RNA methyltransferase, TrmH family	291	4045252	4046133	44.26787741	40.1350738	0.90664
Conserved protein	290	4046151	4046573	63.98104265	41.8945498	0.6548
2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.-)	289	4046655	4047419	95.54973822	80.3835079	0.84127
EBSC protein	288	4047438	4047935	94.56740443	63.6559356	0.67313
hypothetical protein	287	4047976	4048449	131.0782241	125.902748	0.96052
hypothetical protein	286	4048495	4048989	52.63157895	50.8572874	0.96629
Ferric iron ABC transporter, permease protein	285	4049052	4050626	29.2249047	35.4701398	1.2137
Ferric iron ABC transporter, ATP-binding protein	284	4050623	4051387	176.7015707	215.573953	1.21999
Ferric iron ABC transporter, iron-binding protein	283	4051400	4052428	242.2178988	263.400292	1.08745
DNA gyrase subunit A (EC 5.99.1.3)	282	4052428	4054974	216.4179104	227.691084	1.05209
diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	281	4055144	4056181	99.32497589	81.6542912	0.82209
Sensory box histidine kinase/response regulator	280	4056213	4057883	58.68263473	54.6041916	0.9305
DNA gyrase subunit B (EC 5.99.1.3)	279	4057920	4059827	187.2050341	205.422391	1.09731

Chromosomal replication initiator protein dnaA	2339	301	1716	215.9010601	248.056537	1.14894
DNA polymerase III beta subunit (EC 2.7.7.7)	2338	1958	3058	313.1818182	355.909091	1.13643
DNA recombination and repair protein RecF	2337	3084	4196	160.971223	171.98741	1.06844
Uncharacterized protein TP_0004	2336	4193	4675	255.186722	256.742739	1.0061
radical activating enzyme	2335	4720	5655	85.02673797	72.1925134	0.84906
Similarities with tr|Q8EAT4 Shewanella oneidensis	2334	5669	6718	328.884652	302.430887	0.91957
hypothetical protein	2333	6721	8817	147.1851145	115.935115	0.78768
DNA modification methylase (Adenine-specific methyltransferase) (EC 2.1.1.72)	2332	8828	9970	45.97197898	41.3747811	0.9
hypothetical protein	2331	9983	10666	81.99121523	23.0600293	0.28125
Shikimate kinase (EC 2.7.1.71)	2329	10708	11271	80.81705151	59.946714	0.74176
TPR domain protein, putative component of TonB system	2330	11231	13984	116.6000726	84.1808936	0.72196
Periplasmic sugar-binding protein of sugar ABC transporter	2328	14046	15293	61.34723336	63.1515638	1.02941
L-asparaginase (EC 3.5.1.1)	2327	15352	16242	93.25842697	75.8426966	0.81325
RNA methyltransferase, TrmH family	2325	16269	17093	35.80097087	16.3834951	0.45763
DNA-binding response regulator	2326	17083	18642	24.05388069	12.9890956	0.54
Two-component sensor histidine kinase	2324	18642	20135	43.87139987	31.6476892	0.72137
Methylcobalamin:coenzyme M methyltransferase, methanol-specific	2323	20149	21177	109.922179	102.86965	0.93584
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	2322	21257	22243	669.8782961	695.993915	1.03899
D-xylose transport ATP-binding protein xylG	2321	22287	23831	135.6865285	135.524611	0.99881
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	2320	23821	24837	153.0511811	205.954724	1.34566
hypothetical protein	2319	24898	25077	2.793296089	0	0
Multiple sugar ABC transporter, substrate-binding protein	2318	25167	26672	536.8770764	430.564784	0.80198
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	2317	26701	27615	223.7417943	157.549234	0.70416
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	2316	27612	28463	131.6098707	116.333725	0.88393
Conserved protein	2315	28471	28827	106.741573	145.365169	1.36184
Inactive homolog of metal-dependent proteases, putative molecular chaperone / Beta-phosphoglucomutase (EC 5.4.2.6)	2314	28853	29524	220.5663189	211.251863	0.95777
Oxidoreductase, aldo/keto reductase family	2313	29587	30738	195.9165943	207.211121	1.05765
Ferredoxin	2312	30777	31790	119.94077	86.6238894	0.72222
hypothetical protein	2311	32157	32477	0	0	#DIV/0!
Response regulator receiver modulated metal dependent phosphohydrolase	2310	32658	33056	36.4321608	11.3065327	0.31034
Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3)	2309	33191	34285	3655.850091	3681.44424	1.007
Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17)	2308	34357	35892	175.8957655	240.390879	1.36667
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	2307	35889	36890	186.8131868	193.306693	1.03476

Methylmalonate-semialdehyde dehydrogenase [inositol] (EC 1.2.1.27)	2306	36891	38402	142.9516876	171.244209	1.19792
5-keto-2-deoxygluconokinase B (EC 2.7.1.92)		38399	39175	48.32474227	34.7938144	0.72
Transaldolase (EC 2.2.1.2)	2304	39188	40282	109.6892139	76.0968921	0.69375
Osmosensitive K+ channel histidine kinase kdpD (EC 2.7.3.-)	2303	40336	42030	33.9433294	9.29752066	0.27391
Phosphate regulon transcriptional regulatory protein phoB	2302	42027	42722	42.44604317	16.1870504	0.38136
Phosphate transport system regulatory protein PhoU	2301	42719	43375	83.07926829	37.7286585	0.45413
Phosphate transport ATP-binding protein pstB (TC 3.A.1.7.1)	2300	43375	44133	52.11081794	14.8416887	0.28481
Phosphate transport system permease protein pstA (TC 3.A.1.7.1)	2299	44130	44978	56.01415094	21.2264151	0.37895
Phosphate transport system permease protein pstC (TC 3.A.1.7.1)	2298	44975	45826	39.36545241	7.93184489	0.20149
Phosphate ABC transporter, periplasmic phosphate-binding protein pstS (TC 3.A.1.7.1)	2297	45864	46715	46.4159812	29.0834313	0.62658
hypothetical protein	2296	46813	47544	195.622435	135.430917	0.69231
Clumping factor ClfA, fibrinogen-binding protein	2295	47683	50826	152.4021635	103.086223	0.67641
hypothetical protein	2294	50777	50896	67.22689076	18.907563	0.28125
hypothetical protein	2292	51148	52395	81.39534884	173.215718	2.12808
hypothetical protein	2291	52469	52981	60.546875	21.9726563	0.3629
Cell division protein ftsH (EC 3.4.24.-)	2290	53077	55128	305.7045344	228.181375	0.74641
transposase, mutator family	2289	55232	56473	70.10475423	65.2699436	0.93103
putative NADH-dependent flavin oxidoreductase	2288	56570	57544	38.6996904	25.5417957	0.66
Alpha-galactosidase (EC 3.2.1.22)	2287	57698	59932	183.3034915	105.752014	0.57692
hypothetical protein	2286	60003	60434	138.0510441	161.832947	1.17227
Glutamate synthase [NADPH] small chain (EC 1.4.1.13)		60463	61302	204.4100119	179.678188	0.87901
Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	2284	61317	62819	194.4074567	206.724368	1.06336
Oxidoreductase, Gfo/Idh/MocA family	2283	62835	64094	219.618745	235.901509	1.07414
TPR domain protein	2282	64082	64750	135.4790419	121.257485	0.89503
Sugar diacid utilization regulator SdaR	2281	64777	65955	60.27164686	26.7402377	0.44366
D-glycerate transporter (predicted)	2280	66130	67464	48.72563718	13.4932534	0.27692
Methylcobalamin:coenzyme M methyltransferase, methanol-specific	2279	67493	68533	44.71153846	15.1442308	0.33871
Methylcobalamin:coenzyme M methyltransferase, methanol-specific	2278	68556	69590	94.29400387	50.0483559	0.53077
ATPase	2277	69605	70786	54.19136325	40.0084674	0.73828
FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8)	2276	70891	71430	401.6697588	496.753247	1.23672
Fe-S OXIDOREDUCTASE (1.8.-.-)	2275	71591	73369	131.3273341	144.263217	1.0985
NifU-like domain protein	2274	73376	73600	774.5535714	823.660714	1.0634
hypothetical protein	2273	73797	74606	220.0247219	144.622991	0.6573
hypothetical protein	2272	74628	74858	747.826087	567.391304	0.75872
hypothetical protein	2271	74870	75121	278.8844622	197.211155	0.70714
hypothetical protein	2270	75472	76140	103.2934132	67.3652695	0.65217
DNA-damage-inducible protein J	2269	76337	76609	34.92647059	8.27205882	0.23684
hypothetical protein	2268	76800	76919	21.00840336	0	0

hypothetical protein	2267	76985	77557	298.951049	444.493007	1.48684
Glutaminyl-tRNA synthetase (EC 6.1.1.18)	2266	77615	79369	221.4611872	362.157534	1.63531
Ferredoxin	2265	79407	80537	399.5575221	629.20354	1.57475
Cobalamin synthase	2264	80627	81436	43.26328801	19.4684796	0.45
Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)	2263	81436	82482	41.58699809	27.9636711	0.67241
hypothetical protein	2262	82484	83230	4.021447721	6.03217158	1.5
Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	2261	83230	83748	18.33976834	13.030888	0.71053
Nitrogenase vanadium-cofactor synthesis protein VnfN	2260	83757	85106	15.93773165	8.33951075	0.52326
Nitrogenase iron protein (EC 1.18.6.1)	2259	85057	87252	29.61275626	13.3257403	0.45
Vitamin B12 ABC transporter, ATPase component BtuD	2258	87245	88012	29.98696219	23.4680574	0.78261
Vitamin B12 ABC transporter, permease component BtuC	2257	88013	89026	49.85192498	15.5478776	0.31188
Vitamin B12 ABC transporter, B12-binding component BtuF	2256	89013	89915	42.1286031	22.4501109	0.53289
Outer membrane vitamin B12 receptor BtuB	2255	89924	91933	43.80288701	50.3982081	1.15057
hypothetical protein	2254	91930	92526	83.05369128	154.781879	1.86364
hypothetical protein	2253	92597	92782	59.45945946	206.756757	3.47727
hypothetical protein	2252	92845	92973	11.71875	0	0
hypothetical protein	2251	93018	94169	48.21894005	25.4126846	0.52703
hypothetical protein	2250	94339	94458	21.00840336	0	0
Uncharacterized protein TP_1001	2249	94457	95482	131.7073171	111.95122	0.85
Thioredoxin	2248	95486	95815	613.9817629	649.696049	1.05817
PilT protein, N-terminal	2247	95902	96300	115.5778894	73.4924623	0.63587
hypothetical protein	2246	96297	96542	432.6530612	541.836735	1.25236
Multiple antibiotic resistance (MarC) -related proteins	2245	96684	97334	127.6923077	117.692308	0.92169
Peptidase, U32 family	2244	97331	99586	161.6407982	208.536585	1.29012
Single-stranded DNA-binding protein	2243	99788	100249	48.80694143	24.4034707	0.5
hypothetical protein	2242	100416	102368	150.102459	138.319672	0.9215
Cobalt-zinc-cadmium resistance protein	2241	102389	103333	160.4872881	85.8050847	0.53465
Dephospho-CoA kinase (EC 2.7.1.24)	2240	103372	103986	131.1074919	124.592834	0.95031
Cell division protein	2239	103988	104716	381.8681319	287.431319	0.7527
Response regulator receiver precursor	2238	104735	107617	70.4078076	36.0752876	0.51238
Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	2237	107752	109368	251.396648	275.139665	1.09444
hypothetical protein	2236	109439	110347	137.5690608	96.961326	0.70482
hypothetical protein	2235	110600	110719	33.61344538	0	0
Methyl-accepting chemotaxis protein	2234	110718	112874	36.19489559	4.17633411	0.11538
hypothetical protein	2233	112890	113951	35.34401508	19.0857681	0.54
TRAP-type C4-dicarboxylate transport system, large permease component	2232	113963	115252	32.97129558	29.674166	0.9
TRAP-type transport system, large permease component, predicted N-acetylneuraminate transporter / TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter	2231	115262	115738	37.81512605	14.1806723	0.375
TRAP-type C4-dicarboxylate transport system, periplasmic component	2230	115751	116764	79.60199005	89.5522388	1.125

Transcriptional regulator, GntR family	2229	116906	117640	47.0027248	67.4386921	1.43478
Uncharacterized protein TP_0983 precursor	2228	117687	118376	123.3671988	111.030479	0.9
Rhomboid family protein	2227	118384	119025	84.24336973	38.6115445	0.45833
Hydroxypyruvate isomerase (EC 5.3.1.22)	2226	119022	119774	138.2978723	158.577128	1.14663
tRNA dihydrouridine synthase B (EC 1.-.-.-)	2225	119789	120787	68.63727455	83.4168337	1.21533
Putative deoxyribonuclease YcfH	2224	120788	121621	158.4633854	248.4994	1.56818
fructose response regulator of fruA and EII fructose/mannose	2223	121741	122424	71.74231332	49.4143485	0.68878
Xylulose kinase (EC 2.7.1.17)	2222	122461	123948	304.3039677	276.899798	0.90994
hypothetical protein		123953	124102	43.62416107	75.5033557	1.73077
HIPA PROTEIN		124111	124431	89.0625	63.28125	0.71053
hypothetical protein	2219	124424	124750	61.34969325	55.2147239	0.9
Undecaprenyl-diphosphatase (EC 3.6.1.27)	2218	124894	125730	199.1626794	126.495215	0.63514
Phosphoenolpyruvate phosphomutase (EC 5.4.2.9)	2217	125737	127035	315.8705701	107.473035	0.34024
2-aminoethylphosphonate:pyruvate aminotransferase (EC 2.6.1.37)	2216	127046	128641	245.1410658	87.460815	0.35678
Phosphonopyruvate decarboxylase (EC 4.1.1.82)	2215	128641	129825	197.2128378	55.1097973	0.27944
putative integral membrane protein	2214	129925	130695	92.85714286	90.5844156	0.97552
Heat shock protein GrpE	2213	130801	131475	335.3115727	480.712166	1.43363
Chaperone protein DnaK	2212	131512	133458	763.8164755	974.843587	1.27628
Chaperone protein DnaJ	2211	133541	134677	552.8169014	683.318662	1.23607
Pantothenate kinase type II, eukaryotic (EC 2.7.1.33)	2210	134674	135477	156.8123393	216.902314	1.3832
Oxidoreductase, aldo/keto reductase family	2208	135493	136521	272.8599222	341.439689	1.25134
hypothetical protein	2209	136482	137981	46.69779853	16.5110073	0.35357
hypothetical protein	2207	137948	138070	24.59016393	0	0
hypothetical protein	2205	138088	138501	93.22033898	59.9273608	0.64286
hypothetical protein	2206	138498	139193	418.705036	271.942446	0.64948
membrane protein, putative	2203	139271	140104	154.2617047	135.054022	0.87549
Integral membrane protein	2204	140099	140704	201.6528926	189.669421	0.94057
hypothetical protein	2202	141470	142213	14.80484522	9.08479139	0.61364
6-aminohexanoate-dimer hydrolase (EC 3.5.1.46)	2201	142210	143313	40.79782412	16.3191296	0.4
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	2200	143455	144813	263.622975	236.929308	0.89874
membrane protein, putative	2199	144825	145496	44.70938897	23.4724292	0.525
Putative transport protein	2198	145551	146681	141.1504425	85.619469	0.60658
hypothetical protein	2197	146746	147903	333.6214347	410.328436	1.22992
sensory box histidine kinase/response regulator	2195	147926	149662	186.3479263	233.294931	1.25193
glutamate transporter, putative	2196	149659	150831	187.7133106	188.139932	1.00227
Nucleoside diphosphate kinase (EC 2.7.4.6)	2194	151005	151448	94.80812641	66.027088	0.69643
Putative Heme-regulated two-component response regulator	2193	151525	152673	71.42857143	54.8780488	0.76829
GGDEF domain protein	2191	152670	153872	116.8885191	74.875208	0.64057
Flagellar hook-length control protein fliK	2192	153869	155209	108.9552239	124.253731	1.14041
hypothetical protein	2189	155208	155345	65.69343066	32.8467153	0.5
Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)	2190	155338	156687	246.8495182	246.849518	1

hypothetical protein	2188	156782	156973	26.17801047	47.1204188	1.8
Large repetitive protein	2187	156942	162152	508.5412668	628.790787	1.23646
Flagellar hook-length control protein fliK	2186	162254	172549	606.6537154	725.594949	1.19606
hypothetical protein	2185	172658	173719	74.45805844	97.5494816	1.31013
hypothetical protein	2184	173752	173964	99.05660377	74.2924528	0.75
Membrane spanning protein	2183	174098	175678	222.4683544	166.613924	0.74893
Nitrogen regulatory protein P-II	2182	175671	176483	187.1921182	169.027094	0.90296
LysM domain protein	2181	176550	177053	2147.117296	2419.98012	1.12708
S-adenosylmethionine synthetase (EC 2.5.1.6)	2180	177078	178247	688.1950385	831.479897	1.2082
methylated-DNA--protein-cysteine methyltransferase-related protein	2179	178683	178991	212.6623377	189.935065	0.89313
Aquaporin Z	2178	179204	179866	218.2779456	156.344411	0.71626
Methyl-accepting chemotaxis protein	2177	180040	182217	419.7416974	408.902214	0.97418
hypothetical protein	2176	182346	182789	217.8329571	264.108352	1.21244
Peptidase, M48 family	2175	182789	183679	187.6404494	151.685393	0.80838
Adenylate cyclase (EC 4.6.1.1)	2174	183676	185931	87.36141907	54.8780488	0.62817
hypothetical protein	2173	185943	186419	154.4117647	118.172269	0.76531
Peptidase, M48 family	2172	186416	187336	236.4130435	225	0.95172
Flagellin protein flaA	2171	187584	188513	5786.111111	4022.5	0.6952
Predicted L-rhamnose ABC transporter, substrate-binding component	2169	188531	189670	273.046532	308.165057	1.12862
FOG: CheY-like receiver	2170	189667	192240	98.32879907	57.7147299	0.58696
Probable AAA family ATPase	2168	192289	194463	57.26770929	14.4894204	0.25301
Transcriptional regulator, DeoR family	2167	194466	195461	179.2547835	190.332326	1.0618
hypothetical protein	2166	195521	195832	356.9131833	311.093248	0.87162
hypothetical protein	2165	195786	196103	223.9747634	262.618297	1.17254
hypothetical protein	2164	196165	196338	69.36416185	117.052023	1.6875
hypothetical protein	2162	196530	196952	33.17535545	21.3270142	0.64286
DNA-binding protein	2161	197040	197372	28.61445783	6.77710843	0.23684
hypothetical protein	2160	197542	198585	1090.12464	1162.75168	1.06662
Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain	2159	198607	201048	370.7496927	329.065957	0.88757
type 4 fimbrial biogenesis protein PilY1	2158	201060	204890	297.5195822	217.950392	0.73256
hypothetical protein	2157	204932	205552	62.90322581	61.6935484	0.98077
hypothetical protein	2156	205549	206211	39.27492447	33.9879154	0.86538
ATPase	2155	206305	207774	35.73859769	13.7848877	0.38571
hypothetical protein	2154	207921	208061	25	0	0
hypothetical protein	2153	208027	212130	68.60833536	40.0316841	0.58348
methyltransferase	2152	212251	212916	6.015037594	3.38345865	0.5625
sensory box histidine kinase/response regulator	2151	212956	215367	69.75772765	53.5714286	0.76796
Mg-protoporphyrin IX monomethyl ester oxidative cyclase	2150	215475	216992	38.5629532	5.93276203	0.15385
Putative 5'(3')-deoxyribonucleotidase (EC 3.1.3.-)	2149	217019	217621	167.7852349	169.88255	1.0125
Glycogen debranching enzyme (EC 3.2.1.-)	2148	217631	219787	160.7142857	146.103896	0.90909
hypothetical protein	2147	219829	220002	20.23121387	13.0057803	0.64286
Hypothetical Cytosolic Protein	2146	220006	220701	51.07913669	51.7985612	1.01408
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	2145	220904	221611	57.28429986	35.0070721	0.61111
hypothetical protein	2144	221633	223492	98.17105971	104.088219	1.06027
LSU ribosomal protein L34p	2143	223628	223783	619.3548387	1364.51613	2.20313

Ribonuclease P protein component (EC 3.1.26.5)	2142	223803	224180	457.5596817	757.95756	1.65652
YidD	2141	224180	224398	160.5504587	340.59633	2.12143
OxaI/YidC membrane insertion protein	2140	224411	226258	174.0660531	309.420682	1.7776
Jag protein	2139	226281	227048	235.3324641	445.89309	1.89474
hypothetical protein	2138	227092	227877	165.6050955	252.229299	1.52308
sensory box histidine kinase/response regulator	2137	227914	229914	113.5	169.875	1.4967
hypothetical protein	2136	229935	230600	348.8721805	321.428571	0.92134
Uracil permease	2135	230614	231849	126.7206478	114.777328	0.90575
Na+ driven multidrug efflux pump	2134	231946	233301	74.1697417	78.0442804	1.05224
Zinc protease PqqL (EC 3.4.-.-)	2133	233301	236189	169.1481994	137.898199	0.81525
Exopolyphosphatase-related protein	2132	236278	237195	701.1995638	1050.16358	1.49767
polysaccharide deacetylase family protein	2131	237224	238048	40.65533981	46.4199029	1.14179
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	2130	238050	238811	55.84756899	76.8725361	1.37647
Predicted dehydrogenases and related proteins	2129	238824	239915	88.45096242	65.9945005	0.74611
Beta-glucosidase (EC 3.2.1.21)	2128	239970	241319	209.414381	228.502595	1.09115
Acetyl xylan esterase 1; Cephalosporin-C deacetylase (EC 3.1.1.41)	2127	241358	242314	115.0627615	103.556485	0.9
Orotate phosphoribosyltransferase (EC 2.4.2.10)	2126	242355	242960	134.7107438	85.5371901	0.63497
Dihydroorotate dehydrogenase, catalytic subunit (EC 1.3.3.1)	2125	243051	244010	64.65067779	56.3086548	0.87097
Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1)	2124	244007	244765	104.2216359	112.796834	1.08228
Carbon starvation protein A	2123	244890	246392	96.5379494	80.8921438	0.83793
hypothetical protein	2122	246563	246775	4.716981132	0	0
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	2121	246805	247686	103.8592509	66.4018161	0.63934
Aldo/keto reductase	2120	247716	248873	68.71218669	91.4001729	1.33019
hypothetical protein	2119	248884	249402	36.67953668	17.3745174	0.47368
Dihydroorotase (EC 3.5.2.3)	2118	249418	250695	180.8927173	28.1910728	0.15584
Aspartate carbamoyltransferase regulatory chain (pyrI)	2117	250702	251148	304.9327354	25.2242152	0.08272
Aspartate carbamoyltransferase (EC 2.1.3.2)	2116	251161	252084	297.3997833	29.2524377	0.09836
hypothetical protein	2115	252210	252494	181.3380282	118.838028	0.65534
Maltose/maltodextrin ABC transporter, permease protein MalG	2114	252627	253481	52.69320843	5.26932084	0.1
Possible alpha-xyloside ABC transporter, permease component	2113	253495	254403	30.28634361	4.95594714	0.16364
Multiple sugar ABC transporter, ATP-binding protein	2112	254415	255557	29.77232925	13.7915937	0.46324
hypothetical protein	2111	255559	256035	44.11764706	14.1806723	0.32143
hypothetical protein	2110	256026	257318	32.12074303	10.4489164	0.3253
Sugar ABC transporter, periplasmic sugar-binding protein USSDB1B	2109	257351	258661	117.5572519	42.9389313	0.36526
hypothetical protein	2108	258856	259077	9.049773756	0	0
Outer membrane autotransporter barrel	2107	259158	261098	61.08247423	28.9948454	0.47468
DNA-binding protein	2106	261254	261583	53.19148936	27.3556231	0.51429
Adenylate cyclase (EC 4.6.1.1)	2105	261622	262980	133.2842415	99.4108984	0.74586

Two-component response regulator SA14-24	2104	263050	263754	112.9261364	73.5085227	0.65094
Two component system histidine kinase (EC 2.7.3.-)	2103	263751	265010	316.918189	287.728356	0.90789
Outer membrane protein A precursor	2102	265031	265948	2456.924755	2345.69248	0.95473
hypothetical protein	2101	265908	266042	216.4179104	218.283582	1.00862
Heavy-metal-associated domain (N-terminus) and membrane-bounded cytochrome biogenesis cycZ-like domain, possible membrane copper tolerance protein	2100	266107	267864	42.97097325	11.5253273	0.26821
Conserved domain protein	2099	267923	268399	42.01680672	28.3613445	0.675
Copper-translocating P-type ATPase (EC 3.6.3.4)	2098	268400	270736	72.9880137	44.3065068	0.60704
hypothetical protein	2097	270767	271438	119.9701937	103.949329	0.86646
2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	2096	271451	272575	195.2846975	172.153025	0.88155
hypothetical protein	2095	272591	273523	11.26609442	14.4849785	1.28571
hypothetical protein	2094	273537	275093	74.55012853	43.3804627	0.5819
hypothetical protein	2093	275154	276266	87.23021583	80.9352518	0.92784
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	2092	276283	277734	153.6871123	179.875948	1.1704
BNR repeat domain protein	2091	277731	278942	249.3806771	299.132948	1.1995
DNA-3-methyladenine glycosylase (EC 3.2.2.20)	2090	279044	279622	66.60899654	38.9273356	0.58442
hypothetical protein	2089	279626	280384	69.92084433	50.4617414	0.7217
methanol dehydrogenase regulatory protein	2088	280426	281379	89.19202518	49.5802728	0.55588
Probable membrane protein	2087	281376	282638	55.07131537	26.7432647	0.48561
hypothetical protein	2085	282625	284244	40.45707227	13.8974676	0.34351
hypothetical protein	2086	284219	285463	38.98713826	12.6607717	0.32474
Probable ABC transporter permease protein PH1216	2084	285475	286314	20.85816448	5.36352801	0.25714
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	2083	286325	287200	32.57142857	0	0
probable ABC transporter, periplasmic solute-binding protein SMa2305	2082	287307	288596	121.7998448	90.7680372	0.74522
Mlc, transcriptional repressor of MalT (the transcriptional activator of maltose regulon) and manXYZ operon	2081	288645	289799	50.25996534	5.8492201	0.11638
hypothetical protein	2080	289827	289955	11.71875	17.578125	1.5
MoxR-like ATPases	2079	290076	291026	294.2105263	312.631579	1.06261
hypothetical protein	2078	291094	292299	140.6639004	164.315353	1.16814
Plasmid maintenance system antidote protein, XRE family	2077	292355	292777	2131.516588	4697.27488	2.20372
Ribose operon repressor	2076	292944	293966	57.72994129	46.2328767	0.80085
hypothetical protein	2075	294118	294270	49.34210526	59.2105263	1.2
Alpha-rhamnosidase	2074	294316	296955	34.86169003	23.0200834	0.66033
Multiple sugar ABC transporter, substrate-binding protein	2073	297069	298313	47.42765273	65.1125402	1.37288
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	2072	298345	299241	38.50446429	12.5558036	0.32609
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	2071	299290	300126	14.95215311	2.69138756	0.18
Ribose 5-phosphate isomerase B (EC 5.3.1.6)	2070	300129	300743	58.63192182	62.2964169	1.0625

hypothetical protein	2069	300781	301005	258.9285714	170.758929	0.65948
Transglutaminase-like domain protein	2068	301064	304993	49.37643166	34.9325528	0.70747
Integrase domain protein	2067	305085	306320	46.96356275	18.2186235	0.38793
Transcriptional regulator, MerR family, near polyamine transporter	2066	306493	307059	115.7243816	143.109541	1.23664
3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	2065	307102	308385	52.2213562	99.9610288	1.91418
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	2064	308398	308922	35.30534351	38.6450382	1.09459
Conserved protein	2063	308935	309345	60.97560976	60.3658537	0.99
Chromate transport protein	2062	309372	309923	46.27949183	44.9183303	0.97059
Chromate transport protein	2061	309920	310498	66.60899654	81.7474048	1.22727
Aspartyl-tRNA synthetase (EC 6.1.1.12)	2060	310501	312369	207.9764454	233.672377	1.12355
hypothetical protein	2059	312413	313276	92.69988413	59.9652375	0.64688
hypothetical protein	2058	313314	314429	52.91479821	32.2869955	0.61017
Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	2057	314477	315058	320.9982788	329.173838	1.02547
hypothetical protein	2056	315224	315460	2902.542373	3613.34746	1.24489
Ser/Thr protein phosphatase family protein	2055	315543	316412	66.16800921	59.5512083	0.9
Tryptophan synthase beta chain like (EC 4.2.1.20)	2054	316557	317945	292.1469741	269.092219	0.92109
hypothetical protein	2053	318014	318427	290.5569007	495.762712	1.70625
Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)	2052	318757	319899	608.5814361	606.830123	0.99712
Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)	2051	319919	320728	386.8974042	481.149567	1.24361
hypothetical protein	2050	320825	321022	144.6700508	194.162437	1.34211
CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)	2049	321019	321831	139.7783251	108.066502	0.77313
Phosphatidylserine decarboxylase (EC 4.1.1.65)	2048	321828	322469	119.3447738	136.895476	1.14706
hypothetical protein	2047	322456	323118	61.93353474	44.18429	0.71341
COG1272: Predicted membrane protein hemolysin III homolog	2046	323265	324098	123.0492197	78.3313325	0.63659
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	2045	324125	324880	217.8807947	125.165563	0.57447
Permeases of the major facilitator superfamily		324919	325260	95.30791789	92.3753666	0.96923
Permeases of the major facilitator superfamily		325269	326123	52.69320843	36.8852459	0.7
Sensory box histidine kinase/response regulator	2042	326130	328313	215.3704556	261.965025	1.21635
hypothetical protein	2041	328323	329474	193.3101651	228.714162	1.18315
Serine hydroxymethyltransferase (EC 2.1.2.1)	2040	329602	331137	240.0651466	297.557003	1.23948
hypothetical protein	2039	331304	331888	76.19863014	50.0856164	0.6573
Uncharacterized protein TP_0836	2038	331889	332641	57.18085106	38.8962766	0.68023
Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	2037	332638	333318	122.0588235	79.4117647	0.6506
Thiazole biosynthesis protein ThiH	2036	333333	334493	125	104.741379	0.83793
Thiazole biosynthesis protein ThiG	2035	334486	335463	127.9426817	99.0276356	0.774
Uncharacterized conserved protein	2034	335534	336724	203.3613445	236.344538	1.16219
Sensory box histidine kinase/response regulator	2033	336745	338835	221.0526316	236.842105	1.07143
Acyl-ACP thioesterase	2032	338851	339720	95.51208285	85.443038	0.89458
Sugar phosphate isomerases/epimerases	2031	339703	340464	112.3521682	88.6990802	0.78947

Methyl-accepting chemotaxis protein	2030	340512	342332	172.5274725	217.582418	1.26115
Nitroreductase family protein	2029	342344	342913	204.745167	217.486819	1.06223
hypothetical protein	2028	343200	344282	108.5951941	135.166359	1.24468
Alpha-mannosidase (EC 3.2.1.24)	2027	344303	347500	116.5154833	228.026275	1.95705
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	2026	347552	348424	32.68348624	46.4449541	1.42105
Sugar ABC transporter permease	2025	348436	349332	66.96428571	77.8459821	1.1625
Sugar ABC transporter, sugar-binding protein	2024	349441	350781	1961.19403	3230.59701	1.64726
sugar-binding transcriptional regulator, GntR family	2023	350916	351995	69.50880445	43.7905468	0.63
Metallo-beta-lactamase family protein, RNA-specific	2022	352130	353539	186.3023421	142.122072	0.76286
rRNA methylases	2021	353581	354309	230.7692308	188.53022	0.81696
Aminoglycoside 6-adenylyltransferase (EC 2.7.7.-)	2020	354311	355156	47.92899408	37.2781065	0.77778
hypothetical protein	2019	355184	355306	12.29508197	0	0
Phosphomethylpyrimidine kinase (EC 2.7.4.7)	2018	355326	356141	472.392638	472.08589	0.99935
Integrase domain protein	2017	356321	357556	52.22672065	23.6842105	0.45349
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	2015	357956	358900	2026.483051	2423.99364	1.19616
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	2014	358953	359984	290.9796314	384.093113	1.32
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	2013	359994	361496	214.0479361	301.098535	1.40669
Endo-beta-N-acetylglucosaminidase (EC 3.2.1.96)	2012	361587	362876	240.8844065	188.518231	0.78261
Dipeptide transport ATP-binding protein dppF (TC 3.A.1.5.2)		362916	363683	32.67973856	0	0
Dipeptide transport ATP-binding protein dppD (TC 3.A.1.5.2)		363680	364504	31.55339806	8.19174757	0.25962
Binding-protein-dependent transport systems inner membrane component	2009	364501	365313	29.55665025	2.77093596	0.09375
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)		365412	366263	49.94124559	10.5757932	0.21176
ABC transporter, periplasmic substrate-binding protein	2007	366260	367774	123.5138705	29.7225892	0.24064
Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10)	2006	368078	370699	1043.304082	525.371995	0.50357
hypothetical protein	2005	370696	371445	1176.902537	549.732977	0.4671
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	2004	371525	371701	500	281.25	0.5625
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	2003	371722	373449	541.1117545	282.715692	0.52247
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	2002	373458	374975	246.5392221	137.936717	0.55949
hypothetical protein	2001	374950	376203	307.2625698	166.999202	0.54351
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	2000	376215	376460	63.26530612	45.9183673	0.72581
Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	1999	376355	377083	177.1978022	89.6291209	0.50581
Multiple polyol-specific dehydrogenase (EC 1.1.1.-)	1998	377087	378619	257.8328982	126.305483	0.48987
hypothetical protein	1997	378636	378839	68.96551724	44.3349754	0.64286
hypothetical protein	1996	379065	379457	63.7755102	45.9183673	0.72

ABC transporter, ATP-binding protein	1994	379450	380223	74.385511	58.2147477	0.78261
hypothetical protein	1995	380204	380326	0	0	#DIV/0!
ABC transporter, permease protein	1993	380220	381047	41.71704958	40.8101572	0.97826
Na+/H+ antiporter		381072	382358	19.44012442	10.4976672	0.54
Na+/H+ antiporter		382436	383065	22.25755167	10.7313196	0.48214
DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	1990	383071	383628	39.497307	8.07899461	0.20455
Predicted membrane protein	1989	383675	384439	31.41361257	32.395288	1.03125
Uncharacterized protein TP_0073		384496	385755	69.2124105	73.3890215	1.06034
Uncharacterized protein TP_0073		385727	385996	65.05576208	100.371747	1.54286
hypothetical protein	1986	386122	387522	77.85714286	32.1428571	0.41284
Hypothetical protein ybgI	1985	387530	388300	118.8311688	111.038961	0.93443
Lipoprotein signal peptidase (EC 3.4.23.36)	1984	388314	388850	176.3059701	226.679104	1.28571
hypothetical protein	1983	388834	389124	151.7241379	147.413793	0.97159
hydrolase, putative	1982	389158	390000	7.125890736	0	0
hypothetical protein		390240	390422	68.68131868	61.8131868	0.9
hypothetical protein	1980	390506	390667	27.95031056	13.9751553	0.5
Protein of unknown function DUF262 family	1979	390700	392055	12.91512915	1.66051661	0.12857
Protein of unknown function DUF262 family	1978	392045	393886	7.061379685	1.22216187	0.17308
hypothetical protein	1977	393933	394124	28.79581152	23.5602094	0.81818
hypothetical protein	1976	394198	395871	164.6706587	173.802395	1.05545
hypothetical protein	1975	395916	396086	38.23529412	0	0
Probable AAA family ATPase	1973	396132	397847	58.89212828	48.5422741	0.82426
Xylulose kinase (EC 2.7.1.17)	1974	397844	399229	70.75812274	61.732852	0.87245
Endonuclease/exonuclease/phosphatase family protein	1972	399357	400457	53.63636364	12.2727273	0.22881
Transcriptional regulator, DeoR family	1971	400460	401221	219.4480946	476.018397	2.16916
Nitroreductase	1970	401424	401948	6234.732824	8321.56489	1.33471
Threonyl-tRNA synthetase (EC 6.1.1.3)	1969	401992	403776	864.9103139	276.205157	0.31935
hypothetical protein	1968	403775	403903	640.625	386.71875	0.60366
plasmid stability protein	1967	404462	404884	93.60189573	58.6492891	0.62658
6-phospho-3-hexuloisomerase	1966	404894	405463	84.35852373	63.2688928	0.75
ABC transporter, permease protein	1965	405501	408662	49.03511547	18.5068016	0.37742
ABC transporter, ATP-binding protein	1964	408652	409353	89.87161198	38.5164051	0.42857
Glycosyltransferase	1963	409367	410578	39.63666391	29.7274979	0.75
hypothetical protein	1962	410596	411330	47.0027248	24.5231608	0.52174
hypothetical protein	1961	411359	411622	11.40684411	0	0
Calcium-binding acidic-repeat protein precursor		411623	412969	22.65973254	3.34323923	0.14754
Adenylate cyclase (EC 4.6.1.1)	1959	412985	415642	25.59277381	0	0
hypothetical protein	1958	415639	416046	54.05405405	11.0565111	0.20455
Calcium-binding acidic-repeat protein precursor	1957	416079	417953	33.92094017	6.00961538	0.17717
hypothetical protein	1956	418020	419696	29.23627685	6.7124105	0.22959
Integrase domain protein	1955	420125	421360	43.72469636	14.5748988	0.33333
hypothetical protein	1954	421513	421878	121.8836565	43.6288089	0.35795
hypothetical protein	1953	422141	422290	22.72727273	17.0454545	0.75
hypothetical protein	1952	422711	422863	6.578947368	0	0
hypothetical protein	1951	423305	423448	13.98601399	0	0
putative DNA primase/helicase	1950	423743	425137	35.48153512	6.51701665	0.18367
hypothetical protein	1949	425137	425472	37.31343284	0	0
hypothetical protein	1948	425664	425954	18.90756303	0	0

hypothetical protein	1947	425965	427755	24.29514097	6.74865027	0.27778
hypothetical protein	1946	427752	428303	34.43113772	6.73652695	0.19565
hypothetical protein	1945	428304	428585	11.9047619	0	0
hypothetical protein	1944	428545	428832	11.96172249	0	0
hypothetical protein	1943	428825	429091	41.26213592	0	0
hypothetical protein	1942	429110	429283	43.35260116	0	0
Cell wall-associated hydrolases (invasion-associated proteins)	1941	429286	429810	28.43601896	5.33175355	0.1875
hypothetical protein	1940	429814	430071	41.83266932	0	0
hypothetical protein	1939	430081	431577	38.77005348	1.5040107	0.03879
hypothetical protein	1938	431574	432434	32.23140496	0	0
hypothetical protein	1937	432431	432895	23.33333333	0	0
hypothetical protein	1936	432892	433494	25.40650407	4.57317073	0.18
37-kD nucleoid-associated bacterial protein	1935	433830	434858	18.48249027	0	0
putative phage-related membrane protein	1934	434846	436051	8.713692946	3.73443983	0.42857
hypothetical protein	1933	436325	436561	90.90909091	61.3636364	0.675
hypothetical protein	1932	436558	437040	107.8838174	107.365145	0.99519
hypothetical protein	1931	437140	437313	0	14.8026316	#DIV/0!
hypothetical protein	1930	437899	438171	82.72058824	223.345588	2.7
Putative membrane protein	1929	438267	439148	15.32349603	2.553916	0.16667
sensor histidine kinase	1928	439502	440656	25.12998267	7.79896014	0.31034
DNA-binding response regulator	1927	440669	441361	21.67630058	13.0057803	0.6
hypothetical protein	1926	441351	441464	17.69911504	0	0
helix-turn-helix, Fis-type	1925	441769	443046	165.6225529	137.43148	0.82979
hypothetical protein	1924	443142	443390	16.73640167	9.41422594	0.5625
hypothetical protein	1922	443534	443815	320.2846975	296.263345	0.925
hypothetical protein	1923	443808	444290	3.112033195	0	0
hypothetical protein	1921	444481	445380	3.337041157	2.50278087	0.75
Transcriptional regulator, Cro/CI family	1920	445381	445740	54.31754875	37.6044568	0.69231
hypothetical protein	1919	445838	446044	109.223301	76.4563107	0.7
hypothetical protein	1918	446124	446402	71.94244604	40.4676259	0.5625
hypothetical protein	1917	446613	446726	13.27433628	0	0
hypothetical protein	1916	446888	447259	40.43126685	0	0
hypothetical protein	1915	447306	447563	13.61867704	0	0
hypothetical protein	1914	447575	448081	20.75098814	0	0
Major capsid protein, HK97 family	1913	448145	449452	36.58536585	15.9323367	0.43548
hypothetical protein	1912	449511	450173	42.29607251	0	0
DNA-binding response regulator, LuxR family	1911	450186	450836	23.07692308	0	0
Portal protein	1910	450829	452076	26.65589661	3.63489499	0.13636
Phage DNA Packaging Protein	1909	452073	453296	25.49342105	0	0
hypothetical protein	1908	453299	453841	43.35793358	0	0
hypothetical protein	1907	453828	453965	47.44525547	0	0
hypothetical protein	1905	454426	454584	47.46835443	14.2405063	0.3
Integrase	1906	454581	455972	32.35082674	3.23508267	0.1
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	1903	456411	458345	231.1271975	324.58635	1.40436
Molybdopterin-guanine dinucleotide biosynthesis protein B	1904	458327	458845	65.63706564	117.277992	1.78676
4-hydroxybenzoyl-CoA thioesterase family active site	1901	458901	459302	182.0448878	252.493766	1.38699
D-alanine--D-alanine ligase (EC 6.3.2.4)	1902	459299	460396	138.1039198	164.083865	1.18812
Fatty acid degradation regulator YsiA, TetR family	1900	460499	461113	90.39087948	65.9609121	0.72973

Methyltransferase (EC 2.1.1.-); N6-adenine-specific DNA methylase	1899	461122	462279	207.8651685	210.025929	1.0104
Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, alpha subunit (EC 2.7.1.90)	1898	462380	463723	357.7810871	464.072971	1.29709
hypothetical protein	1897	463740	465032	167.5696594	193.304954	1.15358
hypothetical protein	1896	465091	465339	36.29032258	27.2177419	0.75
hypothetical protein	1895	465492	465626	7.462686567	0	0
hypothetical protein	1894	465709	466233	40.07633588	72.9961832	1.82143
hypothetical protein	1893	466238	466972	39.50953678	42.9155313	1.08621
NADH-dependent dehydrogenase	1891	467019	468107	450.8272059	390.854779	0.86697
hypothetical tRNA/rRNA methyltransferase yfiF [EC:2.1.1.-]	1892	468104	468889	129.9363057	117.515924	0.90441
Alanyl-tRNA synthetase family protein	1890	468934	470145	155.2436003	113.336086	0.73005
hypothetical protein	1889	470182	470847	72.18045113	47.3684211	0.65625
Mce family protein	1888	470866	472326	120.890411	103.253425	0.85411
Methionine ABC transporter ATP-binding protein	1887	472323	473075	85.7712766	47.8723404	0.55814
ABC-type transport system involved in resistance to organic solvents, permease component	1886	473072	473836	64.13612565	41.2303665	0.64286
Proline-rich protein	1885	473925	474788	205.0984936	284.183082	1.38559
hypothetical protein	1884	474913	475209	94.59459459	114.02027	1.20536
B. burgdorferi predicted coding region BB0418	1883	475512	476522	167.8217822	189.356436	1.12832
Membrane proteins related to metalloendopeptidases	1882	476643	477686	424.2569511	526.366251	1.24068
hypothetical protein	1881	477694	478140	329.5964126	479.26009	1.45408
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	1880	478172	478711	121.5213358	146.103896	1.20229
Signal peptidase-like protein	1878	478704	479669	217.0301142	226.635514	1.04426
Transcriptional regulator, ArsR family	1879	479644	479934	74.13793103	77.5862069	1.04651
hypothetical protein	1877	479928	480137	4.784688995	0	0
Helix-turn-helix domain protein	1876	480217	480540	201.2383901	202.012384	1.00385
CTP synthase (EC 6.3.4.2)	1875	480590	482224	223.9358421	306.755089	1.36983
hypothetical protein	1874	482226	482834	203.125	325.657895	1.60324
Lipopolysaccharide ABC transporter, ATP-binding protein LptB	1873	482836	483588	105.0531915	116.68883	1.11076
Periplasmic sugar-binding proteins	1872	483585	484562	64.48311157	27.6356192	0.42857
two-component sensor histidine kinase	1871	484559	486079	49.67105263	31.0855263	0.62583
DNA-binding response regulator	1870	486064	487572	38.12997347	26.8567639	0.70435
L-arabinose-binding periplasmic protein precursor araF (TC 3.A.1.2.2)	1869	487725	488873	8839.368617	10203.3426	1.15431
L-arabinose transport ATP-binding protein araG (TC 3.A.1.2.2)	1868	489002	490528	521.0740993	746.430999	1.43249
L-arabinose transport system permease protein (TC 3.A.1.2.2)	1867	490540	491733	302.3156089	360.849057	1.19362
Uroporphyrinogen decarboxylase (EC 4.1.1.37)	1866	491752	492753	262.2377622	352.897103	1.34571
Xylose ABC transporter, periplasmic xylose-binding protein xylF	1865	492814	493920	110.7594937	122.061483	1.10204
Alpha-glucosidase (EC 3.2.1.20)		494758	495849	47.66269478	26.8102658	0.5625
Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)		495878	496459	33.56282272	50.3442341	1.5

Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1862	496463	497836	66.27822287	39.3299345	0.59341
hypothetical protein	1861	497889	498197	76.2987013	58.4415584	0.76596
Integrase domain protein	1860	498325	499560	39.27125506	5.46558704	0.13918
hypothetical protein	1859	499708	501207	69.04603069	37.5250167	0.54348
hypothetical protein	1858	501217	501825	69.90131579	40.7072368	0.58235
MukB N-terminal domain/M protein repeat protein	1857	501822	505034	42.96388543	23.1164384	0.53804
hypothetical protein	1856	505031	506257	42.82218597	9.17618271	0.21429
Transcriptional regulator	1855	506293	506880	34.07155026	15.3321976	0.45
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1854	506877	508223	27.90178571	8.37053571	0.3
sensory box histidine kinase/response regulator	1852	508377	509798	36.94581281	17.4173118	0.47143
diguanylate cyclase (GGDEF domain) with PAS/PAC sensor		509795	510850	91.46919431	110.900474	1.21244
sensory box histidine kinase/response regulator	1851	510831	512555	86.13689095	66.5603248	0.77273
hypothetical protein	1849	512776	513678	78.15964523	52.383592	0.67021
hypothetical protein	1850	513667	513825	25.3164557	28.4810127	1.125
Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	1848	513835	514974	101.8437226	114.574188	1.125
hypothetical protein	1846	515041	515412	397.574124	436.657682	1.09831
hypothetical protein	1847	515405	515527	61.47540984	55.3278689	0.9
TRNA/rRNA methyltransferase	1845	515481	516287	96.77419355	72.5806452	0.75
DinB family protein	1844	516308	516826	37.64478764	34.7490347	0.92308
Beta-galactosidase (EC 3.2.1.23)	1843	516907	518958	35.59239395	10.9702584	0.30822
Maltose/maltodextrin ABC transporter, permease protein MalG	1842	518972	519856	7.918552036	2.54524887	0.32143
Possible alpha-xyloside ABC transporter, permease component	1841	519853	520800	28.51108765	4.75184794	0.16667
ABC-type sugar transport system, periplasmic component	1840	520862	522199	74.42034405	80.7778609	1.08543
Beta-galactosidase (EC 3.2.1.23)	1839	522258	525533	34.35114504	20.610687	0.6
MSM (multiple sugar metabolism) operon regulatory protein	1838	525697	526722	32.19512195	19.7560976	0.61364
PUTATIVE ZINC PROTEASE PROTEIN	1837	526726	527820	79.06764168	63.7568556	0.80636
hypothetical protein	1836	527839	528609	458.4415584	391.558442	0.85411
Aldehyde dehydrogenase B (EC 1.2.1.22)	1835	528694	530175	36.12424038	15.1924375	0.42056
Methyl-accepting chemotaxis protein	1834	530312	532423	213.8796779	293.107532	1.37043
hypothetical protein	1833	532481	532933	117.2566372	84.6238938	0.7217
Tetrapyrrole (Corrin-Porphyrin) methylase family protein UPF0011	1832	532935	533639	178.2670455	150.213068	0.84263
hypothetical protein	1831	533676	533960	1394.366197	1584.50704	1.13636
Alcohol dehydrogenase (EC 1.1.1.1)	1830	534035	535180	134.9344978	149.344978	1.1068
hypothetical protein	1829	535195	535326	41.98473282	34.351145	0.81818
hypothetical protein	1828	535281	536429	115.4181185	117.595819	1.01887
hypothetical protein	1827	536464	536607	10.48951049	31.4685315	3
sensory box histidine kinase/response regulator	1826	537864	539819	176.6275347	188.500534	1.06722

Lysyl-tRNA synthetase (class I) (EC 6.1.1.6)	1825	539910	541538	166.1528977	196.979038	1.18553
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)		541561	542559	79.15831663	65.3807615	0.82595
Beta-mannosidase (EC 3.2.1.25)	1823	542566	545016	191.6326531	180	0.9393
hypothetical protein		545133	545378	202.0408163	211.22449	1.04545
Ferrous iron transport protein B	1821	545375	547450	95.96695821	95.1166181	0.99114
Putative RNA 2'-O-ribose methyltransferase mtfA (EC 2.1.1.-)	1820	547453	548394	99.36238045	124.335813	1.25134
hypothetical protein	1819	548391	548795	233.9108911	317.450495	1.35714
Transcriptional regulator, MerR family	1818	548839	549423	214.8972603	331.335616	1.54183
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	1817	549444	551093	229.2298363	290.630685	1.26786
hypothetical protein	1816	551097	551216	281.512605	189.07563	0.67164
2-oxoglutarate oxidoreductase, gamma subunit (EC 1.2.7.3)	1815	551327	551860	380.8630394	346.153846	0.90887
2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3)	1814	551857	552627	485.0649351	412.012987	0.8494
2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3)	1813	552627	553721	516.4533821	526.508227	1.01947
2-oxoglutarate oxidoreductase, delta subunit, putative (EC 1.2.7.3)	1812	553718	553948	210.8695652	244.565217	1.15979
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	1811	554033	555505	131.7934783	148.267663	1.125
Isochorismatase (EC 3.3.2.1)	1810	555517	556020	23.85685885	13.4194831	0.5625
RNA polymerase sigma factor RpoD	1809	556337	557227	66.85393258	106.179775	1.58824
ankyrin repeat protein, putative	1808	557218	557757	776.4378479	818.181818	1.05376
Phosphate butyryltransferase (EC 2.3.1.19)	1807	557775	558704	177.0721206	155.005382	0.87538
Probable oxidoreductase protein	1806	558764	559936	220.9897611	190.059727	0.86004
Sugar phosphate isomerases/epimerases	1805	559945	560937	236.8951613	235.887097	0.99574
Ribose ABC transporter, periplasmic ribose-binding protein rbsB (TC 3.A.1.2.1)	1804	560984	561997	55.77492596	48.8647581	0.87611
Transcriptional regulator, TetR family	1803	562090	563331	246.9782434	458.702659	1.85726
Acriflavin resistance protein	1802	563480	564862	551.3748191	905.209841	1.64173
Probable Co/Zn/Cd efflux system membrane fusion protein	1801	564876	565844	535.6404959	869.318182	1.62295
RND multidrug efflux transporter; Acriflavin resistance protein	1800	565854	569108	441.1493546	761.985249	1.72727
ortholog to Borrelia burgdorferi BB0139	1799	569108	569401	373.7201365	575.938567	1.5411
hypothetical protein	1798	569445	569651	262.1359223	349.514563	1.33333
hypothetical protein	1797	569723	570496	258.0853816	419.146184	1.62406
Probable peptidyl-prolyl cis-trans isomerase	1796	570551	571540	530.8392315	625.631951	1.17857
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	1795	571703	572872	311.3772455	329.127459	1.05701
Recombination protein RecR	1794	572898	573506	95.39473684	92.5164474	0.96983
conserved protein of unknown function likely to be involved in DNA repair	1793	573503	573841	217.4556213	166.420118	0.76531
DNA polymerase III subunits gamma and tau (EC 2.7.7.7)	1792	573843	575255	232.1299639	181.949458	0.78383
hypothetical protein	1791	575558	576067	28.48722986	13.2612967	0.46552
Uncharacterized protein aq_aa25	1790	576153	576761	16.44736842	11.1019737	0.675
hypothetical protein	1789	576764	577045	39.14590747	16.0142349	0.40909
Transcriptional regulator, MerR family	1788	577114	577491	13.26259947	5.96816976	0.45
Small multidrug export protein	1787	577513	578004	92.66802444	77.9022403	0.84066
5-nitroimidazole antibiotic resistance protein	1786	578102	578572	222.3404255	277.659574	1.2488

L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	1785	578613	579347	279.2915531	337.19346	1.20732
Ribulokinase (EC 2.7.1.16)	1784	579347	581026	349.6128648	361.822513	1.03492
hypothetical protein	1783	581051	581962	307.9034029	303.787047	0.98663
Thymidylate synthase thyX (EC 2.1.1.-)	1782	582034	582870	93.89952153	67.284689	0.71656
hypothetical protein	1781	582887	583231	56.68604651	71.9476744	1.26923
Chitinase (EC 3.2.1.14)	1780	583232	584944	94.04205607	143.253505	1.52329
unknown	1779	584957	585904	159.9788807	142.555438	0.89109
hypothetical protein	1775	586382	586570	138.2978723	71.8085106	0.51923
4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	1774	586594	587253	69.04400607	47.7996965	0.69231
Glucose-6-phosphate isomerase (EC 5.3.1.9)	1773	587241	587378	40.1459854	0	0
hypothetical protein		587623	587754	86.95652174	122.282609	1.40625
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	1769	587867	588853	201.8255578	219.066937	1.08543
Transketolase (EC 2.2.1.1)	1768	588885	590855	466.751269	529.949239	1.1354
DNA binding protein/PTS system, IIA component	1767	590906	591391	123.7113402	129.896907	1.05
ORF encoded in ISPre3	1766	591405	593381	166.7510121	169.660931	1.01745
Collagen binding protein Cna	1765	593572	595089	152.9334212	468.6882	3.06466
hypothetical protein	1764	595452	595664	28.30188679	10.6132075	0.375
TRAP-type C4-dicarboxylate transport system, periplasmic component	1763	595910	596923	308.6053412	364.985163	1.18269
TRAP-type C4-dicarboxylate transport system, large permease component	1762	596923	598788	100.4849138	110.317888	1.09786
hypothetical protein	1761	598801	599625	128.1895504	155.832321	1.21564
hypothetical protein	1760	599654	601600	90.44193217	105.215827	1.16335
hypothetical protein	1759	601629	603746	27.86962683	19.1308455	0.68644
hypothetical protein	1758	603743	607720	49.40910234	25.4588886	0.51527
hypothetical protein	1757	608169	608333	18.29268293	13.7195122	0.75
Kinesin light chain	1756	608437	613572	31.1587147	27.1665044	0.87188
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	1755	613643	614206	87.92184725	83.9253996	0.95455
Homolog of plant auxin-responsive GH3-like protein	1754	614290	615990	470.3748489	472.037485	1.00353
Homolog of plant auxin-responsive GH3-like protein	1753	616029	617729	294.8870392	346.462545	1.1749
Hsp20/alpha crystallin family protein	1752	618218	618667	6596.88196	5131.40312	0.77785
FOG: WD40 repeat	1751	618744	621686	56.25424881	24.4731475	0.43505
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	1750	621723	622997	107.9277865	98.9010989	0.91636
hypothetical protein	1749	623053	623253	20	0	0
hypothetical protein	1748	623360	623500	0	0	#DIV/0!
Plasmid stabilization system	1747	623504	623839	2.985074627	0	0
RNP-1 like RNA-binding protein	1746	624362	624664	2554.421769	3053.57143	1.19541
hypothetical protein	1745	624709	624900	531.4136126	659.685864	1.24138
DNA repair protein RadA	1744	624978	626354	130.7356154	73.7436271	0.56407
Adenine deaminase (EC 3.5.4.2)	1742	626411	628156	58.16618911	47.7077364	0.8202
Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen-III synthase (EC 4.2.1.75)	1743	628134	629669	81.43322476	41.0423453	0.504
Porphobilinogen deaminase (EC 2.5.1.61)	1741	629666	630616	91.57894737	66.3157895	0.72414

Siroheme synthase / Precorrin-2 oxidase (EC 1.3.1.76)	1740	630613	631194	139.4148021	89.070568	0.63889
Mov34/MPN/PAD-1	1739	631201	631605	201.7326733	100.247525	0.49693
ThiS, thiamine-biosynthesis	1738	631599	631808	124.4019139	64.5933014	0.51923
Sulfate-binding protein sbp	1737	631985	633055	228.0373832	10.5140187	0.04611
Sulfate transport system permease protein cysT	1736	633067	633927	38.91509434	0	0
Sulfate transport system permease protein cysW	1735	633924	634754	36.74698795	0	0
Sulfate and thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)	1734	634751	635824	103.4482759	18.8723206	0.18243
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10)	1733	635814	636512	138.9684814	64.469914	0.46392
Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	1732	636520	637422	100	32.5	0.325
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25)	1731	637422	638783	101.7634093	47.9426892	0.47112
Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	1730	638836	639660	291.2621359	229.368932	0.7875
hypothetical protein	1729	639660	639929	433.0855019	443.30855	1.02361
Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits	1728	639926	640792	271.9399538	280.600462	1.03185
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1727	640851	642227	33.52769679	9.83965015	0.29348
S-adenosylmethionine synthetase (EC 2.5.1.6)	1726	642364	643539	22.55319149	1.91489362	0.08491
Radical SAM domain protein	1725	643536	644756	29.50819672	7.37704918	0.25
hypothetical protein	1724	644784	645806	21.037182	8.80626223	0.4186
Taurine transport ATP-binding protein tauB	1723	645816	646664	34.19811321	10.6132075	0.31034
Taurine transport system permease protein tauC	1722	646676	647473	29.48557089	2.82308657	0.09574
Nitrogenase iron protein (EC 1.18.6.1)	1721	647477	648352	34.28571429	5.14285714	0.15
Nitrogenase vanadium-cofactor synthesis protein VnfE	1720	648353	649774	16.18578466	1.58339198	0.09783
Nitrogenase vanadium-cofactor synthesis protein VnfN	1719	649774	651114	27.98507463	25.1865672	0.9
Chaperone protein HtpG	1718	651138	653051	534.7621537	728.044956	1.36144
hypothetical protein	1717	653077	653193	17.24137931	19.3965517	1.125
transcriptional regulator, Cro/CI family	1716	653636	653932	60.81081081	22.8040541	0.375
hypothetical protein	1715	654108	654332	17.85714286	10.0446429	0.5625
VapC toxin protein	1714	654329	654724	17.72151899	0	0
transcriptional regulator, Cro/CI family	1713	654931	655227	45.60810811	38.0067568	0.83333
Beta-lactamase (EC 3.5.2.6)	1712	655224	655604	10.52631579	0	0
hypothetical protein	1711	655631	656251	21.77419355	0	0
hypothetical protein	1710	656414	656623	19.13875598	0	0
hypothetical protein	1709	656727	657281	5.165289256	0	0
hypothetical protein	1708	657284	657550	22.72727273	12.7840909	0.5625
transposase, mutator family	1707	657616	658857	48.34810637	38.0741338	0.7875
Large extracellular alpha-helical protein	1706	659203	665115	87.87212449	70.4076455	0.80125
Small-conductance mechanosensitive channel	1705	665133	665954	53.59317905	46.589525	0.86932

Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	1704	665941	668322	48.50902982	43.4691306	0.8961
hypothetical protein	1703	668347	670581	49.01521934	19.1360788	0.39041
Uracil-DNA glycosylase (EC 3.2.2.-)	1702	670578	670787	162.6794258	75.3588517	0.46324
Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)	1701	670836	672581	172.7793696	242.406877	1.40299
GTP-binding protein EngA	1700	672578	673945	107.1689832	125.091441	1.16724
Transcriptional regulator, MerR family	1699	673947	674300	63.73937677	76.4872521	1.2
Conserved domain protein	1698	674287	675510	49.05968929	33.1152903	0.675
D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	1697	675565	676452	69.33483653	48.1961669	0.69512
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1696	676453	677889	84.26183844	84.6100279	1.00413
hypothetical protein	1695	677905	678018	0	0	#DIV/0!
Transcriptional regulator, ArsR family	1694	678069	678419	34.28571429	45	1.3125
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	1692	678420	680405	49.37027708	43.0730479	0.87245
hypothetical protein	1693	680380	680502	0	0	#DIV/0!
hypothetical protein	1691	680503	681153	774.6153846	1810.38462	2.33714
hypothetical protein	1690	681256	682269	131.2931885	333.168806	2.53759
hypothetical protein	1689	682501	682620	4.201680672	0	0
hypothetical protein		682623	684758	17.56440281	12.64637	0.72
Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1)	1687	684801	691094	27.09359606	16.0893056	0.59384
Kinesin light chain	1686	691106	695242	22.12282398	9.24806576	0.41803
hypothetical protein	1684	695520	696794	71.03610675	75.9419152	1.06906
RNA polymerase sigma-54 factor rpoN	1683	696697	698238	56.78131084	36.5022713	0.64286
Ribosome hibernation protein YhbH	1682	698266	698556	87.93103448	46.5517241	0.52941
Glutathione peroxidase (EC 1.11.1.9)	1681	698574	699104	73.58490566	84.9056604	1.15385
transcriptional regulator, MarR family	1680	699172	699675	25.84493042	13.4194831	0.51923
Nitroreductase	1679	699743	700279	56.90298507	50.3731343	0.88525
Excinuclease ABC subunit C	1978	700313	702328	86.35235732	45.7816377	0.53017
Conserved protein	1677	702358	702885	56.9259962	42.6944972	0.75
Corrinoid methyltransferase protein	1676	703029	703664	672.4409449	818.503937	1.21721
probable electron transfer protein	1675	703725	705215	60.40268456	45.3020134	0.75
CO dehydrogenase accessory protein CooC (nickel insertion)	1674	705230	706000	44.80519481	26.2987013	0.58696
probable electron transfer protein	1673	706000	707988	37.9778672	16.9768612	0.44702
hypothetical protein	1672	707985	708626	24.96099844	7.02028081	0.28125
hypothetical protein	1671	708742	708867	0	0	#DIV/0!
hypothetical protein	1670	708870	709061	0	0	#DIV/0!
PIN domain protein	1669	709058	709441	9.868421053	0	0
Ig domain protein, group 2 domain protein	1668	709691	711643	34.32377049	2.30532787	0.06716
hypothetical protein	1667	711909	712055	10.2739726	0	0
hypothetical protein	1666	712097	712462	10.95890411	0	0
hypothetical protein	1664	712461	712595	0	0	#DIV/0!
BarA-associated response regulator UvrY (= GacA = SirA)	1665	712590	713216	23.1629393	10.7827476	0.46552
hypothetical protein	1663	713209	713838	38.95071542	7.15421304	0.18367

Sensor histidine kinase	1661	713925	715127	54.0765391	20.5906822	0.38077
Oxidoreductase (EC 1.1.1.-)	1662	715117	716265	85.80139373	54.8780488	0.63959
Inosose dehydratase (EC 4.2.1.44)	1660	716262	717086	87.37864078	43.6893204	0.5
hypothetical protein	1659	717103	718317	46.54036244	11.1202636	0.23894
Catabolite control protein A	1658	718319	719380	30.1602262	12.7238454	0.42188
Maltose/maltodextrin ABC transporter, permease protein MalF	1657	719689	720609	23.91304348	12.2282609	0.51136
Maltose/maltodextrin ABC transporter, permease protein MalG	1656	720625	721485	34.30232558	15.6976744	0.45763
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	1655	721550	722845	83.3976834	93.8223938	1.125
Sugar phosphate isomerase/epimerase	1654	722863	723699	32.29665072	40.3708134	1.25
hypothetical protein	1653	723724	724788	49.81203008	42.2932331	0.84906
hypothetical protein	1651	724820	725662	736.935867	908.551069	1.23288
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	1652	725659	726465	189.2059553	212.158809	1.12131
Carbon monoxide dehydrogenase CooS subunit (EC 1.2.99.2)	1650	726682	728577	83.11345646	49.8680739	0.6
CO dehydrogenase accessory protein CooC (nickel insertion)	1649	728574	729356	39.64194373	11.5089514	0.29032
CO dehydrogenase/acetyl-CoA synthase, acetyl-CoA synthase subunit (EC 2.3.1.169)	1648	729392	731521	54.25082198	44.3870362	0.81818
Acetyl-CoA synthase corrinoid iron-sulfur protein, small subunit	1647	731567	732508	137.6195537	126.726886	0.92085
Acetyl-CoA synthase corrinoid iron-sulfur protein, large subunit	1645	732530	733861	228.7753569	218.069121	0.9532
hypothetical protein	1646	733842	733964	0	0	#DIV/0!
5-methyltetrahydrofolate:corrinoid iron-sulfur protein methyltransferase	1644	733929	734714	168.1528662	183.43949	1.09091
hypothetical protein	1643	734726	734995	100.3717472	58.5501859	0.58333
hypothetical protein	1642	734995	735198	44.33497537	33.2512315	0.75
hypothetical protein	1641	735251	735373	20.49180328	0	0
hypothetical protein	1640	735342	735455	26.54867257	0	0
hypothetical protein		735724	736380	108.2317073	89.1768293	0.82394
Fibronectin type III domain protein		736340	737284	107.5211864	100.105932	0.93103
TPR Domain containing protein	1637	737299	739896	170.3889103	129.091259	0.75763
Metal-dependent phosphohydrolase, HD subdomain	1636	739886	740746	97.09302326	75.872093	0.78144
Metal-dependent hydrolases of the beta-lactamase superfamily I	1635	740757	741668	83.4248079	79.0340285	0.94737
Sensory box histidine kinase/response regulator	1634	741677	743947	64.0969163	35.6828194	0.5567
Transcriptional regulator, LuxR family	1633	743966	744580	51.3029316	14.6579805	0.28571
hypothetical protein	1632	744610	745635	108.7804878	100.97561	0.92825
Putative malate dehydrogenase (EC 1.1.1.37), similar to archaeal MJ1425	1631	745651	746769	504.4722719	428.667263	0.84973
Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP-specific)	1630	746813	747931	76.47584973	40.2504472	0.52632
Low-specificity L-threonine aldolase (EC 4.1.2.5)	1629	747928	748977	215.4432793	242.373689	1.125
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	1628	748997	750838	169.6672122	139.934534	0.82476

Mannose-6-phosphate isomerase	1627	750848	751147	272.5752508	255.852843	0.93865
hypothetical protein	1626	751121	751270	483.2214765	302.013423	0.625
Flagellar biosynthesis protein fliL	1625	751296	751748	51.99115044	29.8672566	0.57447
hypothetical protein	1624	751827	752162	88.05970149	53.7313433	0.61017
RNA polymerase sigma factor RpoE	1623	752159	752761	73.92026578	29.9003322	0.40449
hypothetical protein	1622	752740	753228	45.08196721	13.8319672	0.30682
Glycogen phosphorylase (EC 2.4.1.1)	1620	753320	755860	506.1143984	568.934911	1.12412
Proteophosphoglycan	1621	755847	756236	1359.897172	1636.88946	1.20369
Putative preQ0 transporter	1618	756399	757124	109.6551724	71.3793103	0.65094
Sugar (Glycoside-Pentoside-Hexuronide) transporter		757105	757476	115.902965	97.0350404	0.83721
Predicted b-glucoside transporter, GPH family		757476	758459	87.99593082	57.2227874	0.65029
Antiholin-like protein LrgA	1616	758526	758882	21.06741573	44.241573	2.1
lrgA-associated membrane protein LrgB	1615	758885	759565	46.32352941	9.92647059	0.21429
Cysteine synthase (EC 2.5.1.47)	1614	759639	760532	167.9731243	100.783875	0.6
Mov34/MPN/PAD-1	1613	760529	760954	161.1764706	111.176471	0.68978
9.5 kDa culture filtrate antigen cfp10A	1612	760945	761223	196.0431655	226.618705	1.15596
Sulfur carrier protein adenylyltransferase ThiF	1610	761230	762402	352.8156997	203.498294	0.57678
Conserved domain protein	1611	762399	763658	71.88244639	51.8268467	0.72099
Alkaline phosphodiesterase I (EC 3.1.4.1) / Nucleotide pyrophosphatase (EC 3.6.1.9)	1609	763715	764638	119.7183099	92.6327194	0.77376
Major membrane protein I	1608	764817	765758	573.8575983	346.705632	0.60417
Cysteine desulfurase (EC 2.8.1.7)	1607	765745	767220	334.9152542	213.559322	0.63765
hypothetical protein	1606	767235	767453	105.5045872	30.9633028	0.29348
hypothetical protein	1605	767533	767754	11.31221719	20.361991	1.8
Serine acetyltransferase (EC 2.3.1.30)	1604	767738	768691	80.27282267	68.4679958	0.85294
Methionine gamma-lyase (EC 4.4.1.11)	1603	768679	769908	75.26444264	51.261188	0.68108
hypothetical protein	1602	769917	770507	30.50847458	7.62711864	0.25
Cysteine synthase (EC 2.5.1.47)	1601	770504	771481	43.50051177	2.30296827	0.05294
ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	1600	771493	772371	24.48747153	5.12528474	0.2093
ABC transporter permease protein with unknown substrate	1599	772448	773284	4.784688995	0	0
putative nitrate transport system substrate-binding protein	1598	773388	774440	44.20152091	19.2490494	0.43548
hypothetical protein	1597	774604	774723	50.42016807	18.907563	0.375
hypothetical protein	1596	774759	774917	132.9113924	142.405063	1.07143
hypothetical protein	1595	775182	775433	29.88047809	53.7848606	1.8
Chromosome (plasmid) partitioning protein ParB / Stage 0 sporulation protein J	1594	775458	776333	171.4285714	228.857143	1.335
Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein soj	1593	776323	777087	167.539267	220.876963	1.31836
hydrolase, haloacid dehalogenase-like family	1592	777156	777974	180.3178484	145.782396	0.80847
anti-sigma B factor RsbT	1591	777978	778958	125.5102041	149.234694	1.18902
hypothetical protein	1590	778955	779299	140.9883721	98.1104651	0.69588
hypothetical protein	1589	779283	780071	83.12182741	51.3959391	0.61832
Probable lipoprotein nlpC precursor	1588	780084	781226	51.66374781	21.6725044	0.41949
Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	1587	781436	786145	221.0840802	381.241997	1.72442
Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	1585	786155	787609	266.5061898	490.543329	1.84065

Thiol:disulfide oxidoreductase related to ResA	1586	787606	788154	86.67883212	61.5875912	0.71053
Protein crcB homolog	1583	788233	788610	17.24137931	17.9045093	1.03846
Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)	1584	788591	789286	31.65467626	16.1870504	0.51136
Hydrolase (HAD superfamily)	1581	789315	790178	76.4774044	93.8586327	1.22727
Ribokinase (EC 2.7.1.15)	1582	790175	791074	55.61735261	110.122358	1.98
Ribose operon repressor	1580	791071	792093	70.45009785	158.51272	2.25
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	1579	792325	793317	9.576612903	47.6310484	4.97368
maltose/maltodextrin transport permease	1578	793317	794204	22.54791432	88.7824126	3.9375
ABC transporter substrate-binding protein - sugar transport	1577	794228	795781	38.31294269	547.64971	14.2941
hypothetical protein	1576	795901	798039	23.85406922	203.110384	8.51471
putative membrane protein	1575	798115	799464	6.671608599	75.0555967	11.25
Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)	1574	799701	800621	23.36956522	100.271739	4.2907
hypothetical protein		800794	801102	12.98701299	0	0
Putative cytoplasmic protein	1572	801426	802460	58.0270793	65.2804642	1.125
putative membrane protein	1571	802536	803888	62.13017751	99.852071	1.60714
Acetyltransferase, GNAT family	1570	803906	805063	61.36560069	89.4554883	1.45775
hypothetical protein	1569	805095	806372	72.04385278	52.8582616	0.7337
Adenylosuccinate lyase (EC 4.3.2.2)	1568	806428	807894	97.67759563	169.057377	1.73077
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	1567	807887	809323	235.3760446	401.114206	1.70414
hypothetical protein	1566	809396	810088	98.98843931	152.817919	1.5438
Adenylosuccinate synthetase (EC 6.3.4.4)	1565	810172	811398	227.1615008	291.80261	1.28456
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	1564	811420	813009	137.1932033	143.014475	1.04243
Magnesium transporter	1563	813227	814564	71.05459985	74.0463725	1.04211
ATP-dependent DNA helicase pcrA (EC 3.6.1.-)	1562	814574	817801	42.31246125	33.4779913	0.79121
ATP:Cob(I)alamin adenosyltransferase (EC 2.5.1.17), ethanolamine utilization	1560	817838	818359	92.13051823	47.5047985	0.51563
putative membrane protein	1561	818349	818957	43.58552632	7.40131579	0.16981
hypothetical protein	1558	818937	819077	7.142857143	0	0
hypothetical protein	1559	819074	820114	1483.653846	1821.63462	1.2278
Chromosome partition protein smc	1557	820322	823339	190.0894929	346.784886	1.82432
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19); Multiple sugar ABC transporter, ATP-binding protein	1556	823568	824686	850.1788909	1376.5653	1.61915
Cold-shock DEAD-box protein A	1554	824789	826690	270.9100473	207.127827	0.76456
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	1555	826662	827327	26.31578947	20.3007519	0.77143
Transcriptional regulator, AraC family	1553	827358	828737	15.59100798	3.26323423	0.2093
Transcriptional regulator, AraC family	1552	828734	829843	18.48512173	0	0
Transcriptional activator of maltose regulon, MalT	1551	829927	832437	51.19521912	34.9601594	0.68288
Flagellar motor switch protein fliG	1550	832504	833712	101.8211921	121.067881	1.18902
Metalloprotease, insulinase family	1549	833709	836738	66.02839221	58.6827336	0.88875
hypothetical protein	1548	836763	837005	115.7024793	55.785124	0.48214
MG(2+) CHELATASE FAMILY PROTEIN / ComM-related protein	1547	837125	838732	32.66957063	7.00062228	0.21429

hypothetical protein	1546	838813	839121	95.77922078	102.272727	1.0678
hypothetical protein	1544	839081	839386	75.40983607	88.5245902	1.17391
COG0613, Predicted metal-dependent phosphoesterases (PHP family)	1545	839370	840221	128.6721504	100.470035	0.78082
hypothetical protein	1543	840328	840699	54.49591281	12.2615804	0.225
Peroxide stress regulator PerR, FUR family	1542	841069	841590	34.54894434	34.5489443	1
Chlorohydrolase family protein		841656	842882	403.3442088	475.326264	1.17846
transcriptional regulator, Crp/Fnr family	1540	842895	843887	339.2137097	369.707661	1.0899
transcriptional regulator, Crp/Fnr family	1539	843888	844532	340.0621118	310.947205	0.91438
LPXTG anchored putative adhesin	1538	844954	846927	1412.569691	2074.37912	1.46851
Iron-sulfur flavoprotein	1537	847136	847831	142.4460432	168.345324	1.18182
Rrf2 family transcriptional regulator	1536	847831	848229	18.84422111	11.3065327	0.6
Carbon monoxide dehydrogenase CooS subunit (EC 1.2.99.2)	1535	848295	850181	117.709438	84.7030753	0.71959
Nitrite reductase probable electron transfer 4Fe-S subunit (EC 1.7.1.4)	1534	850192	850659	61.02783726	48.1798715	0.78947
Nitrite reductase probable [NAD(P)H] subunit (EC 1.7.1.4)	1533	850661	851884	107.9313164	69.9100572	0.64773
hypothetical protein	1531	852183	852704	63.33973129	51.8234165	0.81818
INTEGRAL MEMBRANE PROTEIN (Rhomboid family)	1530	852704	853453	89.45260347	51.0680908	0.5709
Uncharacterized membrane protein	1529	853450	854406	46.0251046	16.4748954	0.35795
5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases	1528	854403	855887	28.97574124	7.58086253	0.26163
hypothetical protein	1527	855880	856998	29.96422182	34.2128801	1.14179
MoxR-like ATPase	1526	856995	858002	89.87090367	87.1400199	0.96961
POSSIBLE CONSERVED MEMBRANE PROTEIN	1525	858009	859349	43.65671642	33.5820896	0.76923
NAD(P)H oxidoreductase YRKL (EC 1.6.99.-); Putative NADPH-quinone reductase (modulator of drug activity B); Flavodoxin 2	1524	859362	859952	46.61016949	22.8813559	0.49091
Hydroxyethylthiazole kinase (EC 2.7.1.50)	1523	859970	860779	50.0618047	33.3745365	0.66667
hypothetical protein	1522	860829	861203	28.07486631	18.0481283	0.64286
hypothetical protein	1521	861296	861559	15.20912548	8.55513308	0.5625
Predicted N6-adenine-specific RNA methylase containing THUMP domain	1520	861615	862640	35.12195122	10.9756098	0.3125
Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)	1519	862659	867281	97.74599046	124.837451	1.27716
hypothetical protein	1518	867292	867432	14.28571429	16.0714286	1.125
hypothetical protein	1517	867432	867587	90.32258065	29.0322581	0.32143
hypothetical protein	1516	867690	867836	95.89041096	61.6438356	0.64286
Cell surface protein	1515	867837	869153	38.37386018	11.9680851	0.31188
Transposase (class II)	1514	869275	870306	37.82735209	21.8234724	0.57692
Cell surface protein	1513	870413	873301	12.11911357	0	0
hypothetical protein	1512	873375	873728	43.90934844	25.4957507	0.58065
hypothetical protein	1511	873841	876009	69.18819188	51.8911439	0.75
hypothetical protein	1510	876074	877204	77.43362832	49.7787611	0.64286
RNA polymerase sigma-70 factor, group 3	1509	877271	877582	48.23151125	7.23472669	0.15
ActD		877579	877890	32.15434084	0	0
Ferrichrome-iron receptor	1506	877902	879908	21.68494516	6.72981057	0.31034
Virulence factor mviN homolog	1507	879886	881478	38.31658291	9.89321608	0.2582

Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	1505	881471	882247	74.74226804	66.6881443	0.89224
PspA/IM30 family protein	1504	882247	882741	78.94736842	50.1012146	0.63462
Glycerate kinase (EC 2.7.1.31)	1503	882734	883876	115.58669	66.9877408	0.57955
Putative predicted metal-dependent hydrolase	1502	883914	884606	42.6300578	19.5086705	0.45763
Alkanesulfonates ABC transporter ATP-binding protein	1501	884661	885443	44.75703325	11.5089514	0.25714
Alkanesulfonates transport system permease protein	1500	885440	886441	91.90809191	22.4775225	0.24457
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1499	886456	887469	188.0552813	68.8548865	0.36614
hypothetical protein	1498	887598	887873	23.63636364	8.18181818	0.34615
O-acetylhomoserine sulfhydrylase (EC 4.2.99.10) / O-succinylhomoserine sulfhydrylase (EC 4.2.99.9)	1497	888099	889409	80.15267176	51.5267176	0.64286
Nitrogenase (EC 1.18.6.1)	1496	889412	890878	70.94133697	47.5784447	0.67067
Nitrogenase (EC 1.18.6.1)	1495	890882	892234	61.76035503	34.9482249	0.56587
Histone acetyltransferase HPA2 and related acetyltransferases	1494	892255	892725	2.127659574	0	0
hypothetical protein	1493	892719	892850	7.633587786	17.1755725	2.25
transposase, mutator family	1492	893082	894323	55.19742143	43.5132957	0.78832
Transcriptional regulator, MarR family	1491	894397	894735	35.50295858	19.9704142	0.5625
Transposase	1490	895015	896124	40.57709648	16.2308386	0.4
hypothetical protein	1488	896188	896529	10.26392962	0	0
FeMo cofactor biosynthesis protein NifB	1489	896526	897446	58.15217391	2.44565217	0.04206
Nitrogenase iron protein (EC 1.18.6.1)	1487	897462	898340	154.3280182	30.7517084	0.19926
Cysteine synthase (EC 2.5.1.47)	1486	898388	899338	94.21052632	16.5789474	0.17598
hypothetical protein	1485	899391	899528	0	0	#DIV/0!
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1484	899596	900666	56.07476636	8.41121495	0.15
ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	1483	900753	901589	31.10047847	0	0
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	1482	901586	902521	13.90374332	4.81283422	0.34615
Methylcobalamin:coenzyme M methyltransferase, methylamine-specific	1481	902532	903575	24.44870566	4.31447747	0.17647
Nitrogenase (EC 1.18.6.1)	1480	903568	905073	15.28239203	1.49501661	0.09783
Nitrogenase vanadium-cofactor synthesis protein VnfN	1479	905073	906470	23.62204724	3.22118826	0.13636
Dimethylamine methyltransferase corrinoid protein	1478	906483	907145	34.74320242	13.5951662	0.3913
Methylcobalamin:coenzyme M methyltransferase, methylamine-specific	1477	907145	908179	30.46421663	0	0
probable electron transfer protein	1476	908181	909800	22.85361334	0	0
Methylcobalamin:coenzyme M methyltransferase, methylamine-specific	1475	909806	910645	17.28247914	2.681764	0.15517
Predicted molybdate-responsive regulator YvgK in bacilli	1474	910694	911605	31.28430296	7.40944018	0.23684
Spermidine/putrescine-binding protein	1473	911612	912655	32.11888782	17.2579099	0.53731
ABC transporter, ATP-binding protein	1472	912657	913448	22.12389381	14.2225032	0.64286
Ni2+-binding GTPase involved in regulation of expression and maturation of hydrogenase	1471	913441	914163	31.1634349	9.34903047	0.3

methlytransferase, UbiE/COQ5 family	1470	914160	914801	42.90171607	14.0405616	0.32727
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1)	1469	914788	915537	36.04806409	24.0320427	0.66667
BNR repeat domain protein	1468	915698	916789	86.15948671	82.4931256	0.95745
Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain	1467	916841	918664	63.35710368	69.1168404	1.09091
TonB-dependent receptor	1466	918685	920823	19.87839102	4.20954163	0.21176
Ferric siderophore transport system, periplasmic binding protein TonB	1465	920855	921484	109.6979332	85.8505564	0.78261
ABC transporter, solute-binding protein	1464	921561	922631	42.52336449	27.3364486	0.64286
Vitamin B12 ABC transporter, permease component BtuC	1463	922621	923622	36.46353646	22.4775225	0.61644
ABC transporter related	1462	923619	924407	19.03553299	5.7106599	0.3
Outer membrane lipoprotein omp16 precursor	1461	924472	925647	81.27659574	57.4468085	0.70681
Ferritin-like protein 2	1460	925723	926247	435.1145038	541.030534	1.24342
hypothetical protein	1459	926271	926387	60.34482759	19.3965517	0.32143
Heat shock protein 60 family chaperone GroEL	1458	926411	928057	4053.918495	5684.95298	1.40234
NAD binding oxidoreductase	1457	928326	929324	250.501002	288.577154	1.152
Ribonuclease HI (EC 3.1.26.4)	1456	929330	929788	206.3318777	235.80786	1.14286
Treponemal membrane protein A precursor (Antigen tmpA) (Membrane protein A)	1455	929914	931014	1138.181818	1210.90909	1.0639
Treponemal membrane protein B precursor (Antigen tmpB)	1454	931011	931961	2471.578947	1726.57895	0.69857
ADP-ribose pyrophosphatase (EC 3.6.1.13)	1453	932029	932583	134.4765343	174.638989	1.29866
Cytidylate kinase (EC 2.7.4.14)	1452	932730	933551	244.2143727	219.244823	0.89776
ATPase	1451	933591	934829	40.79159935	34.5315024	0.84653
Integrase domain protein	1450	934978	936213	57.89473684	10.9311741	0.18881
Thermostable carboxypeptidase 1 (EC 3.4.17.19)	1448	936361	937893	216.383812	279.046997	1.28959
hypothetical protein	1449	937850	937972	65.57377049	36.8852459	0.5625
hypothetical protein	1447	938042	938497	140.6593407	118.681319	0.84375
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	1446	938540	939124	43.66438356	26.9691781	0.61765
hypothetical protein		940960	941085	0	0	#DIV/0!
hypothetical protein	1443	941158	941277	0	0	#DIV/0!
Hypothetical lipoprotein	1439	944937	946172	926.7206478	1032.99595	1.11468
tRNA nucleotidyltransferase, A-adding (EC 2.7.7.-)	1438	946311	947654	65.89724497	55.2866716	0.83898
Glycyl-tRNA synthetase (EC 6.1.1.14)	1437	947701	949074	346.6860889	358.885652	1.03519
Fe-S oxidoreductase	1435	949180	950775	37.93103448	22.5705329	0.59504
Esterase/lipase	1436	950770	951972	42.01331115	33.6938436	0.80198
Chloride channel protein		951971	952882	48.84742042	27.1679473	0.55618
Voltage-gated chloride channel		952873	953292	53.69928401	21.4797136	0.4
DNA polymerase II (EC 2.7.7.7)	1432	953289	955760	36.44136808	14.6579805	0.40223
oxidoreductase, short-chain dehydrogenase/reductase family	1431	955778	956545	106.2581486	76.2711864	0.71779
SN-glycerol-3-phosphate transport system permease protein ugpA (TC 3.A.1.1.3)	1430	956604	957473	36.24856157	20.7134638	0.57143
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	1429	957470	958309	49.4636472	34.8629321	0.70482

Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	1428	958325	959698	219.592134	140.932265	0.64179
Cardiolipin synthetase (EC 2.7.8.-)		959739	961235	86.56417112	75.2005348	0.86873
YciO family	1426	961235	961855	182.2580645	163.306452	0.89602
Uncharacterized protein TP_0552	1425	961862	962305	130.9255079	132.054176	1.00862
RNA polymerase sigma factor RpoD	1424	962528	963388	126.1627907	170.05814	1.34793
Possible divergent polysaccharide deacetylase	1423	963436	964533	271.6499544	201.002735	0.73993
Endopeptidase essential in most Bacteria (E. coli YgjD/B. subtilis YdiE)	1422	964533	965585	156.3688213	147.576046	0.94377
Kef-type K+ transport systems (NAD-binding component fused to domain related to exopolyphosphatase)	1421	965600	966580	203.0612245	236.479592	1.16457
LSU ribosomal protein L28p	1419	966648	966839	1287.958115	2356.02094	1.82927
Metal-dependent hydrolases of the beta-lactamase superfamily I; PhnP protein	1420	966823	967713	106.741573	106.179775	0.99474
hypothetical protein	1418	967746	967916	97.05882353	13.2352941	0.13636
Alpha-L-fucosidase (EC 3.2.1.51)	1417	967952	969439	48.08338937	43.8802959	0.91259
Xylose repressor XylR (ROK family)	1416	969440	970654	45.30477759	20.3871499	0.45
Hypothetical zinc-type alcohol dehydrogenase-like protein YphC	1415	970717	971778	137.606032	122.997172	0.89384
Aldo-keto reductase family 1 member B10 (EC 1.1.1.-)	1414	971778	972791	213.2280355	153.257651	0.71875
Uncharacterized protein TP_0677	1413	972849	973424	180	117.391304	0.65217
ABC transporter, periplasmic spermidine putrescine-binding protein potD (TC_3.A.1.11.1)	1412	973460	974512	223.8593156	295.152091	1.31847
Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	1411	974531	975400	71.92174914	124.280783	1.728
Spermidine Putrescine ABC transporter permease component potB (TC_3.A.1.11.1)	1410	975397	976299	63.74722838	87.3059867	1.36957
Spermidine Putrescine transport ATP-binding protein potA (TC_3.A.1.11.1)	1409	976299	977432	267.493357	312.887511	1.1697
Possible DNA-binding protein	1408	977542	980652	94.69453376	86.0932476	0.90917
Acetylornithine deacetylase (EC 3.5.1.16)	1407	980687	981910	181.5208504	167.41619	0.9223
UDP-glucose 4-epimerase (EC 5.1.3.2)	1406	981900	982913	220.1382034	244.323791	1.10987
hypothetical protein	1405	983473	984132	578.1487102	949.165402	1.64173
COG0488: ATPase components of ABC transporters with duplicated ATPase domains	1404	984199	986283	144.6737044	134.956814	0.93284
Uncharacterized protein TP_0260	1403	986287	987834	191.6612799	191.984486	1.00169
hypothetical protein		987873	990200	197.6794156	129.565965	0.65543
Alpha-mannosidase (EC 3.2.1.24)	1401	990207	993023	166.5482955	142.223011	0.85394
hypothetical protein	1400	993124	994161	120.0578592	112.825458	0.93976
Probable HIT family protein	1399	994171	994515	188.9534884	209.302326	1.10769
sensory box histidine kinase/response regulator	1397	994475	996850	95.57894737	94.7368421	0.99119
tRNA uridine 5-carboxymethylaminomethyl modification enzyme gidA	1398	996841	998631	55.30726257	41.4804469	0.75
Alpha-xylosidase (EC 3.2.1.-)	1396	998670	1000679	64.21105027	49.2782479	0.76744
Na+ driven multidrug efflux pump	1395	1000680	1002035	50.55350554	31.5498155	0.62409
GTPase and tRNA-U34 5-formylation enzyme TrmE	1394	1002063	1003586	51.54300722	31.0242942	0.60191

Phosphatidylglycerophosphatase B (EC 3.1.3.27)	1393	1003586	1004599	52.81342547	39.9802567	0.75701
hypothetical protein	1392	1004609	1005319	17.6056338	3.16901408	0.18
hypothetical protein	1391	1005316	1006869	28.33226014	23.1809401	0.81818
Alanine racemase (EC 5.1.1.1)	1390	1006944	1008041	79.76298997	73.8377393	0.92571
Formate--tetrahydrofolate ligase (EC 6.3.4.3)	1389	1008038	1009777	90.28177113	77.6308223	0.85987
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	1388	1009817	1010602	458.5987261	601.910828	1.3125
Peptidyl-tRNA hydrolase (EC 3.1.1.29)	1387	1010655	1011248	193.0860034	295.952782	1.53275
Beta-lactamase class C and other penicillin binding proteins	1386	1011324	1012718	71.37733142	75.8608321	1.06281
hypothetical protein	1385	1012720	1013583	91.54113557	70.3939745	0.76899
tetrapyrrole methylase family protein/MazG family protein	1383	1013587	1014369	91.43222506	46.0358056	0.5035
B. burgdorferi predicted coding region BB0351	1384	1014362	1015906	215.6735751	234.617876	1.08784
Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	1382	1015967	1019530	949.1910304	1174.49617	1.23737
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	1381	1019630	1020832	217.9700499	211.522463	0.97042
hypothetical protein	1380	1020899	1021042	34.96503497	31.4685315	0.9
Conserved domain protein	1379	1021071	1021367	16.89189189	7.60135135	0.45
Prevent-host-death family protein	1378	1021357	1021641	61.61971831	39.6126761	0.64286
hypothetical protein	1377	1021631	1021780	33.55704698	15.1006711	0.45
hypothetical protein	1376	1021940	1022266	49.0797546	55.2147239	1.125
Mucin-associated surface protein	1375	1022409	1022990	1113.597246	1095.95525	0.98416
hypothetical protein	1374	1023076	1025529	43.82388912	34.8552792	0.79535
hypothetical protein	1373	1025583	1026671	97.42647059	122.012868	1.25236
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	1372	1026679	1027470	189.6333755	270.22756	1.425
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	1371	1027486	1028640	248.7001733	306.109185	1.23084
Anaerobic nitric oxide reductase flavorubredoxin		1028727	1029734	238.3316783	321.747766	1.35
Metallo-beta-lactamase family protein		1029797	1029940	293.7062937	534.965035	1.82143
Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	1368	1029999	1030436	337.5286041	324.370709	0.96102
tRNA dihydrouridine synthase B (EC 1.-.-.-)	1367	1030408	1031577	101.7964072	90.4619333	0.88866
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	1366	1031583	1032554	81.87435633	71.8331617	0.87736
Adenylate kinase (EC 2.7.4.3)	1365	1032575	1033201	447.284345	456.469649	1.02054
Metal transporter, ZIP family	1364	1033290	1034105	134.9693252	110.429448	0.81818
hypothetical protein	1363	1034153	1034704	70.78039927	65.3357532	0.92308
L-rhamnose isomerase (EC 5.3.1.14)	1362	1034799	1036034	510.5263158	615.789474	1.20619
Rhamnulokinase (EC 2.7.1.5)	1361	1036071	1037474	255.8802566	362.437634	1.41643
Pheromone shutdown protein	1360	1037497	1038696	175.5629691	217.681401	1.2399
TPR repeat		1038716	1040155	141.0701876	217.338429	1.54064
hypothetical protein	1358	1040253	1042061	102.8761062	78.4015487	0.7621
TPR domain protein	1357	1042064	1044289	54.83146067	47.5280899	0.8668
Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-)	1356	1044301	1046748	94.80997139	94.7078055	0.99892

hypothetical protein	1355	1046787	1046900	35.39823009	0	0
Trehalase (EC 3.2.1.28)	1354	1046983	1048407	268.5512367	512.014134	1.90658
Superfamily II DNA/RNA helicases, SNF2 family	1353	1048812	1049270	43.66812227	14.7379913	0.3375
Exopolyphosphatase (EC 3.6.1.11)	1352	1049412	1050944	125.9791123	93.9947781	0.74611
Polyphosphate kinase (EC 2.7.4.1)	1351	1050956	1053082	86.99763593	88.2978723	1.01495
COG1092 family predicted tRNA methylase	1350	1053084	1054418	179.1604198	114.692654	0.64017
Na+/H+ antiporter	1349	1054512	1056605	68.08408982	55.9006211	0.82105
hypothetical protein	1348	1056627	1057235	65.78947368	25.9046053	0.39375
DNA polymerase III delta subunit (EC 2.7.7.7)	1347	1057243	1058223	104.5918367	130.867347	1.25122
SOS-response repressor and protease LexA (EC 3.4.21.88)	1346	1058220	1058846	405.7507987	427.715655	1.05413
Two component, sigma54 specific, transcriptional regulator, Fis family	1345	1058857	1060248	89.50395399	63.0841121	0.70482
Nitrogen regulation protein NtrY	1344	1060245	1062002	52.64655663	46.101309	0.87568
Phosphocarrier protein, nitrogen regulation associated	1343	1061999	1062265	148.4962406	219.924812	1.48101
HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)	1342	1062277	1063266	216.8857432	270.728008	1.24825
hypothetical protein	1341	1063279	1063392	17.69911504	0	0
Amino-acid ABC transporter ATP-binding protein PebC	1340	1063367	1064089	128.1163435	190.096953	1.48378
Major cell-binding factor precursor PebA	1339	1064104	1064907	264.6326276	308.219178	1.16471
Putative ABC-type amino-acid transporter permease protein	1338	1064926	1065645	109.8748261	134.561892	1.22468
Putative ABC-type amino-acid transporter permease protein	1337	1065642	1066334	34.68208092	42.2687861	1.21875
hypothetical protein	1336	1066747	1066986	89.958159	94.1422594	1.04651
Conserved domain protein	1335	1067094	1067969	77.71428571	90	1.15809
ATP-dependent DNA helicase RecQ	1334	1068058	1069653	29.78056426	1.41065831	0.04737
hypothetical protein	1333	1069630	1069746	4.310344828	0	0
Cystine-binding periplasmic protein precursor	1332	1069829	1070644	363.190184	303.680982	0.83615
Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine	1331	1070659	1071336	158.0502216	112.998523	0.71495
Glutamine transport ATP-binding protein glnQ (TC 3.A.1.3.2)	1330	1071352	1072110	209.762533	189.973615	0.90566
Indolepyruvate oxidoreductase subunit iorA (EC 1.2.7.8)	1329	1072107	1074137	117.2413793	90.8866995	0.77521
Indolepyruvate oxidoreductase, subunit B	1328	1074134	1074751	115.0729335	105.753647	0.91901
Phenylacetate-coenzyme A ligase (EC 6.2.1.30); Coenzyme F390 synthetase	1327	1074838	1076067	43.93816111	75.0610252	1.70833
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)	1326	1076094	1076834	102.7027027	136.824324	1.33224
Branched-chain amino acid transport ATP-binding protein livG (TC 3.A.1.4.1)	1325	1076844	1077617	62.09573092	98.9650712	1.59375
Branched-chain amino acid transport system permease protein livM (TC 3.A.1.4.1)	1324	1077614	1078660	52.20306513	60.3448276	1.15596
High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	1323	1078668	1079579	47.59238522	52.9115342	1.11176
Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	1322	1079598	1080764	329.7598628	364.708405	1.10598

Iron-sulfur cluster regulator IscR	1321	1080892	1081326	243.0875576	186.635945	0.76777
Iron-sulfur cluster regulator IscR	1320	1081323	1081754	196.0556845	187.935035	0.95858
Cystathionine gamma-synthase (EC 2.5.1.48)	1319	1081751	1082950	295.2460384	208.298582	0.70551
Cystathionine beta-lyase (EC 4.4.1.8)	1318	1082988	1084148	324.137931	281.25	0.86769
Carotenoid cis-trans isomerase (EC 5.2.-.-)	1317	1084222	1085700	70.70365359	42.6251691	0.60287
Sucrose transport protein	1316	1085710	1087008	74.34514638	31.201849	0.41969
GTP-binding and nucleic acid-binding protein YchF	1315	1087033	1088163	161.0619469	225	1.39698
ATP-dependent DNA helicase RecQ	1314	1088172	1090130	65.1174668	64.351379	0.98824
cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	1313	1090194	1090643	142.5389755	175.389755	1.23047
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)	1312	1090758	1092593	1541.21179	1720.66048	1.11643
HtrA protease/chaperone protein	1311	1092665	1094362	77.78432528	60.9899823	0.78409
Methyl-accepting chemotaxis protein	1310	1094976	1095431	179.1208791	360.989011	2.01534
LL-diaminopimelate aminotransferase	1309	1095939	1097144	173.0290456	210.995851	1.21942
Diaminopimelate decarboxylase (EC 4.1.1.20)	1308	1097207	1098481	260.5965463	342.621664	1.31476
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	1307	1098478	1099578	257.7272727	259.772727	1.00794
hypothetical protein	1305	1099665	1100126	104.1214751	97.6138829	0.9375
Dihydrodipicolinate synthase (EC 4.2.1.52)	1306	1100113	1101018	186.7403315	238.674033	1.27811
Dihydrodipicolinate reductase (EC 1.3.1.26)	1304	1101015	1101800	150.3184713	146.178344	0.97246
Aspartokinase (EC 2.7.2.4)	1303	1101810	1103150	127.8026906	164.798206	1.28947
hypothetical protein	1302	1103420	1103554	242.5373134	251.865672	1.03846
hypothetical protein	1301	1103595	1103807	247.6415094	382.075472	1.54286
Ribonuclease II family protein	1299	1103937	1105910	99.84794729	101.495185	1.0165
hypothetical protein	1300	1105897	1106796	102.8921023	127.641824	1.24054
hypothetical protein	1298	1106799	1107950	89.48740226	107.515204	1.20146
Chemotaxis protein CheA (EC 2.7.3.-)	1297	1108040	1110433	487.8711836	745.294856	1.52765
Positive regulator of CheA protein activity (CheW)	1296	1110458	1111807	487.3980726	878.984433	1.80342
Chemotaxis protein CheX	1295	1111845	1112330	972.0430108	1437.09677	1.47843
Cell surface protein	1293	1112471	1113376	95.5801105	77.0718232	0.80636
LSU ribosomal protein L33p	1291	1113659	1113805	2267.123288	3883.56164	1.71299
Preprotein translocase subunit SecE (TC 3.A.5.1.1)	1289	1113932	1114111	351.9553073	653.631285	1.85714
Transcription antitermination protein NusG	1288	1114129	1114686	468.5816876	1009.87433	2.15517
LSU ribosomal protein L11p (L12e)	1287	1114820	1115251	2354.988399	3659.51276	1.55394
LSU ribosomal protein L1p (L10Ae)	1286	1115248	1115931	1262.079063	1769.03367	1.40168
LSU ribosomal protein L10p (P0)	1285	1115933	1116481	1439.781022	2373.17518	1.64829
LSU ribosomal protein L7/L12 (L23e)	1284	1116613	1116993	1002.631579	2007.23684	2.00197
DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	1283	1117146	1120781	497.3655019	1028.91015	2.06872
DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	1282	1120792	1125546	545.7991156	1093.01958	2.0026
Glutamine transport ATP-binding protein glnQ (TC 3.A.1.3.2)	1281	1125564	1126316	171.8538566	270.97429	1.57677
amino acid ABC transporter, permease protein	1280	1126332	1127033	97.71754636	118.758916	1.21533
Amino acid ABC transporter, amino acid-binding protein	1279	1127034	1127852	375.9168704	528.117359	1.40488
Diaminopimelate epimerase homolog	1278	1127937	1128737	67.5	70.3125	1.04167

hypothetical protein	1277	1128802	1129743	82.35919235	117.162593	1.42258
hypothetical protein	1276	1129775	1129921	3.424657534	0	0
hypothetical protein	1275	1130118	1131407	4907.292475	10307.4088	2.10043
Copper chaperone	1274	1131692	1131892	552.5	427.5	0.77376
hypothetical protein	1273	1131864	1131983	8.403361345	0	0
Acyltransferase domain protein	1272	1131989	1133338	78.94736842	91.7346182	1.16197
Zinc ABC transporter, periplasmic-binding protein ZnuA	1271	1133316	1134272	99.89539749	98.8493724	0.98953
Zinc ABC transporter, ATP-binding protein ZnuC	1270	1134269	1135066	101.0037641	124.215809	1.22981
Zinc ABC transporter, inner membrane permease protein ZnuB	1268	1135063	1135905	60.57007126	80.1662708	1.32353
Sugar/maltose fermentation stimulation protein homolog	1269	1135891	1136937	49.71319312	36.5678776	0.73558
Permease of the drug/metabolite transporter (DMT) superfamily	1267	1137086	1137988	69.84478936	94.789357	1.35714
RlpA-like lipoprotein precursor	1266	1138024	1138806	317.7749361	304.987212	0.95976
Transaldolase (EC 2.2.1.2)	1265	1138847	1139599	123.0053191	131.648936	1.07027
Substrate-specific component TrpP of tryptophan ECF transporter	1264	1139679	1140248	81.72231986	102.811951	1.25806
ATPase component of general energizing module of ECF transporters / ATPase component of general energizing module of ECF transporters		1140263	1141117	69.08665105	39.5199063	0.57203
ATPase component of general energizing module of ECF transporters / ATPase component of general energizing module of ECF transporters		1141120	1141962	48.6935867	50.7719715	1.04268
Transmembrane component of general energizing module of ECF transporters	1261	1141959	1142720	30.22339028	23.653088	0.78261
Fe-S-cluster-containing hydrogenase components 1	1260	1142730	1143131	201.9950125	140.274314	0.69444
Legionella vir region protein	1259	1143263	1144378	189.2376682	163.452915	0.86374
Excinuclease ABC subunit B	1258	1144737	1146794	90.42294604	129.071463	1.42742
hypothetical protein	1257	1146929	1148062	37.51103266	25.8164166	0.68824
hypothetical protein	1256	1148199	1148768	981.5465729	1126.97715	1.14816
hypothetical protein	1255	1148770	1149609	44.69606675	61.6805721	1.38
Putative lipoprotein	1254	1149654	1150283	252.782194	343.402226	1.35849
putative lipoprotein	1253	1150304	1151629	75.09433962	98.490566	1.31156
hypothetical protein	1252	1151617	1152840	92.8045789	128.781684	1.38767
Cell division protein ftsH (EC 3.4.24.-)	1251	1152870	1154636	142.412231	159.258211	1.11829
Beta-galactosidase (EC 3.2.1.23)	1250	1154734	1158063	186.5425053	274.406729	1.47101
Prolyl-tRNA synthetase (EC 6.1.1.15)	1249	1158135	1159976	230.8527974	265.209125	1.14882
serine/threonine protein phosphatase family protein	1248	1160050	1161399	66.34544107	48.3691623	0.72905
hypothetical protein	1247	1161519	1161815	128.3783784	167.22973	1.30263
Predicted cell-wall-anchored protein SasA (LPXTG motif)		1161944	1162945	31.46853147	17.982018	0.57143
Conserved domain protein	1245	1163290	1163598	27.5974026	0	0
hypothetical protein	1244	1163639	1163770	0	0	#DIV/0!
hypothetical protein	1243	1163809	1164822	17.76900296	0	0

TPR domain protein, putative component of TonB system	1242	1164825	1165496	20.86438152	0	0
hypothetical protein	1241	1165493	1166002	14.73477407	0	0
Type I secretion outer membrane protein, TolC precursor	1240	1166002	1167381	25.01812908	1.63161711	0.06522
Probable Co/Zn/Cd efflux system membrane fusion protein	1239	1167406	1168743	14.58489155	1.6828721	0.11538
hypothetical protein	1238	1169045	1170196	22.589053	0	0
conserved hypothetical lipoprotein	1237	1170186	1171730	14.24870466	0	0
RND multidrug efflux transporter; Acriflavin resistance protein	1236	1171739	1174789	19.01639344	2.95081967	0.15517
RND multidrug efflux transporter; Acriflavin resistance protein	1235	1174782	1177769	12.55440241	0	0
hypothetical protein	1234	1177792	1179999	14.72587222	0	0
Chromosome partition protein smc	1233	1180087	1186572	10.40863531	1.73477255	0.16667
hypothetical protein	1232	1186583	1187047	2.155172414	0	0
5'-methylthioadenosine phosphorylase (EC 2.4.2.28)	1231	1187090	1187836	270.1072386	340.817694	1.26179
hypothetical protein	1230	1187849	1188451	185.2159468	246.677741	1.33184
Methylthioribose-1-phosphate isomerase (EC 5.3.1.23)	1229	1188441	1189559	251.3416816	326.028623	1.29715
Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)	1228	1189590	1190510	492.9347826	645.652174	1.30981
Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)	1227	1190510	1191289	510.9114249	563.22208	1.10239
Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)	1226	1191279	1192616	568.4367988	637.808527	1.12204
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	1225	1192626	1193084	641.9213974	805.676856	1.2551
Short-chain alcohol dehydrogenase family	1224	1193081	1194349	555.5993691	640.57571	1.15295
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-)	1223	1194346	1194774	214.953271	273.364486	1.27174
3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41)	1222	1194776	1196056	739.0625	796.289063	1.07743
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	1221	1196069	1196803	497.9310345	642.413793	1.29017
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	1220	1196822	1197787	391.1917098	424.352332	1.08477
3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)	1219	1197831	1198856	664.8780488	627.804878	0.94424
hypothetical protein	1218	1198992	1199723	132.6949384	144.664843	1.09021
Uncharacterized protein TP_0273	1217	1199744	1200517	190.8150065	180.465718	0.94576
hypothetical protein	1216	1200553	1200810	2163.424125	2425.09728	1.12095
hypothetical protein	1215	1200918	1201808	52.80898876	15.1685393	0.28723
SSU ribosomal protein S21p	1214	1201828	1202001	526.0115607	1417.63006	2.69505
Membrane proteins related to metalloendopeptidases	1213	1202079	1203203	127.6690391	146.129893	1.1446
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	1212	1203200	1205341	131.2470808	139.771135	1.06495
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	1211	1205338	1206648	136.6412214	142.557252	1.0433
Recombination protein O	1210	1206666	1207403	113.2971506	91.587517	0.80838

Uncharacterized protein TP_0285	1209	1207467	1209059	66.89698492	70.6658291	1.05634
hypothetical protein	1208	1209127	1210056	52.20667384	53.2831001	1.02062
N-Acetylneuraminate cytidylyltransferase (EC 2.7.7.43)	1207	1210053	1210733	133.8235294	119.117647	0.89011
Cytidylyltransferase domain protein		1210730	1212523	46.01226994	27.607362	0.6
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	1205	1212584	1214143	91.08402822	60.6157793	0.66549
N-acetylmuramoyl-L-alanine amidase	1204	1214140	1215204	78.94736842	46.5225564	0.58929
hypothetical protein	1203	1215201	1215758	211.8491921	282.764811	1.33475
Flagellar filament outer layer protein precursor (Sheath protein)	1202	1215834	1216868	3212.282398	4308.51064	1.34126
GTP pyrophosphokinase (EC 2.7.6.5)	1200	1216967	1218190	88.71627146	158.217498	1.78341
Na+-driven multidrug efflux pump	1201	1218156	1219520	30.05865103	14.8460411	0.4939
Dipeptide transport ATP-binding protein dppF (TC 3.A.1.5.2)	1199	1219537	1220370	53.42136855	10.8043217	0.20225
Dipeptide transport ATP-binding protein dppD (TC 3.A.1.5.2)	1198	1220357	1221406	54.81410867	36.4632984	0.66522
DppC-3 ABC transporter, permease component	1197	1221409	1222380	59.21730175	32.4407827	0.54783
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	1196	1222382	1223395	46.39684107	46.6436328	1.00532
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	1195	1223457	1225220	153.7152581	151.871809	0.98801
hypothetical protein	1194	1225286	1226284	29.05811623	24.7995992	0.85345
Trimethylamine corrinoid protein 2	1193	1226281	1227339	29.30056711	19.1398866	0.65323
oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	1192	1227424	1229196	198.6455982	159.988713	0.8054
hypothetical protein	1191	1229354	1231375	109.351806	80.1583375	0.73303
hypothetical protein	1190	1231956	1233185	48.82017901	18.3075671	0.375
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	1189	1233223	1234503	103.125	110.742188	1.07386
4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	1188	1234497	1235558	158.3411876	148.444863	0.9375
hypothetical protein	1187	1235559	1236122	476.0213144	563.499112	1.18377
TPR domain protein, putative component of TonB system	1186	1236213	1238036	117.1146462	123.422929	1.05386
Phosphate acetyltransferase (EC 2.3.1.8)	1185	1238174	1239169	761.3065327	682.914573	0.89703
hypothetical protein	1184	1239197	1239313	8.620689655	0	0
hypothetical protein	1183	1239332	1239541	0	0	#DIV/0!
hypothetical protein	1182	1239634	1240242	711.3486842	1324.83553	1.86243
hypothetical protein	1181	1240610	1240975	246.5753425	258.90411	1.05
TPR domain protein	1180	1240972	1241595	166.9341894	292.536116	1.7524
MiaB family protein, possibly involved in tRNA or rRNA modification	1179	1241601	1242983	86.46888567	86.2879884	0.99791
hypothetical protein	1178	1243030	1243791	352.1681997	360.709593	1.02425
hypothetical protein	1177	1243803	1244966	130.266552	174.118659	1.33663
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	1175	1245472	1246314	26.12826603	24.0498812	0.92045
hypothetical protein	1174	1246349	1247113	24.86910995	29.4502618	1.18421
hypothetical protein	1173	1247115	1247912	21.32998745	16.9385194	0.79412
Multicopper oxidase	1172	1247925	1249382	23.33562114	16.9869595	0.72794
hypothetical protein	1171	1249409	1250824	56.18374558	52.4734982	0.93396

hypothetical protein	1170	1250905	1251705	56.25	39.375	0.7
hypothetical protein	1169	1251727	1252704	27.12384852	16.1207779	0.59434
Periplasmic binding protein precursor	1168	1252701	1253846	34.93449782	17.6855895	0.50625
Vitamin B12 ABC transporter, permease component BtuC	1167	1253847	1254926	24.09638554	6.2557924	0.25962
Vitamin B12 ABC transporter, permease component BtuC	1166	1254929	1255954	27.80487805	8.7804878	0.31579
Iron ABC transporter, ATP-binding protein	1165	1255945	1256742	26.9761606	5.64617315	0.2093
Fibronectin type III domain protein	1164	1257156	1262294	29.58349552	3.94122227	0.13322
hypothetical protein	1163	1262310	1263083	29.7542044	2.91073739	0.09783
Fibronectin type III domain protein	1162	1263268	1267059	23.60854656	4.74808758	0.20112
hypothetical protein	1161	1267167	1267298	0	0	#DIV/0!
hypothetical protein	1160	1267443	1268177	78.33787466	91.9618529	1.17391
DNA polymerase IV (EC 2.7.7.7)	1159	1268245	1269414	56.03079555	26.9461078	0.48092
Oxidoreductase, short chain dehydrogenase/reductase family	1158	1269449	1270237	786.1675127	759.517766	0.9661
FOG: CheY-like receiver	1157	1270242	1273970	195.8051802	208.403716	1.06434
hypothetical protein	1156	1273957	1274109	9.868421053	0	0
Flagellar hook-length control protein fliK	1155	1274168	1278517	104.966659	138.652564	1.32092
Flagellar hook-length control protein fliK	1154	1278519	1282337	94.2902043	111.380304	1.18125
Adenylate cyclase (EC 4.6.1.1)	1153	1282349	1284232	79.39458311	84.8380244	1.06856
hypothetical protein	1152	1284229	1287156	94.97779296	104.543902	1.10072
hypothetical protein	1151	1287146	1288414	67.42902208	53.2334385	0.78947
hypothetical protein	1150	1288415	1289959	56.99481865	52.4611399	0.92045
Cellulose synthase catalytic subunit [UDP-forming] (EC 2.4.1.12)	1149	1289975	1292434	52.25701505	71.3704758	1.36576
hypothetical protein	1148	1292431	1292628	65.98984772	11.4213198	0.17308
Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	1147	1292658	1294100	29.12621359	26.5256588	0.91071
hypothetical protein		1294111	1295427	64.96960486	58.1306991	0.89474
hypothetical protein	1145	1295424	1296770	77.63744428	76.8945022	0.99043
hypothetical protein	1144	1296788	1298293	32.55813953	34.3853821	1.05612
Beta-glucanase precursor (EC 3.2.1.73)	1143	1298309	1299256	83.94931362	80.781415	0.96226
Xanthan biosynthesis acetyltransferase GumF	1142	1299253	1301559	17.99653079	14.6357329	0.81325
Acyl-CoA thioesterase I	1141	1301552	1302292	49.32432432	42.5675676	0.86301
Beta-glucosidase (EC 3.2.1.21)		1302302	1303096	26.44836272	51.0075567	1.92857
Beta-glucosidase (EC 3.2.1.21)	1139	1303050	1303955	44.19889503	42.2651934	0.95625
hypothetical protein	1138	1303994	1304119	20	54	2.7
hypothetical protein	1137	1304229	1304588	59.88857939	62.6740947	1.04651
hypothetical protein	1136	1304601	1306805	46.27949183	37.7722323	0.81618
D amino acid oxidase (DAO) family (EC 1.4.3.3)	1135	1306821	1307906	146.0829493	197.004608	1.34858
hypothetical protein	1134	1308083	1310962	64.08475165	85.1858284	1.32927
5'-nucleotidase (EC 3.1.3.5)	1133	1310968	1314312	85.37679426	97.562799	1.14273
Outer membrane protein	1132	1314350	1317397	65.14604529	73.1046931	1.12217
Aminotransferase	1130	1317470	1318582	402.8776978	459.307554	1.14007
hypothetical protein	1131	1318579	1318692	61.94690265	39.8230088	0.64286
FOG: TPR repeat	1129	1318676	1320202	101.2450852	85.5176933	0.84466
type 4 fimbrial biogenesis protein PilY1	1127	1320288	1323590	931.2537856	845.623864	0.90805
hypothetical protein	1128	1323574	1323696	209.0163934	73.7704918	0.35294
Uncharacterized protein, related to enterotoxins of other Clostridiales	1126	1323669	1328528	212.5951842	259.775674	1.22193

Glycosyltransferase	1125	1328568	1329512	18.53813559	14.3008475	0.77143
hypothetical protein	1124	1329545	1330528	11.69888098	4.57782299	0.3913
hypothetical protein	1123	1330551	1331528	25.58853634	6.90890481	0.27
Polymyxin resistance protein ArnC, glycosyl transferase (EC 2.4.-.-)	1122	1331532	1332281	18.69158879	6.00801068	0.32143
Putative sugar translocase in surface polysaccharides biosynthesis	1121	1332297	1332737	12.5	0	0
Ser/Thr protein phosphatase family protein	1120	1332747	1333586	16.09058403	0	0
Cell surface protein IsdA, transfers heme from hemoglobin to apo-IsdC	1119	1333594	1335216	411.837238	151.202219	0.36714
Aspartyl-tRNA synthetase (EC 6.1.1.12); Aspartyl-tRNA(Asn) synthetase	1118	1335400	1336740	170.1492537	152.798507	0.89803
Putative sugar transporter	1117	1336737	1338146	55.35841022	27.1469127	0.49038
Putative sugar transporter	1116	1338154	1339521	71.3240673	39.5025604	0.55385
Hexokinase (EC 2.7.1.1)	1115	1339580	1340932	205.2514793	231.323964	1.12703
Fibronectin/fibrinogen-binding protein	1114	1340939	1342378	84.08617095	68.7977762	0.81818
Beta-hexosaminidase (EC 3.2.1.52)	1113	1342432	1343688	64.49044586	41.2022293	0.63889
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	1112	1343685	1344332	184.698609	128.670788	0.69665
Mll4958 protein	1111	1344363	1345616	203.1125299	143.655227	0.70727
hypothetical protein	1110	1345653	1346537	52.0361991	38.178733	0.7337
Oxidoreductase, aldo/keto reductase family	1109	1346635	1347555	229.8913043	100.271739	0.43617
hypothetical protein	1108	1347565	1348254	76.19738752	52.2496372	0.68571
hypothetical protein	1107	1348382	1348606	7.211538462	21.6346154	3
hypothetical protein	1106	1348965	1349573	289.4736842	510.690789	1.7642
hypothetical protein	1105	1349558	1349728	20.58823529	52.9411765	2.57143
Predicted cell-wall-anchored protein SasA (LPXTG motif)	1104	1349801	1351684	31.33297929	7.16941052	0.22881
Permease of the major facilitator superfamily	1103	1351690	1352976	74.65007776	68.2348367	0.91406
Methyl parathion hydrolase	1102	1353012	1353869	102.1003501	57.7596266	0.56571
FKBP-type peptidyl-prolyl cis-trans isomerase fkpA precursor (EC 5.2.1.8)	1101	1353938	1354870	220.4935622	246.244635	1.11679
Macrophage infectivity potentiator/GldI	1100	1354871	1355599	338.5989011	343.063187	1.01318
Nucleoside diphosphate kinase (EC 2.7.4.6)	1099	1355624	1356811	157.1187869	176.284751	1.12198
Translation elongation factor G	1098	1356916	1358991	137.5903614	119.277108	0.8669
Kynurenine formamidase, bacterial (EC 3.5.1.9)	1097	1359007	1359735	91.34615385	132.898352	1.45489
sensory box histidine kinase/response regulator	1096	1359750	1363502	88.30612791	134.265454	1.52045
Chromosome partitioning protein parB / Stage 0 sporulation protein J	1095	1363519	1363911	89.28571429	149.234694	1.67143
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)	1094	1363922	1366594	170.4715569	217.252994	1.27442
hypothetical protein	1093	1366629	1366850	214.953271	10.5140187	0.04891
hypothetical protein	1092	1366825	1367805	175	183.673469	1.04956
Membrane proteins related to metalloendopeptidases	1091	1367830	1368780	124.7368421	111.315789	0.89241
Ferredoxin	1090	1368780	1368950	2461.764706	3877.94118	1.57527
Fatty acid degradation regulator YsiA, TetR family	1089	1368990	1369871	129.3984109	183.881952	1.42105
hypothetical protein	1088	1369861	1370130	63.19702602	66.9144981	1.05882
MEMBRANE PROTEIN MOSC		1370197	1371339	199.2119089	242.338004	1.21648

UDP-glucose 4-epimerase (EC 5.1.3.2)	1086	1371345	1372379	1234.042553	1214.21663	0.98393
Integrase domain protein	1085	1372512	1373747	49.39271255	9.10931174	0.18443
hypothetical protein	1084	1373789	1373905	38.79310345	19.3965517	0.5
Aldo/keto reductase	1083	1373900	1375081	119.8137172	85.7324301	0.71555
Oxidoreductase (EC 1.1.1.-)	1082	1375151	1376014	502.3174971	474.507532	0.94464
hypothetical protein	1080	1376021	1376719	145.4154728	93.4813754	0.64286
hypothetical protein	1081	1376684	1379353	25.29037093	5.05807419	0.2
hypothetical protein	1079	1379380	1380459	43.09545876	16.6821131	0.3871
ACT domain containing transcriptional regulators, related to gcvR of E.coli		1380498	1383593	25.84814216	13.085622	0.50625
Chaperone protein DnaK	1077	1383595	1385766	48.36480884	37.3099954	0.77143
Chaperone protein DnaK	1076	1385770	1387413	109.2513694	87.6445526	0.80223
GrpE protein HSP-70 cofactor	1075	1387415	1388056	70.20280811	49.1419657	0.7
hypothetical protein	1074	1388076	1389677	37.78888195	32.3235478	0.85537
Integrase	1073	1389974	1391389	18.28358209	3.35820896	0.18367
hypothetical protein	1072	1391523	1391798	34.22053232	0	0
hypothetical protein	1071	1391782	1392387	41.32231405	0	0
Phage DNA Packaging Protein	1070	1392390	1393613	27.63819095	0	0
Portal protein	1069	1393610	1394866	14.95553759	0	0
BarA-associated response regulator UvrY (= GacA = SirA)	1068	1394856	1395578	24.33936022	3.12934631	0.12857
hypothetical protein	1067	1395559	1396233	28.18991098	0	0
Major capsid protein, HK97 family	1066	1396238	1397545	35.87962963	3.47222222	0.09677
hypothetical protein	1065	1397666	1397806	14.28571429	0	0
Bpl06	1064	1397867	1398289	17.1990172	5.52825553	0.32143
conserved domain protein	1063	1398339	1398845	8.893280632	0	0
hypothetical protein	1062	1398898	1399152	11.81102362	0	0
hypothetical protein	1061	1399210	1399509	21.73913043	0	0
hypothetical protein	1060	1399684	1399899	25.58139535	52.3255814	2.04545
hypothetical protein	1059	1400056	1400196	39.28571429	0	0
Type III restriction-modification system methylation subunit (EC 2.1.1.72)	1058	1400399	1402363	31.31364562	29.7861507	0.95122
Type III restriction-modification system DNA endonuclease res (EC 3.1.21.5)	1057	1402360	1404930	17.89883268	7.87937743	0.44022
hypothetical protein	1055	1404933	1406984	5.607020965	0	0
hypothetical protein	1056	1406968	1407099	0	0	#DIV/0!
hypothetical protein	1054	1407065	1407235	14.70588235	0	0
hypothetical protein	1052	1407270	1407437	86.82634731	94.3113772	1.08621
hypothetical protein	1053	1407426	1408196	7.142857143	17.5324675	2.45455
hypothetical protein	1051	1408333	1408725	108.4183673	143.494898	1.32353
probable transcription regulator NMA0738	1050	1408739	1409362	50.75593952	68.0345572	1.34043
COG1801: Uncharacterized conserved protein	1049	1409475	1410308	93.63525092	201.040392	2.14706
DNA polymerase IV (EC 2.7.7.7)	1048	1410274	1411491	83.26359833	82.8451883	0.99497
DNA polymerase III alpha subunit (EC 2.7.7.7)	1047	1411475	1414432	54.09202669	36.3540569	0.67208
protein of unknown function DUF262	1046	1414539	1416665	11.05362183	2.11665099	0.19149
hypothetical protein	1045	1417109	1417711	27.77777778	0	0
hypothetical protein	1044	1417708	1418136	26.86915888	0	0
hypothetical protein	1043	1418133	1418996	40.32258065	2.79156328	0.06923
hypothetical protein	1042	1418993	1420513	20.77151335	3.33827893	0.16071
hypothetical protein	1041	1420562	1420786	17.85714286	0	0
Putative lipoprotein	1040	1420790	1421299	8.84086444	0	0
hypothetical protein	1039	1421311	1421571	27.90697674	0	0

hypothetical protein	1038	1421568	1421855	20.7253886	0	0
hypothetical protein	1037	1421815	1422096	22.16748768	0	0
hypothetical protein	1036	1422097	1422648	41.81184669	0	0
hypothetical protein	1035	1422645	1424441	20.34482759	1.55172414	0.07627
hypothetical protein	1034	1424464	1424754	40.28436019	0	0
hypothetical protein	1033	1424941	1425294	18.41359773	0	0
putative DNA primase/helicase	1032	1425279	1426673	33.21167883	4.9270073	0.14835
hypothetical protein	1031	1427691	1427828	14.59854015	0	0
hypothetical protein	1030	1428039	1428173	74.62686567	16.7910448	0.225
hypothetical protein	1029	1428896	1429291	184.8101266	136.708861	0.73973
Putative cytoplasmic protein	1028	1429263	1431290	74.49432659	66.600888	0.89404
hypothetical protein	1026	1431472	1432566	66.72760512	71.9835466	1.07877
2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	1025	1432568	1434250	447.6190476	472.767857	1.05618
L-fucose isomerase related protein	1024	1434314	1435810	742.9812834	795.621658	1.07085
Menaquinone biosynthesis related protein, putative DHNA-CoA thioesterase	1023	1435863	1436747	102.3755656	78.9027149	0.77072
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)		1436748	1440104	235.998802	258.760108	1.09645
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)		1440114	1441280	273.5682819	295.374449	1.07971
Methyl-accepting chemotaxis protein	1020	1441519	1442010	122.1995927	160.386965	1.3125
hypothetical protein	1019	1442323	1442454	83.96946565	68.7022901	0.81818
Glucokinase (EC 2.7.1.2)	1018	1442540	1443436	156.25	148.158482	0.94821
ADP-heptose synthase (EC 2.7.-.-) / D-glycero-beta-D-manno-heptose 7-phosphate kinase	1017	1443484	1444584	192.2727273	192.272727	1
Phosphoheptose isomerase (EC 5.-.-.-)	1016	1444594	1445172	160.899654	194.636678	1.20968
hypothetical protein	1015	1445182	1446159	193.4493347	285.568066	1.47619
Haloacid dehalogenase domain protein hydrolase	1014	1446149	1446982	257.5030012	326.830732	1.26923
Ribose ABC transporter, periplasmic ribose-binding protein rbsB (TC 3.A.1.2.1)	1013	1447079	1448095	1707.677165	2263.2874	1.32536
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	1012	1448201	1449700	270.8472315	375.250167	1.38547
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	1011	1449697	1450668	154.9948507	143.666323	0.92691
NADH-dependent dehydrogenase	1010	1450673	1451761	125.4595588	163.373162	1.3022
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	1009	1451783	1452991	173.3001658	223.880597	1.29187
hypothetical protein	1008	1453041	1453355	57.32484076	28.6624204	0.5
hypothetical protein	1007	1453348	1453944	55.36912752	56.6275168	1.02273
hypothetical protein	1006	1454013	1454828	82.20858896	99.3865031	1.20896
Chromosome 14 contig 1, DNA sequence	1004	1454825	1456507	41.91438763	18.7277051	0.44681
Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	1005	1456504	1457121	160.4538088	138.573744	0.86364
Pentapeptide repeat family protein	1003	1457118	1457711	55.64924115	30.3541315	0.54545
hypothetical protein	1002	1457775	1458071	59.12162162	83.6148649	1.41429
Ribosome small subunit-stimulated GTPase EngC	1001	1458087	1459004	56.16139586	51.5267176	0.91748
Recombination inhibitory protein MutS2	1000	1459011	1461416	41.58004158	35.5509356	0.855
Alpha-galactosidase (EC 3.2.1.22)	999	1461425	1462849	29.84550562	37.9213483	1.27059
Lactoylglutathione lyase and related lyases	998	1462874	1463335	54.22993492	43.9262473	0.81
Ribose operon repressor	997	1463363	1464445	61.92236599	31.1922366	0.50373

L-xylulose 5-phosphate 3-epimerase (EC 5.1.3.-)	996	1464455	1465336	48.80817253	33.2009081	0.68023
Putative carbohydrate kinase, FGGY family	995	1465339	1466850	97.94837856	53.6068829	0.5473
hypothetical protein	994	1466860	1468077	26.29416598	7.39523418	0.28125
alpha-arabinosides ABC transport system, substrate-binding protein araN	993	1468358	1469689	17.28024042	10.1427498	0.58696
Sugar ABC transporter permease	992	1469775	1470671	8.928571429	2.51116071	0.28125
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	991	1470770	1471540	10.38961039	0	0
Dehydrogenase	990	1471597	1472739	11.82136602	1.97022767	0.16667
Sugar phosphate isomerases/epimerases	989	1472770	1473558	12.05583756	0	0
Sugar phosphate isomerases/epimerases	988	1473581	1474396	17.17791411	0	0
oxidoreductase of aldo/keto reductase family, subgroup 1	987	1474447	1475313	20.7852194	20.7852194	1
hypothetical protein	986	1475654	1477795	12.37739374	7.35637553	0.59434
hypothetical protein	985	1477813	1479027	14.82701812	7.41350906	0.5
Alpha-L-fucosidase (EC 3.2.1.51)	984	1479045	1481174	11.27289807	4.22733678	0.375
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	983	1481208	1482032	11.52912621	0	0
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	982	1482032	1482904	16.05504587	0	0
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	981	1482972	1484228	17.11783439	3.58280255	0.2093
Transcriptional (co)regulator CytR	980	1484451	1485488	40.50144648	26.0366442	0.64286
TM2 domain protein	979	1485568	1486086	230.3149606	225.885827	0.98077
hypothetical protein	978	1486119	1487501	149.4211288	73.2633864	0.49031
hypothetical protein	977	1487534	1487647	0	0	#DIV/0!
Arginine pathway regulatory protein ArgR, repressor of arg regulon	976	1487629	1488102	84.56659619	57.0824524	0.675
Glucose-6-phosphate isomerase (EC 5.3.1.9)	975	1488229	1489818	156.2696912	188.563327	1.20665
hypothetical protein	974	1489828	1490388	80.35714286	80.3571429	1
Predicted beta-xyloside ABC transporter, substrate-binding component	973	1490454	1491803	679.6116505	858.663181	1.26346
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	972	1491869	1492774	27.62430939	12.4309392	0.45
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	971	1492778	1493620	40.38004751	24.0498812	0.59559
hypothetical protein	970	1493643	1494536	55.43113102	42.8331467	0.77273
Transcriptional regulator	969	1494533	1495474	36.7803838	57.5692964	1.56522
hypothetical protein	968	1495467	1496135	51.64670659	63.997006	1.23913
TPR domain protein, putative component of TonB system	967	1496132	1497130	100.2004008	114.97996	1.1475
Adenylate cyclase (EC 4.6.1.1)	966	1497210	1497926	159.2178771	254.539106	1.59868
TPR domain protein	965	1497961	1499964	185.7214179	268.472292	1.44556
ACT domain protein	964	1499991	1500260	128.2527881	234.200743	1.82609
Glycerol-3-phosphate dehydrogenase (NAD(P)+) (EC 1.1.1.94)	963	1500264	1501625	224.112426	444.341716	1.98267
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)		1501635	1502381	78.41823056	81.4343164	1.03846
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	961	1502365	1503336	72.60556128	41.7095778	0.57447

Dipeptide transport system permease protein dppC (TC 3.A.1.5.2)	960	1503338	1504138	61.25	45	0.73469
Dipeptide transport system permease protein dppB (TC 3.A.1.5.2)	959	1504135	1505100	67.87564767	58.2901554	0.85878
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	958	1505104	1506651	121.5255333	120.717518	0.99335
Hybrid sensory kinase	957	1506907	1507257	502.8571429	565.714286	1.125
Metal dependent phosphohydrolase		1507247	1507954	625	830.818966	1.32931
Response regulator receiver modulated metal dependent phosphohydrolase		1507951	1508307	623.5955056	821.629213	1.31757
Intergenic (highly expressed)		1508370	1508650	127801.7857	164515.179	1.28727
Uncharacterized protein TP_0813	954	1508765	1509715	90	82.8947368	0.92105
hypothetical protein	952	1509787	1510035	54.43548387	90.7258065	1.66667
Methyl-accepting chemotaxis protein	953	1510025	1511434	65.29453513	35.1312988	0.53804
Deoxycytidylate deaminase	951	1511406	1511948	96.86346863	66.4206642	0.68571
Tagatose-6-phosphate kinase (EC 2.7.1.144) / 1-phosphofructokinase (EC 2.7.1.56)	949	1511985	1512911	84.23326134	51.0259179	0.60577
Adenylate cyclase (EC 4.6.1.1)	950	1512889	1513467	48.44290657	31.1418685	0.64286
hypothetical protein	948	1513534	1513710	42.61363636	25.5681818	0.6
Lipoprotein nlpD	947	1513687	1514475	246.8274112	314.086294	1.27249
RNA polymerase sigma factor RpoD	946	1514527	1515528	42.88597376	45.4086781	1.05882
ABC transporter, ATP-binding protein	945	1515538	1516515	59.87717503	16.1207779	0.26923
putative integral membrane protein	944	1516512	1517345	36.01440576	10.8043217	0.3
ABC transporter permease protein	943	1517346	1518125	43.00385109	37.5481386	0.87313
TRAP-type C4-dicarboxylate transport system, large permease component	942	1518140	1520023	83.64312268	93.2023367	1.11429
TRAP-type transport system, periplasmic component, predicted N-acetylneuraminate-binding protein	941	1520027	1521067	351.4423077	437.019231	1.2435
hypothetical protein	940	1521078	1522043	308.2901554	359.067358	1.16471
DNA polymerase III alpha subunit (EC 2.7.7.7)	939	1522135	1522698	103.9076377	87.9218472	0.84615
Phosphoglucomutase (EC 5.4.2.2)	938	1522698	1524446	186.4553314	149.135447	0.79985
hypothetical protein	937	1524587	1524841	598.4251969	504.92126	0.84375
Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	936	1524902	1526947	714.1809291	1109.04645	1.55289
Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	935	1526957	1528363	612.5356125	862.179487	1.40756
Sensory box histidine kinase/response regulator	934	1528457	1531090	106.5324725	95.7083175	0.8984
Response regulator containing a CheY-like receiver domain and a GGDEF domain	933	1531104	1532009	220.9944751	228.729282	1.035
hypothetical protein	932	1532002	1533303	62.64411991	58.8009224	0.93865
Lipoate synthase	931	1533316	1534164	53.06603774	31.8396226	0.6
lipoate-protein ligase A		1534154	1534468	23.88535032	7.1656051	0.3
Lipoate-protein ligase A	929	1534461	1535240	39.15275995	5.77663671	0.14754
hypothetical protein	928	1535282	1536265	216.6836216	222.024415	1.02465
hypothetical protein	927	1536262	1536531	152.4163569	259.29368	1.70122
Foldase protein prsA precursor (EC 5.2.1.8)	926	1536533	1536811	408.2733813	428.956835	1.05066
GAF domain/HD domain protein	925	1536864	1538120	378.9808917	438.893312	1.15809
UPF0178 protein TDE_2151	924	1538133	1538603	129.787234	172.340426	1.32787
Mannose-6-phosphate isomerase (EC 5.3.1.8)	923	1538603	1540255	131.6585956	168.886199	1.28276
Surface protein pspA precursor	922	1540260	1540772	674.8046875	773.4375	1.14616

LSU ribosomal protein L20p	921	1540774	1541133	1005.633803	1635.21127	1.62605
LSU ribosomal protein L35p	920	1541152	1541352	1104.166667	1746.09375	1.58137
Translation initiation factor 3	919	1541371	1541907	384.3283582	575.093284	1.49636
hypothetical protein	917	1542070	1542684	128.6644951	98.9413681	0.76899
PTS system, cellobiose-specific IIC component (EC 2.7.1.69)	918	1542641	1545586	96.0950764	92.4448217	0.96201
Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	916	1545740	1546738	1922.690763	2417.16867	1.25718
hypothetical protein	915	1546790	1547737	47.51847941	45.1425554	0.95
flagellar filament outer layer protein FlaA, putative	914	1547869	1548696	1096.130593	1382.10399	1.26089
Flagellar filament outer layer protein	913	1548708	1549433	584.137931	822.413793	1.40791
T. pallidum predicted coding region TP0665	912	1549479	1550144	81.95488722	54.1353383	0.66055
Uncharacterized protein TP_0666	911	1550179	1550424	287.755102	247.959184	0.8617
Cell division protein mraZ	910	1550643	1551095	282.079646	532.632743	1.88824
S-adenosyl-methyltransferase mraW (EC 2.1.1.-)	909	1551115	1552059	164.1949153	202.595339	1.23387
cell division protein FtsL, putative	908	1552063	1552338	274.5454545	556.363636	2.02649
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D- alanyl ligase (EC 6.3.2.10)	907	1552351	1553784	150.3838102	219.818562	1.46172
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	906	1553774	1554847	43.33643989	48.2292637	1.1129
Cell division protein ftsW	905	1554858	1556015	75.62662057	87.5108038	1.15714
Cell division protein ftsQ	904	1556017	1556835	56.84596577	123.777506	2.17742
Cell division protein ftsA	903	1556843	1558081	94.10339257	94.5072698	1.00429
Cell division protein ftsZ (EC 3.4.24.-)	902	1558057	1559337	255.078125	402.539063	1.5781
Site-specific recombinase XerD	901	1559345	1560277	144.8497854	229.345494	1.58333
TPR domain protein		1560267	1561013	103.8873995	126.675603	1.21935
Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake	899	1561006	1561959	126.4428122	172.350472	1.36307
DNA topoisomerase I (EC 5.99.1.2)	898	1561995	1564121	124.2937853	176.90678	1.4233
Site-specific tyrosine recombinase	897	1564118	1565026	155.8370044	240.363436	1.5424
ATP-dependent protease hslV (EC 3.4.25.-)	896	1565023	1565574	192.3774955	289.927405	1.50708
ATP-dependent hsl protease ATP-binding subunit hslU	895	1565584	1567149	199.4851995	305.501931	1.53145
Flagellar basal-body rod protein flgB	894	1567199	1567621	387.4407583	330.56872	0.85321
Flagellar basal-body rod protein flgC	893	1567628	1568089	327.5488069	351.409978	1.07285
Flagellar hook-basal body complex protein fliE	892	1568194	1568502	152.5974026	336.038961	2.20213
Flagellar M-ring protein fliF	891	1568513	1570240	156.7944251	207.752613	1.325
Flagellar motor switch protein fliG	890	1570244	1571305	218.66164	330.819981	1.51293
Flagellar assembly protein fliH	889	1571316	1572275	130.8654849	152.502607	1.16534
Flagellum-specific ATP synthase fliI	888	1572279	1573739	105.8219178	134.075342	1.26699
Flagellar protein fliJ	887	1573736	1574179	51.91873589	66.027088	1.27174
Uridine kinase (EC 2.7.1.48)	886	1574243	1575913	93.41317365	74.1017964	0.79327
Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	885	1575937	1577385	72.51381215	43.5082873	0.6
Nicotinamidase (EC 3.5.1.19)	884	1577382	1578029	69.55177743	66.0741886	0.95
Response regulator	883	1578143	1579243	56.36363636	14.3181818	0.25403
sensory box histidine kinase/response regulator	882	1579255	1582062	42.57214108	8.81724261	0.20711

Transcriptional activator of maltose regulon, MalT	881	1582185	1584728	17.89225324	19.4651986	1.08791
Response regulator	880	1584730	1585833	42.15775159	63.2366274	1.5
Sensory box histidine kinase/response regulator	879	1585837	1588686	53.91640323	50.5795574	0.93811
hypothetical protein	877	1589461	1589574	8.849557522	0	0
hypothetical protein	876	1589571	1589714	6.993006993	0	0
hypothetical protein	875	1589945	1590256	382.6366559	289.389068	0.7563
Transposase and inactivated derivatives	874	1590268	1591221	133.7880378	73.1899265	0.54706
hypothetical protein	873	1591232	1591357	20	0	0
hypothetical protein	872	1591488	1591760	12.86764706	8.27205882	0.64286
Putative arylsulfatase regulatory protein	871	1591969	1593108	32.48463565	27.6558385	0.85135
Microsomal dipeptidase (EC 3.4.13.19)	870	1593121	1594083	33.26403326	18.7110187	0.5625
Neuraminidase NanP	869	1594078	1595892	63.67144432	23.5667034	0.37013
Outer membrane protein tpn50 precursor (Antigen tpp57)	868	1595900	1597099	41.28440367	33.7781485	0.81818
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	867	1597182	1598360	148.1324278	221.561969	1.4957
Phosphoglycolate phosphatase (EC 3.1.3.18)	866	1598380	1599036	62.5	72.027439	1.15244
Transcription regulator [contains diacylglycerol kinase catalytic domain]	864	1599033	1600154	55.75379126	44.1570027	0.792
MgtC family protein	865	1600151	1600837	80.90379009	85.2769679	1.05405
hypothetical protein	862	1601223	1601369	89.04109589	77.0547945	0.86538
Uncharacterized protein TP_0851	863	1601349	1603604	64.07982262	49.8891353	0.77855
Putative enzyme	861	1603680	1606010	106.0085837	111.051502	1.04757
Trp Operon Repressor	860	1606023	1606325	155.6291391	260.761589	1.67553
Phosphoglycolate phosphatase (EC 3.1.3.18)	859	1606327	1606977	96.15384615	65.7692308	0.684
Na+-driven multidrug efflux pump	857	1607030	1608397	25.60351134	24.6891002	0.96429
Methyltransferase/methylase	858	1608394	1609248	44.49648712	39.5199063	0.88816
Uncharacterized protein TP_0781	856	1609249	1610133	59.95475113	76.3574661	1.27358
Uncharacterized protein TP_0783	855	1610135	1611220	192.1658986	197.004608	1.02518
Cytidine deaminase (EC 3.5.4.5)	854	1611254	1611664	46.34146341	43.902439	0.94737
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	853	1611719	1612372	227.4119449	182.618683	0.80303
hypothetical protein	852	1612386	1613618	59.65909091	54.788961	0.91837
hypothetical protein	851	1613655	1613825	67.64705882	66.1764706	0.97826
Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	850	1613851	1614516	107.518797	91.3533835	0.84965
Uncharacterized protein TP_0359	849	1614519	1615202	101.7569546	128.477306	1.26259
Glycogen branching enzyme, archaeal type (EC 2.4.1.18)	848	1615204	1616766	128.0409731	194.462228	1.51875
UPF0164 protein TP_0859/TP_0860 precursor	847	1616768	1618066	102.0801233	64.1371341	0.6283
Uncharacterized protein TP_0855 precursor	846	1618191	1621256	96.9004894	93.9641109	0.9697
Serine phosphatase RsbU, regulator of sigma subunit	845	1621253	1625881	78.26369344	72.0935267	0.92116
hypothetical protein	844	1625892	1626212	121.875	105.46875	0.86538
hypothetical protein	843	1626226	1627956	70.80924855	74.132948	1.04694
PIN domain protein	842	1627962	1628219	24.89626556	9.33609959	0.375
hypothetical protein	841	1628296	1628439	27.97202797	0	0
unique zas9 16S rRNA 6		1628953	1628963	477850	460575	0.96385

unique zas9 16S rRNA 3		1629371	1629381	3083500	5220000	1.69288
unique zas9 23S rRNA 8	838	1630786	1630796	182950	263475	1.44015
Transcriptional regulator of rhamnose utilization, AraC family	834	1633944	1634816	39.56422018	56.766055	1.43478
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	833	1634947	1635891	27.54237288	47.6694915	1.73077
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	832	1635982	1637472	31.54362416	28.6912752	0.90957
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	831	1637484	1638482	33.56713427	31.5631263	0.9403
Trimethylamine corrinoid protein 2	830	1638479	1639585	40.68716094	6.10307414	0.15
Oxalate/formate antiporter	829	1639720	1640928	94.78476821	100.57947	1.06114
Acetylornithine deacetylase (EC 3.5.1.16)	828	1640937	1642079	87.56567426	55.1663748	0.63
Positive regulator of CheA protein activity (CheW)	827	1642193	1642663	255.3191489	186.702128	0.73125
4-keto-6-deoxy-N-Acetyl-D-hexosaminyl-(Lipid carrier) aminotransferase	826	1642695	1643726	250.7274491	226.964113	0.90522
NAD kinase (EC 2.7.1.23)	825	1643734	1644585	81.08108108	79.3184489	0.97826
DNA repair protein RecN	824	1644589	1646337	159.0389016	148.026316	0.93076
hypothetical protein	823	1646339	1647151	105.2955665	105.295567	1
Ankyrin repeat protein	822	1647206	1650061	237.3029772	168.651489	0.7107
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	820	1650182	1651585	161.6702355	158.993576	0.98344
sensory box histidine kinase/response regulator	819	1651582	1654530	71.91316147	82.4287653	1.14623
spore peptidoglycan hydrolase (N-acetylglucosaminidase)	818	1654532	1655596	137.2180451	173.402256	1.2637
Transcriptional regulator, TetR family	817	1655741	1656442	75.60627675	99.5007133	1.31604
membrane protein, putative	816	1656429	1659101	51.08532934	44.629491	0.87363
Outer membrane lipoprotein-sorting protein	815	1659098	1659880	70.33248082	86.3171355	1.22727
hypothetical protein	814	1659877	1661406	49.70568999	54.4473512	1.09539
hypothetical protein	813	1661588	1661716	0	0	#DIV/0!
hypothetical protein	812	1661762	1662304	0	0	#DIV/0!
Nicotinamide-nucleotide adenylyltransferase, NadR family (EC 2.7.7.1) / Ribosylnicotinamide kinase (EC 2.7.1.22)		1662636	1663007	59.29919137	6.06469003	0.10227
hypothetical protein	810	1663195	1663731	48.50746269	12.5932836	0.25962
UNC-44 ankyrins	809	1663728	1664720	54.43548387	31.7540323	0.58333
Ankyrin repeat proteins	808	1664733	1666433	108.5294118	71.4705882	0.65854
Molybdate metabolism regulator	807	1666430	1668031	160.8369769	88.5384135	0.55049
molybdate metabolism regulator		1668274	1670439	103.0023095	80.0230947	0.77691
hypothetical protein	805	1671033	1671728	37.41007194	16.1870504	0.43269
hypothetical protein	804	1671737	1672339	35.71428571	11.2126246	0.31395
hypothetical protein	803	1672408	1673508	36.36363636	18.4090909	0.50625
hypothetical protein	802	1673535	1674368	48.01920768	21.6086435	0.45
HD_GYP hydrolase domain fused to HD hydrolase domain	800	1674436	1675695	35.34551231	33.9555203	0.96067
hypothetical protein	801	1675667	1677421	41.90421893	33.3523375	0.79592
hypothetical protein	799	1677527	1679047	35.52631579	14.8026316	0.41667
hypothetical protein	798	1679057	1680868	52.45720596	18.6361126	0.35526
hypothetical protein	797	1680890	1681189	35.11705686	7.52508361	0.21429
zinc finger, SWIM domain protein		1681186	1682994	34.84513274	16.1780973	0.46429

Mg-chelatase subunit ChlD	795	1682970	1684169	41.70141785	26.2718932	0.63
hypothetical protein	794	1684166	1686637	59.49008499	27.3168758	0.45918
hypothetical protein	793	1686598	1687713	118.3856502	50.4484305	0.42614
hypothetical protein	792	1688140	1688622	8.298755187	0	0
hypothetical protein	791	1688613	1688729	77.5862069	0	0
hypothetical protein	790	1688735	1688878	34.61538462	17.3076923	0.5
hypothetical protein	789	1688959	1689993	10.15473888	4.35203095	0.42857
Transposase		1690170	1691444	27.08006279	15.8948195	0.58696
Transposase		1691517	1691708	20.94240838	0	0
Transposase IS116/IS110/IS902	786	1691984	1693018	22.68244576	17.7514793	0.78261
Tetratricopeptide TPR_2	785	1693437	1694531	133.9122486	174.817185	1.30546
Transposase	784	1694578	1695687	35.61767358	22.3174031	0.62658
hypothetical protein	783	1696186	1696551	63.01369863	18.4931507	0.29348
hypothetical protein	782	1696676	1696894	57.33944954	41.2844037	0.72
Molybdate metabolism regulator	781	1697038	1697850	67.73399015	69.273399	1.02273
hypothetical protein	780	1697909	1701217	75.87666264	80.9401451	1.06673
unknown	779	1701223	1702161	63.43283582	88.7526652	1.39916
hypothetical protein	778	1702265	1702399	0	0	#DIV/0!
hypothetical protein	777	1702468	1704462	29.42668696	21.6894977	0.73707
hypothetical protein	776	1704501	1706612	181.193747	176.930365	0.97647
Pyrophosphate--fructose 6-phosphate 1-phosphotransferase, beta subunit (EC 2.7.1.90)	775	1706639	1708294	397.8851964	543.806647	1.36674
Uridylate kinase (EC 2.7.4.-)	774	1708361	1709047	155.2478134	193.51312	1.24648
Transglutaminase-like	773	1709060	1710688	148.3415233	172.757985	1.1646
hypothetical protein	772	1710688	1711227	700.3710575	655.380334	0.93576
hypothetical protein	771	1711224	1711808	924.6575342	1082.61986	1.17083
RNA polymerase sigma-54 factor rpoN	770	1711798	1712367	631.8101933	945.079086	1.49583
Cysteinyl-tRNA synthetase (EC 6.1.1.16)	769	1712408	1713889	198.630137	291.267123	1.46638
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	768	1714112	1714987	34.28571429	36	1.05
hypothetical protein	767	1715012	1715623	31.09656301	25.7774141	0.82895
transcriptional regulator, Crp/Fnr family	766	1715687	1716922	279.3522267	340.688259	1.21957
Serine/threonine protein kinase	765	1716960	1718291	95.11278195	113.345865	1.1917
hypothetical protein	764	1718313	1718942	76.31160572	50.0794913	0.65625
Exported protein	763	1718932	1719390	88.4279476	58.9519651	0.66667
ATP-dependent Clp protease ATP-binding subunit clpA	761	1719432	1721984	169.4749216	175.450627	1.03526
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	762	1721981	1723252	418.9833201	373.510723	0.89147
ATP-dependent RNA helicase	760	1723376	1725676	122.173913	159.456522	1.30516
hypothetical protein	758	1725708	1726835	656.6104703	541.038154	0.82399
hypothetical protein	759	1726822	1726944	204.9180328	110.655738	0.54
ATPase	757	1727188	1728432	21.3022508	10.85209	0.50943
unknown	756	1728478	1729800	28.36611195	5.10590015	0.18
Predicted amino-acid acetyltransferase (EC 2.3.1.1) complementing ArgA function in Arginine Biosynthesis pathway	755	1729790	1730221	38.28306265	0	0
Helicase PriA essential for oriC/DnaA-independent DNA replication	754	1730256	1732253	67.6014021	50.7010516	0.75
DNA polymerase, bacteriophage-type	753	1732240	1732803	55.95026643	35.9680284	0.64286
hypothetical protein		1732861	1733073	21.22641509	0	0

hypothetical protein	751	1733113	1733274	142.8571429	69.8757764	0.48913
UDP-glucose 4-epimerase (EC 5.1.3.2)	750	1733549	1734400	70.5052879	66.0987074	0.9375
Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)	749	1734410	1735084	53.41246291	46.735905	0.875
Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)		1735134	1735676	249.0774908	199.261993	0.8
Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)	747	1735692	1737737	229.0953545	162.836186	0.71078
Ribonucleotide reductase transcriptional regulator NrdR	746	1737743	1738201	245.6331878	191.593886	0.78
Alpha-galactosidase (EC 3.2.1.22)	745	1738421	1739755	461.7691154	446.964018	0.96794
Glycosyltransferase	744	1739759	1740892	170.7855252	188.658429	1.10465
Uroporphyrinogen-III decarboxylase	743	1740906	1741934	98.73540856	67.8501946	0.68719
filamentous haemagglutinin family outer membrane protein	742	1742042	1742728	29.88338192	6.55976676	0.21951
hypothetical protein	741	1743026	1743181	9.677419355	14.516129	1.5
Methyl-accepting chemotaxis protein	740	1743199	1745283	131.7178503	105.806142	0.80328
NADPH:quinone oxidoreductase	739	1745414	1745974	83.03571429	52.2321429	0.62903
ATP-dependent protease La (EC 3.4.21.53) Type I	738	1746019	1748565	152.7886881	239.493323	1.56748
ATP-dependent Clp protease ATP-binding subunit clpX	737	1748576	1749829	568.7851971	626.307321	1.10113
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	736	1749813	1750427	350.9771987	469.055375	1.33643
Cell division trigger factor (EC 5.2.1.8)	735	1750437	1751810	475.600874	658.776402	1.38515
Core component MtsA of methionine-regulated ECF transporter	733	1752092	1752649	95.15260323	88.8689408	0.93396
ATPase component MtsB of energizing module of methionine-regulated ECF transporter	732	1752606	1754390	76.79372197	46.6647982	0.60766
Transmembrane component MtsC of energizing module of methionine-regulated ECF transporter	731	1754387	1755217	31.92771084	18.9759036	0.59434
ATPase	730	1755284	1756522	27.86752827	19.9919225	0.71739
Nitroreductase	729	1756616	1757170	404.33213	430.505415	1.06473
hypothetical protein	728	1757214	1758173	66.73618352	61.0010428	0.91406
hypothetical protein	727	1758188	1758370	24.72527473	0	0
hypothetical protein	726	1758491	1759129	47.80564263	31.7398119	0.66393
D-alanine aminotransferase (EC 2.6.1.21)	725	1759211	1760059	202.8301887	180.424528	0.88953
hypothetical protein	724	1760062	1761168	106.6907776	97.6491863	0.91525
Allophanate hydrolase subunit 1 (EC 3.5.1.54)	723	1761137	1761862	82.06896552	62.0689655	0.7563
Allophanate hydrolase subunit 2 (EC 3.5.1.54)	722	1761853	1762815	62.88981289	56.1330561	0.89256
Protein c14orf159 homolog, mitochondrial precursor	721	1762834	1763619	91.08280255	91.7197452	1.00699
Lactam utilization protein LAMB	720	1763630	1764415	121.0191083	100.318471	0.82895
Membrane protein	719	1764440	1765312	151.9495413	159.977064	1.05283
Flagellar basal-body rod protein flgF	718	1765312	1766202	324.1573034	310.955056	0.95927
Flagellar basal-body rod protein flgG	717	1766217	1767017	315.7560356	297.331639	0.94165
Flagellar protein flgJ [peptidoglycan hydrolase] (EC 3.2.1.-)	715	1767042	1767482	165.9090909	122.727273	0.73973
hypothetical protein	716	1767473	1767598	48	54	1.125
Collagen binding protein Cna	714	1767659	1769179	163.1578947	513.651316	3.14819

hypothetical protein	713	1769399	1769518	0	0	#DIV/0!
hypothetical protein	712	1769654	1770256	58.13953488	22.4252492	0.38571
Uncharacterized protein aq_1917	711	1770395	1771540	147.1615721	137.554585	0.93472
hypothetical protein	710	1771540	1772736	89.46488294	71.4882943	0.79907
ComEC/Rec2-related protein	709	1772760	1774214	31.63686382	15.474553	0.48913
Dimethyladenosine transferase (EC 2.1.1.-)	708	1774195	1775088	45.91265398	17.6371781	0.38415
FIG018583: protein of unknown function	707	1775081	1775788	60.11315417	60.466761	1.00588
hypothetical protein	706	1775785	1776273	28.68852459	18.442623	0.64286
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	704	1776273	1777172	30.03337041	25.0278087	0.83333
Ribonuclease BN (EC 3.1.-.-)	705	1777156	1778493	36.64921466	16.828721	0.45918
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	702	1778523	1779290	35.85397653	23.4680574	0.65455
Dihydrofolate synthase (EC 6.3.2.12) / Folylpolyglutamate synthase (EC 6.3.2.17)	703	1779259	1780611	34.39349112	24.9630178	0.72581
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	701	1780596	1782095	113.0753836	97.5650434	0.86283
Protein yicC	700	1782092	1782958	48.49884527	49.3648961	1.01786
Cytidylate kinase (EC 2.7.4.14)	699	1782948	1783499	83.4845735	77.5862069	0.92935
A/G-specific adenine glycosylase (EC 3.2.2.-)	698	1783472	1784284	64.03940887	58.1896552	0.90865
hypothetical protein	696	1784419	1785213	107.0528967	96.3476071	0.9
Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)	695	1785213	1786655	85.29819695	107.662968	1.2622
putative (R)-2-hydroxyglutaryl-CoA dehydratase activator-related protein	694	1786703	1791037	71.75819105	110.059991	1.53376
hypothetical protein	692	1791159	1792793	153.6107711	143.206854	0.93227
CTP:Inositol-1-phosphate cytidylyltransferase (2.7.7.-) / Phospho-di-inositol-1-phosphate synthase (EC 2.7.8.-)	693	1792783	1793475	80.20231214	97.5433526	1.21622
Glycosyltransferase	691	1793530	1794573	74.78427613	88.4467881	1.18269
OxaI/YidC membrane insertion protein	690	1794560	1797217	35.19006398	28.7918705	0.81818
putative bifunctional polymerase	689	1797217	1798503	81.25972006	90.9797823	1.11962
hypothetical protein	688	1798522	1800174	108.6561743	98.062954	0.90251
hypothetical protein	687	1800187	1801263	35.31598513	23.0018587	0.65132
hypothetical protein	686	1801260	1802093	16.80672269	16.2064826	0.96429
hypothetical protein	685	1802102	1802341	46.0251046	9.41422594	0.20455
Alpha-1,4-N-acetylgalactosamine transferase PglJ (EC 2.4.1.-)	684	1802380	1803573	17.18357083	11.3160101	0.65854
hypothetical protein	683	1803570	1804448	7.972665148	2.56264237	0.32143
OxaI/YidC membrane insertion protein	682	1804445	1807222	11.5232265	6.48181491	0.5625
putative bifunctional polymerase	681	1807215	1808444	34.58096013	42.1074044	1.21765
hypothetical protein	680	1808623	1808847	4.464285714	0	0
Glycosyl transferase, group 1	679	1808934	1810055	27.65388046	28.0999108	1.01613
UDP-glucose 4-epimerase (EC 5.1.3.2)	678	1810059	1811000	15.40913921	0	0
D,D-heptose 7-phosphate kinase	677	1811023	1811997	22.07392197	25.4106776	1.15116
D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.-); possible Histidinol-phosphatase (EC 3.1.3.15)	676	1811994	1813304	13.74045802	6.87022901	0.5
Beta-1,3-glucosyltransferase	675	1813311	1814375	11.7481203	6.34398496	0.54
Putative mannosyltransferase involved in polysaccharide biosynthesis	674	1814378	1815148	5.844155844	0	0
transposase, IS30 family	673	1815169	1816197	130.8365759	100.680934	0.76952

Beta-1,3-glucosyltransferase	672	1816287	1817264	5.117707267	4.60593654	0.9
hypothetical protein	671	1817338	1818978	20.73170732	23.3231707	1.125
Phospholipid-lipopolysaccharide ABC transporter		1818968	1820008	24.51923077	21.6346154	0.88235
Phospholipid-lipopolysaccharide ABC transporter		1820001	1820675	7.418397626	3.33827893	0.45
UDP-glucose dehydrogenase (EC 1.1.1.22)	668	1820772	1822103	77.76108189	101.427498	1.30435
ATP-dependent DNA helicase	667	1822146	1823324	44.99151104	36.2903226	0.8066
hypothetical protein	666	1823352	1824887	124.1042345	136.319218	1.09843
3-dehydroquinate synthase (EC 4.2.3.4)	665	1824887	1825975	185.2022059	210.9375	1.13896
Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4)	664	1826100	1826972	483.9449541	361.238532	0.74645
Xanthine dehydrogenase iron-sulfur subunit (EC 1.17.1.4)	663	1826956	1827441	109.2783505	171.649485	1.57075
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	662	1827438	1829537	237.9704621	275.488328	1.15766
Putative aminotransferase, DegT family	661	1829539	1830720	113.0397968	78.1117697	0.69101
UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-)	660	1830710	1832203	139.3168118	122.069658	0.8762
Transcription antitermination protein NusG	659	1832242	1832775	111.6322702	80.206379	0.71849
hypothetical protein	658	1832850	1833341	122.1995927	50.407332	0.4125
Extensin precursor	657	1833345	1834631	322.3172628	281.687403	0.87394
Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1)	656	1834641	1837397	277.6965265	331.535649	1.19388
hypothetical protein	655	1837484	1837669	256.7567568	182.432432	0.71053
hypothetical protein	654	1837977	1838303	176.3803681	262.269939	1.48696
transcriptional regulator, PemK family	653	1838508	1838837	24.31610942	27.3556231	1.125
hypothetical protein	652	1838825	1839073	22.17741935	27.2177419	1.22727
hypothetical protein	651	1839118	1839246	7.8125	0	0
hypothetical protein	650	1839239	1840048	217.552534	180.778739	0.83097
Ferric iron ABC transporter, iron-binding protein	649	1840118	1841098	577.0408163	215.816327	0.37401
Ferric iron ABC transporter, ATP-binding protein	648	1841086	1841874	300.7614213	154.187817	0.51266
Ferric iron ABC transporter, permease protein	647	1841886	1843454	64.41326531	24.3941327	0.37871
Cholinephosphate cytidylyltransferase (EC 2.7.7.15)	646	1843454	1844332	136.6742597	123.006834	0.9
lipoprotein, putative	645	1844351	1845550	250.2085071	215.804837	0.8625
YjeF protein, function unknown	644	1845550	1847145	303.4482759	242.633229	0.79959
hypothetical protein	643	1847145	1847711	166.0777385	143.109541	0.8617
ortholog to Borrelia burgdorferi BB0157	642	1847771	1848175	164.6039604	206.064356	1.25188
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	640	1848178	1848594	76.92307692	81.1298077	1.05469
hypothetical protein	641	1848565	1849551	52.73833671	29.6653144	0.5625
hypothetical protein	639	1849613	1849981	176.6304348	299.592391	1.69615
hypothetical protein	638	1849978	1850925	75.50158395	80.781415	1.06993
23S rRNA methyltransferase and Florfenicol/chloramphenicol resistance protein / Radical SAM family enzyme, UPF0063 family	637	1850969	1852042	161.5312792	176.470588	1.09249
TPR-repeat-containing protein	636	1852046	1853200	233.9688042	345.103986	1.475
Uncharacterized protein TP_0066	635	1853193	1853537	116.2790698	156.976744	1.35

Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-)	634	1853610	1854158	29.19708029	16.4233577	0.5625
hypothetical protein	633	1854163	1854606	102.7088036	71.1060948	0.69231
SSU ribosomal protein S6p	632	1854711	1854992	622.7758007	1169.03915	1.87714
Single-stranded DNA-binding protein	631	1854998	1855474	552.5210084	1073.0042	1.94202
SSU ribosomal protein S18p	630	1855500	1855817	1126.182965	2207.41325	1.96008
hypothetical protein	629	1855804	1856811	166.3356504	406.653426	2.44478
LSU ribosomal protein L9p	628	1856910	1857572	329.305136	628.776435	1.9094
Replicative DNA helicase (EC 3.6.1.-) [SA14-24]	627	1857588	1858937	128.613788	213.491475	1.65994
hypothetical protein	626	1858949	1859245	128.3783784	281.25	2.19079
Uncharacterized protein TP_0598	625	1859264	1861264	77.5	106.875	1.37903
Uncharacterized protein TP_0599	624	1861261	1861890	89.03020668	135.930048	1.52679
Membrane-associated zinc metalloprotease	623	1861894	1863252	75.11045655	87.8129602	1.16912
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	622	1863239	1864384	65.06550218	43.231441	0.66443
Phosphatidate cytidylyltransferase (EC 2.7.7.41)	621	1864387	1865241	75.52693208	76.4051522	1.01163
Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	620	1865238	1865948	260.5633803	545.070423	2.09189
Ribosome recycling factor	619	1865960	1866514	562.2743682	1189.98195	2.11637
Translation elongation factor Ts	618	1866516	1867370	665.6908665	1285.71429	1.9314
SSU ribosomal protein S2p (SAe)	617	1867440	1868333	788.1455399	1539.61268	1.95346
Septum formation protein Maf	616	1868478	1869065	256.3884157	195.48552	0.76246
hypothetical protein	615	1869218	1869424	169.9029126	349.514563	2.05714
hypothetical protein	614	1869489	1869761	257.3529412	231.617647	0.9
hypothetical protein	613	1869733	1870242	47.90419162	94.3113772	1.96875
hypothetical protein	612	1870239	1870454	141.8604651	209.302326	1.47541
hypothetical protein	611	1870457	1870627	2.941176471	0	0
hypothetical protein	610	1870948	1871136	39.89361702	0	0
hypothetical protein	609	1871211	1871357	17.12328767	0	0
hypothetical protein	608	1871318	1871617	10.03344482	0	0
hypothetical protein	607	1871656	1871919	22.81368821	8.55513308	0.375
hypothetical protein	606	1871909	1872331	8.293838863	0	0
hypothetical protein	605	1872328	1872612	35.21126761	7.92253521	0.225
hypothetical protein	604	1872659	1872850	0	0	#DIV/0!
hypothetical protein	603	1873068	1873277	7.177033493	0	0
Phage-related protein		1873308	1875848	20.47244094	2.65748031	0.12981
hypothetical protein		1875852	1876370	22.2007722	4.34362934	0.19565
Major capsid protein, HK97 family	600	1876409	1877323	41.02844639	9.84682713	0.24
hypothetical protein	599	1877388	1878011	32.90529695	43.3386838	1.31707
hypothetical protein	598	1878087	1878395	4.87012987	0	0
hypothetical protein	597	1878392	1878595	0	0	#DIV/0!
hypothetical protein	596	1878592	1878909	9.463722397	7.0977918	0.75
hypothetical protein	595	1879139	1879318	19.55307263	0	0
Predicted ATPase	594	1879275	1880810	24.75570033	1.46579805	0.05921
hypothetical protein	593	1880864	1881508	34.16149068	34.9378882	1.02273
prophage LambdaSo, DNA modification methyltransferase, putative	592	1881505	1882221	21.64804469	6.2849162	0.29032
Excisionase	591	1882218	1882454	8.474576271	0	0
hypothetical protein	590	1882565	1883233	11.9760479	16.8413174	1.40625

Site-specific recombinase, phage integrase family	589	1883230	1884354	85.40925267	106.094306	1.24219
hypothetical protein		1884397	1884531	0	0	#DIV/0!
DinG family ATP-dependent helicase YoaA	586	1884734	1887259	66.73267327	57.9207921	0.86795
hypothetical protein	585	1887299	1888831	50.91383812	57.2780679	1.125
Iron-sulfur cluster regulator IscR		1888828	1889253	45.88235294	52.9411765	1.15385
hypothetical protein	583	1889397	1889942	682.5688073	862.844037	1.26411
Transposase		1890390	1890689	85.28428094	67.7257525	0.79412
Transposase	581	1890689	1890988	95.31772575	150.501672	1.57895
Transposase		1891141	1891443	51.32450331	7.45033113	0.14516
Integrase domain protein	579	1891716	1892366	36.15384615	6.92307692	0.19149
Uracil phosphoribosyltransferase (EC 2.4.2.9)	578	1892517	1893587	208.8785047	220.794393	1.05705
TPR domain protein, putative component of TonB system	576	1893584	1894543	116.2669447	114.963504	0.98879
hypothetical protein		1894499	1899448	39.40189937	28.6421499	0.72692
YlxP-like protein	575	1899507	1899794	39.0070922	39.893617	1.02273
hypothetical protein	574	1899798	1900430	85.44303797	99.6835443	1.16667
hypothetical protein	573	1900467	1902527	29.61165049	13.1067961	0.44262
Endoribonuclease L-PSP	572	1902509	1902895	174.8704663	355.569948	2.03333
hypothetical protein	571	1902882	1903550	205.8383234	191.991018	0.93273
tRNA (guanine46-N7-)-methyltransferase (EC 2.1.1.33)	570	1903547	1904224	39.88183161	43.2053176	1.08333
DNA ligase (EC 6.5.1.2)	569	1904249	1906258	57.24240916	71.6774515	1.25217
ATP-dependent helicase HrpB	568	1906227	1908806	36.06048856	22.6832105	0.62903
hypothetical protein	567	1908877	1909035	6.329113924	0	0
Transposase	566	1909091	1910200	39.67538323	16.2308386	0.40909
sensory box histidine kinase/response regulator	565	1910537	1912087	19.35483871	4.35483871	0.225
amino acid ABC transporter, amino acid-binding protein		1912200	1913033	1003.0012	359.243697	0.35817
Amino acid ABC transporter, permease protein	563	1913062	1913778	328.2122905	157.122905	0.47872
ABC-type polar amino acid transport system, ATPase component	562	1913775	1914530	102.6490066	38.7417219	0.37742
L-serine dehydratase, alpha subunit (EC 4.3.1.17)	561	1914548	1916155	228.9719626	138.785047	0.60612
hypothetical protein	560	1916445	1916558	0	0	#DIV/0!
Integrase domain protein	559	1916595	1917854	83.39952343	26.8069897	0.32143
hypothetical protein	558	1917883	1917996	8.849557522	79.6460177	9
Transposase	557	1918078	1919187	36.97024346	20.2885482	0.54878
Helix-turn-helix domain protein	556	1919420	1919767	40.34582133	12.9682997	0.32143
Thymidylate kinase (EC 2.7.4.9)	555	1919984	1920625	63.9625585	98.2839314	1.53659
hypothetical protein	554	1920762	1921001	94.14225941	112.970711	1.2
hypothetical protein	553	1921059	1925552	45.07010906	48.575562	1.07778
Outer membrane protein assembly factor YaeT precursor	552	1925611	1928148	383.7209302	867.363027	2.2604
Outer membrane protein H precursor	551	1928159	1928686	304.5540797	717.267552	2.35514
DNA mismatch repair protein MutS	550	1928727	1931381	133.7603617	299.26526	2.23732
Competence protein F	549	1931365	1932123	66.62269129	74.2084433	1.11386
Methyl-accepting chemotaxis protein	548	1932278	1934353	158.778626	188.931298	1.1899
COG0779: clustered with transcription termination protein NusA	547	1934486	1934980	175.1012146	391.700405	2.23699
Transcription termination protein NusA	546	1934993	1936480	298.3706721	581.97556	1.95051

Translation initiation factor 2	545	1936489	1939293	527.9957204	871.433666	1.65046
Ribosome-binding factor A	544	1939290	1939652	209.9447514	379.143646	1.80592
tRNA pseudouridine synthase B (EC 4.2.1.70)	543	1939636	1940607	84.44902163	113.542739	1.34451
SSU ribosomal protein S15p (S13e)	542	1940659	1940928	288.1040892	334.572491	1.16129
Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)	541	1940929	1943100	999.769479	1438.79668	1.43913
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	540	1943100	1943567	159.5289079	173.447537	1.08725
membrane protein, putative	539	1943569	1944855	61.81959565	59.4867807	0.96226
hypothetical protein	538	1944852	1945916	72.36842105	67.6691729	0.93506
tRNA-guanine transglycosylase (EC 2.4.2.29)	537	1945928	1947070	31.98948291	41.4110429	1.29452
FOG: HEAT repeat	535	1947067	1948566	77.71847899	75.0500334	0.96567
Transcriptional regulator, AraC family	536	1948563	1949843	27.734375	26.3671875	0.9507
76K protein	534	1949869	1951608	386.7165037	478.723404	1.23792
Transcription elongation factor GreA	533	1951641	1954385	324.5262391	480.502915	1.48063
TPR domain protein	532	1954397	1955338	309.7768332	408.873539	1.3199
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	531	1955430	1956089	117.6024279	143.39909	1.21935
hypothetical protein	530	1956110	1957075	187.5647668	240.15544	1.28039
hypothetical protein	529	1957099	1958148	122.9742612	102.955195	0.83721
hypothetical protein	528	1958150	1959289	160.2282704	171.861282	1.0726
D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	527	1959307	1959813	205.5335968	31.1264822	0.15144
Zinc ABC transporter, inner membrane permease protein ZnuB	526	1959915	1960754	343.2657926	61.6805721	0.17969
Zinc ABC transporter, ATP-binding protein ZnuC	525	1960747	1961478	563.6114911	107.729138	0.19114
Periplasmic solute binding protein precursor	524	1961479	1962249	1031.168831	254.220779	0.24654
hypothetical protein	523	1962257	1962655	1070.351759	158.291457	0.14789
RTX toxin, putative	522	1962657	1964027	1202.919708	205.291971	0.17066
hypothetical protein	521	1964041	1964163	90.16393443	36.8852459	0.40909
hypothetical protein	520	1964271	1964387	0	0	#DIV/0!
hypothetical protein	519	1964464	1965210	513.4048257	150.80429	0.29373
serine/threonine kinase	518	1965188	1966228	676.9230769	157.932692	0.23331
TonB-dependent receptor		1966243	1968273	250.2463054	48.7684729	0.19488
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	516	1968343	1969443	188.1818182	204.545455	1.08696
hypothetical protein	515	1969507	1969629	8.196721311	0	0
RecA protein	514	1969648	1970949	630.6687164	584.550346	0.92687
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	512	1970986	1971477	231.1608961	270.366599	1.1696
Prokaryotic ATPase	513	1971474	1972619	30.13100437	7.86026201	0.26087
hypothetical protein	511	1972611	1972817	9.708737864	0	0
Segregation and condensation protein A	510	1972774	1973529	168.2119205	199.668874	1.18701
Segregation and condensation protein B	509	1973510	1974061	490.0181488	567.604356	1.15833
Ribosomal large subunit pseudouridine synthase B (EC 5.4.99.-)	508	1974108	1974827	148.8178025	206.536857	1.38785
SSU ribosomal protein S1p	507	1974821	1977244	621.6383947	929.975176	1.49601
Acetoacetate metabolism regulatory protein atoC	506	1977256	1978767	188.1254169	228.152101	1.21277
TPR repeat-containing protein TP_0282	505	1978776	1979477	263.1954351	263.195435	1
hypothetical protein	504	1979513	1980259	69.70509383	111.595174	1.60096
hypothetical protein	503	1980304	1980519	16.27906977	10.4651163	0.64286

transposase, mutator family	502	1980567	1981808	66.88154714	38.0741338	0.56928
hypothetical protein	501	1981891	1982433	1.84501845	0	0
PIN domain protein	500	1982768	1983163	2.53164557	0	0
hypothetical protein	499	1983160	1983306	0	0	#DIV/0!
Transposase IS4 family protein	498	1983757	1985295	42.58777633	20.4811443	0.48092
hypothetical protein	497	1985482	1985613	0	0	#DIV/0!
Potassium uptake protein TrkH	496	1985671	1987122	13.43900758	6.20261888	0.46154
Integrase	495	1987490	1988536	45.41108987	34.416826	0.75789
Radical SAM domain protein	494	1988700	1990988	35.18356643	30.4851399	0.86646
Rod shape-determining protein rodA	493	1991140	1992459	31.84230478	20.4700531	0.64286
Cell division protein ftsI [Peptidoglycan synthetase] (EC 2.4.1.129)	492	1992461	1994317	111.1111111	103.15534	0.9284
Rod shape-determining protein mreD	491	1994317	1994820	49.70178926	35.7852883	0.72
Rod shape-determining protein mreC	490	1994813	1995697	117.081448	83.9932127	0.71739
Rod shape-determining protein mreB	489	1995702	1996730	348.973607	398.093842	1.14076
TPR domain protein	488	1996740	1997603	169.1772885	250.289687	1.47945
hypothetical protein	487	1997610	1997732	86.06557377	165.983607	1.92857
Intergenic (RNaseP Like)		1997820	1998040	33766.00985	25769.7044	0.76318
Zn-ribbon protein, possibly nucleic acid-binding	486	1998094	1998930	331.3397129	433.313397	1.30776
RNA polymerase sigma factor RpoD	485	1999016	2000779	345.150312	372.660238	1.0797
DNA primase (EC 2.7.7.-)	484	2000776	2002638	194.4146079	194.548872	1.00069
COG1559 protein yceG like	483	2002639	2003715	85.96654275	66.9144981	0.77838
hypothetical protein	482	2003758	2003928	129.4117647	39.7058824	0.30682
Metal-dependent hydrolases of the beta-lactamase superfamily I	481	2003931	2004872	194.2369264	177.694771	0.91484
hypothetical protein	480	2004872	2005432	87.5	84.375	0.96429
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)	479	2005429	2006478	81.50619638	72.9265968	0.89474
Holliday junction DNA helicase RuvB	478	2006494	2007561	145.267104	126.522962	0.87097
Holliday junction DNA helicase RuvA	477	2007569	2008171	106.3122924	104.651163	0.98438
Ferredoxin 3 fused to uncharacterized domain	476	2008407	2009015	13.98026316	0	0
Hcp transcriptional regulator HcpR (Crp/Fnr family)		2009232	2009783	9.98185118	0	0
UPF0173 metal-dependent hydrolase PF1764	474	2009870	2010484	39.90228013	40.3094463	1.0102
Crossover junction endodeoxyribonuclease ruvC (EC 3.1.22.4)	473	2010648	2011184	160.4477612	159.514925	0.99419
hypothetical protein	472	2011165	2011905	746.6216216	1064.18919	1.42534
Uncharacterized protein TP_0777	471	2012043	2012282	1615.062762	2730.12552	1.69041
N-acetylneuraminate synthase (EC 2.5.1.56)	469	2012356	2013474	45.16994633	36.2254025	0.80198
hypothetical protein		2013482	2013595	30.97345133	39.8230088	1.28571
hypothetical protein	467	2013589	2014383	208.4382872	263.539043	1.26435
Histidyl-tRNA synthetase (EC 6.1.1.21)	466	2014398	2015723	190.1886792	183.396226	0.96429
Aspartate aminotransferase (EC 2.6.1.1)	465	2015735	2016946	360.4459125	343.724195	0.95361
Arabinose operon protein araM	464	2016996	2018378	145.0795948	128.617945	0.88653
hypothetical protein	463	2018392	2018538	75.34246575	107.876712	1.43182
hypothetical protein	462	2018585	2019247	39.27492447	40.7854985	1.03846
Aspartokinase (EC 2.7.2.4) / Homoserine dehydrogenase (EC 1.1.1.3)	461	2019277	2021775	128.5028022	125.20016	0.9743
Transcriptional regulator, ArsR family	460	2021775	2022080	80.32786885	88.5245902	1.10204
Cysteine desulfurase (EC 2.8.1.7)	459	2022138	2023283	98.68995633	98.2532751	0.99558
Thiamine biosynthesis protein thiI	458	2023280	2024458	107.8098472	129.881154	1.20472
Hemerythrin-like iron-binding protein	457	2024471	2024878	493.8574939	519.65602	1.05224

hypothetical protein	456	2024906	2026990	125.4798464	110.12476	0.87763
TPR domain protein, putative component of TonB system	455	2026987	2027712	204.137931	192.413793	0.94257
5'-nucleotidase surE (EC 3.1.3.5)	454	2027714	2028502	187.1827411	202.728426	1.08305
Galactokinase (EC 2.7.1.6)	453	2028504	2029673	233.1052181	279.084688	1.19725
hypothetical protein	452	2029689	2029820	15.26717557	17.1755725	1.125
Adenylate cyclase (EC 4.6.1.1)	451	2029860	2032577	61.09679794	40.5778432	0.66416
Multimeric flavodoxin WrbA family protein	450	2032613	2033233	174.1935484	188.709677	1.08333
lipoprotein, putative	449	2033567	2033938	187.3315364	133.423181	0.71223
Adenylate cyclase (EC 4.6.1.1)	448	2033949	2035868	66.18030224	53.9343408	0.81496
Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor	447	2035955	2036974	447.0068695	50.7850834	0.11361
Core component BioY of biotin ECF transporter	446	2037027	2037605	141.0034602	23.3564014	0.16564
ATPase component CbiO of energizing module of cobalt ECF transporter	445	2037595	2038347	202.7925532	20.9441489	0.10328
Transmembrane component of general energizing module of ECF transporters	444	2038340	2038981	78.78315133	3.51014041	0.04455
putative outer membrane protein probably involved in nutrient binding	443	2039003	2041588	33.0754352	5.22243714	0.15789
hypothetical protein	442	2041594	2042355	24.96714849	20.696452	0.82895
MotA/TolQ/ExbB proton channel family protein	441	2042365	2043021	33.53658537	17.1493902	0.51136
hypothetical protein	440	2043018	2043419	19.95012469	5.61097257	0.28125
Biopolymer transport protein ExbD/TolR	439	2043416	2043814	21.35678392	16.959799	0.79412
Ferric siderophore transport system, periplasmic binding protein TonB	437	2043807	2044430	41.73354735	18.0577849	0.43269
Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB	438	2044423	2045172	29.37249666	15.0200267	0.51136
ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	436	2045169	2045909	22.97297297	21.2837838	0.92647
ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	435	2045913	2046920	129.59285	122.889772	0.94828
Transcriptional regulator, TetR family	434	2047012	2047728	55.86592179	31.424581	0.5625
Putative efflux protein	433	2047703	2048917	154.4481054	203.871499	1.32
Oxidoreductase, aldo/keto reductase family	432	2049011	2050165	337.9549393	368.500867	1.09038
Pyruvate,phosphate dikinase (EC 2.7.9.1)	431	2050375	2053275	514.8531952	450.777202	0.87555
RNA helicase, putative	430	2053379	2055904	189.0873016	158.035714	0.83578
hypothetical protein		2055935	2056195	221.1538462	181.730769	0.82174
hypothetical protein		2056321	2056554	17.16738197	9.65665236	0.5625
hypothetical protein	427	2056553	2056774	9.049773756	0	0
hypothetical protein	426	2056862	2056975	26.54867257	0	0
hypothetical protein	425	2057071	2057481	40.24390244	21.9512195	0.54545
hypothetical protein	424	2057671	2058492	132.7649208	172.655298	1.30046
Two component transcriptional regulator, LuxR family	423	2058563	2059183	152.4193548	148.790323	0.97619
Sensor histidine kinase	422	2059180	2059932	196.8085106	185.505319	0.94257
hypothetical protein	421	2059911	2060705	99.49622166	107.68262	1.08228
hypothetical protein	420	2060729	2060866	65.69343066	82.1167883	1.25
hypothetical protein	419	2060949	2061461	223.6328125	175.78125	0.78603
Similar to coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)	418	2061486	2062661	28.08510638	17.2340426	0.61364

Signal peptidase I (EC 3.4.21.89)	417	2062665	2063387	60.94182825	49.8614958	0.81818
Signal peptidase I (EC 3.4.21.89)	416	2063391	2064386	195.4773869	241.959799	1.23779
S-layer protein	415	2064454	2065941	104.5729657	96.8392737	0.92605
SsrA-binding protein	414	2065938	2066396	335.1528384	397.925764	1.1873
Uncharacterized protein TP_0183 precursor	413	2066472	2067338	106.2355658	114.318707	1.07609
Septum formation initiator family protein	412	2067343	2067783	131.8181818	92.0454545	0.69828
Topoisomerase IV subunit A (EC 5.99.1.-)	411	2067923	2069941	223.9841427	205.153617	0.91593
hypothetical protein	410	2069943	2070800	70.01166861	78.7631272	1.125
Uncharacterized protein TP_0177	409	2070804	2072243	30.22932592	18.7630299	0.62069
hypothetical protein		2072266	2073876	32.60869565	15.3726708	0.47143
COG1355, Predicted dioxygenase	408	2073871	2074737	36.95150115	25.9815242	0.70313
Uncharacterized protein TP_0172	405	2074815	2075936	107.4933095	102.363961	0.95228
hypothetical protein	406	2075924	2076853	74.27341227	84.7685684	1.1413
gliding motility protein GldG		2076843	2078456	88.34469932	119.962802	1.35789
gliding motility protein GldF	403	2078458	2079192	38.82833787	39.8501362	1.02632
ABC-type multidrug transport system, ATPase component	402	2079189	2080130	219.4473964	208.023379	0.94794
Ribonuclease Z (EC 3.1.26.11)	401	2080144	2081157	111.5498519	122.161895	1.09513
putative enzyme; Not classified	400	2081196	2083676	18.5483871	6.35080645	0.34239
hypothetical protein	398	2083938	2084180	45.45454545	65.0826446	1.43182
hypothetical protein	399	2084161	2084277	17.24137931	0	0
hypothetical protein	397	2084301	2084423	39.13043478	0	0
hypothetical protein	396	2084851	2084994	24.47552448	0	0
hypothetical protein	395	2085041	2085364	26.31578947	0	0
hypothetical protein	394	2085384	2085659	20	0	0
hypothetical protein	393	2086349	2086498	33.55704698	0	0
hypothetical protein	392	2087180	2087356	2.840909091	0	0
hypothetical protein	391	2087632	2087898	22.55639098	16.9172932	0.75
ATP-dependent DNA helicase	390	2088094	2089452	38.78406709	18.8679245	0.48649
Nucleotidyltransferase domain protein	389	2089445	2089777	6.060606061	13.6363636	2.25
hypothetical protein	388	2089770	2090192	8.293838863	0	0
Nucleotidyltransferase domain protein	387	2090185	2090505	6.25	7.03125	1.125
trans-Golgi membrane protein p230	386	2090593	2092761	11.0701107	3.11346863	0.28125
Putative type IIS restriction /modification enzyme, N-terminal half	385	2092758	2095904	22.40940877	15.0190718	0.67021
Superfamily II DNA/RNA helicases, SNF2 family	384	2095904	2099170	50.67360686	57.1800367	1.1284
Integrase domain protein	383	2099318	2100553	46.55870445	18.2186235	0.3913
Conserved protein	382	2100805	2101203	32.66331658	22.6130653	0.69231
Chromosome undetermined scaffold_92, whole genome shotgun sequence	381	2101200	2102015	10.42944785	5.52147239	0.52941
putative membrane protein	380	2102018	2102908	17.41573034	12.6404494	0.72581
hypothetical protein	379	2102997	2103179	30.21978022	12.3626374	0.40909
hypothetical protein	378	2103578	2103775	32.99492386	22.8426396	0.69231
Transposase (class II)	377	2104050	2105081	47.04170708	24.0058196	0.51031
hypothetical protein	376	2105211	2105699	26.63934426	4.61065574	0.17308
Phage integrase	375	2105711	2107000	29.09231963	12.2187742	0.42
hypothetical protein	374	2107329	2107487	0	0	#DIV/0!
hypothetical protein	373	2107487	2107972	52.57731959	18.556701	0.35294
hypothetical protein	372	2107969	2108229	119.2307692	103.846154	0.87097
hypothetical protein	371	2108341	2108553	4.716981132	10.6132075	2.25
hypothetical protein	370	2108693	2109919	29.77161501	5.50570962	0.18493

hypothetical protein	369	2109956	2110630	17.06231454	0	0
hypothetical protein	368	2110693	2111190	18.10865191	4.52716298	0.25
hypothetical protein	367	2111302	2111664	13.8121547	37.2928177	2.7
hypothetical protein	366	2111709	2111897	10.63829787	0	0
Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein soj	365	2112034	2112804	6.493506494	0	0
hypothetical protein	364	2112809	2113087	3.597122302	0	0
hypothetical protein	363	2113336	2114040	13.49431818	0	0
hypothetical protein	362	2114030	2114272	0	0	#DIV/0!
Plasmid recombination enzyme	361	2114521	2115603	11.09057301	2.07948244	0.1875
DNA repair protein RadA domain protein	360	2115657	2116676	23.06182532	4.41609421	0.19149
hypothetical protein	359	2116660	2116800	7.142857143	0	0
hypothetical protein	358	2117205	2117591	0	0	#DIV/0!
hypothetical protein	357	2117625	2118119	2.024291498	4.55465587	2.25
Phage integrase	356	2118209	2119390	22.86198137	7.62066046	0.33333
Response regulator	353	2119815	2120825	232.1782178	153.712871	0.66205
Response regulator	352	2120822	2121880	132.7977316	146.73913	1.10498
Chorismate mutase II (EC 5.4.99.5)	351	2121951	2122319	139.9456522	128.396739	0.91748
hypothetical protein	350	2122316	2122663	79.25072046	45.389049	0.57273
Uncharacterized protein TP_0788	349	2122738	2123562	90.41262136	60.0728155	0.66443
Uncharacterized protein TP_0733	348	2123691	2124326	387.4015748	584.645669	1.50915
hypothetical protein	347	2124341	2125471	661.5044248	1290.26549	1.9505
ATPase, AAA family	346	2125494	2127821	180.7047701	351.955307	1.94768
Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	345	2127831	2130191	119.9152542	94.3855932	0.7871
hypothetical protein	344	2130254	2131144	69.66292135	35.3932584	0.50806
Endo-1,4-beta-xylanase B precursor	343	2131198	2132019	101.0962241	120.584653	1.19277
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	342	2132023	2133372	32.24610823	21.6827279	0.67241
Flagellin protein flaA	341	2133592	2134452	2394.988067	2706.44391	1.13004
Flagellin protein flaA	340	2134725	2135579	5607.142857	5733.02108	1.02245
hypothetical protein	339	2135696	2135836	492.8571429	578.571429	1.17391
Flagellin protein flaG	338	2135793	2136110	984.2271293	887.223975	0.90144
Flagellar hook-associated protein fliD	337	2136200	2138179	272.3597777	165.992926	0.60946
hypothetical protein	336	2138183	2139025	80.16627078	48.0997625	0.6
hypothetical protein	335	2139090	2140211	82.06958073	50.1784121	0.61141
hypothetical protein	334	2140254	2140520	99.62406015	93.0451128	0.93396
ATPase YjeE, predicted to have essential role in cell wall biosynthesis	333	2140498	2140968	230.8510638	186.702128	0.80876
Inactive homolog of metal-dependent proteases, putative molecular chaperone	332	2140965	2141660	95.68345324	48.5611511	0.50752
Response regulator	331	2141677	2142753	187.267658	127.555762	0.68114
Carbon storage regulator homolog	330	2142768	2143001	51.50214592	96.5665236	1.875
Transmembrane protein	329	2143004	2143453	216.0356347	185.412027	0.85825
Flagellar hook-associated protein flgL	328	2143477	2144724	256.0192616	216.693419	0.84639
Flagellar hook-associated protein flgK	327	2144744	2146642	207.3234984	175.44784	0.84625
hypothetical protein	326	2146664	2147167	221.6699801	174.45328	0.787
Integrase	321	2147869	2149083	76.19439868	63.014827	0.82703
hypothetical protein	320	2149152	2149295	3.496503497	0	0
hypothetical protein	319	2149442	2149684	0	0	#DIV/0!

hypothetical protein	318	2149769	2150080	397.1061093	340.032154	0.85628
Transposase and inactivated derivatives	317	2150092	2151045	132.2140609	75.5508919	0.57143
hypothetical protein	316	2151047	2151292	6.12244898	0	0
Transposase and inactivated derivatives	315	2151853	2152806	107.5550892	82.633788	0.76829
hypothetical protein	314	2152818	2153129	400.3215434	303.858521	0.75904
hypothetical protein	313	2154900	2155031	0	0	#DIV/0!
DNA polymerase III alpha subunit (EC 2.7.7.7)	312	2155207	2158170	23.79345258	2.27809652	0.09574
DNA polymerase IV (EC 2.7.7.7)	311	2158163	2159380	29.17009039	14.7904684	0.50704
COG1801: Uncharacterized conserved protein	310	2159364	2160167	45.51122195	8.41645885	0.18493
hypothetical protein	309	2160286	2160408	0	0	#DIV/0!
Integrase domain protein	308	2160815	2162050	51.01214575	16.3967611	0.32143
hypothetical protein	307	2162362	2163312	39.47368421	42.6315789	1.08
hypothetical protein	306	2163322	2163519	78.68020305	79.9492386	1.01613
hypothetical protein	305	2163586	2164812	29.77161501	18.3523654	0.61644
hypothetical protein	304	2164970	2165266	32.09459459	38.0067568	1.18421
hypothetical protein	303	2165611	2165994	236.2924282	346.605744	1.46685
Pirin	302	2166022	2166729	61.23919308	48.6311239	0.79412
hypothetical protein	300	2167097	2167294	10.15228426	22.8426396	2.25
Outer membrane autotransporter barrel		2167151	2179324	28.91645445	5.72989403	0.19815
TPR repeat precursor	299	2179395	2180057	32.47734139	10.1963746	0.31395
Ferredoxin	298	2180371	2181159	26.64974619	14.2766497	0.53571
FemA protein	297	2181152	2182306	176.3431542	228.119584	1.29361
Methionyl-tRNA synthetase (EC 6.1.1.10)	296	2182308	2184656	226.362862	305.68569	1.35042
Alpha-amylase (EC 3.2.1.1)	295	2184703	2186481	91.1136108	101.237345	1.11111
hypothetical protein	294	2186440	2186562	8.196721311	0	0
hypothetical protein	293	2186584	2187165	98.10671256	81.3253012	0.82895
hypothetical protein	292	2187162	2187779	52.67423015	83.8735818	1.59231
hypothetical protein	291	2187776	2188225	158.1291759	225.501114	1.42606
Electron transport complex protein rnfD	290	2188222	2189313	87.07607699	113.428048	1.30263
Electron transport complex protein rnfC	289	2189313	2190638	234.3396226	326.037736	1.3913
hypothetical protein	288	2190649	2192049	93.21428571	151.071429	1.62069
hypothetical protein	287	2192057	2192545	168.0327869	216.70082	1.28963
Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	286	2192606	2193586	64.79591837	34.4387755	0.5315
hypothetical protein	285	2193600	2194127	336.8121442	345.825427	1.02676
Deoxyribonuclease-1 precursor (EC 3.1.21.1)	284	2194151	2195029	108.7699317	74.3166287	0.68325
hypothetical protein	283	2195038	2195772	18.39237057	30.653951	1.66667
Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	282	2195846	2197306	54.45205479	63.1849315	1.16038
hypothetical protein	281	2197366	2198229	158.7485516	146.002317	0.91971
hypothetical protein	280	2198241	2199407	135.5060034	133.147513	0.98259
hypothetical protein	279	2199506	2200231	128.9655172	158.275862	1.22727
hypothetical protein	278	2200256	2200408	16.44736842	14.8026316	0.9
Poly(A) polymerase (EC 2.7.7.19)	277	2200413	2201636	183.5650041	195.012265	1.06236
Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23); putative	276	2201651	2202610	252.8675704	279.19708	1.10412
23S rRNA (Uracil-5-) -methyltransferase rumA (EC 2.1.1.-)	275	2202682	2203845	339.2089424	265.047291	0.78137
hypothetical protein	274	2203835	2205565	140.1734104	124.855491	0.89072
Antigen, p83/100		2205633	2207252	658.4311303	717.109327	1.08912
conserved hypothetical protein; possible membrane protein	272	2207356	2207769	16.94915254	5.44794189	0.32143

hypothetical protein	271	2208070	2208219	6.711409396	0	0
hypothetical protein	270	2208648	2208818	30.76923077	0	0
hypothetical protein	269	2208860	2209735	6.320224719	0	0
hypothetical protein	268	2209772	2210635	23.46570397	16.2454874	0.69231
transposase, mutator family	267	2210672	2211913	71.71635778	45.3263497	0.63202
Transposase (class II)	266	2212223	2213254	44.13191077	19.6411251	0.44505
hypothetical protein	265	2213310	2213846	9.009009009	0	0
FOG: TPR repeat	264	2213848	2214588	13.56852103	3.05291723	0.225
hypothetical protein	263	2214676	2215821	2.620087336	0	0
hypothetical protein	262	2215870	2216097	77.09251101	0	0
hypothetical protein	261	2216216	2216980	10.01335113	0	0
hypothetical protein	260	2217022	2217135	123.8938053	39.8230088	0.32143
hypothetical protein	259	2217417	2217671	9.842519685	8.85826772	0.9
Transcriptional regulator, MerR family	258	2217672	2218385	7.713884993	9.46704067	1.22727
hypothetical protein	257	2218385	2218513	11.71875	17.578125	1.5
Iron-sulfur cluster assembly scaffold protein NifU	256	2218544	2219137	203.2040472	227.655987	1.12033
Cysteine desulfurase (EC 2.8.1.7)	255	2219152	2220312	155.4404145	172.927461	1.1125
Phosphomannomutase (EC 5.4.2.8) / Phosphoglucosamine mutase (EC 5.4.2.10)	254	2220429	2222225	104.1202673	250.556793	2.40642
hypothetical protein	252	2222249	2222650	132.1695761	263.715711	1.99528
hypothetical protein	253	2222647	2223198	34.48275862	53.0852995	1.53947
hypothetical protein	251	2223218	2223466	32.25806452	0	0
hypothetical protein	250	2223465	2223596	49.61832061	0	0
Ribonuclease HII (EC 3.1.26.4)	249	2223752	2224327	26.08695652	19.5652174	0.75
hypothetical protein	248	2224324	2227281	70.84883328	50.2198174	0.70883
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	247	2227290	2227919	70.74721781	57.2337043	0.80899
GlpG protein (membrane protein of glp regulon)	246	2227951	2228511	45.53571429	32.1428571	0.70588
Exodeoxyribonuclease III (EC 3.1.11.2)	245	2228508	2229287	101.4120668	138.639281	1.36709
hypothetical protein	244	2229407	2229529	8.196721311	0	0
hypothetical protein	243	2229743	2236333	22.91350531	11.6084977	0.50662
PIN (PilT N terminus) domain	242	2236917	2237255	72.4852071	39.9408284	0.55102
ATP-dependent Clp protease adaptor protein clpS	241	2237364	2237678	81.21019108	42.9936306	0.52941
ATP-dependent Clp protease ATP-binding subunit clpA	240	2237694	2240084	198.9112228	180.904523	0.90947
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	239	2240094	2240888	113.9798489	102.015113	0.89503
Probable M18-family aminopeptidase 1 (EC 3.4.11.-)	238	2240893	2242353	149.3150685	146.40411	0.9805
Glutamyl-tRNA synthetase (EC 6.1.1.17); Glutamyl-tRNA(Gln) synthetase	237	2242276	2243880	107.8553616	98.19202	0.9104
hypothetical protein	236	2243928	2244719	138.4323641	156.447535	1.13014
NAD-dependent protein deacetylase of SIR2 family	235	2244757	2245512	143.7086093	104.304636	0.72581
Putative ankyrin repeat-containing protein TP_0502	234	2245514	2246488	63.6550308	53.1314168	0.83468
Adenylate cyclase (EC 4.6.1.1)	233	2246533	2247510	47.59467758	39.1504606	0.82258
Inosose dehydratase (EC 4.2.1.44)	232	2247556	2248455	61.7352614	72.5806452	1.17568
Epi-inositol hydrolase	231	2248456	2250336	89.09574468	84.9734043	0.95373
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	230	2250368	2251387	96.17271835	88.3218842	0.91837

hypothetical protein	229	2251418	2252719	40.73789393	39.7770945	0.97642
hypothetical protein	228	2252735	2254291	31.16966581	21.6902314	0.69588
hypothetical protein	227	2254310	2255710	37.85714286	27.3214286	0.7217
hypothetical protein	226	2255713	2256498	77.07006369	68.7898089	0.89256
hypothetical protein	225	2256507	2257715	48.01324503	52.1523179	1.08621
hypothetical protein	224	2257708	2258199	137.4745418	146.639511	1.06667
hypothetical protein	223	2258243	2258437	54.12371134	57.9896907	1.07143
Xylulose kinase (EC 2.7.1.17)	222	2258471	2259952	100.9453072	91.1546253	0.90301
Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	221	2259954	2260859	136.4640884	221.270718	1.62146
L-fucose isomerase related protein	220	2260871	2262265	111.9081779	85.5451937	0.76442
Ribose operon repressor	219	2262280	2263293	29.12142152	6.66337611	0.22881
Transposase subunit		2263945	2264172	0	9.91189427	#DIV/0!
Transposase subunit		2264176	2264295	8.403361345	0	0
transposase, IS30 family	216	2264471	2265157	59.76676385	49.1982507	0.82317
hypothetical protein	215	2265243	2265632	16.70951157	11.5681234	0.69231
hypothetical protein	214	2265738	2265854	4.310344828	0	0
ABC transporter, substrate binding protein	213	2265919	2267229	101.9083969	84.1603053	0.82584
Predicted rhamnose oligosaccharide ABC transport system, permease component	212	2267260	2268108	26.53301887	10.6132075	0.4
Predicted rhamnose oligosaccharide ABC transport system, permease component 2	211	2268105	2269037	31.11587983	28.9699571	0.93103
transcriptional regulator, AraC family	210	2269115	2270002	50.16910936	35.5129651	0.70787
Putative isomerase	208	2270059	2271558	72.04803202	60.0400267	0.83333
Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99)	209	2271548	2272471	148.4290358	117.009751	0.78832
Alpha-galactosidase (EC 3.2.1.22)	207	2272483	2273892	118.5237757	108.587651	0.91617
possible Bacterial Ig-like domain (group 1)	206	2274059	2276404	18.97654584	4.79744136	0.25281
hypothetical protein	205	2276474	2276920	30.2690583	10.0896861	0.33333
hypothetical protein	204	2276933	2280070	30.92126235	2.15173733	0.06959
hypothetical protein	203	2280144	2281556	21.60056657	3.18696884	0.14754
hypothetical protein	202	2281678	2282871	14.66890193	0	0
Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	201	2282882	2284327	19.03114187	4.67128028	0.24545
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	200	2284327	2285988	13.84708007	5.41842264	0.3913
Transcriptional regulator	199	2286105	2287007	16.07538803	0	0
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	198	2287097	2288077	21.42857143	6.8877551	0.32143
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	197	2288090	2289010	30.43478261	12.2282609	0.40179
ABC transporter, substrate-binding protein	196	2289036	2290607	51.24124761	34.3730108	0.67081
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)	195	2290614	2292104	40.60402685	24.1610738	0.59504
Sorbitol dehydrogenase (EC 1.1.1.14)		2292312	2293265	182.5813221	203.043022	1.11207
Putative dihydroxyacetone kinase (EC 2.7.1.29), dihydroxyacetone binding subunit	193	2293290	2294285	160.8040201	144.723618	0.9
Putative dihydroxyacetone kinase (EC 2.7.1.29), ADP-binding subunit	192	2294295	2294939	107.9192547	66.3819876	0.61511
Ribose 5-phosphate isomerase B (EC 5.3.1.6)	191	2294942	2295400	141.9213974	68.7772926	0.48462
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	190	2295506	2296756	497.2	541.8	1.0897

N-Acetyl-D-glucosamine ABC transport system, permease protein 1	189	2296767	2297705	105.010661	76.7590618	0.73096
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	188	2297707	2298546	115.613826	174.31466	1.50773
hypothetical protein	186	2298869	2299891	84.63796477	112.279843	1.32659
Uncharacterized protein BB_0265	185	2299910	2300488	104.6712803	81.7474048	0.78099
hypothetical protein	184	2300490	2300831	115.8357771	98.973607	0.85443
hypothetical protein	183	2300812	2302776	180.2443992	183.299389	1.01695
RNA polymerase sigma factor for flagellar operon	182	2302790	2303563	355.7567917	390.03881	1.09636
hypothetical protein	181	2303604	2304323	131.4325452	147.079277	1.11905
Flagellar synthesis regulator fleN	180	2304341	2305276	150.802139	202.139037	1.34043
Flagellar biosynthesis protein flhF	179	2305279	2306598	103.1084155	139.878696	1.35662
Flagellar biosynthesis protein flhA	178	2306616	2308745	118.3654298	154.297792	1.30357
Flagellar biosynthesis protein flhB	177	2308745	2309866	82.96164139	112.399643	1.35484
Flagellar biosynthesis protein fliR	176	2309863	2310678	34.96932515	55.2147239	1.57895
Flagellar biosynthesis protein fliQ	175	2310692	2310958	41.35338346	50.7518797	1.22727
Flagellar biosynthesis protein fliP	174	2310972	2311787	50.61728395	86.1111111	1.70122
Flagellar biosynthesis protein fliZ	173	2311789	2312187	140.7035176	141.331658	1.00446
hypothetical protein	172	2312225	2312422	347.715736	239.847716	0.68978
Flagellar motor switch protein fliN	171	2312578	2313696	392.6654741	374.329159	0.9533
Flagellar motor switch protein fliM	170	2313693	2314724	648.4907498	633.15482	0.97635
Flagellar biosynthesis protein fliL	169	2314737	2315291	156.1371841	158.393502	1.01445
Flagellar motor rotation protein motB	168	2315338	2316069	208.5048011	166.666667	0.79934
Flagellar motor rotation protein motA	167	2316086	2316868	276.2148338	250.319693	0.90625
Flagellar protein flbD	166	2316874	2317071	213.1979695	262.690355	1.23214
Flagellar hook protein flgE	165	2317083	2318483	857.8571429	639.642857	0.74563
Flagellar basal-body rod modification protein flgD	164	2318509	2318946	544.6224256	458.237986	0.84139
Flagellar hook-length control protein fliK	163	2318964	2320385	289.9366643	213.757917	0.73726
Flagellar protein flbB	162	2320457	2321095	583.8557994	507.836991	0.8698
hypothetical protein	161	2321132	2322202	29.43925234	16.8224299	0.57143
Gluconokinase (EC 2.7.1.12) / oxidoreductase domain	160	2322202	2323317	81.16591928	58.5201794	0.72099
D-mannonate oxidoreductase (EC 1.1.1.57)	159	2323411	2325009	78.8485607	47.8723404	0.60714
Autoinducer 2 (AI-2) ABC transport system, periplasmic AI-2 binding protein LsrB	158	2325036	2326115	82.94717331	47.9610751	0.57821
Putative pheromone precursor lipoprotein	157	2326125	2326586	68.329718	34.164859	0.5
Sensory box histidine kinase/response regulator	156	2326590	2329376	30.50969131	7.26848528	0.23824
Xanthosine/inosine triphosphate pyrophosphatase ; HAM1 protein homolog	155	2329422	2330027	57.85123967	59.5041322	1.02857
ATP-dependent DNA helicase Rep	154	2330094	2332196	50.26202954	39.6617437	0.7891
Iron-dependent repressor IdeR/DtxR	153	2332230	2332607	181.6976127	226.790451	1.24818
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.-)	152	2332757	2333392	64.56692913	24.8031496	0.38415
tRNA pseudouridine synthase A (EC 4.2.1.70)	151	2333393	2334139	74.39678284	45.2412869	0.60811
hypothetical protein	150	2334154	2335014	84.88372093	91.5697674	1.07877
Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	149	2335029	2335409	96.05263158	130.263158	1.35616
hypothetical protein		2335406	2336377	134.9124614	122.811535	0.91031

ABC transporter, permease protein ybbP / Tlr1762 protein	147	2336367	2337215	123.2311321	92.865566	0.75359
Dihydropteroate synthase (EC 2.5.1.15)	146	2337254	2338096	105.7007126	96.1995249	0.91011
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)	145	2338093	2340030	69.69540527	95.2503872	1.36667
Methylmalonyl-CoA epimerase (EC 5.1.99.1)	144	2340381	2340848	387.5802998	342.077088	0.8826
hypothetical protein	143	2341038	2341280	33.05785124	46.4876033	1.40625
Death on curing protein	142	2341277	2341663	93.2642487	69.9481865	0.75
putative autotransporter protein	141	2341894	2346528	61.8256366	42.7276651	0.6911
Outer membrane protein		2346543	2348147	55.48628429	29.457606	0.5309
helix-turn-helix, type 11 domain protein	139	2348384	2349199	46.01226994	35.8895706	0.78
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	138	2349206	2350192	135.9026369	203.093306	1.4944
DNA-directed RNA polymerase omega chain (EC 2.7.7.6) (RNAP omega subunit) (Transcriptase omega chain) (RNA polymerase omega subunit)	137	2350198	2350473	385.4545455	540	1.40094
HflK protein	136	2350451	2351422	324.92276	319.773429	0.98415
HflC protein	135	2351422	2352399	320.3684749	368.474923	1.15016
hypothetical protein	134	2352402	2353862	171.9178082	140.239726	0.81574
Fumarate hydratase class I, aerobic (EC 4.2.1.2)	133	2353859	2355505	53.15917375	35.5407047	0.66857
NADH pyrophosphatase (EC 3.6.1.22)	132	2355519	2356301	55.62659847	37.4040921	0.67241
hypothetical protein	131	2356375	2356758	124.0208877	105.744125	0.85263
COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like	130	2356789	2357628	43.50417163	48.2717521	1.10959
hypothetical protein	129	2358002	2358301	528.4280936	594.481605	1.125
hypothetical protein	128	2358314	2359228	77.68052516	39.3873085	0.50704
Isoleucyl-tRNA synthetase (EC 6.1.1.5)	127	2359251	2362454	132.8835896	139.08064	1.04664
Endonuclease III (EC 4.2.99.18)	126	2362491	2363180	39.18722787	19.5936139	0.5
Transposase IS4 family		2363437	2363610	0	0	#DIV/0!
hypothetical protein	124	2363658	2363774	4.310344828	0	0
hypothetical protein	123	2363902	2364591	19.59361393	16.3280116	0.83333
Legionella vir region protein	122	2364825	2365262	22.88329519	15.4462243	0.675
hypothetical protein	121	2365315	2365521	70.38834951	43.6893204	0.62069
hypothetical protein	120	2365550	2366017	52.46252677	48.1798715	0.91837
type I phosphodiesterase/nucleotide pyrophosphatase family protein	119	2366270	2367559	83.39798293	66.3304888	0.79535
23S rRNA (guanine-N-2-) -methyltransferase rlmL EC 2.1.1.-)	118	2367626	2368639	42.44817374	28.8746298	0.68023
hypothetical protein	117	2368632	2369171	88.12615955	125.231911	1.42105
LSU ribosomal protein L31p	116	2369249	2369452	485.2216749	886.699507	1.82741
Transcription termination factor Rho	115	2369525	2371405	421.1941904	479.289941	1.13793
Similar to C-terminal domain of competence/damage-inducible protein CinA	114	2371430	2371924	103.2388664	100.202429	0.97059
hypothetical protein	113	2371917	2372333	346.1538462	367.788462	1.0625
Phosphate regulon transcriptional regulatory protein phoB	112	2372336	2373010	170.6231454	193.620178	1.13478
Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE	111	2373011	2374672	141.180012	173.389524	1.22814
Integration host factor alpha subunit	110	2374669	2374983	457.0063694	566.082803	1.23868
SSU ribosomal protein S20p	109	2375011	2375286	850.9090909	1464.54545	1.72115

hypothetical protein	108	2375369	2375539	305.8823529	410.294118	1.34135
Uncharacterized protein TP_0447 precursor	107	2375631	2376779	106.7073171	101.916376	0.9551
hypothetical protein	106	2376818	2376955	43.79562044	0	0
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.4.3)	105	2376963	2378072	165.4643823	233.318305	1.41008
V-type ATPase, subunit K	104	2378087	2378494	401.7199017	469.90172	1.16972
V-type ATP synthase subunit I (EC 3.6.3.14)	103	2378576	2380510	270.6065319	372.083981	1.375
V-type ATP synthase subunit D 1 (EC 3.6.3.14) (V type ATPase subunit D 1)	102	2380515	2381135	783.8709677	874.596774	1.11574
V-type ATP synthase beta chain 1 (EC 3.6.3.14) (V-type ATPase subunit B 1)	101	2381150	2382448	1023.137255	1252.94118	1.22461
V-type ATP synthase subunit A (EC 3.6.3.14)	100	2382460	2384220	688.5813149	829.152249	1.20415
hypothetical protein	99	2384217	2384762	622.9357798	792.66055	1.27246
V-type ATP synthase subunit E (EC 3.6.3.14) (V-type ATPase subunit E)	98	2384766	2385377	602.2913257	754.909984	1.2534
L-arabinose-specific 1-epimerase (mutarotase)	97	2385473	2386504	322.9873909	467.022308	1.44595
DnaJ domain protein	96	2386553	2386978	145.8823529	132.352941	0.90726
oxidoreductase, Gfo/Idh/MocA family	95	2386984	2388009	292.6829268	232.682927	0.795
Uncharacterized sugar kinase yegV	94	2388013	2388909	65.29017857	42.6897321	0.65385
Response regulator of zinc sigma-54-dependent two-component system	93	2388906	2390270	64.38557763	64.5695364	1.00286
two-component sensor PilS	92	2390271	2391482	35.92072667	24.1535921	0.67241
DNA polymerase III delta prime subunit (EC 2.7.7.7)	91	2391484	2392836	97.26331361	73.2248521	0.75285
Uncharacterized protein TP_0522	90	2392838	2393353	64.0776699	39.3203883	0.61364
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	89	2393353	2394423	100.4672897	79.9065421	0.79535
GGDEF domain/EAL domain protein	88	2394442	2395917	19.3220339	0	0
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	87	2395901	2397358	10.63829787	1.54426905	0.14516
hypothetical protein	86	2397355	2397525	11.76470588	0	0
hypothetical protein	85	2397565	2397690	12	0	0
hypothetical protein	84	2397844	2399235	24.08339324	4.85262401	0.20149
Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-)	83	2399282	2400763	80.68872384	100.270088	1.24268
Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.-); Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-)	82	2400779	2402284	120.5980066	195.847176	1.62397
hypothetical protein	81	2402299	2402622	54.17956656	48.7616099	0.9
hypothetical protein	80	2402725	2402961	127.1186441	85.8050847	0.675
branched-chain amino acid transport	79	2402991	2403338	11.52737752	6.48414986	0.5625
branched-chain amino acid transport	78	2403335	2404066	43.09165527	40.0136799	0.92857
Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake	77	2404115	2404831	77.51396648	56.5642458	0.72973
COG2078: Uncharacterized ACR	76	2404881	2405456	73.04347826	97.826087	1.33929
Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis, PTPS-III	75	2405466	2405840	98.93048128	48.1283422	0.48649
hypothetical protein	74	2405799	2405927	39.0625	0	0

UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	73	2405924	2407636	106.6004673	86.7406542	0.8137
hypothetical protein	72	2407657	2408685	90.46692607	94.114786	1.04032
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	71	2408743	2410188	109.3425606	84.083045	0.76899
Lysyl-tRNA synthetase-related protein	69	2410192	2411181	57.12841254	38.6754297	0.67699
hypothetical protein	70	2411178	2412095	38.16793893	26.9901854	0.70714
Oligoendopeptidase F (EC 3.4.24.-)	68	2412094	2413893	242.881072	242.462312	0.99828
Homolog of plant auxin-responsive GH3-like protein	67	2414049	2415758	746.0410557	849.853372	1.13915
hypothetical protein	66	2415976	2416722	69.70509383	120.643432	1.73077
hypothetical protein	65	2416901	2417056	54.83870968	14.516129	0.26471
transcriptional regulator, PemK family	64	2417098	2417445	129.6829971	90.778098	0.7
hypothetical protein	63	2417432	2417590	91.7721519	113.924051	1.24138
hypothetical protein	62	2417726	2417881	19.35483871	0	0
Translation elongation factor P; Translation initiation factor 5A	61	2417950	2418513	277.0870337	411.634103	1.48558
hypothetical protein	60	2418704	2419828	46.70818505	50.044484	1.07143
Leucyl-tRNA synthetase (EC 6.1.1.4)	59	2419900	2422365	198.3353634	210.109622	1.05937
Putative kinase	58	2422407	2423408	134.3656344	112.387612	0.83643
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	56	2423418	2424623	138.1742739	186.721992	1.35135
Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) # NAD-specific	57	2424620	2425483	364.4264195	696.118192	1.91017
2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	55	2425480	2426505	695.6097561	1200.73171	1.72616
hypothetical protein	54	2426618	2426740	45.08196721	0	0
late embryogenesis abundant family protein / LEA family protein / similar to ethylene-responsive late embryogenesis-like protein [Lycopersicon esculentum] GI:1684830; contains Pfam profile PF03168: Late embryogenesis abundant protein; go_process: response to dessication [goid 0009269]; go_process: embryonic development (sensu Magnoliophyta) [goid 0009793]	53	2426772	2428007	96.3562753	103.846154	1.07773
Seryl-tRNA synthetase (EC 6.1.1.11)	52	2428016	2429308	218.6532508	195.04644	0.89204
Isochorismatase (EC 3.3.2.1)	50	2429360	2429848	101.4344262	69.1598361	0.68182
Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor	51	2429845	2430624	50.06418485	17.3299101	0.34615
Homoserine kinase (EC 2.7.1.39)	49	2430666	2431271	68.59504132	78.0991736	1.13855
GTP-binding protein Era	48	2431272	2432195	64.46370531	56.0671723	0.86975
Flagellar hook-length control protein fliK	47	2432198	2437672	56.90537084	48.5020095	0.85233
Flagellar hook-length control protein fliK		2437629	2440109	517.5403226	430.947581	0.83268
hypothetical protein	45	2440951	2441088	14.59854015	49.270073	3.375
hypothetical protein	44	2441263	2441445	5.494505495	0	0
hypothetical protein	43	2441608	2441877	94.79553903	58.5501859	0.61765
Plasmid stability protein	41	2441861	2442271	19.51219512	10.9756098	0.5625
hypothetical protein	42	2442253	2442384	11.45038168	0	0
hypothetical protein	40	2442367	2442840	19.02748414	4.75687104	0.25
hypothetical protein	39	2442846	2443055	47.84688995	21.5311005	0.45

Serine acetyltransferase (EC 2.3.1.30)	38	2443073	2443963	253.9325843	260.393258	1.02544
(R)-2-hydroxyglutaryl-CoA dehydratase activator-related protein		2443987	2444445	350.5494505	445.054945	1.26959
(R)-2-hydroxyglutaryl-CoA dehydratase activator-related protein		2444477	2448382	239.1749936	311.299001	1.30155
Peroxide stress regulator PerR, FUR family	35	2448619	2449032	46.00484262	70.8232446	1.53947
Rubrerythrin	33	2449061	2449600	727.0168856	1025.79737	1.41097
transcriptional regulator	34	2449597	2450559	97.19334719	154.365904	1.58824
L-rhamnose mutarotase	32	2450614	2450931	26.81388013	7.0977918	0.26471
Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1)	31	2450942	2452444	22.96937417	4.49400799	0.19565
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	30	2452453	2453397	16.41949153	0	0
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	29	2453390	2454388	20.04008016	4.50901804	0.225
Predicted L-rhamnose ABC transporter, substrate-binding component	28	2454433	2455506	75.02329916	27.2600186	0.36335
hypothetical protein	27	2455524	2456618	24.68007313	10.2833638	0.41667
hypothetical protein	26	2456715	2459564	26.32502633	26.0617761	0.99
probable ATP /GTP binding protein	25	2459537	2460847	48.47328244	46.3740458	0.95669
ATP-dependent helicase	23	2460828	2463026	30.02729754	11.2602366	0.375
N-acetylhexosamine 1-kinase	24	2463023	2464153	66.37168142	57.7433628	0.87
Alpha-L-fucosidase (EC 3.2.1.51)	22	2464218	2465513	109.6525097	92.0849421	0.83979
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	21	2465558	2467372	116.4914222	158.13503	1.35748
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	20	2467381	2468478	57.88514129	65.633546	1.13386
Peptide/opine/nickel uptake family ABC transporter, permease/ATP- binding protein	19	2468478	2470625	75.68700512	68.1183046	0.9
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	18	2470622	2471629	42.20456802	44.6871897	1.05882
putative ATP-dependent DNA helicase		2471666	2475223	44.70059039	25.9347765	0.58019
ATP-dependent helicase		2475244	2476116	26.37614679	5.16055046	0.19565
Response regulator	15	2476166	2476786	71.77419355	36.2903226	0.50562
Lipoprotein releasing system transmembrane protein LolC	14	2476788	2478050	41.99683043	17.8288431	0.42453
Lipoprotein releasing system ATP-binding protein lolD	13	2478051	2478755	36.22159091	35.15625	0.97059
Lipoprotein releasing system transmembrane protein LolC	12	2478748	2480088	27.23880597	21.8283582	0.80137
hypothetical protein	11	2480085	2481242	63.52636128	68.0639585	1.07143
Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	10	2481235	2482110	112	118.285714	1.05612
PEGA domain protein	9	2482111	2483637	59.30537353	58.9777195	0.99448
Peptide chain release factor 2; programmed frameshift-containing	8	2483630	2484574	268.528464	319.011815	1.188
hypothetical protein	7	2484742	2485059	282.3343849	255.520505	0.90503
hypothetical protein	6	2485110	2486297	142.3757372	130.791912	0.91864
hypothetical protein	5	2486483	2486743	73.52941176	77.2058824	1.05
hypothetical protein	4	2486740	2487219	0	46.9728601	#DIV/0!
hypothetical protein	3	2487783	2487905	8.196721311	0	0

putative autotransporter protein	2	2487978	2491139	40.17715913	17.7950016	0.44291
Probable hemagglutinin-related autotransporter protein	1	2491142	2493544	54.12156536	29.0383014	0.53654
hypothetical protein	3666	2493800	2494207	104.4226044	44.2260442	0.42353
hypothetical protein	3665	2494204	2494446	179.7520661	269.628099	1.5
TPR domain protein	3664	2494585	2496585	93	104.625	1.125
Magnesium and cobalt efflux protein corC	3663	2496585	2497370	78.98089172	91.7197452	1.16129
predicted metal-dependent hydrolase	3662	2497367	2497822	52.74725275	69.2307692	1.3125
Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog	3661	2497819	2500041	70.4320432	67.8442844	0.96326
Phosphate starvation-inducible protein PhoH, predicted ATPase	3660	2500025	2500966	215.727949	236.716259	1.09729
Organic solvent tolerance protein precursor	3659	2501029	2504460	50.2768872	32.7892743	0.65217
Excinuclease ABC subunit A	3658	2504457	2507333	119.9582754	129.085535	1.07609
Iron-sulfur flavoprotein	3657	2507368	2508024	123.4756098	157.77439	1.27778
Methyl-accepting chemotaxis protein	3656	2508027	2510129	118.9343482	131.660324	1.107
Transcriptional regulator		2510259	2511311	44.20152091	36.3593156	0.82258
Alcohol dehydrogenase (EC 1.1.1.1)	3654	2511549	2512847	63.55932203	55.4699538	0.87273
Glyoxylate carboligase (EC 4.1.1.47)	3653	2512865	2514526	31.90848886	21.6736905	0.67925
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	3652	2514703	2515539	11.96172249	0	0
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	3651	2515543	2516493	15.78947368	2.36842105	0.15
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	3650	2516595	2517977	30.39073806	35.8176556	1.17857
Invasion protein IbeA	3649	2518058	2519398	39.55223881	38.619403	0.97642
Invasion protein IbeA	3648	2519660	2520991	23.29075883	6.76183321	0.29032
Invasion protein IbeA	3647	2521033	2522370	18.32460733	6.73148841	0.36735
Sorbitol dehydrogenase (EC 1.1.1.14)	3646	2522817	2523893	22.76951673	18.8197026	0.82653
oxidoreductase, short-chain dehydrogenase/reductase family	3645	2523908	2524675	29.98696219	17.601043	0.58696
Dihydroxyacetone kinase, ATP-dependent (EC 2.7.1.29)	3644	2524685	2525680	29.64824121	9.04522613	0.30508
Putative dihydroxyacetone kinase (EC 2.7.1.29), ADP-binding subunit	3643	2525698	2526333	30.70866142	17.7165354	0.57692
Ribose 5-phosphate isomerase B (EC 5.3.1.6)	3642	2526347	2526805	38.20960699	0	0
hypothetical protein		2526843	2527046	7.389162562	0	0
hypothetical protein	3640	2527151	2527294	6.993006993	0	0
Transposase subunit	3639	2527456	2527806	41.42857143	6.42857143	0.15517
type III effector Hrp-dependent outer	3638	2528228	2528821	29.51096121	0	0
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	3637	2528829	2530073	33.76205788	5.42604502	0.16071
4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	3636	2530067	2531128	13.19509896	0	0
Transcriptional regulator, IclR family	3634	2531140	2531940	77.5	75.9375	0.97984
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	3635	2531937	2532686	46.06141522	39.0520694	0.84783
Acyl-CoA dehydrogenase (EC 1.3.99.3)	3633	2532696	2533310	97.71986971	76.9543974	0.7875
Transcription-repair coupling factor	3632	2533397	2536822	83.55243938	78.878177	0.94406
hypothetical protein	3631	2536883	2537866	293.4893184	256.358087	0.87348
Uncharacterized protein TP_0454	3630	2537875	2538648	226.3906856	148.447607	0.65571
hypothetical protein	3629	2538691	2538846	16.12903226	0	0

transcriptional regulator, PadR family	3628	2538845	2539192	30.25936599	19.4524496	0.64286
CDS_ID OB0393		2539420	2540007	30.66439523	34.4974446	1.125
Phosphomethylpyrimidine kinase (EC 2.7.4.7)	3626	2540111	2540911	126.25	104.0625	0.82426
Alkaline phosphatase like protein	3625	2540908	2541609	42.79600571	25.6776034	0.6
Putative deoxyribonuclease YcfH	3624	2541602	2542402	47.5	47.8125	1.00658
DNA integration/recombination/invertion protein	3623	2542402	2542962	57.14285714	32.1428571	0.5625
hypothetical protein	3622	2543135	2543551	439.9038462	481.370192	1.09426
Asparaginyl-tRNA synthetase (EC 6.1.1.22)	3621	2543557	2545002	132.0361362	140.722724	1.06579
D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	3620	2545008	2546234	69.73898858	53.2218597	0.76316
Polysaccharide deacetylase precursor	3619	2546292	2548541	73.14361939	45.0200089	0.6155
hypothetical protein	3618	2548525	2548728	307.8817734	243.842365	0.792
hypothetical protein	3617	2548725	2548850	180	216	1.2
Membrane proteins related to metalloendopeptidases	3616	2548888	2550162	253.5321821	233.124019	0.9195
Signal peptidase I (EC 3.4.21.89)	3615	2550239	2550613	76.20320856	84.2245989	1.10526
Cell division protein ftsI [Peptidoglycan synthetase] (EC 2.4.1.129)	3614	2550610	2552478	185.4925054	168.62955	0.90909
hypothetical protein	3613	2552493	2553551	146.5028355	204.15879	1.39355
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	3612	2553576	2554415	66.74612634	37.5446961	0.5625
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	3611	2554425	2555291	80.25404157	62.3556582	0.77698
Multiple sugar ABC transporter, substrate-binding protein	3610	2555377	2556774	253.758053	227.093772	0.89492
Conserved domain protein	3609	2556808	2558730	79.0842872	87.7991675	1.1102
Aspartate aminotransferase (EC 2.6.1.1)	3608	2558867	2560084	127.3623665	134.963024	1.05968
Uncharacterized protein TP_0763	3607	2560099	2560920	129.7198538	139.768575	1.07746
HD domain protein	3606	2560966	2562180	217.0510708	224.258649	1.03321
Hemolysins and related proteins containing CBS domains	3605	2562191	2563519	55.80693816	44.1176471	0.79054
ATP-dependent RNA helicase YfmL	3604	2563552	2564787	85.82995951	61.9433198	0.7217
Glycosyltransferase	3603	2564777	2566135	130.7069219	107.69514	0.82394
Sodium/proline symporter	3602	2566218	2567684	173.2876712	211.130137	1.21838
Glutathione peroxidase (EC 1.11.1.9)	3601	2567697	2568176	76.20041754	84.5511482	1.10959
hypothetical protein	3600	2568234	2568371	105.8394161	65.6934307	0.62069
hypothetical protein	3599	2568557	2572069	30.46697039	22.4231207	0.73598
similar to TPR repeat-containing protein	3598	2572128	2572391	17.11026616	17.1102662	1
Indolepyruvate oxidoreductase, subunit A	3597	2572601	2574298	217.7895981	202.12766	0.92809
Pyruvate kinase (EC 2.7.1.40)	3596	2574295	2576130	182.5613079	147.138965	0.80597
Indolepyruvate oxidoreductase, subunit B	3595	2576157	2576729	78.67132867	59.0034965	0.75
Phenylacetate-coenzyme A ligase (EC 6.2.1.30)	3594	2576726	2578039	169.2073171	180.068598	1.06419
hypothetical protein	3593	2578064	2578654	51.69491525	34.3220339	0.66393
Mlr3463 protein	3592	2578651	2580054	57.37704918	27.2630078	0.47516
Cell surface protein	3591	2580069	2583068	52.01733911	16.5055018	0.31731
hypothetical protein	3590	2583088	2585025	57.56324213	40.6556531	0.70628
hypothetical protein	3589	2585136	2586533	37.2226199	17.7165354	0.47596
Phenylacetate-coenzyme A ligase (EC 6.2.1.30)	3588	2586661	2587962	304.0958269	403.400309	1.32656
Amino acid-binding ACT	3587	2588045	2588461	152.6442308	194.711538	1.27559

Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)	3586	2588415	2589950	220.8469055	222.801303	1.00885
UDP-sugar hydrolase (EC 3.6.1.45); 5'-nucleotidase (EC 3.1.3.5)	3585	2589955	2591508	167.961165	103.398058	0.61561
Transcriptional regulator	3584	2591561	2592046	20.6185567	0	0
Iron-sulfur cluster-binding protein	3583	2592088	2593200	32.82374101	14.1636691	0.43151
Methyl-accepting chemotaxis sensory transducer precursor	3582	2593320	2595083	130.7430516	100.822462	0.77115
Signal transduction histidine kinase	3581	2595121	2597820	62.4768261	35.0389321	0.56083
Transcription regulator [contains diacylglycerol kinase catalytic domain]	3580	2597813	2598808	51.75879397	38.4422111	0.74272
Circadian input kinase A / Phytochrome-like protein	3579	2598870	2600096	81.56606852	108.278956	1.3275
sensory box histidine kinase/response regulator	3578	2600109	2602037	60.6846473	63.0186722	1.03846
sensory box histidine kinase/response regulator	3577	2602052	2605270	52.05096333	56.6345556	1.08806
hypothetical protein	3576	2605298	2606458	121.1206897	172.62931	1.42527
Sugar phosphate isomerases/epimerases	3574	2606710	2607531	516.4433618	701.583435	1.35849
Flavodoxin	3573	2607696	2608184	145.4918033	147.540984	1.01408
Peptidase U32	3572	2608186	2609385	58.38198499	54.4203503	0.93214
Protein RtcB	3571	2609407	2610603	22.57525084	15.0501672	0.66667
Peptide chain release factor homolog	3570	2610593	2611369	40.59278351	31.8943299	0.78571
Virulence associated protein	3569	2611672	2611830	37.97468354	0	0
Purine nucleoside phosphorylase (EC 2.4.2.1)	3567	2612398	2613144	35.5227882	33.1769437	0.93396
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	3566	2613175	2614089	41.02844639	29.5404814	0.72
Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1)	3565	2614082	2615227	34.06113537	13.7554585	0.40385
ABC transporter, ATP-binding protein	3564	2615220	2616740	111.1842105	90.2960526	0.81213
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	3563	2616875	2618476	710.1811368	713.928795	1.00528
Oligopeptide transport system permease protein oppB (TC 3.A.1.5.1)	3562	2618498	2619427	94.18729817	84.7685684	0.9
Oligopeptide transport system permease protein oppC (TC 3.A.1.5.1)	3561	2619440	2620510	43.45794393	23.1308411	0.53226
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3560	2620519	2621523	100.5976096	53.7848606	0.53465
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	3559	2621520	2622524	74.20318725	80.6772908	1.08725
hypothetical protein	3558	2622529	2622897	248.6413043	238.451087	0.95902
lipoprotein, Bmp family	3557	2622924	2624072	641.1149826	664.416376	1.03635
hypothetical protein	3556	2624002	2624172	5.882352941	0	0
OmpA family protein	3555	2624246	2628319	440.4615762	560.70464	1.27299
hypothetical protein	3554	2628442	2629203	84.09986859	68.0026281	0.80859
Bsr0038 protein	3553	2629314	2629703	56.55526992	34.7043702	0.61364
S-layer protein	3552	2629707	2631314	94.58618544	82.6073429	0.87336
Methionine ABC transporter ATP-binding protein	3551	2631508	2632296	29.82233503	8.56598985	0.28723
Methionine ABC transporter permease protein	3550	2632293	2632982	44.99274311	3.26560232	0.07258

Methionine ABC transporter substrate-binding protein	3549	2633029	2633862	36.61464586	5.40216086	0.14754
DNA repair protein RadC	3548	2633912	2634604	33.23699422	13.0057803	0.3913
Alfa-L-rhamnosidase (EC 3.2.1.40)	3547	2634698	2637346	223.3761329	229.418429	1.02705
hypothetical protein	3545	2637363	2638052	92.88824383	39.1872279	0.42188
hypothetical protein	3546	2638049	2639314	48.22134387	24.9011858	0.51639
hypothetical protein	3544	2639365	2640387	219.1780822	158.51272	0.72321
TPR domain protein, putative component of TonB system	3543	2640399	2641565	179.6740995	189.108062	1.05251
ortholog to Borrelia burgdorferi BB0097	3542	2641591	2641989	165.8291457	209.170854	1.26136
ATP-dependent protease La (EC 3.4.21.53) Type I	3541	2641996	2644374	417.442845	575.359865	1.3783
AAA+ superfamily protein	3540	2644584	2645795	25.18579686	9.2898431	0.36885
NimC/NimA family protein	3539	2645857	2646252	115.1898734	131.012658	1.13736
Cysteine synthase (EC 2.5.1.47)	3538	2646421	2647341	1936.413043	481.793478	0.24881
Outer membrane protein	3537	2647346	2649511	143.187067	75.8660508	0.52984
FeMo cofactor biosynthesis protein NifB	3536	2649584	2649946	143.6464088	136.740331	0.95192
Glycosyl hydrolase, family 5	3535	2649956	2651314	258.1001473	336.340206	1.30314
hypothetical protein	3534	2651317	2651751	781.1059908	1000.57604	1.28097
hypothetical protein	3533	2652021	2652671	107.6923077	138.461538	1.28571
hypothetical protein	3532	2652694	2653125	77.7262181	57.424594	0.73881
hypothetical protein	3531	2653225	2654172	118.2682154	130.675818	1.10491
Peptidase M18, aminopeptidase I:Peptidase M20	3528	2654731	2656152	201.9704433	196.340605	0.97213
Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	3527	2656166	2657773	387.0566273	418.637212	1.08159
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	3526	2657812	2658747	97.32620321	69.7860963	0.71703
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3525	2658744	2659706	180.7291667	131.25	0.72622
Oligopeptide ABC transporter, permease	3524	2659703	2660641	91.68443497	95.9488273	1.04651
Putative glutathione transporter, permease component	3523	2660645	2661604	123.5662148	166.579771	1.3481
Citrate synthase (si) (EC 2.3.3.1)	3522	2661626	2662984	91.67893962	77.8718704	0.8494
Carbon starvation protein A	3521	2663091	2664788	91.33765468	74.2486741	0.8129
sensory box histidine kinase/response regulator	3520	2664815	2666596	161.8725324	171.319797	1.05836
hypothetical protein	3519	2666617	2666793	28.40909091	38.3522727	1.35
hypothetical protein	3518	2666790	2666990	55	101.25	1.84091
Methyl-accepting chemotaxis protein	3517	2667186	2667668	1380.705394	1638.48548	1.1867
Cell surface protein	3516	2668308	2669912	441.084788	506.390274	1.14806
hypothetical protein	3515	2670012	2670131	210.0840336	226.890756	1.08
hypothetical protein	3514	2670183	2670407	73.66071429	20.0892857	0.27273
hypothetical protein	3513	2670463	2671995	359.9869452	625.652742	1.73799
Uncharacterized protein TP_0930	3512	2672009	2673658	58.82352941	105.063675	1.78608
ATP synthase delta chain (EC 3.6.3.14)	3511	2673678	2674361	232.7964861	233.894583	1.00472
Translation elongation factor LepA	3510	2674362	2676176	224.0802676	334.866221	1.4944
Flagellar biosynthesis protein flhA	3509	2676179	2677507	304.2168675	398.15512	1.30879
Serine protease precursor MucD/AlgY associated with sigma factor RpoE	3508	2677520	2679364	220.9869848	491.729935	2.22515
Uncharacterized protein TP_0374	3507	2679377	2681053	391.1097852	861.873508	2.20366
Cell division protein ftsH (EC 3.4.24.-)	3506	2681055	2682944	305.9820011	440.70937	1.44031

tRNA(Ile)-lysidine synthetase	3505	2682922	2684256	97.45127436	139.992504	1.43654
LSU ribosomal protein L25p	3504	2684556	2685251	870.5035971	1430.93525	1.6438
SpoVG family protein	3502	2685432	2685713	60.49822064	112.099644	1.85294
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	3501	2685748	2686683	88.23529412	86.631016	0.98182
hypothetical protein	3499	2686807	2687112	667.2131148	826.229508	1.23833
COG0799: Uncharacterized homolog of plant Iojap protein	3500	2687070	2687429	215.8774373	225.626741	1.04516
Transcriptional regulator	3498	2687434	2688648	41.59802306	51.8945634	1.24752
Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18) / Hydrolase (HAD superfamily), yqeK # fusion with NadD	3497	2688645	2689847	77.78702163	99.2096506	1.2754
COG0536: GTP-binding protein Obg	3496	2689844	2690839	120.6030151	174.120603	1.44375
LSU ribosomal protein L27p	3495	2690854	2691111	649.8054475	1006.80934	1.5494
hypothetical protein	3494	2691113	2691442	411.8541033	594.984802	1.44465
LSU ribosomal protein L21p	3493	2691442	2691765	498.4520124	912.5387	1.83075
oxidoreductase, aldo/keto reductase family	3492	2691848	2692822	175.5646817	247.176591	1.40789
hypothetical protein	3491	2692845	2694002	30.68280035	11.6681072	0.38028
Trimethylamine corrinoid protein 2	3490	2694053	2695102	37.65490944	23.593899	0.62658
hypothetical protein	3489	2695183	2696439	33.43949045	17.9140127	0.53571
Alpha-galactosidase (EC 3.2.1.22)	3488	2696443	2697786	77.06626955	58.637379	0.76087
hypothetical protein	3487	2697810	2698187	35.80901857	5.96816976	0.16667
Oligopeptide transport ATP-binding protein oppF (TC 3.A.1.5.1)	3486	2698189	2699193	31.37450199	35.8565737	1.14286
Possible rhamnose ABC transporter, permease component 2	3485	2699203	2700297	35.19195612	14.3967093	0.40909
ABC transporter, permease protein	3484	2700310	2701308	44.58917836	15.7815631	0.35393
ABC transporter, periplasmic alpha-galactoside binding protein	3483	2701378	2703477	116.9604574	100.762268	0.86151
Oligopeptide transport ATP-binding protein oppD (TC 3.A.1.5.1)	3482	2703522	2704517	34.17085427	47.4874372	1.38971
Transcriptional regulator, AraC/XylS family	3481	2704646	2705530	93.89140271	124.717195	1.32831
Arginyl-tRNA synthetase (EC 6.1.1.19)	3480	2705533	2707296	151.0238908	152.303754	1.00847
COG1496: Uncharacterized conserved protein	3479	2707342	2708136	71.15869018	48.1738035	0.67699
Uncharacterized protein TP_0110	3478	2708136	2709842	58.90973036	44.8417351	0.76119
hypothetical protein	3477	2709948	2710214	45.11278195	67.6691729	1.5
hypothetical protein	3476	2710216	2710455	23.0125523	28.2426778	1.22727
hypothetical protein	3475	2710452	2710673	36.19909502	0	0
hypothetical protein	3474	2710831	2710944	39.82300885	59.7345133	1.5
Outer membrane autotransporter barrel	3471	2711398	2712405	75.47169811	35.7497517	0.47368
Transcriptional regulator, MerR family	3470	2712531	2712857	35.27607362	0	0
Glycosyltransferase	3469	2713049	2715379	35.19313305	21.2446352	0.60366
hypothetical protein	3468	2715376	2716677	90.69946195	83.0130669	0.91525
Oxidoreductase, short chain dehydrogenase/reductase family	3467	2716684	2717451	357.8878748	378.422425	1.05738
Adenine phosphoribosyltransferase (EC 2.4.2.7)	3466	2717473	2718003	436.7924528	513.679245	1.17603
hypothetical protein	3465	2718021	2718425	194.3069307	178.217822	0.9172
Translation initiation factor 1	3463	2718500	2718724	140.625	251.116071	1.78571
Recombination inhibitory protein MutS2	3464	2718721	2719116	315.1898734	751.898734	2.38554
hypothetical protein	3462	2719128	2720651	176.2967827	317.629678	1.80168
BatB	3461	2720663	2722306	58.73402313	53.4083993	0.90933

BatA (Bacteroides aerotolerance operon)	3460	2722303	2723304	41.95804196	33.7162837	0.80357
hypothetical protein	3459	2723301	2724239	66.09808102	59.9680171	0.90726
hypothetical protein PA3071	3458	2724236	2725111	65.14285714	84.8571429	1.30263
MoxR-like ATPase in aerotolerance operon	3457	2725122	2726162	127.3080661	166.180758	1.30534
Aspartate aminotransferase (EC 2.6.1.1)	3456	2726249	2727571	140.3177005	142.965204	1.01887
hypothetical protein	3455	2727581	2728027	400.2242152	403.587444	1.0084
lipoprotein, putative	3454	2728135	2729397	145.800317	128.36767	0.88043
hypothetical protein	3453	2729463	2729894	78.8863109	93.9675174	1.19118
6-phosphofructokinase (EC 2.7.1.11)	3452	2730120	2731226	176.7631103	71.2025316	0.40281
hypothetical protein	3451	2731318	2731485	26.94610778	26.9461078	1
Conserved domain protein		2731556	2733466	112.565445	89.5287958	0.79535
Alanyl-tRNA synthetase (EC 6.1.1.7)	3449	2733518	2735335	316.8975069	366.481994	1.15647
Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8)	3448	2735423	2736463	548.0769231	1109.85577	2.025
Transcription termination protein NusB	3447	2736466	2736933	240.8993576	534.796574	2.22
hypothetical protein	3446	2736953	2738689	159.2741935	221.630184	1.3915
Heat shock protein 60 family co-chaperone GroES	3445	2738750	2739016	5650.37594	8281.01504	1.46557
hypothetical protein	3444	2739039	2739155	0	0	#DIV/0!
hypothetical protein	3443	2739294	2739407	17.69911504	0	0
RNA polymerase sigma factor RpoD	3441	2739440	2740318	950.4555809	1376.13895	1.44787
Predicted rhamnulose-1-phosphate aldolase (EC 4.1.2.19) / Predicted lactaldehyde dehydrogenase (EC 1.2.1.22)	3442	2740315	2741454	281.3871817	369.402985	1.31279
Galactitol utilization operon repressor	3440	2741590	2742381	67.00379267	62.5790139	0.93396
Dihydrolipoamide acetyltransferase component (E2) of acetoin dehydrogenase complex (EC 2.3.1.-)	3439	2742398	2743810	114.3767705	159.348442	1.39319
Dihydrolipoamide dehydrogenase of acetoin dehydrogenase (EC 1.8.1.4)	3438	2743828	2745195	76.81053402	67.4835406	0.87857
Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) / Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)	3437	2745233	2747692	82.55388369	107.055714	1.2968
hypothetical protein	3436	2747689	2748975	59.48678072	62.9860031	1.05882
Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140)	3435	2749095	2750306	42.52683732	50.1651528	1.17961
Putative oxidoreductase	3434	2750331	2751608	130.7752545	140.955364	1.07784
hypothetical protein		2751730	2751873	27.97202797	78.6713287	2.8125
Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)	3432	2752101	2752568	16.05995717	0	0
ADA regulatory protein	3431	2752619	2753179	25	4.01785714	0.16071
Na+ driven multidrug efflux pump	3430	2753524	2755065	42.8293316	8.7605451	0.20455
hypothetical protein	3428	2755102	2755335	113.7339056	57.9399142	0.50943
hypothetical protein	3429	2755325	2755441	4.310344828	0	0
N-acetylglutamate synthase (EC 2.3.1.1)	3427	2755394	2756716	149.0166415	136.157337	0.91371
Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	3426	2756752	2757984	112.4188312	85.836039	0.76354
Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	3425	2757992	2758255	110.2661597	94.1064639	0.85345
DNA mismatch repair protein MutL	3424	2758252	2759988	90.72580645	60.9158986	0.67143

putative oxidoreductase	3423	2760039	2761028	85.94539939	50.0505561	0.58235
hypothetical protein	3422	2761128	2763761	62.47626282	58.1086213	0.93009
hypothetical protein	3420	2763773	2764906	301.8534863	754.633716	2.5
HtrA protease/chaperone protein	3421	2764903	2766411	1613.72679	5425.06631	3.36182
Methionine aminopeptidase (EC 3.4.11.18)	3419	2766505	2767257	81.78191489	92.7526596	1.13415
Chaperone protein DnaJ	3418	2767244	2768041	119.8243413	149.623588	1.24869
hypothetical protein	3417	2768050	2768460	173.1707317	268.902439	1.55282
Universal stress protein	3416	2768476	2768961	251.5463918	264.43299	1.05123
V-type ATP synthase subunit D (EC 3.6.3.14)	3415	2768958	2769581	178.9727127	202.247191	1.13004
hypothetical protein	3414	2769753	2769986	12.87553648	9.65665236	0.75
hypothetical protein	3413	2770061	2770327	33.83458647	0	0
PIN domain protein	3412	2770498	2770638	7.142857143	0	0
hypothetical protein	3411	2770775	2771071	16.89189189	45.6081081	2.7
hypothetical protein	3410	2771127	2771324	12.69035533	34.2639594	2.7
Cell filamentation protein	3409	2771341	2771679	20.71005917	6.65680473	0.32143
hypothetical protein	3408	2771633	2771791	28.48101266	0	0
V-type ATP synthase subunit B (EC 3.6.3.14)	3407	2771819	2773243	156.2942008	92.291372	0.5905
V-type ATP synthase subunit A (EC 3.6.3.14)	3406	2773251	2775059	227.3987798	143.510815	0.6311
V-type ATPase, subunit E, putative [EC:3.6.3.14]	3405	2775052	2775669	125.6077796	76.5802269	0.60968
V-type ATPase, subunit F, putative	3404	2775679	2776020	101.1730205	65.9824047	0.65217
V-type ATP synthase subunit K (EC 3.6.3.14)	3403	2776024	2776341	123.0283912	42.5867508	0.34615
V-type ATP synthase subunit I (EC 3.6.3.14)	3402	2776371	2778437	98.74152953	66.4327202	0.67279
Uncharacterized protein TP_0534	3401	2778434	2779468	130.0773694	104.448743	0.80297
hypothetical protein	3400	2779470	2779781	329.5819936	318.327974	0.96585
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	3399	2779801	2780274	270.6131078	475.687104	1.75781
Preprotein translocase subunit SecG (TC 3.A.5.1.1)	3398	2780288	2780698	709.7560976	773.780488	1.09021
Acetoin utilization protein AcuB	3397	2780782	2781426	230.5900621	160.714286	0.69697
hypothetical protein	3396	2781426	2781758	131.0240964	149.096386	1.13793
Uroporphyrinogen-III decarboxylase	3395	2781921	2782898	32.24155578	32.2415558	1
hypothetical protein	3394	2782972	2783178	36.40776699	10.9223301	0.3
hypothetical protein	3393	2783197	2784315	38.90876565	32.2003578	0.82759
Xylose repressor XylR (ROK family)	3392	2784317	2785522	34.02489627	7.46887967	0.21951
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)		2785536	2786039	41.74950298	58.1510934	1.39286
Branched-chain amino acid transport ATP-binding protein livF (TC 3.A.1.4.1)		2786045	2786248	32.01970443	0	0
Branched-chain amino acid transport ATP-binding protein livG (TC 3.A.1.4.1)	3389	2786241	2787050	73.54758962	97.342398	1.32353
Branched-chain amino acid transport system permease protein livM (TC 3.A.1.4.1)	3388	2787047	2788036	51.56723964	50.0505561	0.97059
High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	3387	2788039	2788926	81.17249154	76.0992108	0.9375
Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)	3386	2788977	2790119	573.117338	732.924694	1.27884
sensory box histidine kinase/response regulator	3385	2790283	2792733	47.25859247	15.6505728	0.33117

Phosphoglycerate kinase (EC 2.7.2.3)	3384	2792816	2794822	726.4957265	729.638009	1.00433
NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	3383	2794912	2795985	2421.052632	3320.0188	1.37131
Putative sugar transporter	3382	2796035	2797414	66.3524293	55.4749819	0.83607
hypothetical protein	3381	2797415	2797987	133.7412587	247.814685	1.85294
Valyl-tRNA synthetase (EC 6.1.1.9)	3380	2797996	2800677	238.3439015	280.305856	1.17606
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	3379	2800710	2801642	74.57081545	130.364807	1.7482
Protein-export membrane protein secF (TC 3.A.5.1.1)	3378	2801755	2802990	300.8097166	493.724696	1.64132
Protein-export membrane protein secD (TC 3.A.5.1.1)	3377	2802990	2804732	472.1584386	928.673938	1.96687
Preprotein translocase subunit YajC (TC 3.A.5.1.1)	3376	2804757	2805155	413.3165829	853.643216	2.06535
hypothetical protein	3375	2805229	2805516	153.3101045	219.512195	1.43182
Rubredoxin	3374	2805524	2805685	1083.850932	1173.91304	1.08309
TPR domain protein, putative component of TonB system	3373	2805775	2807487	189.8364486	202.39486	1.06615
hypothetical protein	3372	2807484	2808041	67.32495512	40.3949731	0.6
ortholog to Borrelia burgdorferi BB0398	3371	2808106	2809197	102.6581118	63.9321723	0.62277
Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-)	3370	2809181	2810611	46.15384615	40.9090909	0.88636
OmpA family protein	3369	2810616	2811521	117.1270718	116.850829	0.99764
Ferredoxin	3368	2811533	2812621	82.26102941	76.5165441	0.93017
hypothetical protein	3367	2812699	2813610	175.6311745	227.222832	1.29375
ABC transporter substrate binding protein (EC 2.5.1.47)	3366	2813619	2814686	122.7741331	99.1096532	0.80725
Putative ABC transporter ATP-binding protein	3365	2814683	2815417	189.373297	153.269755	0.80935
ABC transporter permease protein	3364	2815428	2816201	75.03234153	46.5717982	0.62069
hypothetical protein	3363	2816088	2816225	0	0	#DIV/0!
Sensory box histidine kinase/response regulator	3362	2816232	2817395	150.0429923	147.033534	0.97994
Argininosuccinate lyase (EC 4.3.2.1)	3361	2817415	2818827	152.266289	141.820113	0.9314
Argininosuccinate synthase (EC 6.3.4.5)	3360	2818855	2820123	360.5845182	341.232227	0.94633
L-serine dehydratase, beta subunit (EC 4.3.1.17)	3359	2820192	2820905	40.67321178	31.5568022	0.77586
L-serine dehydratase, alpha subunit (EC 4.3.1.17)	3358	2820902	2821846	58.26271186	30.9851695	0.53182
hypothetical protein	3357	2821950	2822090	46.42857143	0	0
hypothetical protein	3356	2822398	2822898	356	450	1.26404
ABC transporter, ATP-binding protein	3355	2823309	2824328	47.10500491	30.9126595	0.65625
ABC-type multidrug transport system, permease component	3354	2824328	2825125	25.09410289	2.82308657	0.1125
conserved membrane protein, multidrug efflux associated	3353	2825122	2825916	32.11586902	14.1687657	0.44118
hypothetical protein	3352	2825992	2826159	13.24503311	0	0
transposase, IS30 family	3351	2826309	2827337	54.96108949	41.5856031	0.75664
Acetylornithine aminotransferase (EC 2.6.1.11)	3350	2827432	2828634	127.703827	174.084859	1.36319
Acetylglutamate kinase (EC 2.7.2.8)	3349	2828657	2829538	97.44779582	154.00232	1.58036
Glutamate N-acetyltransferase (EC 2.3.1.35) / N-acetylglutamate synthase (EC 2.3.1.1)	3348	2829554	2830777	113.2461161	132.461161	1.16968

N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	3347	2830797	2831942	106.0473269	205.08326	1.93388
hypothetical protein	3346	2832075	2832461	147.9057592	212.041885	1.43363
Uncharacterized protein TP_0625	3344	2832580	2832918	359.4674556	539.201183	1.5
Expressed protein	3345	2832902	2834002	70.90909091	34.7727273	0.49038
Uncharacterized protein MJ1020	3343	2834022	2834864	117.5771971	104.216152	0.88636
Transcriptional regulator	3342	2834880	2837792	61.3823934	61.8982118	1.0084
Tyrosyl-tRNA synthetase (EC 6.1.1.1)	3341	2837795	2839039	237.1382637	354.501608	1.49492
hypothetical protein	3340	2839101	2839490	194.0874036	161.953728	0.83444
Pyruvate,phosphate dikinase (EC 2.7.9.1)		2839616	2842300	589.6050671	459.388972	0.77915
Uncharacterized protein TP_0747	3338	2842316	2843392	513.9405204	424.488848	0.82595
Cytoplasmic filament protein A	3337	2843469	2845505	2020.628684	2955.05894	1.46245
hypothetical protein	3336	2845722	2846240	357.1428571	416.988417	1.16757
DHH family/DHHA1 domain protein	3335	2846250	2847230	101.0204082	94.1326531	0.93182
Uncharacterized protein BB_0038	3334	2847227	2848723	139.075067	119.135389	0.85663
hypothetical protein	3333	2848724	2849674	140	156.315789	1.11654
hypothetical protein	3332	2849661	2849969	123.3766234	124.188312	1.00658
tRNA-i(6)A37 methylthiotransferase	3331	2850008	2851354	70.95096582	43.46211	0.61257
hypothetical protein	3330	2851364	2851744	76.31578947	29.6052632	0.38793
GTP cyclohydrolase I (EC 3.5.4.16) type 2	3329	2851737	2852561	55.82524272	87.3786408	1.56522
Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	3328	2852558	2853421	106.6048667	104.28737	0.97826
Thiamin pyrophosphokinase (EC 2.7.6.2)	3327	2853405	2854088	123.7188873	177.891654	1.43787
tRNA nucleotidyltransferase (EC 2.7.7.25)	3326	2854140	2855522	144.3560058	174.204052	1.20677
Ribonuclease III (EC 3.1.26.3)	3325	2855527	2856213	222.303207	249.271137	1.12131
Acyl carrier protein	3324	2856272	2856508	1650.423729	3117.58475	1.88896
LSU ribosomal protein L32p	3323	2856520	2856708	1651.595745	2992.02128	1.81159
Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	3322	2856807	2857391	104.4520548	107.876712	1.03279
Uncharacterized lipoprotein TP_0503 precursor	3321	2857410	2858000	530.5084746	575.847458	1.08546
Uncharacterized protein TP_0608	3320	2858036	2858794	863.4564644	1009.23483	1.16883
hypothetical protein	3319	2858826	2859932	316.9077758	347.875226	1.09772
hypothetical protein	3317	2860110	2860961	29.96474736	21.1515864	0.70588
Adenylate cyclase (EC 4.6.1.1)	3316	2861031	2863781	83.69723435	68.7772926	0.82174
Filamentous haemagglutinin domain protein		2863955	2865895	267.2680412	373.453608	1.3973
hypothetical protein		2865896	2866588	117.7745665	201.589595	1.71166
hypothetical protein	3313	2866601	2867881	70.703125	89.6484375	1.26796
hypothetical protein	3312	2867878	2868330	206.8584071	398.230088	1.92513
hypothetical protein	3311	2868485	2868850	47.94520548	18.4931507	0.38571
hypothetical protein	3310	2868868	2870082	39.95057661	37.0675453	0.92784
hypothetical protein	3309	2870079	2870615	52.23880597	20.988806	0.40179
Translation elongation factor Tu	3308	2870625	2871128	36.77932406	35.7852883	0.97297
hypothetical protein	3307	2871165	2872016	52.29142186	50.2350176	0.96067
unknown	3306	2872026	2873120	57.1297989	30.8500914	0.54
hypothetical protein	3305	2873121	2873963	102.7315914	90.8551069	0.88439
Cell surface protein	3304	2874168	2877452	103.5322777	87.6979294	0.84706
Flagellar hook-length control protein fliK		2877468	2880260	120.1647564	127.32808	1.05961
hypothetical protein	3302	2880273	2880392	25.21008403	0	0
hypothetical protein	3301	2880389	2880733	502.9069767	608.284884	1.20954
hypothetical protein	3300	2880730	2881020	224.137931	217.241379	0.96923

hypothetical protein	3299	2881080	2881229	46.97986577	45.3020134	0.96429
hypothetical protein	3298	2881188	2881439	323.8866397	300.607287	0.92813
hypothetical protein	3297	2881449	2881694	475.5102041	293.877551	0.61803
hypothetical protein	3296	2881728	2883092	185.8504399	255.681818	1.37574
hypothetical protein	3295	2883108	2884478	94.16058394	114.963504	1.22093
internalin, putative		2884490	2886433	60.21616058	89.1662378	1.48077
Flagellar hook-length control protein fliK		2886825	2888744	62.79312142	80.9015112	1.28838
putative autotransporter protein	3292	2888798	2889964	134.6483705	164.022298	1.21815
Outer membrane autotransporter barrel	3291	2890066	2891124	153.5916824	163.752363	1.06615
hypothetical protein	3289	2891111	2891308	76.14213198	68.5279188	0.9
putative autotransporter protein	3290	2891301	2892386	102.3041475	151.382488	1.47973
hypothetical protein	3288	2892407	2892811	221.5346535	400.990099	1.81006
conserved hypothetical protein-putative a phopsphoesterase or an exonuclease, fig|138119.3.peg.2719 homolog	3287	2892903	2894117	91.0214168	122.3229	1.34389
hypothetical protein	3286	2894121	2894819	207.0200573	270.773639	1.30796
type 4 fimbrial biogenesis protein PilY1	3285	2894889	2897486	217.3661918	313.631113	1.44287
hypothetical protein	3284	2897646	2899004	620.7658321	843.335788	1.35854
hypothetical protein	3283	2899127	2899405	57.55395683	56.6546763	0.98438
hypothetical protein	3282	2899563	2899787	24.55357143	10.0446429	0.40909
hypothetical protein	3281	2899866	2900135	66.91449814	8.36431227	0.125
hypothetical protein	3280	2900145	2900375	206.5217391	107.608696	0.52105
Transcriptional regulator, LuxR family	3279	2900417	2901808	102.4442847	85.7296909	0.83684
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	3278	2901821	2903149	69.27710843	84.7138554	1.22283
hypothetical protein	3277	2903289	2905703	38.31814416	34.4863297	0.9
Sensor histidine protein kinase UhpB, glucose-6-phosphate specific (EC 2.7.13.3)	3276	2905696	2907075	43.5097897	22.8426396	0.525
Two component transcriptional regulator, LuxR family	3275	2907068	2907724	143.2926829	157.77439	1.10106
sensory box histidine kinase/response regulator	3274	2907736	2910894	64.34699714	52.1925643	0.81111
Two component transcriptional regulator VraR, LuxR family	3273	2910913	2911596	117.8623719	102.122987	0.86646
hypothetical protein	3272	2911669	2913177	195.9549072	223.806366	1.14213
TPR domain protein, putative component of TonB system	3271	2913187	2913804	145.0567261	120.340357	0.82961
Phosphoesterase family protein	3270	2913811	2914641	112.0481928	100.301205	0.89516
hypothetical protein	3269	2914634	2915059	37.64705882	21.1764706	0.5625
hypothetical protein	3268	2915243	2915776	749.5309568	692.307692	0.92365
Sugar phosphate isomerases/epimerases	3267	2915908	2916702	109.5717884	102.015113	0.93103
Choline-sulfatase (EC 3.1.6.6)	3266	2916716	2918113	124.5526127	95.0250537	0.76293
D-galactose 1-dehydrogenase (EC 1.1.1.48)	3265	2918114	2919124	88.11881188	44.5544554	0.50562
AraC-type DNA-binding domain-containing protein	3264	2919172	2919978	26.05459057	2.79156328	0.10714
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	3263	2920001	2921104	57.11695376	36.7180417	0.64286
Choline-sulfatase (EC 3.1.6.6)	3262	2921110	2922483	43.69992717	13.1099782	0.3
ABC transporter, substrate-binding protein	3261	2922493	2924085	36.11809045	9.89321608	0.27391
Predicted beta-xyloside ABC transporter, permease component	3260	2924097	2925035	28.78464819	9.59488273	0.33333
ABC transporter, permease protein	3259	2925045	2925935	41.01123596	27.8089888	0.67808

Dehydrogenase	3258	2925938	2927026	255.9742647	281.25	1.09874
hypothetical protein	3257	2927048	2927776	149.7252747	154.532967	1.03211
Deoxyribose-phosphate aldolase (EC 4.1.2.4)	3256	2927802	2928449	472.9520866	452.086553	0.95588
DinB family protein	3255	2928458	2929000	454.797048	419.280443	0.92191
Xanthine/uracil/thiamine/ascorbate permease family protein	3254	2929015	2930310	233.2046332	244.980695	1.0505
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	3253	2930382	2931236	159.2505855	137.002342	0.86029
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	3252	2931238	2932143	140.3314917	183.977901	1.31102
Multiple sugar ABC transporter, substrate-binding protein	3251	2932155	2933447	1200.851393	1205.10836	1.00354
Periplasmic [Fe] hydrogenase large subunit (EC 1.12.7.2)	3250	2933642	2935399	1111.838361	1046.2436	0.941
NAD-reducing hydrogenase subunit HoxF (EC 1.12.1.2)	3249	2935410	2937215	660.4560623	802.141268	1.21453
NADP-reducing hydrogenase, subunit B	3248	2937229	2937624	745.5696203	1150.63291	1.54329
Flagellar sensor histidine kinase fleS	3247	2937640	2938245	439.6694215	557.85124	1.2688
NAD-dependent formate dehydrogenase gamma subunit	3246	2938313	2938801	935.4508197	1364.7541	1.45893
hypothetical protein	3245	2938872	2938985	4.424778761	0	0
hypothetical protein	3244	2938948	2939190	18.59504132	27.892562	1.5
hypothetical protein	3243	2939657	2940394	50.20352782	27.4762551	0.5473
hypothetical protein	3242	2940519	2940635	267.2413793	271.551724	1.01613
hypothetical protein	3241	2940801	2941772	71.57569516	50.9783728	0.71223
hypothetical protein	3240	2942065	2942811	134.0482574	129.691689	0.9675
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	3239	2942864	2944576	371.4953271	406.103972	1.09316
Putative malate dehydrogenase (EC 1.1.1.37), similar to archaeal MJ1425	3238	2944601	2945683	75.32347505	83.1792976	1.10429
Histidinol dehydrogenase (EC 1.1.1.23)	3237	2945715	2947043	52.71084337	76.2424699	1.44643
Histidinol-phosphate aminotransferase (EC 2.6.1.9)	3236	2947045	2948025	44.89795918	75.7653061	1.6875
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	3235	2948145	2949461	124.2401216	201.74772	1.62385
Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)	3234	2949455	2950225	135.7142857	254.220779	1.87321
Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-)	3233	2950235	2950855	129.0322581	228.629032	1.77188
Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	3232	2950852	2951421	110.7205624	189.806678	1.71429
ATP phosphoribosyltransferase (EC 2.4.2.17)	3231	2951438	2952292	186.1826698	279.274005	1.5
Predicted molybdate-responsive regulator YvgK in bacilli	3230	2952496	2953575	84.80074143	79.2400371	0.93443
Molybdenum ABC transporter, periplasmic molybdenum-binding protein modA (TC 3.A.1.8.1)	3229	2953661	2954485	50.36407767	40.9587379	0.81325
Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1) / Molybdenum transport system permease protein modB (TC 3.A.1.8.1)		2954491	2955156	57.14285714	16.9172932	0.29605
hypothetical protein	3228	2955131	2955289	6.329113924	0	0

Molybdenum transport ATP-binding protein modC (TC 3.A.1.8.1) / Molybdenum transport system permease protein modB (TC 3.A.1.8.1)		2955267	2956223	17.25941423	7.06066946	0.40909
Molybdate-binding domain of ModE	3225	2956270	2956479	200.9569378	236.842105	1.17857
hypothetical protein	3224	2956487	2956879	122.4489796	80.3571429	0.65625
2-isopropylmalate synthase (EC 2.3.3.13)	3223	2956869	2958434	31.30990415	20.1277955	0.64286
Ferredoxin, 2Fe-2S	3222	2958444	2958752	43.83116883	7.30519481	0.16667
FeMo cofactor biosynthesis protein NifB	3221	2958794	2960062	21.68769716	12.4211356	0.57273
Nitrogenase molybdenum-cofactor synthesis protein NifN	3220	2960072	2961463	29.4751977	4.85262401	0.16463
Nitrogenase molybdenum-cofactor synthesis protein NifE	3219	2961460	2962818	19.2165558	9.97782705	0.51923
Nitrogenase (molybdenum-iron) beta chain (EC 1.18.6.1)	3218	2962829	2964205	23.86196769	9.91189427	0.41538
Nitrogenase (molybdenum-iron) alpha chain (EC 1.18.6.1)	3217	2964216	2965853	30.84911423	21.9914478	0.71287
Nitrogen regulatory protein P-II	3216	2965872	2966252	38.15789474	11.8421053	0.31034
Nitrogen regulatory protein P-II	3215	2966249	2966614	28.76712329	6.16438356	0.21429
Nitrogenase iron protein (EC 1.18.6.1)	3214	2966630	2967454	26.44526445	13.8376384	0.52326
Mo/Fe-nitrogenase-specific transcriptional regulator NifA	3213	2967751	2969286	48.20846906	5.86319218	0.12162
hypothetical protein	3212	2969298	2970503	42.73858921	24.2738589	0.56796
hypothetical protein	3211	2970521	2971318	37.64115433	11.2923463	0.3
Uncharacterized protein TP_0584	3210	2971426	2972829	163.2216679	157.163222	0.96288
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA (TC 3.A.1.5.1)	3209	2972839	2974536	137.3011196	148.497348	1.08155
Transcriptional regulator	3208	2974590	2975087	524.1448692	823.943662	1.57198
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	3207	2975094	2975840	263.4048257	331.769437	1.25954
Glycerol kinase (EC 2.7.1.30)	3205	2975857	2977341	100	101.020408	1.0102
Methionine ABC transporter permease protein	3206	2977338	2978018	42.64705882	46.3235294	1.08621
Methionine ABC transporter ATP-binding protein	3204	2978011	2979048	43.87656702	23.8669238	0.54396
Peptide methionine sulfoxide reductase	3203	2979045	2980037	27.72177419	27.2177419	0.98182
Methionine ABC transporter substrate-binding protein	3202	2980066	2980902	80.14354067	129.186603	1.61194
N-acetyl-L,L-diaminopimelate deacetylase homolog (EC 3.5.1.18)	3201	2981071	2982210	100.9657594	69.1395961	0.68478
Cystathionine beta-lyase (EC 4.4.1.8)	3200	2982226	2983374	135.0174216	88.1968641	0.65323
O-acetylhomoserine sulfhydrylase (EC 4.2.99.10) / O-succinylhomoserine sulfhydrylase (EC 4.2.99.9)	3199	2983387	2985525	118.3348924	74.7193639	0.63142
hypothetical protein	3198	2985795	2985917	8.196721311	0	0
cell surface protein	3197	2986047	2987003	48.11715481	23.5355649	0.48913
Asr2958 protein	3196	2987447	2987698	266.9322709	295.816733	1.10821
Asr2959 protein	3195	2987773	2988027	102.3622047	79.7244094	0.77885
HtrA protease/chaperone protein	3194	2988270	2989517	220.9302326	187.650361	0.84936
hypothetical protein	3193	2989538	2990965	176.5942537	137.175893	0.77679
Nucleoside-diphosphate-sugar epimerases	3192	2990999	2991847	202.240566	127.358491	0.62974

hypothetical protein	3191	2991875	2992084	131.5789474	183.014354	1.39091
hypothetical protein	3190	2992122	2992331	122.0095694	75.3588517	0.61765
hypothetical protein	3189	2992321	2992755	58.75576037	98.5023041	1.67647
hypothetical protein	3188	2992763	2992948	35.13513514	0	0
hypothetical protein	3187	2992984	2993151	11.9760479	0	0
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	3186	2993192	2993959	28.68318123	23.4680574	0.81818
Myosin heavy chain, fast skeletal muscle, embryonic	3185	2993967	2996831	123.644631	130.640084	1.05658
Endonuclease III (EC 4.2.99.18)	3184	2996876	2997619	88.15612382	51.4804845	0.58397
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	3183	2997616	2998098	80.91286307	70.0207469	0.86538
Glycine N-methyltransferase (EC 2.1.1.20)	3182	2998119	2998898	75.09627728	86.6495507	1.15385
hypothetical protein	3181	2998901	2999500	98.49749583	135.225376	1.37288
Conserved domain protein		2999565	2999774	629.1866029	409.090909	0.65019
Adenylate cyclase (EC 4.6.1.1)	3179	2999832	3001523	79.8344175	67.8592549	0.85
almost identical to CIP1 (GI:836950) [Arabidopsis thaliana]; go_component: cytoskeleton [goid 0005856]; go_function: protein binding [goid 0005515] / COP1-interactive protein 1 / CIP1	3178	3001545	3002897	152.3668639	161.427515	1.05947
Topoisomerase IV subunit A (EC 5.99.1.-)	3177	3002912	3004831	134.1844711	146.560709	1.09223
Na+ driven multidrug efflux pump	3176	3004887	3006290	32.43050606	24.0555952	0.74176
Topoisomerase IV subunit B (EC 5.99.1.-)	3175	3006313	3008223	169.8113208	188.679245	1.11111
Myosin heavy chain	3174	3008230	3009357	181.8988465	131.76575	0.72439
Translation elongation factor G-related protein	3173	3009464	3011548	424.184261	400.551823	0.94429
Helix-turn-helix motif	3172	3011697	3011912	137.2093023	167.44186	1.22034
hypothetical protein	3171	3011909	3012238	74.46808511	95.7446809	1.28571
Protein hipA	3170	3012231	3013181	60.52631579	30.7894737	0.5087
Citrate synthase (si) (EC 2.3.3.1)	3169	3013187	3014527	161.5671642	226.679104	1.403
hypothetical protein	3168	3014614	3014781	20.95808383	0	0
hypothetical protein	3167	3014802	3014930	27.34375	17.578125	0.64286
hypothetical protein	3166	3015086	3015523	19.45080092	15.4462243	0.79412
hypothetical protein	3165	3015525	3016160	466.9291339	457.086614	0.97892
Acetyl-coenzyme A synthetase (EC 6.2.1.1)	3164	3016162	3017961	367.9822123	425.236242	1.15559
Transcriptional regulator, Hth-3 family	3163	3017973	3018527	210.2888087	203.068592	0.96567
Multidrug resistance ABC transporter ATP-binding and permease protein	3162	3018579	3020420	51.33079848	39.1091798	0.7619
Multidrug resistance ABC transporter ATP-binding and permease protein	3161	3020420	3022231	58.53119823	57.1507454	0.97642
hypothetical protein	3160	3022232	3022888	38.1097561	58.3079268	1.53
Ribose 5-phosphate isomerase A (EC 5.3.1.6)	3159	3022892	3023608	94.97206704	59.7067039	0.62868
3-dehydroquinate dehydratase (EC 4.2.1.10) / Shikimate 5-dehydrogenase (EC 1.1.1.25)	3158	3023623	3025137	67.04095112	111.459709	1.66256
hypothetical protein	3157	3025153	3025599	105.3811659	216.928251	2.05851
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	3156	3025688	3027268	110.443038	88.2911392	0.79943
Transcriptional regulator, TetR family	3155	3027436	3028026	40.6779661	30.5084746	0.75
hypothetical protein	3154	3028051	3028704	55.89586524	51.6845329	0.92466
B. burgdorferi predicted coding region BB0418	3153	3028722	3029645	34.12784399	34.127844	1
Serine/threonine protein kinase PrkC, regulation of stationary phase	3152	3029824	3030870	242.3518164	232.313576	0.95858
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	3151	3030907	3031926	151.1285574	189.892051	1.25649
Peptide deformylase (EC 3.5.1.88)	3150	3031926	3032459	297.3733583	308.161351	1.03628

Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	3149	3032524	3033708	155.4054054	144.425676	0.92935
supporting cDNA gi|11908017|gb|AF326856.1|; contains Pfam profile PF01965:DJ-1/PfpI family; identical to cDNA EST Athsr7 GI:5281061; go_function: catalytic activity [goid 0003824]; go_process: thiamin biosynthesis [goid 0009228] / 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative	3148	3033724	3034290	139.1843972	91.7553191	0.65924
Fructokinase (EC 2.7.1.4)	3147	3034316	3035341	150.7317073	182.195122	1.20874
Acetate kinase (EC 2.7.2.1)	3146	3035342	3036679	642.9107277	592.460615	0.92153
DNA-binding heavy metal response regulator	3145	3036818	3038083	135.1778656	142.29249	1.05263
Circadian input kinase A	3144	3038097	3040643	129.6150825	142.282011	1.09773
Histidinol-phosphatase (EC 3.1.3.15)	3142	3040640	3041503	110.6604867	88.6442642	0.80105
C4-type zinc finger protein, DksA/TraR family	3143	3041457	3041813	466.2921348	613.061798	1.31476
oxidoreductase domain protein	3140	3042109	3043248	334.9429324	418.788411	1.25033
TPR repeat-containing protein TP_0123	3139	3043288	3046002	81.42962417	53.8872513	0.66176
Ornithine carbamoyltransferase (EC 2.1.3.3)		3046317	3047042	306.8965517	245.172414	0.79888
Uncharacterized protein TP_0437	3137	3047182	3047607	555.2941176	651.176471	1.17267
Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP-specific)	3136	3047607	3048779	263.225256	295.648464	1.12318
conserved hypothetical protein-putative a phopsphoesterase or an exonuclease, fig|138119.3.peg.2719 homolog	3135	3048790	3049767	90.0716479	126.663255	1.40625
hypothetical protein	3134	3049856	3050719	23.75434531	5.21436848	0.21951
Protein involved in catabolism of external DNA	3133	3050508	3051593	63.59447005	58.0645161	0.91304
COG1272: Predicted membrane protein hemolysin III homolog	3132	3051604	3052284	66.91176471	56.25	0.84066
COG0488: ATPase components of ABC transporters with duplicated ATPase domains	3131	3052293	3053981	319.3701723	247.326203	0.77442
anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	3130	3053986	3054339	86.40226629	19.121813	0.22131
hypothetical protein	3129	3054341	3055582	69.29895246	52.5785657	0.75872
hypothetical protein	3128	3055599	3056219	220.9677419	188.709677	0.85401
Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)	3127	3056271	3057545	77.3155416	98.9010989	1.27919
hypothetical protein	3126	3057567	3058298	584.1313269	563.269494	0.96429
Oxidoreductase	3124	3058462	3059472	42.07920792	24.5049505	0.58235
RND multidrug efflux transporter; Acriflavin resistance protein	3123	3059486	3062635	52.25106802	49.5399277	0.94811
Probable Co/Zn/Cd efflux system membrane fusion protein	3122	3062645	3063613	70.09345794	79.4392523	1.13333
Outer membrane protein	3121	3063610	3064920	50.91883614	36.179173	0.71053
hypothetical protein	3120	3064981	3065142	0	0	#DIV/0!
Uracil-DNA glycosylase (EC 3.2.2.-)	3119	3065182	3065931	73.43124166	30.0400534	0.40909
Alpha-N-arabinofuranosidase (EC 3.2.1.55)	3118	3066011	3067531	72.36842105	54.7697368	0.75682
Alpha-N-arabinofuranosidase 2 (EC 3.2.1.55)	3117	3067799	3069283	24.25876011	0	0
Oligopeptide ABC transporter, ATP-binding protein	3116	3069280	3070266	22.81947262	2.28194726	0.1
Oligopeptide ABC transporter, ATP-binding protein	3115	3070263	3071255	22.68145161	6.80443548	0.3

ABC-type dipeptide/oligopeptide/nickel transport system, permease component	3114	3071257	3072114	25.08751459	0	0
Oligopeptide ABC transporter, permease protein	3113	3072126	3073136	16.83168317	4.45544554	0.26471
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	3112	3073214	3075172	30.13278856	5.74565884	0.19068
Alpha-N-arabinofuranosidase (EC 3.2.1.55)	3111	3075304	3076797	29.13596785	4.52109846	0.15517
Probable transcriptional regulator protein, ArsR family	3110	3076875	3077822	58.6061246	54.6462513	0.93243
archaeal ATPase, fused to C-terminal DUF234 domain	3109	3077868	3079175	20.65799541	6.88599847	0.33333
hypothetical protein	3108	3079312	3080613	103.3820138	77.8247502	0.75279
Sorbitol dehydrogenase (EC 1.1.1.14)	3107	3080682	3081731	392.7550048	379.647283	0.96663
Fructokinase (EC 2.7.1.4)	3106	3081816	3082991	293.6170213	312.12766	1.06304
Chorismate synthase (EC 4.2.3.5)	3105	3082993	3084105	138.4892086	117.356115	0.8474
hypothetical protein	3104	3084124	3084510	222.7979275	233.160622	1.04651
GGDEF domain protein	3103	3084507	3085514	137.5372393	174.28004	1.26715
Uncharacterized protein MJ0150	3102	3085531	3086061	433.0188679	590.09434	1.36275
DNA polymerase III alpha subunit (EC 2.7.7.7)	3101	3086160	3090185	148.7665088	195.676551	1.31533
conserved hypothetical membrane protein	3100	3090201	3090785	75.34246575	80.9075342	1.07386
ATP-dependent DNA helicase RecG (EC 3.6.1.-)	3099	3090787	3092949	81.40610546	97.826087	1.2017
Sensory box histidine kinase/response regulator	3098	3092964	3095768	74.7146933	73.8231098	0.98807
Response regulator	3097	3095791	3096876	143.3179724	174.193548	1.21543
Methionine ABC transporter ATP-binding protein	3096	3096873	3097592	129.3463143	84.4923505	0.65323
Methionine ABC transporter permease protein	3095	3097585	3098250	109.7744361	91.3533835	0.83219
Methionine ABC transporter substrate-binding protein	3094	3098350	3099144	981.1083123	1005.98237	1.02535
hypothetical protein	3093	3099231	3099350	823.5294118	718.487395	0.87245
hypothetical protein	3092	3099484	3099840	585.6741573	733.146067	1.2518
5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	3091	3099842	3100429	65.58773424	80.4940375	1.22727
Predicted ATPase (AAA+ superfamily)	3090	3100482	3101792	47.32824427	39.5038168	0.83468
Proline/sodium symporter PutP (TC 2.A.21.2.1) @ Propionate/sodium symporter	3089	3101910	3103475	293.2907348	309.105431	1.05392
hypothetical protein	3087	3103549	3104136	214.6507666	229.982964	1.07143
Aspartate aminotransferase (EC 2.6.1.1)	3088	3104094	3105320	168.8417618	209.216966	1.23913
hypothetical protein	3086	3105317	3106858	48.99415964	29.201817	0.59603
L-fucose mutarotase	3085	3106958	3107392	197.0046083	197.004608	1
L-fucose isomerase (EC 5.3.1.25)	3084	3107421	3109235	889.7464168	738.009923	0.82946
Probable glycolate oxidase	3083	3109295	3110185	157.8651685	113.764045	0.72064
Phenylacetic acid degradation protein paaI	3081	3110527	3110949	158.7677725	154.620853	0.97388
tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins	3080	3111022	3111903	344.4948922	332.009081	0.96376
HtrA protease/chaperone protein	3078	3111922	3113910	186.6197183	201.458753	1.07951
ClpB protein	3079	3113907	3116516	212.6965861	229.574223	1.07935
hypothetical protein	3076	3116628	3117638	159.4059406	180.445545	1.13199

Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	3077	3117635	3118723	152.1139706	157.169118	1.03323
Polysialic acid transport protein kpsD precursor	3075	3118739	3120226	128.7827841	133.154001	1.03394
Fic family protein	3074	3120238	3121356	140.8765653	124.776386	0.88571
Tyrosine-protein kinase wzc (EC 2.7.1.112)	3073	3121463	3122500	92.09257473	101.976856	1.10733
GDP-mannose 4,6-dehydratase (EC 4.2.1.47)		3122871	3123509	166.9278997	165.752351	0.99296
GDP-mannose 4,6 dehydratase (EC 4.2.1.47)		3123525	3123878	92.06798867	159.348442	1.73077
hypothetical protein	3070	3124117	3124284	0	0	#DIV/0!
hypothetical protein	3069	3124659	3124784	0	0	#DIV/0!
Glycosyltransferase		3124741	3125220	19.83298539	32.8810021	1.65789
Beta-1,3-glucosyltransferase		3125332	3126210	10.82004556	5.12528474	0.47368
Alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	3066	3126266	3127186	16.30434783	4.89130435	0.3
Oligosaccharide repeat unit polymerase Wzy	3065	3127195	3128400	2.904564315	3.73443983	1.28571
hypothetical protein	3064	3128382	3128504	16.39344262	0	0
Glycosyltransferase	3063	3128681	3129877	8.361204013	5.64381271	0.675
Flippase	3062	3129874	3131403	4.905166776	1.47155003	0.3
Glycosyltransferase	3061	3131393	3132379	71.5010142	59.3306288	0.82979
hypothetical protein	3060	3132345	3132581	4.237288136	0	0
Putative glycosyltransferase	3059	3132588	3133592	14.44223108	11.2051793	0.77586
Putative O-antigen synthesis protein, WbyH	3058	3133620	3134885	32.41106719	30.2371542	0.93293
UDP-glucose 4-epimerase (EC 5.1.3.2)	3057	3134909	3135772	21.4368482	20.8574739	0.97297
hypothetical protein	3056	3135769	3135927	110.7594937	71.2025316	0.64286
hypothetical protein	3054	3136228	3136341	22.12389381	0	0
Similar to CDP-glucose 4,6-dehydratase (EC 4.2.1.45)	3055	3136323	3137399	210.0371747	248.83829	1.18473
Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	3053	3137371	3138150	73.81258023	80.872914	1.09565
hypothetical protein	3052	3138257	3140923	110.0900225	115.622656	1.05026
hypothetical protein	3051	3140925	3141539	333.0618893	282.166124	0.84719
ABC transport protein, ATP-binding subunit	3050	3141536	3142684	148.5191638	148.954704	1.00293
5'-nucleotidase (EC 3.1.3.5)	3049	3142718	3144952	178.8272158	186.324978	1.04193
hypothetical protein	3048	3144964	3145623	243.5508346	279.969651	1.14953
hypothetical protein		3145834	3145965	64.88549618	68.7022901	1.05882
hypothetical protein	3046	3145967	3146122	467.7419355	798.387097	1.7069
hypothetical protein	3045	3146140	3146820	97.79411765	92.6470588	0.94737
ATPase	3044	3147179	3148414	148.582996	127.530364	0.85831
hypothetical protein	3043	3148416	3149261	122.4852071	109.171598	0.8913
unknown	3042	3149258	3149800	180.8118081	141.143911	0.78061
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	3041	3150064	3151182	576.4758497	503.13059	0.87277
dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	3040	3151137	3152012	524.5714286	537.428571	1.02451
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	3039	3152025	3152561	464.5522388	453.358209	0.9759
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	3038	3152561	3153436	343.4285714	290.571429	0.84609
hypothetical protein	3037	3153433	3153846	319.6125908	294.188862	0.92045
hypothetical protein	3036	3153811	3153948	3.649635036	16.4233577	4.5
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	3034	3154077	3155810	340.7386036	482.977496	1.41744

Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	3035	3155807	3156481	90.50445104	116.839763	1.29098
Haloacid dehalogenase-like hydrolase	3033	3156481	3157266	110.1910828	189.171975	1.71676
Sorbitol dehydrogenase (EC 1.1.1.14)	3032	3157263	3158294	106.6925315	196.411251	1.84091
Acetolactate synthase large subunit (EC 2.2.1.6)	3031	3158316	3160067	159.0519703	337.949743	2.12478
Dihydroxy-acid dehydratase (EC 4.2.1.9)	3030	3160069	3161727	131.1821472	294.481303	2.24483
3-isopropylmalate dehydrogenase (EC 1.1.1.85)	3029	3161729	3162880	162.4674196	390.964379	2.40642
2-isopropylmalate synthase (EC 2.3.3.13)	3028	3162892	3164493	127.1455817	257.469803	2.025
2-isopropylmalate synthase (EC 2.3.3.13)	3027	3164497	3166035	280.5591678	580.786736	2.0701
Ketol-acid reductoisomerase (EC 1.1.1.86)	3026	3166059	3167060	278.5642063	520.980789	1.87024
Acetolactate synthase small subunit (EC 2.2.1.6)	3025	3167187	3167717	365.0943396	615.566038	1.68605
Deoxyribose-phosphate aldolase (EC 4.1.2.4)	3024	3167839	3168543	165.4829545	223.721591	1.35193
2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta (EC 2.5.1.54)	3023	3168555	3170546	357.6092416	426.04219	1.19136
Hypothetical NagD-like phosphatase	3022	3170596	3171378	299.8721228	304.987212	1.01706
hypothetical protein	3021	3171453	3172115	224.3202417	832.703927	3.71212
hypothetical protein	3020	3172142	3172276	0	16.7910448	#DIV/0!
Sua5 YciO YrdC YwlC family protein	3019	3172596	3173642	83.17399618	86.042065	1.03448
Magnesium and cobalt transport protein CorA	3018	3173649	3174632	128.6876907	178.535097	1.38735
hypothetical protein	3017	3174619	3174744	16	0	0
Phosphoglycolate phosphatase (EC 3.1.3.18)	3015	3174722	3175351	38.95071542	25.0397456	0.64286
Transcriptional regulator, MerR family	3016	3175322	3175747	94.11764706	68.8235294	0.73125
UPF0272 protein CA_C0774	3014	3175748	3176974	124.7960848	192.699837	1.54412
hypothetical protein	3013	3176971	3177396	150.5882353	254.117647	1.6875
hypothetical protein	3012	3177402	3178058	109.7560976	113.185976	1.03125
hypothetical protein	3010	3178057	3178203	41.09589041	46.2328767	1.125
HAD-superfamily hydrolase, subfamily IA, variant 3 protein family	3011	3178173	3178850	69.4239291	73.1166913	1.05319
Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	3009	3178860	3179486	141.3738019	125.798722	0.88983
Predicted hydroxymethylpyrimidine transporter CytX	3008	3179479	3180645	116.6380789	71.3979417	0.61213
hypothetical protein	3007	3180858	3181601	72.67833109	105.989233	1.45833
Spermidine Putrescine transport ATP-binding protein potA (TC_3.A.1.11.1)	3006	3181682	3182815	76.34598411	67.5198588	0.88439
Spermidine Putrescine ABC transporter permease component potB (TC_3.A.1.11.1)	3005	3182812	3183687	63.42857143	20.5714286	0.32432
Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	3004	3183684	3184496	67.1182266	49.8768473	0.74312
ABC transporter, periplasmic spermidine putrescine-binding protein potD (TC_3.A.1.11.1)	3003	3184493	3185554	186.1451461	129.359095	0.69494
Methyl-accepting chemotaxis protein	3001	3185597	3187789	137.7737226	103.672445	0.75248
amidohydrolase family protein	3002	3187776	3188555	82.79845956	72.2079589	0.87209
membrane protein, putative	3000	3188560	3189438	92.82460137	105.068337	1.1319
Branched-chain amino acid aminotransferase (EC 2.6.1.42)	2999	3189533	3190621	164.0625	161.305147	0.98319
hypothetical protein	2998	3190678	3191970	56.50154799	57.4690402	1.01712
Glycosyltransferase	2997	3191990	3193126	71.3028169	75.2640845	1.05556

hypothetical protein	2996	3193198	3193521	583.5913313	626.934985	1.07427
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	2995	3193592	3194074	147.3029046	214.73029	1.45775
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	2994	3194120	3196042	9.365244537	3.5119667	0.375
Beta-glucosidase (EC 3.2.1.21)	2992	3196291	3198411	229.9528302	238.79717	1.03846
hypothetical protein	2991	3198530	3199033	212.7236581	254.970179	1.1986
Homoserine O-succinyltransferase (EC 2.3.1.46)	2990	3199046	3199966	366.3043478	366.847826	1.00148
O-acetylhomoserine sulfhydrylase (EC 4.2.99.10) / O-succinylhomoserine sulfhydrylase (EC 4.2.99.9)	2989	3200079	3201362	664.9726349	478.498827	0.71958
hypothetical protein	2988	3201792	3201938	0	0	#DIV/0!
hypothetical protein	2987	3202500	3202706	4.854368932	0	0
hypothetical protein	2985	3202735	3203142	15.97051597	0	0
hypothetical protein	2986	3203139	3203774	41.73228346	24.8031496	0.59434
Sensory box histidine kinase	2984	3203998	3205086	107.0772059	35.15625	0.32833
DNA-binding response regulator, LuxR family	2983	3205136	3205741	38.84297521	22.3140496	0.57447
Rubrerythrin	2982	3205810	3206352	525.8302583	552.121771	1.05
sensory box histidine kinase/response regulator	2981	3206447	3209500	37.01277432	25.7943007	0.6969
HDIG domain protein	2980	3209504	3210100	176.1744966	120.805369	0.68571
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)	2978	3210124	3211179	54.50236967	42.6540284	0.78261
Biotin synthase and related enzymes	2979	3211169	3212191	38.64970646	30.8219178	0.79747
Thiazole biosynthesis protein ThiH	2977	3212184	3213608	45.99719101	47.4016854	1.03053
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	2976	3213605	3213874	57.62081784	41.8215613	0.72581
Aspartate ammonia-lyase (EC 4.3.1.1)	2975	3214025	3215344	55.72403336	34.1167551	0.61224
Flavodoxin	2974	3215344	3215823	99.16492693	84.5511482	0.85263
Putative GTP-binding protien TM0445	2973	3215820	3217040	72.54098361	62.704918	0.86441
Multidrug resistance ABC transporter ATP-binding and permease protein	2971	3217092	3218876	45.81225408	31.618887	0.69018
Glutaminase A	2972	3218842	3220944	25.45195052	14.9857279	0.58879
Sugar ABC transporter, sugar permease protein 2 USSDB1D	2970	3220945	3221778	22.80912365	2.70108043	0.11842
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	2969	3221775	3222677	18.29268293	12.4722838	0.68182
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	2968	3222788	3224161	174.4355426	155.680991	0.89248
Beta-galactosidase (EC 3.2.1.23)	2967	3224397	3226199	44.39511654	34.9611543	0.7875
hypothetical protein	2966	3226196	3227131	26.73796791	12.0320856	0.45
Methionine ABC transporter ATP-binding protein	2965	3227149	3227976	79.80652963	54.4135429	0.68182
ABC transporter	2964	3227973	3228875	94.44444444	77.5	0.82059
ABC transporter substrate-binding protein	2963	3228897	3229907	293.0693069	298.514851	1.01858
Glutamine synthetase type III, GlnN (EC 6.3.1.2)	2961	3230164	3232305	197.1830986	45.4225352	0.23036
Transposase subunit	2960	3232851	3233201	17.14285714	0	0
hypothetical protein	2959	3233667	3234209	194.6494465	286.439114	1.47156

hypothetical protein	2958	3234379	3234537	15.82278481	0	0
Nitrogen regulatory protein P-II	2957	3234547	3234888	58.65102639	65.9824047	1.125
Ammonium transporter	2956	3234901	3236262	71.27112417	49.5958854	0.69588
hypothetical protein	2954	3236397	3236546	13.42281879	0	0
Mo/Fe-nitrogenase-specific transcriptional regulator NifA	2955	3236525	3238111	130.8322825	137.61034	1.05181
hypothetical protein	2952	3238284	3239126	228.0285036	229.809976	1.00781
no significant homology.	2951	3239128	3239388	51.92307692	60.5769231	1.16667
hypothetical protein	2950	3239563	3239718	109.6774194	188.709677	1.72059
Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	2949	3239784	3240872	85.01838235	39.2922794	0.46216
Glycine cleavage system H protein	2948	3240902	3241273	87.60107817	42.4528302	0.48462
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2)	2947	3241283	3242605	92.66263238	39.1452345	0.42245
Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2)	2946	3242602	3244017	130.7420495	50.8833922	0.38919
hesA/moeB/thiF family protein	2945	3244036	3244860	104.9757282	73.7257282	0.70231
tRNA(Cytosine32)-2-thiocytidine synthetase	2944	3244857	3245621	51.70157068	32.395288	0.62658
Deoxyribonuclease TatD	2943	3245623	3246408	64.96815287	48.7261146	0.75
COGs COG3146	2942	3246411	3247571	34.9137931	13.5775862	0.38889
Hydantoinase	2941	3247579	3249687	66.17647059	65.1091082	0.98387
Purine nucleoside phosphorylase (EC 2.4.2.1)	2940	3249729	3250433	264.9147727	194.957386	0.73592
hypothetical protein	2938	3251326	3252474	137.630662	150.914634	1.09652
putative protein	2937	3252486	3254195	56.1732007	36.863663	0.65625
hypothetical protein	2936	3254441	3254605	0	0	#DIV/0!
hypothetical protein	2935	3254705	3255988	26.50038971	24.5518316	0.92647
Heat shock protein htpG	2934	3255981	3257549	22.64030612	18.6543367	0.82394
Fe-S oxidoreductase	2933	3257546	3259501	19.69309463	6.90537084	0.35065
hypothetical protein		3259959	3260351	66.32653061	45.9183673	0.69231
hypothetical protein		3260364	3261482	66.63685152	42.2629696	0.63423
hypothetical protein	2930	3261486	3261647	37.26708075	13.9751553	0.375
Hypothetical similar to thiamin biosynthesis lipoprotein ApbE	2929	3261655	3262680	129.7560976	153.658537	1.18421
3-polyprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)	2928	3262698	3264152	128.954608	100.584594	0.78
4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-)	2927	3264142	3265005	79.37427578	31.2862109	0.39416
3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX (EC 4.1.1.-)	2926	3265018	3265587	63.26889279	71.1775044	1.125
thiamine biosynthesis protein, putative	2925	3265590	3266528	93.28358209	57.5692964	0.61714
Taurine transport ATP-binding protein tauB	2924	3266522	3267277	65.56291391	41.7218543	0.63636
Taurine transport system permease protein tauC	2923	3267274	3268029	65.56291391	44.7019868	0.68182
hypothetical protein	2922	3268050	3268268	20.64220183	10.3211009	0.5
hypothetical protein	2921	3268256	3268399	13.98601399	0	0
hypothetical protein	2920	3268581	3269561	726.0204082	941.326531	1.29656
Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	2919	3269635	3270006	1289.757412	1024.93261	0.79467
hypothetical protein	2918	3269984	3270355	500	557.951482	1.1159
hypothetical protein	2917	3270393	3270566	150.2890173	65.0289017	0.43269

Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	2916	3270866	3272656	2734.636872	2255.02793	0.82462
Integrase domain protein	2915	3272902	3274137	53.03643725	12.7530364	0.24046
Ferredoxin	2914	3274324	3275586	494.0570523	1565.37242	3.1684
hypothetical protein	2912	3275605	3275751	30.82191781	15.4109589	0.5
putative membrane protein		3275626	3276528	29.37915743	54.8780488	1.86792
Uncharacterized protein TP_1032	2911	3276604	3276987	65.27415144	82.2454308	1.26
Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)		3276950	3277552	107.1428571	160.714286	1.5
membrane protein, putative		3277549	3278193	65.2173913	80.3571429	1.23214
hypothetical protein	2909	3278171	3278479	457.7922078	336.038961	0.73404
hypothetical protein	2907	3278704	3279609	175.6906077	273.480663	1.5566
Putative pheromone precursor lipoprotein	2906	3279773	3280543	1113.636364	2013.31169	1.80787
NADH dehydrogenase (EC 1.6.99.3) in cluster with putative pheromone precursor	2905	3280562	3282520	611.8488253	1188.20225	1.94199
Heptaprenyl diphosphate synthase component II (EC 2.5.1.30)	2904	3282536	3283501	207.253886	324.093264	1.56375
Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)	2903	3283509	3284297	93.27411168	142.766497	1.53061
Sensory box histidine kinase/response regulator	2902	3284354	3286660	52.19660722	88.0817747	1.6875
Beta-galactosidase (EC 3.2.1.23)	2901	3286684	3288735	39.98049732	12.0672843	0.30183
hypothetical protein	2900	3288748	3289989	49.55680902	27.1958098	0.54878
hypothetical protein	2899	3290006	3291247	14.9073328	0	0
L-threonine 3-dehydrogenase (EC 1.1.1.103)	2898	3291261	3292292	29.09796314	0	0
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	2897	3292345	3293646	29.20830131	17.2943889	0.59211
Predicted beta-xyloside ABC transporter, permease component	2896	3293713	3294606	30.79507279	7.55879059	0.24545
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	2895	3294616	3295449	19.20768307	0	0
hypothetical protein	2894	3295784	3295963	11.17318436	0	0
Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	2893	3296023	3297123	29.09090909	12.2727273	0.42188
Xylose isomerase domain protein TIM barrel precursor	2892	3297139	3297999	23.8372093	20.9302326	0.87805
Xylose repressor XylR (ROK family)	2891	3298151	3299374	66.23058054	53.3524121	0.80556
Possible D-erythrulose 4-phosphate dehydrogenase EryC (EC 1.1.1.-)	2890	3299442	3300338	77.56696429	42.6897321	0.55036
Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	2889	3300344	3301402	71.3610586	55.2930057	0.77483
Sorbitol dehydrogenase (EC 1.1.1.14)	2888	3301399	3302442	124.1610738	110.019175	0.8861
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	2886	3302444	3303115	153.5022355	177.719821	1.15777
hypothetical protein	2887	3303112	3303981	169.735328	243.383199	1.4339
PTS system, fructose-specific IIA component (EC 2.7.1.69) / PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)	2885	3304041	3304487	1012.331839	1079.59641	1.06645
hypothetical protein	2884	3304499	3305689	594.9579832	709.033613	1.19174
hypothetical protein	2883	3305737	3307602	68.63270777	50.6702413	0.73828
pilT protein, putative		3307644	3308330	477.4052478	245.991254	0.51527
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	2881	3308376	3309554	2071.731749	353.353141	0.17056

Phosphoserine aminotransferase (EC 2.6.1.52)	2880	3309588	3310691	1266.092475	242.747053	0.19173
Redox-sensitive transcriptional regulator (AT-rich DNA-binding protein)	2879	3310743	3311315	899.4755245	212.412587	0.23615
hypothetical protein	2878	3311406	3311519	13.27433628	0	0
hypothetical protein	2877	3311569	3311682	8.849557522	0	0
motif=sugar transport proteins signatures	2876	3311826	3312206	125	159.868421	1.27895
hypothetical protein	2875	3312199	3312645	458.5201794	554.932735	1.21027
Enolase (EC 4.2.1.11)	2874	3312753	3314054	1434.63035	1943.57977	1.35476
Propanediol utilization transcriptional activator	2873	3314131	3315003	52.17889908	36.1238532	0.69231
hypothetical protein	2872	3315094	3316113	23.55250245	2.20804711	0.09375
hypothetical protein	2871	3316271	3317095	76.45631068	98.3009709	1.28571
hypothetical protein	2869	3317104	3318891	136.8214885	123.391158	0.90184
Exonuclease SbcC	2870	3318881	3322039	37.68207726	29.2115263	0.77521
Exonuclease SbcD	2868	3322036	3323220	46.03040541	19.0033784	0.41284
L-fuconolactone hydrolase	2867	3323529	3324383	42.15456674	15.8079625	0.375
ABC transporter, ATP-binding/permease protein		3324421	3325164	21.53432032	0	0
ABC transporter, ATP-binding protein, MsbA family		3325372	3325899	23.71916509	0	0
hypothetical protein	2864	3326083	3326202	16.80672269	0	0
uncharacterized conserved secreted protein	2863	3326210	3328531	121.068505	112.45153	0.92883
Uncharacterized protein TP_0480	2862	3328542	3329078	72.76119403	79.7574627	1.09615
TPR domain protein, putative component of TonB system	2861	3329134	3330519	177.6173285	154.33213	0.8689
5'-nucleotidase (EC 3.1.3.5)	2860	3330619	3331647	599.2217899	420.233463	0.7013
soluble lytic murein transglycosylase, putative	2859	3331892	3333865	39.02686265	35.3522554	0.90584
hypothetical protein	2858	3333907	3334281	46.79144385	78.2085561	1.67143
Cell division protein ftsK	2857	3334519	3336729	111.7647059	91.6289593	0.81984
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	2856	3336747	3338282	51.79153094	21.9869707	0.42453
hypothetical protein	2855	3338409	3338924	164.0776699	96.1165049	0.5858
ATP synthase A chain (EC 3.6.3.14)	2854	3338950	3339711	53.21944809	35.4796321	0.66667
ATP synthase C chain (EC 3.6.3.14)	2853	3339753	3339971	245.412844	196.100917	0.79907
ATP synthase B chain (EC 3.6.3.14)	2852	3339981	3340490	154.2239686	141.453831	0.9172
ATP synthase delta chain (EC 3.6.3.14)	2851	3340491	3341027	139.9253731	125.932836	0.9
ATP synthase alpha chain (EC 3.6.3.14)	2850	3341027	3342529	149.3333333	109.5	0.73326
ATP synthase gamma chain (EC 3.6.3.14)	2849	3342539	3343450	142.1514819	121.020856	0.85135
ATP synthase beta chain (EC 3.6.3.14)	2848	3343466	3344851	271.8411552	250.180505	0.92032
ATP synthase epsilon chain (EC 3.6.3.14)	2847	3344860	3345285	171.7647059	127.058824	0.73973
NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase	2846	3345328	3347079	155.6253569	125.928041	0.80917
Ubiquitin-protein ligase	2845	3347419	3348816	11.45311382	8.05297065	0.70313
Nitroreductase family protein	2844	3348824	3349330	74.11067194	31.1264822	0.42
GTP-binding protein HflX	2843	3349352	3350623	178.992919	166.404406	0.92967
Cell division protein ftsK	2842	3350738	3353305	122.3217764	119.205298	0.97452
Membrane proteins related to metalloendopeptidases	2841	3353326	3354294	93.49173554	97.6239669	1.0442
hypothetical protein	2840	3354315	3354869	141.6967509	150.270758	1.06051

Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltranstransferase (EC 2.5.1.10) / Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29)	2839	3354879	3355961	108.5951941	62.3844732	0.57447
Cell division protein ftsJ	2837	3356009	3356647	60.34482759	63.4796238	1.05195
Maebl	2838	3356644	3357429	115.2866242	154.77707	1.34254
Uncharacterized protein TP_0021	2836	3357446	3359569	72.77437588	82.6660386	1.13592
DNA repair helicase	2835	3359566	3361287	109.5293434	129.430564	1.1817
Sulfate permease	2834	3361430	3363109	78.02263252	92.4657534	1.18511
2-dehydropantoate 2-reductase (EC 1.1.1.169)	2833	3363106	3364035	71.58234661	89.6124865	1.25188
Thymidylate synthase (EC 2.1.1.45)	2832	3364032	3364781	67.42323097	81.1081442	1.20297
Putative high-affinity iron permease	2831	3364985	3366196	39.223782	16.7217176	0.42632
Periplasmic protein p19 involved in high-affinity Fe2+ transport	2830	3366211	3366795	63.35616438	73.2020548	1.15541
Putative high-affinity iron permease	2829	3366796	3368055	28.19698173	25.019857	0.88732
ABC transporter permease protein	2828	3368064	3369329	37.1541502	7.11462451	0.19149
ABC transporter permease protein	2827	3369319	3370488	31.65098375	9.62360992	0.30405
Putative ABC transport system ATP-binding protein	2826	3370491	3371162	52.1609538	16.7660209	0.32143
Putative pheromone precursor lipoprotein	2825	3371159	3371566	17.1990172	11.0565111	0.64286
Transposase, IS4	2824	3371730	3372587	71.76196033	68.2613769	0.95122
hypothetical protein	2823	3372770	3372994	0	20.0892857	#DIV/0!
hypothetical protein	2822	3372995	3373291	3.378378378	0	0
hypothetical protein	2821	3373311	3373454	13.98601399	31.4685315	2.25
Uncharacterized protein MJ1673	2820	3373476	3373874	64.07035176	33.919598	0.52941
M. jannaschii predicted coding region MJ1674	2819	3373850	3375172	27.23146747	15.3177005	0.5625
hypothetical protein	2818	3375191	3376255	82.23684211	63.4398496	0.77143
hypothetical protein	2817	3376257	3376631	46.79144385	48.1283422	1.02857
putative protein	2816	3376640	3377533	118.7010078	75.5879059	0.63679
hypothetical protein	2815	3377546	3378529	91.04781282	91.5564598	1.00559
hypothetical protein	2814	3378533	3381004	78.10602995	74.6661271	0.95596
hypothetical protein	2813	3381001	3382104	132.819583	101.99456	0.76792
hypothetical protein	2812	3382105	3383028	117.0097508	95.0704225	0.8125
hypothetical protein	2811	3383211	3383339	703.125	1072.26563	1.525
CRISPR-associated protein Cas1	2810	3384752	3385768	17.22440945	8.85826772	0.51429
CRISPR-associated protein Cas2	2809	3385765	3386040	60	24.5454545	0.40909
hypothetical protein	2808	3386532	3386726	18.04123711	0	0
all_bases.cand.99 - score = 69.41, potential signal peptide		3386765	3387514	5.340453939	0	0
hypothetical protein	2806	3387532	3388143	14.7299509	11.0474632	0.75
hypothetical protein	2805	3388157	3388465	21.1038961	7.30519481	0.34615
hypothetical protein	2804	3388453	3389649	15.05016722	7.52508361	0.5
Transcriptional regulator, DeoR family		3389730	3390425	15.10791367	12.9496403	0.85714
hypothetical protein	2802	3390536	3390811	14.54545455	0	0
Radical SAM domain heme biosynthesis protein	2801	3390970	3391896	25.91792657	7.28941685	0.28125
hypothetical protein	2800	3391922	3392932	28.21782178	13.3663366	0.47368
Radical SAM domain protein	2799	3392935	3393759	25.48543689	10.9223301	0.42857
Dihydropyrimidine dehydrogenase [NADP+] (EC 1.3.1.2)	2798	3393770	3394954	35.05067568	7.60135135	0.21687
hypothetical protein	2797	3395113	3395757	34.16149068	13.9751553	0.40909

unknown	2796	3395831	3396412	22.37521515	30.9810671	1.38462
hypothetical protein	2795	3396446	3396595	10.06711409	0	0
hypothetical protein	2794	3396588	3396887	31.77257525	7.52508361	0.23684
hypothetical protein	2793	3397117	3397245	31.25	0	0
Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC 6.3.5.3) / Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (EC 6.3.5.3)	2790	3397575	3401498	97.37445832	101.516696	1.04254
hypothetical protein	2791	3401491	3402165	123.8872404	140.207715	1.13174
Predicted sucrose permease, MFS family, FucP subfamily	2789	3402230	3403453	33.93295176	31.2755519	0.92169
Hydrolase (HAD superfamily)	2787	3403466	3404245	67.39409499	98.2028241	1.45714
hypothetical protein	2788	3404229	3404939	346.4788732	535.56338	1.54573
Translation elongation factor G, mitochondrial	2786	3404984	3407077	1048.768711	1535.12796	1.46374
hypothetical protein	2785	3407185	3407388	14.77832512	0	0
Sensor protein of zinc sigma-54-dependent two-component system	2784	3407482	3408744	57.05229794	37.4405705	0.65625
Acetoacetate metabolism regulatory protein atoC	2783	3408755	3410149	54.16068867	67.7905308	1.25166
Leucyl aminopeptidase	2782	3410202	3411350	100.6097561	101.916376	1.01299
UPF0088 protein TP_0032	2781	3411369	3412202	118.2472989	97.2388956	0.82234
hypothetical protein		3412212	3413009	149.3099122	124.215809	0.83193
lipoprotein, putative	2779	3413084	3414127	109.7794823	127.277085	1.15939
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	2778	3414135	3415106	140.061792	150.61792	1.07537
Histone acetyltransferase HPA2 and related acetyltransferases	2776	3415136	3415642	52.3715415	17.7865613	0.33962
polysaccharide deacetylase	2777	3415594	3416655	44.76908577	16.9651272	0.37895
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	2775	3416647	3417900	109.3375898	77.2146848	0.7062
Glutamate 5-kinase (EC 2.7.2.11)	2774	3417904	3418695	247.7820025	265.209125	1.07033
Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2773	3418721	3419581	154.6511628	149.127907	0.96429
Phosphate regulon transcriptional regulatory protein phoB	2772	3419584	3420189	156.1983471	119.008264	0.7619
Regulatory protein recX	2771	3420385	3421017	80.69620253	156.64557	1.94118
SSU ribosomal protein S9p (S16e)	2770	3421103	3421495	1091.836735	2146.68367	1.96612
LSU ribosomal protein L13p (L13Ae)	2769	3421496	3422002	742.0948617	1405.13834	1.89348
hypothetical protein	2768	3422029	3422247	222.4770642	144.495413	0.64948
hypothetical protein	2767	3422262	3422564	213.5761589	335.264901	1.56977
Beta-lactamase class C and other penicillin binding proteins	2766	3422643	3423848	234.0248963	216.59751	0.92553
hypothetical protein	2765	3423841	3424866	125.3658537	133.902439	1.06809
Transcriptional repressor of the arabinose operon	2764	3425137	3426192	54.97630332	23.4597156	0.42672
ABC transporter, permease protein	2763	3426258	3427145	32.69447576	12.6832018	0.38793
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	2762	3427157	3428068	35.12623491	12.349067	0.35156
ABC transporter, substrate-binding protein	2761	3428150	3429628	102.165088	57.8484438	0.56623
hypothetical protein	2760	3429705	3430946	43.11039484	29.0088638	0.6729
hypothetical protein	2759	3430943	3431905	40.02079002	28.0665281	0.7013
Uroporphyrinogen-III decarboxylase	2757	3431968	3432987	32.87536801	11.0402355	0.33582

hypothetical protein	2758	3432984	3433262	26.97841727	8.09352518	0.3
Alpha-mannosidase	2756	3433265	3435673	98.62956811	92.5041528	0.93789
Alpha-mannosidase (EC 3.2.1.24)	2755	3435698	3438841	122.9716831	136.016545	1.10608
Phosphoheptose isomerase 2 (EC 5.3.1.-)	2754	3438838	3439479	124.8049922	136.895476	1.09688
Glucokinase (EC 2.7.1.2)	2753	3439496	3440413	67.61177754	88.3315158	1.30645
hypothetical protein	2752	3440406	3441542	34.77112676	63.3802817	1.82278
hypothetical protein	2751	3441547	3442923	112.6453488	206.031977	1.82903
Mucin 2 precursor	2750	3442932	3444383	232.2536182	431.082012	1.85608
gliding motility protein GldF	2749	3444393	3445256	57.93742758	96.4658169	1.665
ABC-type multidrug transport system, ATPase component	2748	3445253	3446197	383.4745763	467.161017	1.21823
hypothetical protein	2747	3446156	3446269	221.2389381	338.495575	1.53
Cell division protein ftsH (EC 3.4.24.-)	2746	3446313	3448274	212.9677089	221.42491	1.03971
hypothetical protein	2745	3448277	3448525	54.43548387	9.07258065	0.16667
T. pallidum predicted coding region TP0592	2744	3448756	3449661	131.4917127	106.906077	0.81303
hypothetical protein	2743	3449666	3449788	639.3442623	461.065574	0.72115
hypothetical protein	2742	3449860	3450861	42.95704296	51.6983017	1.20349
hypothetical protein	2741	3450876	3451739	93.2792584	83.4298957	0.89441
hypothetical protein	2740	3451825	3452529	117.8977273	131.036932	1.11145
hypothetical protein	2739	3452545	3453657	138.0395683	204.361511	1.48046
2-methylthioadenine synthetase	2738	3453683	3455026	48.39910648	36.8577811	0.76154
Exoenzymes regulatory protein aepA precursor	2737	3455105	3456751	83.23207776	72.4483597	0.87044
ATP-dependent DNA helicase UvrD/PcrA	2736	3456798	3459203	133.2640333	96.3617464	0.72309
Uncharacterized protein TP_0678	2735	3459204	3459968	107.3298429	64.7905759	0.60366
Uncharacterized protein TP_0942	2734	3459974	3460459	206.185567	171.649485	0.8325
Flagellar biosynthesis protein fliS	2733	3460469	3460915	328.4753363	287.556054	0.87543
hypothetical protein	2732	3461107	3461448	491.202346	712.609971	1.45075
Galactokinase (EC 2.7.1.6)	2731	3461478	3462836	171.2076583	202.135493	1.18065
ATPase	2730	3462879	3464096	40.26294166	29.5809367	0.73469
GAF domain protein; CDS_ID OB2202	2729	3464204	3464773	58.87521968	63.2688928	1.07463
hypothetical protein	2728	3464837	3465133	59.12162162	0	0
DNA-binding protein	2727	3465138	3465434	23.64864865	0	0
DNA polymerase I (EC 2.7.7.7)	2726	3465507	3468365	73.65290413	63.7683695	0.8658
NADP-dependent malic enzyme (EC 1.1.1.40)	2725	3468368	3469822	446.3548831	509.112792	1.1406
SEC-C motif domain protein	2724	3469858	3470394	142.7238806	188.899254	1.32353
Threonine synthase (EC 4.2.3.1)	2723	3470391	3471716	227.9245283	224.150943	0.98344
Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	2722	3471752	3472849	102.0966272	90.2461258	0.88393
hypothetical protein	2721	3472859	3475786	82.67851042	53.040656	0.64153
Flagellar synthesis regulator fleN	2720	3475796	3476941	158.9519651	141.484716	0.89011
hypothetical protein	2719	3476938	3477303	123.2876712	110.958904	0.9
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)	2718	3477477	3478637	85.77586207	98.9224138	1.15327
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)	2717	3478640	3482137	418.3585931	416.285387	0.99504
Glycoprotein gp2	2716	3482356	3485325	179.0165039	264.482991	1.47742
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)	2715	3485462	3489640	314.2651987	433.520823	1.37947
Ig-like repeat domain protein 1	2714	3489657	3493229	248.4602464	388.647816	1.56423

similar to (EMBL:AL117211) YPMT1.20C, Yersinia pestis CO-92 hypothetical protein from plasmid pMT1; similar to (EMBL:AF074611) Y1035, Yersinia pestis KIM5 hypothetical protein from plasmid pMT1; blastn and dotplot analyses suggest that an insertion event has taken place at this point as compared to Yersinia pestis pMT1	2713	3493248	3495839	217.8695484	343.01428	1.5744
similar to (EMBL:AL117211) YPMT1.20C, Yersinia pestis CO-92 hypothetical protein from plasmid pMT1; similar to (EMBL:AF074611) Y1035, Yersinia pestis KIM5 hypothetical protein from plasmid pMT1; blastn and dotplot analyses suggest that an insertion event has taken place at this point as compared to Yersinia pestis pMT1	2712	3496004	3498055	261.8235007	354.339347	1.35335
RTX toxin, putative	2711	3498123	3499970	329.9945858	495.804006	1.50246
Carboxyl-terminal protease (EC 3.4.21.102)	2710	3500455	3501951	421.4572193	407.586898	0.96709
Small ribosomal subunit 16S rRNA methyltransferase ## U1498-specific in E.coli	2709	3501984	3502790	100.4962779	100.496278	1
hypothetical protein		3503057	3503263	97.08737864	262.135922	2.7
tRNA:Cm32/Um32 methyltransferase	2707	3503657	3504457	150	67.5	0.45
D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	2706	3504495	3505232	258.4803256	235.074627	0.90945
anti-sigma F factor antagonist (spoIIAA-2); anti sigma b factor antagonist RsbV	2705	3505382	3505933	357.5317604	530.852995	1.48477
hypothetical protein	2704	3505990	3506334	792.1511628	1059.59302	1.33761
Phage shock protein A	2703	3506347	3507039	651.0115607	1024.2052	1.57325
2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	2702	3507049	3508071	295.9882583	402.886497	1.36116
hypothetical protein	2701	3508369	3509283	103.3916849	39.3873085	0.38095
hypothetical protein	2700	3509276	3511075	105.0583658	81.295164	0.77381
DnaJ-like protein DjlA	2699	3511167	3511862	64.02877698	45.323741	0.70787
hypothetical protein	2698	3512126	3512320	23.19587629	11.5979381	0.5
hypothetical protein	2697	3512886	3513254	76.08695652	61.1413043	0.80357
hypothetical protein	2696	3513261	3513635	306.1497326	288.770053	0.94323
hypothetical protein	2695	3513651	3514670	269.3817468	260.549558	0.96721
unknown	2694	3514691	3516133	147.3647712	123.266297	0.83647
ATP-dependent RNA helicase RhlB	2693	3516273	3518060	428.7317621	506.313131	1.18096
ABC transporter, ATP-binding protein	2692	3518089	3519723	149.1712707	225.138122	1.50926
Uncharacterized protein TP_0369 precursor	2691	3519730	3521202	184.1032609	134.51087	0.73063
hypothetical protein	2690	3521226	3521702	135.5042017	80.3571429	0.59302
hypothetical protein	2689	3521824	3521970	6.849315068	0	0
Flavodoxin	2688	3521925	3522392	2.141327623	0	0
transposase, mutator family	2687	3522440	3523681	87.42949234	19.9435939	0.22811
hypothetical protein	2686	3523746	3524024	424.4604317	671.76259	1.58263
hypothetical protein	2685	3524255	3524380	0	0	#DIV/0!
hypothetical protein	2684	3524386	3524574	23.93617021	0	0
hypothetical protein	2683	3524546	3524725	273.7430168	452.513966	1.65306
Peptide chain release factor 1	2682	3524718	3525788	525.9433962	560.377358	1.06547
Methylase of polypeptide chain release factors	2681	3525813	3526727	328.7746171	273.249453	0.83111

GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I		3526714	3528747	155.4353173	112.887359	0.72627
Capsule biosynthesis protein capA	2679	3528751	3529920	62.8742515	40.4191617	0.64286
Major facilitator (MFS) superfamily multidrug resistance protein	2677	3529968	3531185	43.96055875	57.3130649	1.30374
Uncharacterized protein TP_0214	2678	3531176	3531397	622.1719457	1802.0362	2.89636
LSU ribosomal protein L17p	2676	3531398	3531856	1042.576419	2775.65502	2.6623
DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)	2675	3531846	3532901	849.1295938	2073.74275	2.4422
SSU ribosomal protein S4p (S9e)	2674	3532911	3533546	829.6178344	1748.40764	2.10749
SSU ribosomal protein S11p (S14e)	2673	3533563	3533946	1214.099217	2743.47258	2.25968
SSU ribosomal protein S13p (S18e)	2672	3533959	3534324	864.3835616	1707.53425	1.97544
Preprotein translocase secY subunit (TC 3.A.5.1.1)	2671	3534522	3535850	335.3566009	839.908953	2.50452
LSU ribosomal protein L15p (L27Ae)	2670	3535843	3536283	352.2727273	680.113636	1.93065
LSU ribosomal protein L30p (L7e)	2669	3536283	3536465	211.5384615	333.791209	1.57792
SSU ribosomal protein S5p (S2e)	2668	3536467	3537048	1213.425129	2823.14974	2.3266
LSU ribosomal protein L18p (L5e)	2667	3537057	3537419	864.640884	1995.16575	2.30751
LSU ribosomal protein L6p (L9e)	2666	3537428	3537967	709.6474954	2149.81447	3.02941
SSU ribosomal protein S8p (S15Ae)	2665	3537980	3538378	468.1933842	1190.83969	2.54348
SSU ribosomal protein S14p (S29e)	2664	3538388	3538573	505.4644809	1241.80328	2.45676
LSU ribosomal protein L5p (L11e)	2663	3538584	3539135	954.6279492	2294.91833	2.40399
LSU ribosomal protein L24p (L26e)	2662	3539135	3539461	960.1226994	2622.69939	2.73163
LSU ribosomal protein L14p (L23e)	2661	3539471	3539842	394.8787062	1024.93261	2.59556
SSU ribosomal protein S17p (S11e)	2660	3539858	3540130	900.7352941	2332.72059	2.5898
LSU ribosomal protein L29p (L35e)	2659	3540134	3540361	1171.806167	2735.68282	2.33459
LSU ribosomal protein L16p (L10e)	2658	3540371	3540796	862.3529412	1990.58824	2.30832
SSU ribosomal protein S3p (S3e)	2657	3540799	3541506	1106.534091	2358.66477	2.13158
LSU ribosomal protein L22p (L17e)	2656	3541507	3541875	720.1086957	1754.75543	2.43679
SSU ribosomal protein S19p (S15e)	2655	3541887	3542168	485.7651246	1249.11032	2.57143
LSU ribosomal protein L2p (L8e)	2654	3542180	3543007	1026.602177	2415.96131	2.35336
LSU ribosomal protein L23p (L23Ae)	2653	3543014	3543301	611.4982578	1348.43206	2.20513
LSU ribosomal protein L4p (L1e)	2652	3543298	3543996	1344.555874	2962.39255	2.20325
LSU ribosomal protein L3p (L3e)	2651	3544001	3544636	788.1889764	1782.28346	2.26124
SSU ribosomal protein S10p (S20e)	2650	3544761	3545165	2334.586466	4719.92481	2.02174
Translation elongation factor Tu	2649	3545189	3546388	4977.898249	8825.47957	1.77293
hypothetical protein	2648	3546514	3546714	110	157.5	1.43182
SSU ribosomal protein S7p (S5e)	2647	3546788	3547258	975.5319149	2163.82979	2.2181
SSU ribosomal protein S12p (S23e)	2646	3547271	3547684	3070.217918	5180.99274	1.6875
Maltose/maltodextrin ABC transporter, permease protein MalG	2645	3547758	3548606	94.92924528	92.865566	0.97826
ABC-type sugar transport systems, permease components	2644	3548603	3549499	102.6785714	72.8236607	0.70924
Sugar ABC transporter, periplasmic sugar-binding protein	2643	3549523	3550794	792.6829268	787.765539	0.9938
hypothetical protein	2642	3550870	3552780	98.42931937	53.0104712	0.53856
diguanylate cyclase (GGDEF domain) with PAS/PAC sensor	2641	3552784	3553791	237.8351539	254.716981	1.07098
Putative Heme-regulated two-component response regulator	2640	3553788	3554828	156.7307692	229.326923	1.46319
hypothetical protein-signal peptide and transmembrane prediction	2639	3554957	3555694	160.7869742	131.275441	0.81646

Sorbitol dehydrogenase (EC 1.1.1.14)	2638	3555705	3556739	149.9032882	110.976789	0.74032
Gluconokinase (EC 2.7.1.12) / oxidoreductase domain	2637	3556747	3557814	106.841612	99.1096532	0.92763
hypothetical protein	2636	3557798	3557953	51.61290323	43.5483871	0.84375
possible Bacterial Ig-like domain (group 1)	2635	3558194	3559915	138.5822196	61.4468332	0.4434
Outer membrane autotransporter barrel	2634	3559928	3564631	248.671061	125.823942	0.50599
Oxidoreductase domain protein	2633	3564640	3565782	124.3432574	100.481611	0.8081
Short-chain dehydrogenase/reductase SDR	2632	3565818	3566570	117.6861702	59.8404255	0.50847
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	2631	3566571	3567452	120.8853575	104.710556	0.8662
Transketolase, C-terminal section (EC 2.2.1.1)	2630	3567469	3568419	93.15789474	54.4736842	0.58475
Transketolase, N-terminal section (EC 2.2.1.1)	2629	3568419	3569255	77.15311005	43.062201	0.55814
Aldehyde dehydrogenase (EC 1.2.1.3)	2628	3569273	3570826	60.8499678	44.9130715	0.7381
Putative sugar ABC transporter	2627	3570843	3571691	36.55660377	10.6132075	0.29032
Multiple sugar ABC transporter, membrane-spanning permease protein MsmF	2626	3571714	3572604	38.20224719	7.58426966	0.19853
Putative sugar-binding protein	2625	3572679	3573962	198.3632112	236.749805	1.19352
hypothetical protein	2624	3574093	3575514	110.8374384	128.25475	1.15714
Electron transport complex protein rnfB	2623	3575514	3576332	217.603912	302.567237	1.39045
Electron transport complex protein rnfA	2622	3576343	3576918	204.3478261	289.565217	1.41702
Electron transport complex protein rnfE	2621	3576918	3577547	162.1621622	186.009539	1.14706
Electron transport complex protein rnfG	2620	3577544	3578152	435.8552632	395.970395	0.90849
Electron transport complex protein rnfD	2619	3578149	3579162	461.994077	330.94768	0.71635
Electron transport complex protein rnfC	2618	3579175	3580581	548.3641536	636.913229	1.16148
Uncharacterized protein TP_0900	2617	3580702	3583560	37.61371589	25.9797061	0.6907
ATP-dependent nuclease, subunit A	2615	3583557	3587177	53.59116022	39.7790055	0.74227
Na+ driven multidrug efflux pump	2616	3587174	3588553	43.14720812	22.8426396	0.52941
Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)	2613	3588722	3589894	341.4422242	383.145091	1.12214
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	2614	3589884	3591626	328.358209	384.902411	1.1722
hypothetical protein	2612	3591725	3592723	87.6753507	63.1262525	0.72
Methyl-accepting chemotaxis protein	2611	3592789	3593223	18.43317972	5.1843318	0.28125
hypothetical protein	2610	3593260	3593469	76.55502392	10.7655502	0.14063
hypothetical protein	2609	3593558	3593776	68.07511737	126.760563	1.86207
Chain A, Crystal Structure Of Yfir, A Putative Transcriptional Regulator From Bacillus Subtilis	2608	3593961	3594593	30.85443038	0	0
unknown		3594597	3594965	33.9673913	0	0
hypothetical protein	2606	3595069	3595188	8.403361345	0	0
Alpha-mannosidase (EC 3.2.1.24)	2605	3595632	3598334	70.13323464	50.7957069	0.72427
2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	2604	3598370	3598609	41.84100418	0	0
hypothetical protein	2603	3598829	3599023	5.154639175	11.5979381	2.25
hypothetical protein	2602	3599023	3599754	1.367989056	0	0
hypothetical protein	2601	3599763	3600941	7.215619694	1.91001698	0.26471
Plectin 8	2600	3601087	3602409	23.82753404	6.80786687	0.28571
Metal-dependent hydrolases of the beta-lactamase superfamily III	2599	3602623	3603549	18.89848812	7.28941685	0.38571
DnaJ-class molecular chaperone CbpA	2598	3603616	3604293	5.908419498	0	0
transposase, mutator family	2597	3604712	3605953	86.62369057	45.3263497	0.52326
hypothetical protein	2596	3606028	3607245	12.3253903	11.0928513	0.9

Transcriptional regulator, DeoR family	2595	3607309	3608295	17.24137931	13.6916836	0.79412
hypothetical protein	2594	3608302	3608445	55.94405594	62.9370629	1.125
Protein of unknown function DUF262 family	2593	3608522	3610228	19.92966002	32.971864	1.65441
Transcription accessory protein (S1 RNA-binding domain)	2592	3610418	3612850	132.4013158	160.053454	1.20885
MloA protein, putative	2591	3612966	3614054	26.65441176	20.6801471	0.77586
Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	2590	3614121	3614525	42.07920792	0	0
hypothetical protein	2589	3614575	3614967	117.3469388	149.234694	1.27174
HEN1 C-terminal domain; double-stranded RNA 3'-methylase	2588	3615023	3616486	117.2248804	70.7450444	0.6035
protein serine-threonine phosphatase	2587	3616483	3619167	124.8137109	109.817437	0.87985
Appr-1-p processing	2586	3619204	3619743	36.17810761	12.5231911	0.34615
transcriptional regulator, MarR family	2585	3619749	3620186	38.00475059	21.3776722	0.5625
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	2584	3620176	3621498	39.15171289	11.0114192	0.28125
hypothetical protein	2583	3621616	3621786	17.64705882	0	0
Methyl-accepting chemotaxis protein	2582	3621777	3623627	62.7027027	24.3243243	0.38793
Multidrug resistance ABC transporter ATP-binding and permease protein	2581	3623664	3625439	119.4366197	103.943662	0.87028
Multidrug resistance ABC transporter ATP-binding and permease protein	2580	3625429	3627234	86.70360111	64.8199446	0.7476
Methyltransferase gidB (EC 2.1.-.-)	2579	3627203	3627901	55.8739255	35.4584527	0.63462
Two-component sensor kinase yesM (EC 2.7.3.-)	2578	3627904	3629460	16.38817481	4.33804627	0.26471
Alpha-galactosidase (EC 3.2.1.22)	2577	3629551	3631560	29.11896466	4.47984072	0.15385
ABC transporter, substrate-binding protein	2576	3631631	3633193	29.76952625	10.0832266	0.33871
ABC-type polysaccharide transport system, permease component	2575	3633208	3634152	32.83898305	2.38347458	0.07258
maltose/maltodextrin transport permease	2574	3634166	3635062	18.97321429	0	0
Two-component response regulator yesN	2573	3635073	3635843	21.42857143	0	0
hypothetical protein		3635876	3636001	32	0	0
PilT protein, N-terminal	2571	3636138	3636524	37.97468354	0	0
hypothetical protein	2570	3636503	3636796	29.41176471	11.0294118	0.375
hypothetical protein	2569	3636939	3638072	56.04589585	23.8305384	0.4252
hypothetical protein	2568	3638148	3638366	231.6513761	340.59633	1.4703
Uroporphyrinogen-III decarboxylase	2567	3638363	3638608	155.1020408	165.306122	1.06579
IolI protein	2566	3638652	3639497	171.0059172	183.727811	1.07439
Two-component response regulator yesN	2565	3639614	3639997	15.66579634	5.87467363	0.375
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG		3640196	3640684	25.6147541	0	0
hypothetical protein	2564	3640681	3640803	0	0	#DIV/0!
Beta-mannosidase (EC 3.2.1.25)	2562	3640903	3643419	83.26709062	83.1677266	0.99881
Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	2561	3643442	3644344	79.26829268	82.3170732	1.03846
Pyruvate formate-lyase (EC 2.3.1.54)	2560	3644332	3646536	102.9945554	96.9827586	0.94163
hypothetical protein	2559	3646546	3647970	117.2752809	126.404494	1.07784
Iron-sulfur cluster-binding protein	2558	3647988	3648824	80.74162679	56.5191388	0.7
Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	2557	3648848	3649327	289.1440501	366.388309	1.26715

Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	2556	3649324	3650043	86.23087622	125.173853	1.45161
Amidophosphoribosyltransferase (EC 2.4.2.14)	2555	3650018	3651439	202.3223082	201.090781	0.99391
Sensory box histidine kinase/response regulator	2554	3651445	3653607	97.36355227	100.948196	1.03682
Transposase subunit	2553	3654227	3654577	15.71428571	6.42857143	0.40909
hypothetical protein	2552	3654851	3655045	48.96907216	0	0
Ribose operon repressor	2551	3655067	3656089	27.88649706	6.60469667	0.23684
N-acylglucosamine 2-epimerase (EC 5.1.3.8)	2550	3656377	3657669	28.25077399	3.48297214	0.12329
hypothetical protein	2549	3657723	3659693	13.70558376	7.99492386	0.58333
N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein	2548	3659739	3661085	34.54680535	8.35809807	0.24194
N-Acetyl-D-glucosamine ABC transport system, permease protein 1	2547	3661166	3662056	16.29213483	5.05617978	0.31034
N-Acetyl-D-glucosamine ABC transport system, permease protein 2	2545	3662068	3662913	26.62721893	0	0
hydrolase, haloacid dehalogenase-like family	2546	3662910	3663758	34.19811321	7.95990566	0.23276
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	2544	3663805	3664923	175.0448833	135.32316	0.77308
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	2543	3664966	3665586	105.6451613	101.612903	0.96183
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	2542	3665583	3667229	84.14337789	61.5127582	0.73105
Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	2541	3667272	3668597	81.50943396	67.9245283	0.83333
Hemolysins and related proteins containing CBS domains	2540	3668590	3669915	55.47169811	35.6603774	0.64286
Radical SAM domain protein	2539	3669908	3670894	62.37322515	27.3833671	0.43902
membrane protein, putative	2538	3671009	3672379	111.3138686	119.890511	1.07705
Fragment flavodoxin oxidoreductase	2537	3672383	3673660	165.6225529	204.385278	1.23404
D-galactose 1-dehydrogenase (EC 1.1.1.48)	2536	3673690	3674724	153.2882012	187.137331	1.22082
Iron-sulfur cluster-binding protein	2535	3674726	3675877	117.7237185	119.244136	1.01292
Threonine synthase (EC 4.2.3.1)	2534	3675915	3677219	128.4509202	115.605828	0.9
Mechanosensitive ion channel family protein	2532	3677261	3678442	80.86367485	87.6375953	1.08377
Multiple sugar ABC transporter, membrane-spanning permease protein MsmG	2533	3678439	3679266	55.01813785	46.2515115	0.84066
N-Acetyl-D-glucosamine ABC transport system, permease protein 1		3679266	3680150	31.10859729	20.361991	0.65455
Multiple sugar ABC transporter, substrate-binding protein	2530	3680216	3681514	73.18952234	39.8690293	0.54474
Two-component sensor histidine kinase	2529	3681532	3683424	103.3298097	77.2991543	0.74808
DNA-binding response regulator	2527	3683412	3684929	96.57218194	63.7771918	0.66041
Prokaryotic ATPase	2528	3684880	3686019	43.02019315	21.7295874	0.5051
tRNA nucleotidyltransferase (EC 2.7.7.25)	2526	3686114	3687271	87.29472774	66.119274	0.75743
hypothetical protein	2525	3687373	3688074	9.985734665	3.20970043	0.32143
Acetyltransferase, GNAT family protein	2524	3688071	3688586	19.41747573	17.4757282	0.9
Protease IV	2523	3688680	3690314	67.31946144	31.6707466	0.47045
Alpha amylase	2522	3690359	3693979	162.0165746	126.174033	0.77877
hypothetical protein	2521	3693966	3694121	112.9032258	58.0645161	0.51429
hypothetical protein	2520	3694149	3696575	25.35037098	12.9843364	0.5122
Protein of unknown function DUF262 family		3696575	3697426	6.462984724	0	0

hypothetical protein		3697515	3698306	29.70922882	8.5335019	0.28723
5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	2517	3698576	3699868	111.4551084	55.7275542	0.5
Cystine-binding periplasmic protein precursor	2516	3699891	3700640	58.07743658	48.0640854	0.82759
hypothetical protein	2515	3700597	3700710	66.37168142	99.5575221	1.5
Endoglucanase D precursor (EC 3.2.1.4)	2513	3700763	3702451	93.60189573	89.306872	0.95411
Very-short-patch mismatch repair endonuclease (G-T specific)	2514	3702429	3702932	43.73757455	8.94632207	0.20455
Ribonuclease D (EC 3.1.26.3)	2512	3702960	3703808	30.07075472	53.0660377	1.76471
Arsenate reductase (EC 1.20.4.1)	2511	3703814	3704149	110.4477612	73.880597	0.66892
hypothetical protein	2510	3704272	3705147	144	136.285714	0.94643
hypothetical protein	2509	3705151	3705945	156.8010076	127.518892	0.81325
Transcriptional regulator, Hth-3 family	2508	3705979	3706536	110.4129264	92.9084381	0.84146
Acetyl-coenzyme A synthetase (EC 6.2.1.1)	2507	3706536	3708230	204.8406139	217.827627	1.0634
Site-specific tyrosine recombinase	2505	3708494	3709720	74.22512235	25.6933116	0.34615
hypothetical protein	2504	3709957	3710142	35.13513514	12.1621622	0.34615
hypothetical protein	2503	3710779	3710895	43.10344828	0	0
hypothetical protein		3711218	3711727	61.88605108	30.9430255	0.5
hypothetical protein	2501	3711738	3712019	49.82206406	16.0142349	0.32143
putative structure; Structural component (Phage or Prophage Related)	2500	3712021	3714291	48.6784141	13.876652	0.28507
hypothetical protein	2499	3714516	3714764	20.16129032	27.2177419	1.35
hypothetical protein	2498	3714761	3715921	63.79310345	11.637931	0.18243
hypothetical protein	2497	3715942	3716319	22.5464191	5.96816976	0.26471
phage terminase, small subunit, putative	2496	3716391	3716900	30.4518664	8.84086444	0.29032
hypothetical protein	2495	3717043	3717477	51.84331797	10.3686636	0.2
hypothetical protein	2494	3717564	3717743	83.79888268	87.9888268	1.05
hypothetical protein	2493	3717718	3717900	134.6153846	74.1758242	0.55102
Integration host factor beta subunit	2492	3717890	3718210	129.6875	42.1875	0.3253
hypothetical protein	2491	3718203	3718385	96.15384615	74.1758242	0.77143
hypothetical protein	2490	3718378	3718608	23.91304348	29.3478261	1.22727
hypothetical protein	2489	3718605	3718880	74.54545455	16.3636364	0.21951
hypothetical protein	2488	3718877	3719167	41.37931034	0	0
hypothetical protein	2487	3719164	3719460	42.22972973	15.2027027	0.36
hypothetical protein	2486	3719618	3719908	37.93103448	23.2758621	0.61364
hypothetical protein	2485	3720038	3720241	54.18719212	22.1674877	0.40909
hypothetical protein	2484	3720238	3720450	30.66037736	31.8396226	1.03846
hypothetical protein	2483	3720529	3720648	63.02521008	0	0
hypothetical protein	2482	3720742	3720963	74.66063348	61.0859729	0.81818
Putative cytoplasmic protein	2481	3721020	3721388	294.7658402	260.330579	0.88318
hypothetical protein	2480	3721385	3721591	587.3786408	567.961165	0.96694
hypothetical protein	2479	3721887	3722090	174.8768473	166.256158	0.9507
hypothetical protein	2478	3722237	3722959	61.63434903	43.6288089	0.70787
S-ribosylhomocysteine lyase (EC 4.4.1.21) / Autoinducer-2 production protein LuxS	2477	3722963	3723439	153.3613445	127.62605	0.83219
5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	2476	3723441	3724151	259.1549296	212.323944	0.81929
GGDEF domain protein	2475	3724161	3725321	186.637931	122.198276	0.65473
hypothetical protein	2474	3725321	3725881	527.6785714	393.75	0.74619
Predicted endonuclease distantly related to archaeal Holliday junction resolvase	2473	3726032	3726379	76.36887608	77.8097983	1.01887

HD domain protein	2472	3726372	3727550	310.2564103	236.538462	0.7624
Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB	2471	3727547	3727822	214.5454545	106.363636	0.49576
hypothetical protein	2470	3727824	3728780	99.37238494	98.8493724	0.99474
LSU ribosomal protein L19p	2469	3728792	3729205	869.2493947	1280.26634	1.47284
tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)	2468	3729183	3729983	171.25	362.8125	2.11861
16S rRNA processing protein RimM	2467	3730018	3730524	103.7549407	137.84585	1.32857
UPF0109 protein CPE1711	2466	3730541	3730774	482.832618	878.755365	1.82
SSU ribosomal protein S16p	2465	3730842	3731093	402.3904382	770.916335	1.91584
hypothetical protein	2464	3731261	3731536	132.7272727	130.909091	0.9863
Serine protease (EC 3.4.21.-)	2463	3731523	3732347	216.0194175	152.912621	0.70787
hypothetical protein	2462	3732347	3732949	157.807309	153.239203	0.97105
hypothetical protein	2461	3732973	3733086	17.69911504	0	0
4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	2460	3733124	3735151	170.6231454	64.5400593	0.37826
NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	2459	3735189	3735548	229.8050139	131.615599	0.57273
Periplasmic [Fe] hydrogenase (EC 1.12.7.2)	2458	3735558	3737645	195.7355055	178.965022	0.91432
GCN5-related N-acetyltransferase	2457	3738018	3738617	20.86811352	15.0250417	0.72
transposase, mutator family	2456	3738722	3739963	68.89605157	39.8871878	0.57895
CDS_ID OB3186	2455	3740081	3740791	5.035971223	3.23741007	0.64286
Phosphoesterase family protein	2454	3741173	3741979	269.8511166	200.992556	0.74483
Hydrolase (HAD superfamily)	2453	3741991	3743520	854.8821549	1136.36364	1.32926
hypothetical protein	2452	3743514	3743687	26.01156069	26.0115607	1
Transposase, mutator type		3743867	3743992	48.67256637	19.9115044	0.40909
transposase, mutator family		3743993	3744565	26.47657841	0	0
Cell surface protein	2449	3744851	3749743	33.01308258	12.8781684	0.39009
hypothetical protein	2448	3749822	3749998	36.93181818	25.5681818	0.69231
hypothetical protein	2447	3750238	3750360	16.39344262	55.3278689	3.375
hypothetical protein	2446	3750325	3750459	14.92537313	0	0
Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	2445	3750587	3750952	38.35616438	18.4931507	0.48214
Chemotaxis protein CheX	2444	3750975	3751454	37.5782881	14.091858	0.375
hypothetical protein	2443	3751473	3752612	32.92361721	13.8279192	0.42
Chemotaxis protein CheA (EC 2.7.3.-)	2442	3752625	3754553	32.41701245	2.3340249	0.072
NrtR-regulated hypothetical OrfX	2441	3754666	3755709	182.6462128	172.579099	0.94488
NrtR-regulated hypothetical OrfY	2440	3755748	3756857	112.7141569	75.0676285	0.666
Nitroreductase family protein	2439	3757067	3757606	36.17810761	8.34879406	0.23077
archaeal ATPase, fused to C-terminal DUF234 domain		3757670	3758866	49.33110368	31.9816054	0.64831
Sensory box histidine kinase/response regulator	2437	3759156	3762251	37.80290792	2.90791599	0.07692
Response regulator	2436	3762238	3763377	26.77787533	3.95083406	0.14754
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	2435	3763472	3765076	171.7581047	159.912718	0.93103
hypothetical protein	2434	3765078	3765419	98.24046921	46.1876833	0.47015
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	2433	3765596	3766708	17.98561151	18.2104317	1.0125
hypothetical protein	2432	3766721	3767578	5.834305718	2.62543757	0.45
hypothetical protein	2431	3767575	3768030	6.593406593	0	0

hypothetical protein	2430	3768141	3768323	32.96703297	12.3626374	0.375
hypothetical protein	2429	3768325	3768519	30.92783505	0	0
hypothetical protein	2428	3768710	3769012	34.76821192	0	0
hypothetical protein	2427	3769082	3769411	234.0425532	225.683891	0.96429
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	2426	3769495	3772776	84.5778726	68.5766535	0.81081
hypothetical protein	2425	3772899	3774053	179.3760832	175.476603	0.97826
Sensor histidine kinase/response regulator (EC 2.7.3.-)	2424	3774085	3776262	56.72944419	47.5424897	0.83806
Potassium uptake protein TrkH	2423	3776295	3777755	52.05479452	36.9863014	0.71053
Trk system potassium uptake protein trkA	2422	3777761	3779209	89.84105045	54.422944	0.60577
hypothetical protein	2421	3779851	3779970	16.80672269	0	0
hypothetical protein	2420	3780015	3780290	65.69343066	0	0
hypothetical protein	2419	3780402	3780608	0	0	#DIV/0!
PIN domain protein	2418	3780605	3781003	29.8013245	37.2516556	1.25
Transposase IS4 family protein	2417	3781146	3782684	32.1846554	13.1664499	0.40909
Transposase IS116/IS110/IS902		3782963	3783700	26.93370166	12.4309392	0.46154
hypothetical protein	2415	3784520	3785404	42.42081448	35.6334842	0.84
Transposase		3785512	3786402	42.69662921	27.8089888	0.65132
Transposase IS4 family protein		3786399	3786647	74.59677419	36.2903226	0.48649
hypothetical protein	2412	3786800	3786958	28.48101266	0	0
Putative transposase	2411	3787026	3787478	44.24778761	24.8893805	0.5625
transposase, mutator family	2410	3787558	3788727	73.56715141	42.3438837	0.57558
transposase, mutator family	2409	3788732	3789544	99.13793103	49.8768473	0.50311
transposase, mutator family	2408	3789549	3790433	92.19457014	33.0882353	0.3589
hypothetical protein	2407	3790554	3790766	33.01886792	21.2264151	0.64286
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	2406	3790930	3792432	11.9840213	11.9840213	1
hypothetical protein	2404	3792433	3793185	7.313829787	0	0
hypothetical protein	2405	3793163	3793462	11.70568562	0	0
hypothetical protein	2403	3793459	3793662	17.24137931	0	0
hypothetical protein	2402	3793774	3793902	35.15625	17.578125	0.5
Fructose-bisphosphate aldolase (EC 4.1.2.13) / Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40); Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	2401	3793992	3795461	50.37440436	32.1647379	0.63851
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	2400	3795471	3796373	33.81374723	34.9223947	1.03279
6-phosphogluconolactonase (EC 3.1.1.31)	2399	3796375	3797454	44.48563485	14.5968489	0.32813
Sorbitol dehydrogenase (EC 1.1.1.14)	2397	3797486	3798559	94.12861137	73.3923579	0.7797
Membrane endopeptidase, M50 family	2398	3798556	3799230	39.31750742	20.0296736	0.50943
Methyl-directed repair DNA adenine methylase (EC 2.1.1.72)	2396	3799227	3800087	34.30232558	18.3139535	0.5339
hypothetical protein	2395	3800165	3801106	95.64293305	54.9946865	0.575
Tripeptide aminopeptidase (EC 3.4.11.4)	2394	3801084	3802406	118.3812405	122.541604	1.03514
hypothetical protein	2393	3802448	3803350	110.864745	127.217295	1.1475
Sodium-dependent phosphate transporter	2392	3803401	3805083	108.2045184	124.40547	1.14973
Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	2391	3805197	3806195	355.8375635	308.375635	0.86662
Hypothetical lipoprotein	2390	3806258	3807490	1819.705642	2071.54538	1.1384
ABC-type sugar transport system, ATP-binding protein (EC 3.6.3.17)	2389	3807572	3809170	123.59199	83.0725907	0.67215
ABC transporter integral membrane protein	2388	3809167	3810237	78.5046729	50.4672897	0.64286

ABC transporter integral membrane protein	2387	3810234	3811355	137.823372	112.399643	0.81553
hypothetical protein	2386	3811470	3811805	95.52238806	73.880597	0.77344
hypothetical protein	2385	3811938	3812702	134.1623037	126.636126	0.9439
Uronate isomerase (EC 5.3.1.12)	2384	3812725	3814164	139.33287	121.959694	0.87531
Beta-glucosidase (EC 3.2.1.21)	2383	3814183	3816585	66.4029975	33.7218984	0.50784
unknown	2382	3816643	3817614	52.00823893	41.7095778	0.80198
hypothetical protein	2381	3817639	3819021	112.5180897	78.1476122	0.69453
Thioredoxin reductase (EC 1.8.1.9)	2380	3819129	3820082	127.4921301	84.9947534	0.66667
Beta-hexosaminidase (EC 3.2.1.52)	2379	3820095	3821783	86.78909953	75.9774882	0.87543
GCN5-related N-acetyltransferase, fig|164756.6.peg.1929 homolog	2378	3821785	3822642	106.7677946	68.2613769	0.63934
Outer membrane protein	2377	3822673	3823803	148.2300885	125.442478	0.84627
Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family	2376	3823938	3824678	47.97297297	27.3648649	0.57042
Phosphoglycolate phosphatase (EC 3.1.3.18)	2375	3824766	3825410	141.3043478	115.295031	0.81593
ABC transporter, permease protein, putative	2374	3825444	3826721	50.1174628	29.9530149	0.59766
hypothetical protein	2372	3826750	3826956	155.3398058	185.679612	1.19531
hypothetical protein	2373	3826953	3827156	128.0788177	177.339901	1.38462
hypothetical protein	2371	3827137	3827694	39.497307	32.3159785	0.81818
DNA-binding protein	2370	3827749	3828018	70.63197026	25.0929368	0.35526
Integrase domain protein	2369	3828815	3830050	49.79757085	9.10931174	0.18293
hypothetical protein	2368	3830581	3830694	8.849557522	0	0
hypothetical protein	2367	3830986	3831273	15.67944251	7.83972125	0.5
PIN domain protein	2366	3831338	3831733	5.063291139	0	0
hypothetical protein		3831876	3832310	108.2949309	25.921659	0.23936
hypothetical protein	2364	3832407	3832547	35.71428571	0	0
hypothetical protein	2363	3832801	3834006	225.3112033	164.315353	0.72928
Sensory box histidine kinase/response regulator	2362	3834025	3836160	70.52186178	61.3540197	0.87
hypothetical protein	2361	3836209	3836343	85.82089552	16.7910448	0.19565
hypothetical protein	2360	3836547	3836675	113.28125	140.625	1.24138
hypothetical protein	2359	3836956	3837180	35.71428571	90.4017857	2.53125
hypothetical protein	2358	3837233	3837364	38.16793893	34.351145	0.9
hypothetical protein	2357	3837398	3837595	65.98984772	68.5279188	1.03846
Conserved domain protein	2356	3837994	3838884	192.6966292	121.348315	0.62974
hypothetical protein	2355	3839019	3839246	165.1982379	99.1189427	0.6
Lipase precursor (EC 3.1.1.3)	2354	3839577	3840377	150	81.5625	0.54375
EBSC protein	2353	3840399	3840884	338.1443299	273.71134	0.80945
hypothetical protein	2352	3841126	3841629	135.1888668	147.614314	1.09191
probable metal-dependent peptidase	2350	3841709	3842392	169.8389458	204.245974	1.20259
DNA gyrase subunit A (EC 5.99.1.3)	2351	3842361	3844898	359.8738668	428.360268	1.19031
alpha-arabinosides ABC transport system, substrate-binding protein araN	2349	3845009	3846313	1688.266871	1634.01074	0.96786
Lactose transport system	2348	3846377	3847255	133.2574032	84.5671982	0.63462
Lactose transport system	2346	3847252	3848061	152.039555	102.904821	0.67683
Leucine-rich-repeat protein	2347	3848054	3849007	90.7660021	66.1070304	0.72832
Von Willebrand factor type A domain protein	2345	3849021	3850907	143.4252386	122.879109	0.85675
GldJ	2344	3850916	3851734	346.5770171	338.325183	0.97619
hypothetical protein	2343	3851733	3852158	55.29411765	5.29411765	0.09574
ATPase	2342	3852221	3853447	61.17455139	51.3866232	0.84
hypothetical protein	2340	3853463	3853687	46.875	30.1339286	0.64286
DNA gyrase subunit B (EC 5.99.1.3)	2341	3853671	3855617	521.5827338	659.044193	1.26355