

Supplemental Table 1: Reciprocal amino acid identities of orthologs for *D. vulgaris* strains DePue and Hildenborough

## CHROMOSOME

locusId_1VIMSS	locusId_2VIMSS	ident	align	len	mismatches	gaps	Description
1659754	207168	25.27	463	283	14		N-6 DNA methylase
1660149	206945	25.55	411	265	11		phage major capsid protein, HK97 family
1660151	206948	30.2	404	255	7		phage portal protein, HK97 family
1660329	209163	32.41	145	94	2		transcriptional regulator CII, putative
1660141	207160	34.39	410	223	13		beta-lactamase domain protein
1660755	207189	35.48	93	58	2		plasmid maintenance system killer
1660155	206951	35.65	115	67	1		HNH endonuclease
1660148	206943	44.02	184	100	2		conserved hypothetical protein
1659921	207174	44.71	700	358	11		conserved hypothetical protein
1660783	209157	48	125	64	1		protein of unknown function UPF0150
1660324	207222	48.9	364	175	7		phage integrase family protein
1660152	206949	51.38	543	257	6		phage Terminase
1660147	408328	51.85	108	51	1		phage head-tail adaptor, putative
1660153	206950	53.85	156	66	2		phage terminase, small subunit, putative, P27 family
1662095	206954	55.46	119	48	3		conserved hypothetical protein
1660346	207664	59.15	235	85	4		antirepressor, putative
1660036	209531	61.33	1006	383	5		formate dehydrogenase, alpha subunit
1660340	207671	64.41	177	32	3		conserved hypothetical protein
1659917	207178	64.88	299	103	2		conserved hypothetical protein
1661198	206606	71.91	178	50	0		conserved hypothetical protein
1660355	207645	73.33	165	44	0		Lytic transglycosylase, catalytic
1660363	207636	73.42	933	204	8		tail tape measure protein, putative
1660337	207673	74.48	145	37	0		transcriptional regulator CII, putative
1659681	209233	75.29	680	168	0		anaerobic ribonucleoside-triphosphate reductase
1660344	207668	77.14	70	16	0		phage transcriptional regulator, AlpA
1660751	208357	82.39	176	31	0		tail fiber assembly protein, putative
1661779	408294	83.51	758	64	5		DNA mismatch repair protein MutL
1660334	207677	83.65	159	26	0		conserved hypothetical protein
1662085	209154	83.67	147	22	1		tail fiber assembly protein, putative
1659899	208117	83.87	62	2	1		hypothetical protein
1662143	209096	83.87	186	30	0		lipoprotein, putative
1662079	206533	84.15	246	39	0		DNA methylase N-4/N-6 domain protein
1660883	207004	85.19	297	44	0		Methyltransferase type 11
1661937	207513	86.32	95	13	0		conserved hypothetical protein
1660027	207989	86.86	236	31	0		Phosphoribosylanthranilate isomerase
1661713	209495	87.18	312	40	0		NAD-dependent epimerase/dehydratase
1660022	207994	88.11	244	29	0		lipoprotein, putative
1662202	209028	88.46	390	41	1		TonB family protein
1660339	207672	89.28	830	80	3		phage/plasmid primase, P4 family
1659962	208057	89.84	128	3	1		putative 3R-hydroxymyristoyl ACP dehydrase
1661821	209373	89.91	446	15	1		efflux transporter, RND family, MFP subunit
1660333	207678	90	220	22	0		conserved hypothetical protein
1660227	207802	90.08	242	24	0		protein of unknown function UPF0029
1660428	207568	90.32	444	29	2		thiazole biosynthesis protein ThiH
1661490	206229	90.42	428	34	2		histidine kinase
1661655	209568	90.65	834	73	2		multi-sensor hybrid histidine kinase
1659306	208859	91.45	152	13	0		conserved hypothetical protein
1660123	207876	91.77	316	20	1		MotA/TolQ/ExbB proton channel
1661976	209269	92.26	530	41	0		Three-deoxy-D-manno-octulosonic-acid transferase domain protein
1659869	208148	92.65	68	5	0		conserved hypothetical protein
1659742	208397	92.73	275	14	2		ABC transporter related
1660331	207679	92.94	85	6	0		conserved hypothetical protein
1660128	207871	93.17	879	56	1		TonB-dependent receptor, plug
1659439	208719	93.43	624	31	2		DNA polymerase III, subunits gamma and tau
1660129	207870	93.48	460	24	1		conserved hypothetical protein
1660828	207059	93.62	799	49	2		DNA ligase, NAD-dependent
1660431	207565	93.7	238	6	1		Calcium-binding EF-hand-containing protein
1661410	206317	93.88	376	23	0		Phosphoglycerate mutase
1659748	208391	93.95	496	25	1		FolC bifunctional protein
1660268	207746	94.04	604	36	0		conserved hypothetical protein
1659925	207154	94.08	169	10	0		tail fiber assembly protein, putative
1662053	209191	94.16	154	9	0		GCN5-related N-acetyltransferase
1660869	207017	94.29	70	4	0		conserved hypothetical protein
1661104	206710	94.35	407	23	0		type II secretion system protein
1662011	209231	94.39	107	6	0		conserved hypothetical protein
1660357	207643	94.44	54	3	0		conserved hypothetical protein
1661936	207512	94.51	91	5	0		conserved hypothetical protein
1661782	209416	94.65	243	13	0		protein of unknown function UPF0153
1662235	208998	94.68	451	21	1		metallophosphoesterase

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1661778	209420	94.7	264	14	0	ABC transporter related
1661784	209414	94.85	291	11	1	metallophosphoesterase
1659436	208722	94.9	353	18	0	conserved hypothetical protein
1660387	207613	94.91	393	15	1	conserved hypothetical protein
1660024	207992	94.96	139	7	0	uncharacterized domain 1
1660121	207879	95.03	302	15	0	TonB family protein
1661475	206245	95.06	607	5	1	conserved hypothetical protein
1660193	207839	95.08	122	6	0	conserved hypothetical protein
1659619	208524	95.24	273	4	1	conserved hypothetical protein
1660757	207094	95.24	105	5	0	conserved hypothetical protein
1659631	208512	95.27	275	13	0	formyl transferase domain protein
1659763	208327	95.27	423	14	1	efflux transporter, RND family, MFP subunit
1661813	209381	95.3	574	27	0	putative signal-transduction protein with CBS domains
1660359	207641	95.34	236	11	0	conserved hypothetical protein
1662010	209232	95.38	260	12	0	conserved hypothetical protein
1660358	207642	95.41	109	5	0	conserved hypothetical protein
1659630	208513	95.45	396	18	0	conserved hypothetical protein
1660117	207885	95.52	469	15	1	two component, sigma54 specific, transcriptional regulator, Fis family
1660987	206836	95.52	67	3	0	conserved hypothetical protein
1660356	207644	95.59	136	6	0	lipoprotein, putative
1659411	408363	95.63	206	9	0	flagellar basal body-associated protein FlIL
1660194	207838	95.64	482	9	1	gid protein
1660353	207647	95.65	69	3	0	conserved hypothetical protein
1659618	208525	95.66	599	26	0	conserved hypothetical protein
1659261	208914	95.79	451	19	0	permease
1660259	207762	95.81	191	8	0	conserved hypothetical protein
1661780	209418	95.85	482	20	0	multi-sensor signal transduction histidine kinase
1661975	209270	95.96	446	18	0	DegT/DnrJ/EryC1/StrS aminotransferase
1659916	208101	96	225	9	0	conserved hypothetical protein
1660119	207883	96	150	6	0	Tir chaperone family protein
1659373	208788	96.06	279	11	0	hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha subunit
1662186	209046	96.09	358	14	0	polysaccharide deacetylase
1659963	208056	96.12	541	3	1	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
1659464	208693	96.13	671	26	0	putative CheA signal transduction histidine kinases
1660549	207379	96.17	574	22	0	carbohydrate kinase, YjeF related protein
1661167	206640	96.29	377	14	0	riboflavin biosynthesis protein RibD
1659272	208898	96.31	785	29	0	5-methyltetrahydropteroyltryglutamate--homocysteine S-methyltransferase
1660350	207650	96.32	408	13	1	peptidase S49
1659822	208257	96.39	166	6	0	DoxX family protein
1662185	209047	96.39	305	11	0	glycosyl transferase, family 2
1659724	208416	96.45	423	15	0	DNA-directed DNA polymerase
1660413	207585	96.45	479	9	1	Dinitrogenase iron-molybdenum cofactor biosynthesis
1661196	206608	96.46	113	4	0	conserved hypothetical protein
1661620	206081	96.48	256	9	0	conserved hypothetical protein
1660303	207707	96.49	114	4	0	conserved hypothetical protein
1660375	207628	96.54	578	20	0	protein of unknown function DUF814
1660362	207638	96.55	116	4	0	conserved hypothetical protein
1660159	408343	96.56	349	12	0	Integrase, catalytic region
1659323	208838	96.69	151	5	0	conserved hypothetical protein
1659372	208789	96.72	183	6	0	hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta subunit
1660474	207464	96.73	214	7	0	antibiotic acetyltransferase
1662151	209087	96.75	462	15	0	type I phosphodiesterase/nucleotide pyrophosphatase
1661476	206244	96.77	155	5	0	hypothetical protein
1661814	209380	96.89	740	23	0	putative signal-transduction protein with CBS domains
1659639	208504	96.9	290	9	0	conserved hypothetical protein
1661764	209435	96.9	452	14	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1662214	209016	96.95	164	5	0	protein of unknown function DUF997
1660124	207875	96.96	593	17	1	ABC transporter related
1662251	208982	96.96	427	5	1	dihydrouridine synthase, DuS
1659476	208679	96.97	330	10	0	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))
1660426	207570	96.97	66	2	0	thiamine biosynthesis protein ThiS
1660799	207090	96.97	198	6	0	NAD(P)H dehydrogenase (quinone)
1660686	207231	97.02	470	14	0	fumarate lyase
1659382	208780	97.04	371	5	1	formamidopyrimidine-DNA glycosylase
1662238	208995	97.06	102	3	0	conserved hypothetical protein
1660122	207877	97.08	137	4	0	Biopolymer transport protein ExbD/TolR
1659956	208062	97.1	241	7	0	dethiobiotin synthase
1661815	209379	97.13	244	7	0	Exonuclease, RNase T and DNA polymerase III
1661845	209347	97.13	557	8	1	glycosyl transferase, family 9
1659731	208408	97.14	280	8	0	conserved hypothetical protein
1659957	208061	97.17	424	12	0	aminotransferase, class I and II
1660114	207888	97.17	247	7	0	conserved hypothetical protein

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1660207	207822	97.18	461	6	1	protein of unknown function DUF610, YibQ
1659637	208506	97.19	891	21	1	glycosyl transferase, family 2
1660248	207777	97.19	178	5	0	NADH dehydrogenase (ubiquinone), 30 kDa subunit
1660599	207324	97.19	178	5	0	putative cold-shock DNA-binding domain protein
1659348	208821	97.2	464	13	0	aldehyde dehydrogenase
1661656	209567	97.2	465	13	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659765	208324	97.22	540	11	1	RND efflux system, outer membrane lipoprotein, NodT family
1659770	208317	97.22	144	4	0	cytochrome c, class III
1661227	206515	97.22	180	5	0	nitrite and sulphite reductase 4Fe-4S region
1659819	208260	97.23	325	9	0	Alcohol dehydrogenase, zinc-binding domain protein
1660192	207840	97.25	545	15	0	glycosyl transferase, family 2
1661470	206253	97.27	439	12	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659498	208658	97.29	258	7	0	extracellular solute-binding protein, family 3
1659843	208179	97.3	148	4	0	flavodoxin
1660451	207543	97.31	668	13	1	DNA protecting protein DprA
1660093	207910	97.33	187	2	1	Rhodanese domain protein
1662041	209205	97.38	496	13	0	response regulator receiver sensor signal transduction histidine kinase
1659713	208428	97.44	78	2	0	conserved hypothetical protein
1659886	208131	97.44	78	2	0	conserved hypothetical protein
1662060	209189	97.44	1053	27	0	DEAD/DEAH box helicase domain protein
1662200	209030	97.44	508	13	0	Methyltransferase type 12
1659381	408365	97.45	979	20	1	ComEC/Rec2-related protein
1660820	207068	97.46	197	5	0	nitroreductase
1661392	206335	97.46	985	16	3	conserved hypothetical protein
1660455	207539	97.47	474	10	1	phage integrase family protein
1661199	206603	97.49	439	11	0	NADH dehydrogenase
1661555	206159	97.53	162	4	0	conserved hypothetical protein
1659610	208533	97.54	122	3	0	conserved hypothetical protein
1660351	207649	97.54	122	3	0	conserved hypothetical protein
1661789	209405	97.54	284	7	0	Phosphoribosylanthranilate isomerase
1661385	206343	97.55	245	6	0	cobalamin-5-phosphate synthase CobS
1661974	209271	97.56	656	16	0	conserved hypothetical protein
1660989	206834	97.58	124	3	0	conserved hypothetical protein
1660700	207144	97.59	249	6	0	protein of unknown function DUF558
1660566	207359	97.6	250	4	1	glycosyl transferase, family 2
1660668	207252	97.6	208	5	0	nuclease (SNase domain protein)
1659307	208858	97.62	589	14	0	heavy metal translocating P-type ATPase
1659771	208316	97.63	169	4	0	TonB family protein
1660028	207988	97.64	636	11	1	ABC transporter related
1659636	208507	97.65	341	8	0	glycosyl transferase, family 2
1660537	207394	97.65	213	5	0	lipolytic enzyme, G-D-S-L family
1662014	209228	97.66	641	15	0	glycosyl transferase, family 2
1661872	209319	97.67	129	3	0	conserved hypothetical protein
1659571	208578	97.69	562	13	0	integral membrane protein MviN
1659654	208488	97.69	346	8	0	membrane-bound metal-dependent hydrolase
1659881	208135	97.69	389	9	0	conserved hypothetical protein
1661478	206242	97.72	701	16	0	AsmA family protein
1660354	207646	97.73	132	3	0	toxin secretion/phage lysis holin
1661925	408344	97.73	88	2	0	transposase IS3/IS911 family protein
1659313	208850	97.74	221	5	0	ABC transporter related
1659918	208099	97.74	133	3	0	conserved hypothetical protein
1661737	209464	97.76	223	4	1	transcriptional regulator, MarR family
1659622	208521	97.77	358	8	0	N-acetylneuraminic acid synthase, N-terminal domain
1660361	207639	97.77	314	7	0	conserved hypothetical protein
1661477	206243	97.77	539	12	0	cobyric acid synthase CobQ
1660675	207245	97.78	90	2	0	protein of unknown function DUF1653
1660922	206909	97.81	411	9	0	glycosyl transferase, family 9
1661856	209336	97.81	183	4	0	conserved hypothetical protein
1659550	208602	97.82	597	13	0	cobyric acid a,c-diamide synthase
1660685	207232	97.83	322	7	0	Radical SAM domain protein
1662123	209117	97.84	139	3	0	conserved hypothetical protein
1659955	208063	97.86	421	9	0	diaminopimelate decarboxylase
1660191	207841	97.86	562	12	0	glycosyl transferase, family 2
1661145	206663	97.86	280	6	0	apurinic endonuclease Apn1
1662031	209212	97.86	140	3	0	Glyoxalase/bleomycin resistance protein/dioxygenase
1662199	209031	97.88	330	7	0	periplasmic solute binding protein
1659421	208739	97.89	142	3	0	conserved hypothetical protein
1660132	207867	97.91	1005	21	0	peptidase M16 domain protein
1660623	207302	97.91	383	8	0	Polynucleotide adenyllyltransferase region
1660931	206900	97.92	336	7	0	protein of unknown function DUF34
1659414	208746	97.93	242	5	0	sugar fermentation stimulation protein
1659635	208508	97.93	387	8	0	glycosyl transferase, group 1

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1659803	208278	97.94	436	8	1	protein of unknown function DUF111
1660411	207587	97.96	294	6	0	transcriptional regulator, LysR family
1660606	207318	97.96	98	2	0	conserved hypothetical protein
1660740	207104	97.96	147	3	0	protein tyrosine phosphatase
1661935	207511	97.96	98	2	0	conserved hypothetical protein
1660018	207999	97.97	295	6	0	UDP-N-acetylenolpyruvoylglucosamine reductase
1660343	207669	97.97	641	13	0	phage terminase GpA
1659443	208715	97.98	495	6	1	small GTP-binding protein
1661151	206657	97.98	99	2	0	protein of unknown function DUF77
1660921	206910	98.02	354	7	0	conserved hypothetical protein
1661865	209327	98.02	252	5	0	conserved hypothetical protein
1662265	208968	98.04	204	4	0	conserved hypothetical protein
1659634	208509	98.05	307	6	0	NAD-dependent epimerase/dehydratase
1661138	206674	98.06	206	4	0	conserved hypothetical protein
1660542	207388	98.08	156	3	0	hydrogenase maturation protease
1659693	208444	98.09	472	9	0	two component, sigma54 specific, transcriptional regulator, Fis family
1662121	209120	98.09	366	4	1	diguanylate cyclase
1659371	208790	98.1	263	5	0	conserved hypothetical protein
1659860	208162	98.1	158	3	0	conserved hypothetical protein
1661303	206433	98.11	687	12	1	cytochrome c biogenesis protein, transmembrane region
1661829	209364	98.11	106	2	0	Antibiotic biosynthesis monooxygenase
1659506	208650	98.12	320	1	1	transcriptional regulator, DeoR family
1659549	208603	98.12	213	4	0	Precorin-8X methylmutase CbiC/CobH
1660127	207872	98.12	639	11	1	extracellular solute-binding protein, family 5
1661035	206784	98.13	268	5	0	ABC transporter related
1661558	206156	98.13	321	6	0	conserved hypothetical protein
1661950	209295	98.13	107	2	0	amino acid-binding ACT domain protein
1659743	208396	98.14	322	6	0	protein of unknown function DUF6, transmembrane
1661226	206516	98.14	539	10	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660889	206998	98.15	216	4	0	Phosphoglycerate mutase
1659628	208515	98.17	382	7	0	Methyltransferase type 12
1660183	207851	98.17	219	4	0	thiamine-phosphate pyrophosphorylase
1661805	209388	98.17	438	8	0	conserved hypothetical protein
1660265	207754	98.18	55	1	0	conserved hypothetical protein
1661181	206626	98.18	274	5	0	conserved hypothetical protein
1661462	206261	98.18	220	4	0	Ribonuclease H
1661499	206219	98.18	110	2	0	conserved hypothetical protein
1661783	209415	98.2	499	9	0	protein kinase
1659657	208484	98.21	279	5	0	glycosyl transferase, family 8
1660377	207626	98.21	502	9	0	serine dehydratase alpha chain
1660927	206904	98.21	390	7	0	tRNA(Ile)-lysidine synthetase
1660894	206991	98.23	847	15	0	ATP-dependent helicase HrpB
1661271	206469	98.23	339	6	0	Glucokinase
1661013	206806	98.24	340	6	0	dTDP-glucose 4,6-dehydratase
1659942	208075	98.25	229	4	0	response regulator receiver protein
1659493	208662	98.26	518	9	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659811	208269	98.26	172	3	0	nitroreductase
1659675	208464	98.27	520	9	0	putative transcriptional regulator, GntR family
1659796	208287	98.27	173	3	0	conserved hypothetical protein
1659463	208694	98.28	58	1	0	conserved hypothetical protein
1660285	207725	98.28	406	7	0	4-hydroxythreonine-4-phosphate dehydrogenase
1661338	206397	98.28	58	1	0	conserved hypothetical protein
1661836	209356	98.28	58	1	0	conserved hypothetical protein
1659589	208559	98.29	293	5	0	conserved hypothetical protein
1661630	206069	98.29	351	6	0	transport system permease protein
1660190	207842	98.31	415	7	0	glycosyl transferase, family 2
1661940	207516	98.31	533	9	0	von Willebrand factor, type A
1661333	206402	98.32	179	3	0	lipoprotein, putative
1661629	206070	98.32	297	5	0	anaerobic cobalt chelatase
1659613	208530	98.33	300	5	0	Methyltransferase type 12
1661077	206743	98.33	60	1	0	conserved hypothetical protein
1661941	207518	98.33	60	1	0	conserved hypothetical protein
1660032	207983	98.34	181	3	0	GCN5-related N-acetyltransferase
1660279	207731	98.34	723	12	0	RNA binding S1 domain protein
1660418	207580	98.34	301	5	0	Cobyrinic acid a,c-diamide synthase
1660458	207535	98.35	1152	19	0	UvrD/REP helicase
1659282	208887	98.36	304	5	0	parB-like partition proteins
1659434	208724	98.36	305	5	0	DNA polymerase III, delta prime subunit, putative
1661062	206758	98.36	61	1	0	ribosomal protein S14
1661745	209455	98.36	610	10	0	peptidase M23B
1660970	206856	98.37	430	7	0	conserved hypothetical protein
1659448	208710	98.38	431	7	0	Fmu (Sun) domain protein
1659773	208314	98.39	249	4	0	MotA/TolQ/ExbB proton channel

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1660319	207687	98.39	124	2	0	putative endoribonuclease L-PSP
1660829	207058	98.39	248	4	0	conserved hypothetical protein
1661939	207515	98.39	248	4	0	filamentation induced by cAMP protein Fic
1659892	408360	98.4	125	2	0	conserved hypothetical protein
1659565	408362	98.41	440	7	0	aminodeoxychorismate lyase
1660310	207697	98.41	189	3	0	nuclease (SNase domain protein)
1659300	208865	98.42	569	9	0	potassium-transporting ATPase, A subunit
1662284	208954	98.42	190	3	0	dienelactone hydrolase
1660725	207120	98.44	64	1	0	conserved hypothetical protein
1661787	209407	98.44	257	4	0	tryptophan synthase, alpha subunit
1662004	209239	98.44	64	1	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659558	208592	98.45	193	3	0	Redoxin domain protein
1659633	208510	98.45	258	4	0	conserved hypothetical protein
1661557	206157	98.45	453	7	0	conserved hypothetical protein
1660103	207901	98.47	196	3	0	Superoxide dismutase
1661236	206506	98.47	196	3	0	conserved hypothetical protein
1661384	206344	98.47	262	4	0	protein of unknown function DUF62
1661763	209436	98.47	131	2	0	protein of unknown function UPF0047
1659596	208551	98.48	330	5	0	protein of unknown function DUF362
1661376	206353	98.48	132	2	0	Endoribonuclease L-PSP
1660421	207577	98.49	1783	27	0	protein of unknown function DUF490
1660660	207262	98.5	266	4	0	dimethyladenosine transferase
1661756	209443	98.5	333	5	0	phosphoesterase, RecJ domain protein
1661793	209401	98.5	532	8	0	Anthranilate synthase
1659288	208880	98.51	404	6	0	phosphopantothenoylcysteine decarboxylase/phosphopantothenate-cysteine ligase
1659502	208654	98.51	202	3	0	NAD(P)H dehydrogenase (quinone)
1659762	208328	98.51	202	3	0	transcriptional regulator, TetR family
1660402	207597	98.51	134	2	0	conserved hypothetical protein
1660506	207426	98.51	335	5	0	glycosyl transferase, family 9
1661301	206435	98.51	134	2	0	CoA-binding domain protein
1661369	206362	98.51	268	4	0	phosphomethylpyrimidine kinase
1659960	208059	98.52	135	2	0	acyl carrier protein, putative
1661631	206067	98.52	271	4	0	ABC transporter related
1660483	207454	98.53	407	6	0	conserved hypothetical protein
1659959	208060	98.54	481	7	0	beta-ketoacyl synthase
1660237	207790	98.54	478	4	1	Sel1 domain protein repeat-containing protein
1661189	206617	98.54	205	3	0	conserved hypothetical protein
1660261	207760	98.55	484	7	0	sigma54 specific transcriptional regulator, Fis family
1660422	207575	98.55	138	2	0	UspA domain protein
1661623	206078	98.55	69	1	0	protein of unknown function DUF343
1662209	209021	98.55	1105	16	0	signal transduction histidine kinase, nitrogen specific, NtrB
1661574	206135	98.56	554	8	0	Mg chelatase, subunit ChlI
1662222	209011	98.56	139	2	0	protein of unknown function DUF309
1659818	208261	98.57	280	4	0	protein of unknown function DUF191
1660853	207033	98.57	279	4	0	conserved hypothetical protein
1659680	208458	98.58	282	4	0	flagellin domain protein
1660110	207892	98.58	494	7	0	methyl-viologen-reducing hydrogenase, delta subunit
1661833	209359	98.58	141	2	0	UspA domain protein
1660882	207005	98.59	71	1	0	conserved hypothetical protein
1660998	206823	98.59	71	1	0	conserved hypothetical protein
1661438	206287	98.59	426	6	0	conserved hypothetical protein
1659683	208455	98.6	285	4	0	conserved hypothetical protein
1661096	206719	98.6	286	4	0	dihydropteroate synthase
1661697	209519	98.6	143	2	0	methionine-R-sulfoxide reductase
1662070	209177	98.6	285	4	0	conserved hypothetical protein
1660378	207623	98.61	216	3	0	chloramphenicol acetyltransferase
1660564	207361	98.61	72	1	0	conserved hypothetical protein
1659470	208686	98.62	218	3	0	Threonyl/alanyl tRNA synthetase, SAD
1661191	206615	98.62	145	2	0	conserved hypothetical protein
1662026	209218	98.62	579	8	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1659254	208926	98.63	437	2	1	chromosomal replication initiator protein DnaA
1660348	207652	98.63	73	1	0	conserved hypothetical protein
1660679	207239	98.63	293	4	0	conserved hypothetical protein
1660818	207070	98.63	511	7	0	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
1659587	208561	98.64	368	5	0	glycosyl transferase, group 1
1659689	208449	98.64	295	4	0	conserved hypothetical protein
1661168	206639	98.64	220	3	0	riboflavin synthase, alpha subunit
1659322	208839	98.65	296	4	0	transcriptional regulator, LysR family
1659632	208511	98.65	444	6	0	conserved hypothetical protein
1660262	207757	98.65	817	11	0	Formate C-acetyltransferase
1660263	207756	98.65	297	4	0	glycyl-radical enzyme activating protein family
1661694	209522	98.65	222	3	0	molybdopterin-guanine dinucleotide biosynthesis protein A, putative

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1659862	208160	98.66	521	7	0	twin-arginine translocation pathway signal sequence domain
1660870	207016	98.66	224	3	0	protein
1660968	408316	98.66	1194	13	1	phosphoadenosine phosphosulfate reductase
1662013	209229	98.66	449	6	0	AsmA family protein
1660023	207993	98.67	150	2	0	amine oxidase, flavin-containing
1661144	206665	98.67	150	2	0	lipoprotein, putative
1661830	209362	98.67	450	6	0	conserved hypothetical protein
1659315	208848	98.68	152	2	0	chromate transporter, chromate ion transporter (CHR) family
1659384	208778	98.68	454	6	0	conserved hypothetical protein
1659974	208044	98.68	228	3	0	PDZ/DHR/GLGF domain protein
1661454	206269	98.68	76	1	0	putative transcriptional regulator, Crp/Fnr family
1661753	408295	98.68	76	1	0	conserved hypothetical protein
1659266	208906	98.69	153	2	0	conserved hypothetical protein
1660888	206999	98.69	459	6	0	YbaK/prolyl-tRNA synthetase associated region
1659695	208442	98.7	308	4	0	metal dependent phosphohydrolase
1660292	207718	98.71	389	5	0	domain of unknown function DUF1731
1660420	207578	98.71	776	10	0	HI0933 family protein
1660721	207124	98.71	155	2	0	surface antigen (D15)
1660990	206833	98.71	155	2	0	3-dehydroquinate dehydratase
1661378	206351	98.71	155	2	0	conserved hypothetical protein
1661375	206355	98.72	468	6	0	pyridoxamine 5'-phosphate oxidase-related, FMN-binding
1659567	208582	98.74	792	10	0	RNA methyltransferase, TrmA family
1661654	209570	98.74	159	2	0	[NiFe] hydrogenase maturation protein HypF
1661944	209301	98.74	239	3	0	NapC/NirT cytochrome c family protein
1659480	208674	98.75	963	12	0	metallophosphoesterase
1659682	208456	98.75	80	1	0	methyl-accepting chemotaxis sensory transducer
1661530	206185	98.75	401	5	0	conserved hypothetical protein
1660909	206976	98.76	161	2	0	peptidase M29, aminopeptidase II
1661781	209417	98.76	323	4	0	CMP/dCMP deaminase, zinc-binding
1662019	209223	98.76	161	2	0	ADP-L-glycero-D-manno-heptose-6-epimerase
1659314	208849	98.77	488	6	0	molybdenum cofactor biosynthesis protein C
1659521	208629	98.77	244	3	0	protein of unknown function DUF214
1659574	208574	98.77	488	1	1	putative transcriptional regulator, Crp/Fnr family
1660567	207358	98.77	244	3	0	signal recognition particle-docking protein FtsY
1660576	207349	98.77	162	2	0	conserved hypothetical protein
1661029	206790	98.77	81	1	0	protein of unknown function UPF0054
1661148	206660	98.77	81	1	0	Exonuclease VII, small subunit
1661241	206500	98.77	163	2	0	conserved hypothetical protein
1661431	206294	98.77	408	5	0	Xanthine phosphoribosyltransferase
1661596	206110	98.77	162	2	0	1-deoxy-D-xylulose 5-phosphate reductoisomerase
1659428	208730	98.78	327	4	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660394	207605	98.78	164	2	0	protein of unknown function DUF205
1661299	206437	98.78	328	4	0	TadE family protein
1661803	209390	98.78	82	1	0	heat shock protein DnaJ domain protein
1659764	208325	98.79	1070	13	0	conserved hypothetical protein
1659894	208123	98.79	165	2	0	transporter, hydrophobe/amphiphile efflux-1 (HAE1) family
1661162	206645	98.79	247	3	0	hypothetical protein
1659357	208806	98.8	166	2	0	3-oxoacyl-(acyl-carrier-protein) reductase
1659386	208776	98.8	83	1	0	conserved hypothetical protein
1659722	208418	98.8	250	3	0	conserved hypothetical protein
1659883	208133	98.8	83	1	0	putative cobalt transport system permease protein
1660271	207743	98.8	166	2	0	conserved hypothetical protein
1660992	206831	98.8	251	3	0	crossover junction endodeoxyribonuclease RuvC
1661594	206112	98.8	166	2	0	conserved hypothetical protein
1661956	209290	98.8	167	2	0	conserved hypothetical protein
1659487	208667	98.81	503	6	0	DNA-3-methyladenine glycosylase I
1659646	208497	98.81	335	4	0	4-alpha-glucanotransferase
1660307	207701	98.81	168	2	0	protein of unknown function DUF89
1661332	206403	98.81	168	2	0	GCN5-related N-acetyltransferase
1661809	209385	98.81	1513	18	0	molybdenum cofactor synthesis domain
1662127	209113	98.81	253	3	0	signal transduction histidine kinase with CheB and CheR activity
1660054	207955	98.82	339	4	0	ABC transporter related
1660985	206839	98.82	85	1	0	binding-protein-dependent transport systems inner membrane component
1661275	206466	98.82	169	2	0	conserved hypothetical protein
1659961	208058	98.83	342	4	0	conserved hypothetical protein
1661106	206709	98.83	426	5	0	short-chain dehydrogenase/reductase SDR
1661115	206699	98.83	427	4	1	twitching motility protein
1662298	208938	98.83	341	4	0	membrane protein involved in aromatic hydrocarbon degradation
1659701	208436	98.84	173	2	0	TRAP dicarboxylate transporter, DctP subunit
1661252	206489	98.84	344	4	0	ribosomal protein L10
1661466	206258	98.84	86	1	0	glycosyl transferase, family 9
1659616	208527	98.85	697	8	0	Phosphotransferase system, phosphocarrier protein HPr
						asparagine synthase (glutamine-hydrolyzing)

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1660562	207364	98.85	87	1	0	ribosomal protein S20
1660899	206986	98.85	174	2	0	conserved hypothetical protein
1661777	209421	98.85	260	3	0	conserved hypothetical protein 245
1660705	207139	98.86	263	3	0	inositol monophosphatase
1661215	206528	98.86	176	2	0	HAD-superfamily hydrolase, subfamily IA, variant 3
1661306	206430	98.86	351	4	0	glycosyl transferase, family 9
1660881	207006	98.87	797	9	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1662017	209225	98.87	354	4	0	ABC transporter related
1659638	208505	98.88	538	6	0	glycosyl transferase, family 2
1659645	208498	98.88	357	4	0	3-isopropylmalate dehydrogenase
1659830	208248	98.88	358	4	0	inner-membrane translocator
1659935	208078	98.88	1343	15	0	integral membrane sensor hybrid histidine kinase
1660305	207704	98.88	89	1	0	conserved hypothetical protein
1660717	207128	98.88	267	3	0	pseudouridine synthase
1661758	209441	98.88	89	1	0	ribosomal protein S15
1659799	208284	98.89	90	1	0	conserved hypothetical protein
1660997	206824	98.89	90	1	0	HesB/YadR/YfhF-family protein
1661607	206098	98.89	271	3	0	polar amino acid ABC transporter, inner membrane subunit
1659308	208856	98.9	91	1	0	conserved hypothetical protein
1659579	208569	98.9	364	4	0	Radical SAM domain protein
1659655	208486	98.9	91	1	0	histone family protein DNA-binding protein
1659879	208137	98.9	362	4	0	conserved hypothetical protein
1659972	208046	98.9	91	1	0	hypothetical protein
1660412	207586	98.9	545	6	0	L-lactate transport
1659562	208588	98.91	644	7	0	binding-protein-dependent transport systems inner membrane component
1659890	208128	98.91	183	2	0	conserved hypothetical protein
1660256	207767	98.91	733	8	0	histidine kinase
1660296	207714	98.91	274	3	0	purine nucleoside phosphorylase I, inosine and guanosine-specific
1661031	206788	98.91	459	5	0	exodeoxyribonuclease VII, large subunit
1661926	207483	98.91	274	3	0	Integrase, catalytic region
1662232	209001	98.91	368	4	0	CDP-glucose 4,6-dehydratase
1659302	208863	98.92	185	2	0	potassium-transporting ATPase, C subunit
1659483	208671	98.92	553	6	0	PAS/PAC sensor signal transduction histidine kinase
1659592	208556	98.92	93	1	0	cytochrome c, class I
1660687	207230	98.92	464	5	0	biotin and thiamin synthesis associated
1661436	206289	98.92	372	4	0	glycosyl transferase, group 1
1661650	209574	98.92	372	4	0	acetate and butyrate kinase
1661698	209518	98.92	93	1	0	conserved hypothetical protein
1660454	207540	98.93	373	4	0	diguanylate cyclase
1660736	207109	98.93	374	4	0	Tetratricopeptide domain protein
1662190	209042	98.93	467	5	0	Deoxyribodipyrimidine photo-lyase
1659466	208691	98.94	284	3	0	precorrin-3B C17-methyltransferase
1660258	207763	98.94	283	3	0	protein of unknown function DUF6, transmembrane
1660887	207000	98.94	376	4	0	protein of unknown function DUF182
1661619	206683	98.94	188	2	0	phosphodiesterase, MJ0936 family
1661958	209288	98.94	282	3	0	conserved hypothetical protein
1659449	208709	98.95	191	2	0	NLP/P60 protein
1659922	208094	98.95	191	2	0	conserved hypothetical protein
1660009	208008	98.95	95	1	0	conserved hypothetical protein
1660012	208005	98.95	478	5	0	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase
1660069	207940	98.95	191	2	0	conserved hypothetical protein
1660655	207267	98.95	286	3	0	PGAP1 family protein
1661314	206422	98.95	285	3	0	endonuclease III
1661932	207508	98.95	95	1	0	plasmid stabilization system
1659859	208163	98.96	288	3	0	ABC transporter related
1660867	207019	98.96	578	6	0	pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
1659350	208819	98.97	776	8	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1659392	208771	98.97	389	4	0	efflux transporter, RND family, MFP subunit
1659446	208712	98.97	390	4	0	pseudouridine synthase
1660644	207278	98.97	97	1	0	caa(3)-type oxidase, subunit IV
1660690	207225	98.97	194	2	0	transcriptional regulator, TetR family
1660973	206853	98.97	290	3	0	hypothetical protein
1661835	209357	98.97	290	3	0	putative agmatinase
1659473	208683	98.98	293	3	0	binding-protein-dependent transport systems inner membrane component
1659715	208426	98.98	295	3	0	modification methylase, HemK family
1660189	207843	98.98	196	2	0	tRNA guanosine-2'-O-methyltransferase
1661237	206505	98.98	491	5	0	ABC transporter related
1661491	206227	98.98	688	7	0	excinuclease ABC, C subunit
1659304	208861	98.99	593	6	0	multi-sensor signal transduction histidine kinase
1659353	208813	98.99	597	6	0	glycosyl transferase, family 2
1659467	208689	98.99	398	4	0	cobalamin (vitamin B12) biosynthesis CbiG protein

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1660561	207365	98.99	696	7	0	Glycine--tRNA ligase
1661388	206339	98.99	297	3	0	tRNA pseudouridine synthase A
1661394	206333	98.99	298	3	0	lipoic acid synthetase
1661495	206222	98.99	298	3	0	phosphoribosylaminoimidazole-succinocarboxamidesynthase
1661788	209406	98.99	395	4	0	tryptophan synthase, beta subunit
1659556	208595	99	200	2	0	Glyoxalase/bleomycin resistance protein/dioxygenase
1659730	208409	99	399	4	0	amidohydrolase
1659845	208177	99	400	4	0	pseudouridine synthase
1660975	206850	99	100	1	0	conserved hypothetical protein
1661185	206622	99	299	3	0	putative PAS/PAC sensor protein
1661435	206290	99	301	3	0	flagellar protein FlIS
1662130	209109	99	299	3	0	glycerophosphoryl diester phosphodiesterase
1662187	209045	99	301	3	0	shikimate 5-dehydrogenase
1659279	208890	99.01	507	5	0	NusB/RsmB/TIM44
1660075	207933	99.01	302	3	0	conserved hypothetical protein
1660836	207051	99.01	203	2	0	adenylate cyclase
1661030	206789	99.01	303	3	0	peptidase M23B
1659440	208718	99.02	307	3	0	branched-chain amino acid aminotransferase
1659575	208573	99.02	1223	12	0	multi-sensor hybrid histidine kinase
1662003	209240	99.02	205	2	0	conserved hypothetical protein
1659438	208720	99.03	103	1	0	conserved hypothetical protein 103
1659511	208643	99.03	206	2	0	protein of unknown function DUF306, Meta and HsIJ
1661234	206508	99.03	308	3	0	conserved hypothetical protein
1662286	208953	99.03	719	7	0	signal transduction histidine kinase, nitrogen specific, NtrB
1660556	207370	99.04	312	3	0	conserved hypothetical protein
1659345	208824	99.05	419	4	0	aromatic amino acid transporter
1659369	208792	99.05	420	4	0	conserved hypothetical protein
1659586	208562	99.05	315	3	0	aminotransferase, class IV
1660854	207032	99.05	105	1	0	conserved hypothetical protein
1660429	207567	99.06	213	2	0	thiamine biosynthesis protein ThiF
1660449	207545	99.06	318	3	0	conserved hypothetical protein
1661532	206183	99.06	106	1	0	type IV pilus assembly PilZ
1661573	206136	99.06	213	2	0	conserved hypothetical protein
1662024	209219	99.06	213	2	0	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit
1662248	208985	99.06	213	2	0	transcriptional regulator, TetR family
1660251	207774	99.07	322	1	2	respiratory-chain NADH dehydrogenase, subunit 1
1660810	207077	99.07	214	2	0	conserved hypothetical protein
1660993	206830	99.07	430	4	0	conserved hypothetical protein
1661064	206756	99.07	107	1	0	ribosomal protein L24
1661602	206104	99.07	643	6	0	PAS/PAC sensor signal transduction histidine kinase
1661617	206085	99.07	323	3	0	Serine O-acetyltransferase
1661934	207510	99.07	324	3	0	ATPase associated with various cellular activities, AAA_5
1662211	209019	99.07	323	3	0	NAD-dependent epimerase/dehydratase
1659501	208655	99.08	218	2	0	nitroreductase
1659577	208571	99.08	217	2	0	protein of unknown function DUF208
1660222	207806	99.08	218	2	0	response regulator receiver protein
1660385	207615	99.08	217	2	0	protein of unknown function DUF1121
1660615	207310	99.08	109	1	0	Septum formation initiator
1659327	408366	99.09	110	1	0	Excinuclease ABC, C subunit domain protein
1659402	208759	99.09	547	5	0	small GTP-binding protein
1659798	208285	99.09	439	4	0	extracellular solute-binding protein, putative
1659642	208501	99.1	221	2	0	phage shock protein A, PspA
1659989	208028	99.1	222	2	0	Ribulose-phosphate 3-epimerase
1660379	207621	99.1	333	3	0	glyceraldehyde-3-phosphate dehydrogenase, type I
1660425	207572	99.1	223	2	0	putative transcriptional regulator, Crp/Fnr family
1660463	207528	99.1	663	6	0	methionyl-tRNA synthetase
1661034	206785	99.1	335	3	0	periplasmic solute binding protein
1661222	206520	99.1	221	2	0	phosphate uptake regulator, PhoU
1662273	208960	99.1	111	1	0	branched-chain amino acid transport
1659908	208109	99.11	225	2	0	conserved hypothetical protein
1659924	206932	99.11	112	1	0	conserved hypothetical protein
1660383	207617	99.11	224	2	0	dTMP kinase
1660433	207561	99.11	225	2	0	conserved hypothetical protein
1660886	207001	99.11	449	4	0	AMP-binding protein
1661560	206153	99.11	224	2	0	conserved hypothetical protein
1661766	209433	99.11	1015	9	0	DNA polymerase I
1659624	208519	99.12	453	4	0	acylneuraminate cytidyltransferase
1660430	207566	99.12	226	2	0	thiamine-phosphate pyrophosphorylase
1661634	408298	99.12	679	6	0	methyl-accepting chemotaxis sensory transducer
1662039	209207	99.12	456	4	0	conserved hypothetical protein
1660416	207582	99.13	458	4	0	sigma54 specific transcriptional regulator, Fis family
1661402	206325	99.13	458	4	0	RNA modification enzyme, MiaB family
1661507	206211	99.13	115	1	0	protein of unknown function DUF583



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1661516	206199	99.13	115	1	0	conserved hypothetical protein
1661704	209510	99.13	346	3	0	Rhodanese domain protein
1662170	209066	99.13	345	3	0	glycosyl transferase, family 2
1660593	207332	99.14	233	2	0	conserved hypothetical protein
1660709	207135	99.14	116	1	0	preprotein translocase, SecE subunit
1661082	206735	99.14	232	2	0	protein of unknown function DUF45
1661278	206462	99.14	232	2	0	cytidylate kinase
1661692	209524	99.14	233	2	0	response regulator receiver protein
1661724	209478	99.14	467	4	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661847	209345	99.14	116	1	0	conserved hypothetical protein
1659823	208256	99.15	351	3	0	cobalamin (vitamin B12) biosynthesis CbiD protein
1660628	207295	99.15	354	3	0	conserved hypothetical protein
1660692	207223	99.15	235	2	0	lipoprotein, putative
1661046	206774	99.15	351	3	0	selenide, water dikinase
1661420	206306	99.15	118	1	0	transcriptional regulator, TraR/DksA family
1662256	208977	99.15	352	3	0	OmpA/MotB domain protein
1659328	208835	99.16	239	2	0	beta-lactamase domain protein
1660111	207891	99.16	359	3	0	hydrogenase, putative
1660928	206902	99.16	238	2	0	putative chemotaxis phosphatase, CheZ
1661270	206470	99.16	238	2	0	conserved hypothetical protein
1661705	209508	99.16	359	3	0	Integral membrane protein TerC
1659791	208294	99.17	120	1	0	regulatory protein, ArsR
1659865	208156	99.17	120	1	0	6-pyruvoyl tetrahydropterin synthase and hypothetical protein
1660116	207886	99.17	362	3	0	histidine kinase
1660311	207696	99.17	120	1	0	conserved hypothetical protein
1661118	206695	99.17	362	3	0	glycosyl transferase, family 9
1661269	206471	99.17	480	4	0	pyridine nucleotide-disulphide oxidoreductase dimerisation region
1661931	207507	99.17	121	1	0	conserved hypothetical protein
1662228	209005	99.17	360	3	0	conserved hypothetical protein
1659419	208741	99.18	368	3	0	conserved hypothetical protein
1659861	208161	99.18	245	2	0	conserved hypothetical protein
1660247	207778	99.18	366	3	0	NADH dehydrogenase (ubiquinone)
1660260	207761	99.18	244	2	0	protein of unknown function DUF81
1660294	207716	99.18	122	1	0	conserved hypothetical protein
1660462	207530	99.18	487	4	0	PSP1 domain protein
1661052	206768	99.18	122	1	0	ribosomal protein S13
1661217	206526	99.18	368	3	0	thiamine biosynthesis protein
1661247	206494	99.18	367	3	0	glycosyl transferase, group 1
1662016	209227	99.18	368	3	0	aminoglycoside phosphotransferase
1659267	208905	99.19	124	1	0	diacylglycerol kinase
1659296	208871	99.19	123	1	0	conserved hypothetical protein
1660242	207783	99.19	248	2	0	monofunctional biosynthetic peptidoglycan transglycosylase
1660550	207378	99.19	124	1	0	holo-acyl-carrier-protein synthase
1660641	207281	99.19	246	2	0	conserved hypothetical protein
1660837	207050	99.19	124	1	0	CrcB protein
1661211	206532	99.19	247	2	0	protein of unknown function DUF375
1661428	206297	99.19	247	2	0	undecaprenyl diphosphate synthase
1659692	208445	99.2	250	2	0	phosphoglycerate mutase 1 family
1659737	208402	99.2	125	1	0	protein of unknown function DUF1078 domain protein
1659882	208134	99.2	377	3	0	glycosyl transferase, group 1
1660228	207800	99.2	249	2	0	6-phosphogluconolactonase
1660252	207772	99.2	1253	10	0	NADH dehydrogenase (quinone)
1660991	206832	99.2	377	3	0	conserved hypothetical protein
1661221	206521	99.2	249	2	0	conserved hypothetical protein
1661277	206463	99.2	373	3	0	histidinol-phosphate aminotransferase
1661572	206137	99.2	376	3	0	Extracellular ligand-binding receptor
1661998	209245	99.2	250	2	0	flagellar assembly protein FliH, putative
1662027	209216	99.2	373	3	0	A/G-specific adenine glycosylase
1662263	208970	99.2	249	2	0	RNA methyltransferase, TrmH family, group 3
1659310	208853	99.21	127	1	0	small multidrug resistance protein
1659495	208660	99.21	126	1	0	lipoprotein, putative
1659518	208632	99.21	252	2	0	3-deoxy-D-manno-octulosonate cytidyltransferase
1659526	208624	99.21	630	5	0	diguanylate cyclase
1659557	208593	99.21	253	2	0	Redoxin domain protein
1659608	208536	99.21	1140	8	1	multi-sensor hybrid histidine kinase
1659988	208029	99.21	127	1	0	putative transcriptional regulator, MerR family
1661272	206468	99.21	254	2	0	conserved hypothetical protein
1661315	206421	99.21	127	1	0	CutA1 divalent ion tolerance protein
1659462	208695	99.22	258	2	0	ubiquinone/menaquinone biosynthesis methyltransferases
1659825	208254	99.22	257	2	0	precorrin-4 C11-methyltransferase
1661025	206794	99.22	129	1	0	6-pyruvoyl tetrahydropterin synthase and hypothetical protein
1661425	206300	99.22	255	2	0	glycosyl transferase, family 2
1661802	209391	99.22	255	2	0	conserved hypothetical protein

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1662237	208996	99.22	511	4	0	conserved hypothetical protein
1659415	208745	99.23	390	3	0	aminotransferase, class I and II
1659620	208523	99.23	392	3	0	DegT/DnrJ/EryC1/StrS aminotransferase
1659725	208415	99.23	392	3	0	iron-containing alcohol dehydrogenase
1660349	207651	99.23	517	4	0	phage portal protein, lambda family
1660486	207451	99.23	130	1	0	conserved hypothetical protein
1661054	206766	99.23	259	2	0	methionine aminopeptidase, type I
1661248	206493	99.23	390	3	0	aminotransferase, class I and II
1661422	206303	99.23	259	2	0	5-carboxymethyl-2-hydroxyimuconate delta-isomerase
1661648	209577	99.23	521	4	0	conserved hypothetical protein
1661660	209561	99.23	130	1	0	conserved hypothetical protein
1661760	209439	99.23	130	1	0	conserved hypothetical protein
1661768	209431	99.23	389	3	0	Serine--glyoxylate transaminase
1661837	209355	99.23	390	3	0	carboxynorspermidine decarboxylase
1661949	209296	99.23	259	2	0	putative 4-amino-4-deoxychorismate lyase
1659383	208779	99.24	132	1	0	protein of unknown function UPF0150
1659991	208026	99.24	393	3	0	Phosphoglycerate kinase
1660695	207151	99.24	131	1	0	conserved hypothetical protein
1661414	206313	99.24	262	2	0	amidohydrolase 2
1661472	206250	99.24	393	3	0	arginine biosynthesis bifunctional protein ArgJ
1661653	209571	99.24	524	4	0	Nitrite reductase (cytochrome; ammonia-forming)
1661725	209477	99.24	262	2	0	Xylose isomerase domain protein TIM barrel
1659546	208606	99.25	401	3	0	membrane protein involved in aromatic hydrocarbon degradation
1659629	208514	99.25	265	2	0	conserved hypothetical protein
1659660	208481	99.25	398	3	0	response regulator receiver sensor signal transduction histidine kinase
1661112	206702	99.25	267	2	0	peptidase A24A domain protein
1661127	206685	99.25	267	2	0	protein of unknown function DUF140
1661391	206336	99.25	534	4	0	ferredoxin
1661412	206315	99.25	401	3	0	MltA domain protein
1661767	209432	99.25	398	3	0	conserved hypothetical protein
1662297	208939	99.25	400	3	0	conserved hypothetical protein
1659915	208102	99.26	135	1	0	conserved hypothetical protein
1660082	207926	99.26	135	1	0	hypothetical protein
1660404	207595	99.26	272	2	0	SAF domain
1660892	206995	99.26	537	4	0	putative PAS/PAC sensor protein
1661133	206679	99.26	135	1	0	conserved hypothetical protein
1661341	206393	99.26	1354	10	0	protein of unknown function DUF748
1661413	206314	99.26	136	1	0	thioesterase superfamily protein
1661625	206075	99.26	408	3	0	peptidase U32
1661993	209250	99.26	136	1	0	flagellar basal-body rod protein FlgB
1662044	209200	99.26	408	3	0	conserved hypothetical protein
1662208	209022	99.26	816	6	0	glycosyl transferase, group 1
1659995	208021	99.27	137	1	0	cytochrome c, class III
1660029	207987	99.27	274	2	0	histidinol phosphate phosphatase HisJ family
1660877	207011	99.27	964	7	0	metal dependent phosphohydrolase
1661251	206490	99.27	273	2	0	ABC transporter related
1661255	206485	99.27	137	1	0	cytochrome c-type biogenesis protein CcmE
1661663	209555	99.27	275	2	0	ABC transporter related
1659299	208868	99.28	138	1	0	TadE family protein
1659368	208793	99.28	839	6	0	PAS/PAC sensor hybrid histidine kinase
1660208	207820	99.28	139	1	0	Nucleoside-diphosphate kinase
1660507	207425	99.28	277	2	0	TPR repeat-containing protein
1660600	207323	99.28	695	5	0	methyl-accepting chemotaxis sensory transducer
1661038	206781	99.28	276	2	0	lipoprotein, putative
1661738	209463	99.28	138	1	0	conserved hypothetical protein
1659413	208747	99.29	140	1	0	conserved hypothetical protein
1659644	208499	99.29	140	1	0	phage shock protein C, PspC
1659728	208412	99.29	422	3	0	dihydroorotase, multifunctional complex type
1659779	208309	99.29	421	3	0	putative PAS/PAC sensor protein
1659903	208114	99.29	282	2	0	extracellular solute-binding protein, family 3
1660112	207890	99.29	283	2	0	oxidoreductase FAD/NAD(P)-binding domain protein
1660186	207845	99.29	280	2	0	putative signal transduction protein
1660713	207132	99.29	280	2	0	lipid A biosynthesis acyltransferase
1660816	207072	99.29	140	1	0	conserved hypothetical protein
1661609	206093	99.29	423	3	0	O-antigen polymerase
1661700	209516	99.29	141	1	0	CreA family protein
1659522	208628	99.3	573	4	0	fumarate reductase/succinate dehydrogenase flavoprotein domain protein
1660025	207991	99.3	286	2	0	peptidase M48, Ste24p
1660645	207277	99.3	426	3	0	cytochrome c, monohaem
1660859	207026	99.3	286	2	0	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
1660866	207020	99.3	284	2	0	pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit
1660941	206891	99.3	569	4	0	CgeB family protein

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1660978	206848	99.3	142	1	0	conserved hypothetical protein
1661032	206787	99.3	574	4	0	prolyl-tRNA synthetase
1661330	206405	99.3	287	2	0	4-hydroxybenzoate polyprenyltransferase, putative
1659583	208565	99.31	144	1	0	protein of unknown function DUF606
1659857	208165	99.31	290	2	0	binding-protein-dependent transport systems inner membrane component
1660250	207775	99.31	144	1	0	NADH ubiquinone oxidoreductase, 20 kDa subunit
1660505	207428	99.31	865	6	0	multi-sensor signal transduction histidine kinase
1660821	207067	99.31	435	3	0	Phenylacetate--CoA ligase
1661007	206812	99.31	290	2	0	conserved hypothetical protein
1661014	206805	99.31	291	2	0	dTDP-4-dehydrorhamnose reductase
1661308	206428	99.31	291	2	0	conserved hypothetical protein
1661380	206349	99.31	144	1	0	conserved hypothetical protein
1661494	206223	99.31	436	3	0	Histidinol dehydrogenase
1659486	208668	99.32	296	2	0	signal peptide peptidase SppA, 36K type
1659525	208625	99.32	589	4	0	cytochrome c, class I
1660632	207290	99.32	442	3	0	amidohydrolase
1660738	207106	99.32	146	1	0	lipoprotein, putative
1660925	206906	99.32	440	3	0	Shikimate/quinate 5-dehydrogenase
1660938	206894	99.32	146	1	0	putative signal transduction histidine kinase
1661101	206713	99.32	147	1	0	conserved hypothetical protein
1661298	206438	99.32	294	2	0	protein of unknown function DUF6, transmembrane
1662236	208997	99.32	1467	10	0	conserved hypothetical protein
1660805	207082	99.33	149	1	0	putative PTS IIA-like nitrogen-regulatory protein PtsN
1661319	206416	99.33	449	3	0	RNA modification enzyme, MiaB family
1659561	208589	99.34	303	2	0	conserved hypothetical protein
1659792	208293	99.34	152	1	0	conserved hypothetical protein
1659994	208022	99.34	304	2	0	hydrogenase (NiFe) small subunit HydA
1660217	207811	99.34	905	6	0	heavy metal translocating P-type ATPase
1660624	207300	99.34	304	2	0	biotin--acetyl-CoA-carboxylase ligase
1660733	207112	99.34	904	6	0	Polynucleotide adenylyltransferase region
1661806	209387	99.34	603	4	0	Cl- channel, voltage-gated family protein
1661955	209291	99.34	305	2	0	conserved hypothetical protein
1662269	208964	99.34	151	1	0	conserved hypothetical protein
1659813	208268	99.35	306	2	0	protein of unknown function DUF6, transmembrane
1660038	207974	99.35	309	2	0	phosphate ABC transporter, inner membrane subunit PstA
1660196	207836	99.35	153	1	0	deoxyuridine 5'-triphosphate nucleotidohydrolase Dut
1660360	207640	99.35	155	1	0	conserved hypothetical protein
1660376	207627	99.35	464	3	0	protein of unknown function DUF21
1660432	207562	99.35	306	2	0	protein of unknown function DUF6, transmembrane
1660484	207453	99.35	462	3	0	DEAD/DEAH box helicase domain protein
1660849	207037	99.35	155	1	0	Redoxin domain protein
1661417	206310	99.35	154	1	0	conserved hypothetical protein
1661621	206080	99.35	153	1	0	heat shock protein Hsp20
1660629	207293	99.36	629	4	0	glucose inhibited division protein A
1660942	206890	99.36	467	3	0	glycosyl transferase, family 9
1661469	206254	99.36	471	3	0	D-lactate dehydrogenase (cytochrome)
1661586	206121	99.36	472	3	0	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase
1661851	209341	99.36	468	3	0	cobyrimic acid a,c-diamide synthase
1659729	208411	99.37	317	2	0	aspartate carbamoyltransferase
1659755	208336	99.37	473	3	0	sigma54 specific transcriptional regulator, Fis family
1659904	208113	99.37	159	1	0	Tetratricopeptide TPR_2 repeat protein
1660288	207722	99.37	159	1	0	tRNA/rRNA methyltransferase (SpoU)
1660568	207357	99.37	315	2	0	porphobilinogen deaminase
1660583	207342	99.37	316	2	0	chaperone DnaJ domain protein
1660617	207308	99.37	318	2	0	lipoprotein, putative
1661124	206688	99.37	317	2	0	malonyl CoA-acyl carrier protein transacylase
1661206	408309	99.37	477	3	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661547	206167	99.37	158	1	0	conserved hypothetical protein
1661734	209467	99.37	159	1	0	phosphatidylglycerophosphatase A
1660289	207721	99.38	320	2	0	cobalamin biosynthesis protein CobD
1660293	207717	99.38	325	2	0	alpha/beta hydrolase fold
1660399	207600	99.38	321	2	0	type II secretion system protein
1660434	207560	99.38	480	3	0	putative transcriptional regulator, GntR family
1660536	207395	99.38	162	1	0	conserved hypothetical protein
1660547	207381	99.38	162	1	0	protein of unknown function UPF0079
1660694	207152	99.38	324	2	0	glutamyl-tRNA synthetase, class Ic
1660936	206896	99.38	162	1	0	D-tyrosyl-tRNA(Tyr) deacylase
1661000	206819	99.38	162	1	0	acetolactate synthase, small subunit
1661195	206609	99.38	804	5	0	methyl-accepting chemotaxis sensory transducer
1661279	206461	99.38	323	2	0	conserved hypothetical protein
1659581	208567	99.39	659	4	0	ABC transporter related

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1659723	208417	99.39	164	1	0	putative prophage repressor
1659965	208054	99.39	330	2	0	biotin--acetyl-CoA-carboxylase ligase
1660976	206852	99.39	491	3	0	Radical SAM domain protein
1661273	206467	99.39	164	1	0	CinA domain protein
1661430	206295	99.39	489	3	0	Aromatic-L-amino-acid decarboxylase
1661603	206103	99.39	488	3	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661682	209535	99.39	652	4	0	methyl-accepting chemotaxis sensory transducer
1662025	209217	99.39	164	1	0	Peptidylprolyl isomerase
1662032	209211	99.39	326	2	0	transcription activator, effector binding
1659576	208572	99.4	497	3	0	putative oxygen-independent coproporphyrinogen III oxidase
1659717	208423	99.4	335	2	0	lipoprotein, putative
1659902	208115	99.4	1000	6	0	multi-sensor hybrid histidine kinase
1660238	207789	99.4	672	4	0	sodium/hydrogen exchanger
1660440	207553	99.4	833	5	0	PAS/PAC sensor signal transduction histidine kinase
1660596	207328	99.4	331	2	0	diguanylate cyclase
1660980	206846	99.4	167	1	0	ATP:corrinoic adenosyltransferase BtuR/CobO/CobP
1661618	206084	99.4	332	2	0	dihydrouridine synthase, DuS
1661791	209403	99.4	332	2	0	anthranilate phosphoribosyltransferase
1661938	207514	99.4	331	2	0	conserved hypothetical protein
1662177	209056	99.4	1171	7	0	transcriptional regulator, Fis family
1662229	209004	99.4	334	2	0	glycosyl transferase, family 2
1659975	208043	99.41	512	3	0	PAS/PAC sensor signal transduction histidine kinase
1660254	207770	99.41	170	1	0	conserved hypothetical protein
1660903	206982	99.41	170	1	0	protein of unknown function DUF395, YeeE/YedE
1661575	206132	99.41	338	2	0	TRAP dicarboxylate transporter, DctP subunit
1661707	209506	99.41	338	2	0	glyceraldehyde-3-phosphate dehydrogenase, type I
1661997	209246	99.41	338	2	0	flagellar motor switch protein FlhG
1659262	208912	99.42	173	1	0	zinc resistance-associated protein
1659590	208558	99.42	343	2	0	conserved hypothetical protein
1659821	208258	99.42	173	1	0	Rhodanese domain protein
1659926	208089	99.42	521	3	0	Hemerythrin HHE cation binding domain protein
1660125	207874	99.42	343	2	0	binding-protein-dependent transport systems inner membrane component
1660255	207768	99.42	516	3	0	conserved hypothetical protein
1660382	207618	99.42	345	2	0	metal dependent phosphohydrolase
1660659	207263	99.42	171	1	0	conserved hypothetical protein
1660864	207022	99.42	171	1	0	transcriptional regulator, CarD family
1660955	206874	99.42	868	5	0	peptidase M16 domain protein
1661173	206634	99.42	172	1	0	lipoprotein, putative
1661681	209536	99.42	173	1	0	putative CheW protein
1662260	208973	99.42	173	1	0	flagellar biosynthesis protein, FlhO, putative
1659346	208823	99.43	175	1	0	conserved hypothetical protein
1659475	208681	99.43	349	2	0	ABC transporter related
1659609	208534	99.43	353	2	0	metal dependent phosphohydrolase
1660306	207702	99.43	348	2	0	GTPase EngC
1660503	207430	99.43	697	4	0	CheA signal transduction histidine kinases
1661147	206661	99.43	175	1	0	conserved hypothetical protein
1661166	206641	99.43	176	1	0	CMP/dCMP deaminase, zinc-binding
1661444	206281	99.43	176	1	0	putative transcriptional regulator, AsnC family
1659387	208775	99.44	179	1	0	HPP family protein+B94
1659572	208577	99.44	1080	6	0	multi-sensor hybrid histidine kinase
1661186	206621	99.44	356	2	0	response regulator receiver modulated metal dependent phosphohydrolase
1659349	208820	99.45	547	3	0	thiamine pyrophosphate enzyme TPP binding domain protein
1659393	208769	99.45	541	3	0	RND efflux system, outer membrane lipoprotein, NodT family
1659407	208753	99.45	365	2	0	flagellar biosynthesis protein FlhF, putative
1659505	208651	99.45	546	3	0	FAD dependent oxidoreductase
1659597	208550	99.45	550	3	0	methyl-accepting chemotaxis sensory transducer
1659656	208485	99.45	183	1	0	CheD, stimulates methylation of MCP proteins
1659741	208398	99.45	182	1	0	BioY protein
1659868	208149	99.45	183	1	0	conserved hypothetical protein
1659946	208072	99.45	366	2	0	peptidase M20
1660175	207859	99.45	543	3	0	N-acetylmuramoyl-L-alanine amidase
1660388	207612	99.45	183	1	0	conserved hypothetical protein
1660654	207268	99.45	362	2	0	glycosyl transferase, group 1
1660701	207143	99.45	362	2	0	glycine cleavage system T protein
1660979	206847	99.45	362	2	0	Radical SAM domain protein
1661282	206458	99.45	541	3	0	pseudouridine synthase, RluA family
1661510	206205	99.45	183	1	0	ATP synthase F1, delta subunit
1662247	208986	99.45	366	2	0	efflux transporter, RND family, MFP subunit
1659271	208900	99.46	554	3	0	dihydroxy-acid dehydratase
1659615	208528	99.46	185	1	0	Methyltransferase type 11
1659920	208097	99.46	184	1	0	conserved hypothetical protein

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1660442	207552	99.46	367	2	0	response regulator receiver modulated CheB methyltransferase
1660492	207445	99.46	367	2	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1660742	207100	99.46	371	2	0	permease
1660826	207061	99.46	559	3	0	NAD+ synthetase
1661427	206298	99.46	186	1	0	ribosome recycling factor
1661521	206194	99.46	368	2	0	Serine--pyruvate transaminase
1661649	209575	99.46	186	1	0	transcriptional regulator, TetR family
1662048	209196	99.46	184	1	0	conserved hypothetical protein
1662176	209057	99.46	370	2	0	ABC-2 type transporter
1659494	208661	99.47	567	3	0	sigma54 specific transcriptional regulator, Fis family
1659612	208531	99.47	377	2	0	Radical SAM domain protein
1660272	207741	99.47	187	1	0	Holliday junction DNA helicase RuvA
1660405	207594	99.47	188	1	0	peptidase A24A, prepilin type IV
1660494	207441	99.47	187	1	0	Sel1 domain protein repeat-containing protein
1660540	207391	99.47	566	3	0	nickel-dependent hydrogenase, large subunit
1661016	206803	99.47	376	2	0	lipid-A-disaccharide synthase
1661992	209252	99.47	187	1	0	TPR repeat-containing protein
1662230	209003	99.47	377	2	0	DegT/DnrJ/EryC1/StrS aminotransferase
1662299	208937	99.47	188	1	0	Tripartite ATP-independent periplasmic transporter, DctQ component
1659401	408364	99.48	773	4	0	Pyruvate, water dikinase
1659445	208713	99.48	386	2	0	glycosyl transferase, group 1
1659891	208127	99.48	192	1	0	Tetratricopeptide TPR_2 repeat protein
1659976	208042	99.48	386	2	0	iron-containing alcohol dehydrogenase
1660844	207043	99.48	580	3	0	methyl-accepting chemotaxis sensory transducer
1661103	206711	99.48	573	3	0	type II secretion system protein E
1661387	206340	99.48	194	1	0	conserved hypothetical protein
1661810	209384	99.48	381	2	0	GDP-mannose 4,6-dehydratase
1661817	209377	99.48	575	3	0	adenine deaminase
1659952	208065	99.49	394	2	0	amidohydrolase
1660457	207536	99.49	984	5	0	conserved hypothetical protein
1660656	207266	99.49	389	2	0	conserved hypothetical protein
1661261	206479	99.49	198	1	0	Tetratricopeptide domain protein
1661266	206474	99.49	198	1	0	Imidazoleglycerol-phosphate dehydratase
1661368	206363	99.49	391	2	0	histidine kinase
1661615	206087	99.49	394	2	0	aminotransferase, class V
1662064	209183	99.49	195	1	0	conserved hypothetical protein
1659403	208758	99.5	200	1	0	Phosphoribosylaminoimidazolecarboxamideformyltransferase
1659437	208721	99.5	201	1	0	recombination protein RecR
1659452	208706	99.5	402	2	0	beta-lactamase domain protein
1659720	208420	99.5	201	1	0	protein of unknown function DUF204
1659745	208394	99.5	397	2	0	iron-containing alcohol dehydrogenase
1659987	208030	99.5	798	4	0	phenylalanyl-tRNA synthetase, beta subunit
1659997	208019	99.5	200	1	0	conserved hypothetical protein
1660575	207350	99.5	800	4	0	methyl-accepting chemotaxis sensory transducer
1660605	207319	99.5	202	1	0	conserved hypothetical protein
1660893	206992	99.5	807	4	0	MscS Mechanosensitive ion channel
1661339	206396	99.5	997	5	0	Glu/Leu/Phe/Val dehydrogenase, C terminal
1661445	206280	99.5	399	2	0	protein of unknown function UPF0027
1661688	209528	99.5	797	4	0	CoA-binding domain protein
1661816	209378	99.5	398	2	0	PhoH family protein
1662018	209224	99.5	202	1	0	lipoprotein, putative
1662162	209076	99.5	200	1	0	rfaE bifunctional protein
1659275	208894	99.51	610	3	0	aspartyl-tRNA synthetase
1659507	208647	99.51	205	1	0	protein of unknown function DUF330
1659767	208320	99.51	1012	5	0	formate dehydrogenase, alpha subunit
1659808	208273	99.51	204	1	0	iron-sulfur flavoprotein, putative
1659911	208106	99.51	206	1	0	conserved hypothetical protein
1660684	207233	99.51	410	2	0	small GTP-binding protein
1661249	206492	99.51	204	1	0	cobalamin (vitamin B12) biosynthesis CbiM protein
1661288	206453	99.51	406	2	0	conserved hypothetical protein
1661293	206443	99.51	204	1	0	conserved hypothetical protein
1661302	206434	99.51	407	2	0	peptidase M24
1661474	206246	99.51	205	1	0	NADPH-dependent FMN reductase
1661662	209556	99.51	406	2	0	protein of unknown function DUF140
1659274	208895	99.52	417	2	0	histidyl-tRNA synthetase
1659380	208782	99.52	417	2	0	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
1659459	208699	99.52	207	1	0	conserved hypothetical protein
1659482	208673	99.52	207	1	0	non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family
1659566	208584	99.52	827	4	0	diguanylate cyclase with PAS/PAC sensor
1659648	208495	99.52	419	2	0	3-isopropylmalate dehydratase, large subunit
1659757	208333	99.52	828	4	0	Formate C-acetyltransferase
1659851	208171	99.52	207	1	0	protein of unknown function UPF0126
1659930	208083	99.52	626	3	0	methyl-accepting chemotaxis sensory transducer

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1660570	207355	99.52	208	1	0	phosphoheptose isomerase
1660714	207131	99.52	208	1	0	protein of unknown function DUF374
1661050	206770	99.52	208	1	0	ribosomal protein S4
1661099	206715	99.52	622	3	0	conserved hypothetical protein
1661130	206682	99.52	210	1	0	toluene tolerance family protein
1661280	206460	99.52	419	2	0	uracil-xanthine permease
1661281	206459	99.52	208	1	0	uracil phosphoribosyltransferase
1661331	206404	99.52	421	2	0	metal dependent phosphohydrolase
1661800	209393	99.52	416	2	0	diguanylate phosphodiesterase
1661820	209374	99.52	1041	5	0	acriflavin resistance protein
1661881	209309	99.52	832	4	0	pyruvate ferredoxin/ferredoxin oxidoreductase
1659347	208822	99.53	215	1	0	channel protein, hemolysin III family
1659430	208728	99.53	426	2	0	Phosphoribosylaminoimidazolecarboxamideformyltransferase
1659433	208725	99.53	426	2	0	Adenylosuccinate synthase
1659544	208609	99.53	215	1	0	conserved hypothetical protein
1659735	208405	99.53	1070	5	0	Tetratricopeptide TPR_2 repeat protein
1659780	208306	99.53	633	3	0	heavy metal translocating P-type ATPase
1660249	207776	99.53	211	1	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660283	207727	99.53	640	3	0	1,4-alpha-glucan branching enzyme
1660678	207240	99.53	214	1	0	3,4-dihydroxy-2-butanone 4-phosphate synthase
1660728	207117	99.53	215	1	0	putative transaldolase
1661019	206800	99.53	215	1	0	HAD-superfamily hydrolase, subfamily IA, variant 1
1661253	206488	99.53	212	1	0	histidinol-phosphate phosphatase family protein
1661267	206473	99.53	213	1	0	lipoprotein, putative
1661409	206318	99.53	424	2	0	Homoserine dehydrogenase
1661541	206173	99.53	212	1	0	ABC transporter related
1661804	209389	99.53	1070	5	0	UvrD/REP helicase
1661973	209273	99.53	213	1	0	Haloacid dehalogenase domain protein hydrolase
1659651	208492	99.54	217	1	0	phosphatidylserine decarboxylase related protein
1659864	208157	99.54	216	1	0	conserved hypothetical protein
1659944	208074	99.54	216	1	0	two component transcriptional regulator, LuxR family
1660302	207708	99.54	216	1	0	conserved hypothetical protein
1660448	408349	99.54	1089	5	0	CheA signal transduction histidine kinases
1660722	207123	99.54	216	1	0	GTP-binding protein, HSR1-related
1661257	206483	99.54	216	1	0	ABC transporter related
1661795	209399	99.54	439	2	0	3-phosphoshikimate 1-carboxyvinyltransferase
1662045	209199	99.54	219	1	0	conserved hypothetical protein
1662201	209029	99.54	649	3	0	TonB-dependent receptor, plug
1659424	208736	99.55	884	4	0	Pyruvate, water dikinase
1659873	208143	99.55	223	1	0	transcriptional regulator, GntR family
1660130	207869	99.55	222	1	0	conserved hypothetical protein
1660316	207690	99.55	223	1	0	YheO domain protein
1660392	207607	99.55	220	1	0	conserved hypothetical protein
1660529	207402	99.55	223	1	0	adenylate kinase
1660608	207317	99.55	440	2	0	peptidase M23B
1660674	207246	99.55	221	1	0	protein of unknown function DUF162
1660801	207086	99.55	223	1	0	conserved hypothetical protein
1661235	206507	99.55	220	1	0	conserved hypothetical protein
1661350	206383	99.55	445	2	0	molybdenum cofactor synthesis domain
1661545	206169	99.55	665	3	0	PAS/PAC sensor signal transduction histidine kinase
1661556	206158	99.55	884	4	0	valyl-tRNA synthetase
1661592	206114	99.55	223	1	0	type IV pilus assembly PilZ
1661818	209376	99.55	443	2	0	protein of unknown function DUF1063
1661867	209325	99.55	224	1	0	polar amino acid ABC transporter, inner membrane subunit
1662173	209060	99.55	220	1	0	HAD-superfamily hydrolase, subfamily IA, variant 3
1659263	208910	99.56	679	3	0	signal transduction histidine kinase, nitrogen specific, NtrB
1659264	208909	99.56	459	2	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659848	208174	99.56	227	1	0	two component transcriptional regulator, LuxR family
1660100	207904	99.56	680	3	0	Radical SAM N-terminal domain protein
1660464	207526	99.56	226	1	0	conserved hypothetical protein
1660573	207352	99.56	225	1	0	conserved hypothetical protein
1660923	206908	99.56	225	1	0	siroheme synthase
1661108	206706	99.56	227	1	0	conserved hypothetical protein
1661140	206672	99.56	906	4	0	metal dependent phosphohydrolase
1661440	206286	99.56	227	1	0	lipoprotein, putative
1661523	206191	99.56	454	2	0	Hydroxypyruvate reductase
1661597	206109	99.56	453	2	0	Phosphomannomutase
1661962	209284	99.56	227	1	0	acylneuraminate cytidyltransferase
1662174	209059	99.56	452	2	0	putative PAS/PAC sensor protein
1659427	208732	99.57	470	2	0	threonine synthase
1659442	208716	99.57	462	2	0	lipoprotein, putative
1659489	208665	99.57	230	1	0	conserved hypothetical protein
1659512	208641	99.57	231	1	0	metal dependent phosphohydrolase

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1659747	208392	99.57	469	2	0	L-seryl-tRNA(Sec) selenium transferase
1659778	208310	99.57	231	1	0	regulatory protein GntR, HTH
1659970	208049	99.57	463	2	0	glutamyl-tRNA synthetase
1660133	207866	99.57	230	1	0	helix-turn-helix- domain containing protein, AraC type
1660201	207828	99.57	233	1	0	polar amino acid ABC transporter, inner membrane subunit
1660508	207424	99.57	234	1	0	nicotinate (nicotinamide) nucleotide adenylyltransferase
1660510	207422	99.57	231	1	0	conserved hypothetical protein
1660698	207146	99.57	235	1	0	glycosyl transferase, group 2 family protein
1661492	206225	99.57	466	2	0	conserved hypothetical protein
1661563	206150	99.57	468	2	0	amino acid carrier protein
1661600	206106	99.57	232	1	0	putative phage repressor
1661883	209307	99.57	230	1	0	conserved hypothetical protein
1662062	209186	99.57	941	4	0	D-lactate dehydrogenase (cytochrome)
1662126	209114	99.57	233	1	0	molybdate ABC transporter, inner membrane subunit
1662132	209106	99.57	698	3	0	molybdopterin oxidoreductase
1662261	208972	99.57	235	1	0	flagellar biosynthetic protein FlIP
1659269	208903	99.58	238	1	0	cell division ATP-binding protein FtsE
1659432	208726	99.58	481	2	0	Lytic transglycosylase, catalytic
1659598	208547	99.58	717	3	0	protein of unknown function DUF224, cysteine-rich region domain protein
1659607	208537	99.58	472	2	0	putative two component, sigma54 specific, transcriptional regulator, Fis family
1659849	208173	99.58	239	1	0	succinate dehydrogenase and fumarate reductase iron-sulfur protein
1659967	208052	99.58	473	2	0	MATE efflux family protein
1660041	207971	99.58	476	2	0	glutamate synthase (NADPH), homotetrameric
1660219	207809	99.58	479	2	0	UTP--glucose-1-phosphate uridylyltransferase
1660466	207525	99.58	240	1	0	glycosyl transferase, family 2
1661244	206497	99.58	477	2	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659293	208875	99.59	245	1	0	thiamine pyrophosphate enzyme domain protein TPP-binding
1659880	208136	99.59	487	2	0	putative PAS/PAC sensor protein
1660011	208006	99.59	486	2	0	UDP-N-acetylmuramyl-tripeptide synthetases
1660298	207712	99.59	244	1	0	OmpA/MotB domain protein
1660808	207079	99.59	241	1	0	ABC transporter related
1660856	207030	99.59	485	2	0	cysteinyI-tRNA synthetase
1660918	206913	99.59	482	2	0	protease Do
1661139	206673	99.59	243	1	0	protein of unknown function DUF81
1661283	206457	99.59	246	1	0	Rhomboid family protein
1661535	206179	99.59	243	1	0	ABC transporter related
1661979	209265	99.59	973	4	0	multi-sensor signal transduction histidine kinase
1662196	209035	99.59	244	1	0	ABC transporter related
1659374	208787	99.6	247	1	0	succinate dehydrogenase and fumarate reductase iron-sulfur protein
1660270	207744	99.6	247	1	0	protein of unknown function DUF28
1660320	207686	99.6	505	2	0	extracellular solute-binding protein, family 3
1660381	207619	99.6	250	1	0	stationary-phase survival protein SurE
1660636	207286	99.6	251	1	0	glutamate synthase, alpha subunit domain protein
1660890	206997	99.6	250	1	0	Methyltransferase type 11
1660932	206899	99.6	247	1	0	protein of unknown function DUF164
1661110	206704	99.6	249	1	0	conserved hypothetical protein
1661268	206472	99.6	249	1	0	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
1661334	206401	99.6	248	1	0	Lysine exporter protein (LYSE/YGGA)
1661946	209299	99.6	251	1	0	protein of unknown function DUF152
1661953	209292	99.6	247	1	0	conserved hypothetical protein
1662068	209179	99.6	744	3	0	pyruvate phosphate dikinase, PEP/pyruvate-binding
1662255	208978	99.6	252	1	0	MotA/TolQ/ExbB proton channel
1662292	208945	99.6	749	3	0	methyl-accepting chemotaxis sensory transducer
1659378	208783	99.61	257	1	0	exodeoxyribonuclease III
1659417	208743	99.61	508	2	0	integral membrane sensor signal transduction histidine kinase
1659500	208656	99.61	258	1	0	short-chain dehydrogenase/reductase SDR
1659841	208183	99.61	516	2	0	L-lactate permease family protein
1660044	207967	99.61	779	3	0	glycoside hydrolase, family 57
1660450	207544	99.61	257	1	0	Tetratricopeptide TPR_2 repeat protein
1661136	206676	99.61	256	1	0	polar amino acid ABC transporter, inner membrane subunit
1661182	206625	99.61	257	1	0	MazG family protein
1661245	206496	99.61	256	1	0	conserved hypothetical protein
1661250	206491	99.61	256	1	0	cobalt ABC transporter, inner membrane subunit CbiQ
1661633	206065	99.61	256	1	0	precorrin-2 C20-methyltransferase
1661794	209400	99.61	255	1	0	Prephenate dehydrogenase
1661841	209351	99.61	507	2	0	Leucyl aminopeptidase
1661868	209324	99.61	255	1	0	ABC transporter related
1661882	209308	99.61	770	3	0	CoA-binding domain protein
1661966	209280	99.61	512	2	0	polysaccharide biosynthesis protein
1659268	208904	99.62	524	2	0	sulfatase
1659738	208401	99.62	264	1	0	protein of unknown function DUF198

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1659806	208275	99.62	260	1	0	conserved hypothetical protein
1660209	207819	99.62	265	1	0	pyrroline-5-carboxylate reductase
1660427	408350	99.62	265	1	0	thiazole biosynthesis family protein
1660525	207406	99.62	265	1	0	phosphonate ABC transporter, ATPase subunit
1660589	207336	99.62	265	1	0	cyclase family protein
1660726	207119	99.62	265	1	0	putative undecaprenol kinase
1660846	207040	99.62	262	1	0	MJ0042 family finger-like protein
1661411	206316	99.62	526	2	0	signal transduction histidine kinase
1661433	206292	99.62	261	1	0	peptidase M22, glycoprotease
1661606	206099	99.62	261	1	0	extracellular solute-binding protein, family 3
1662240	208993	99.62	265	1	0	conserved hypothetical protein
1662271	208962	99.62	261	1	0	DSBA oxidoreductase
1662294	208942	99.62	263	1	0	prolipoprotein diacylglycerol transferase
1659320	208841	99.63	272	1	0	Oxidoreductase FAD-binding domain protein
1659351	208818	99.63	544	2	0	ferredoxin-dependent glutamate synthase
1659807	208274	99.63	269	1	0	phosphoribosyltransferase
1659979	208038	99.63	269	1	0	putative CoA-substrate-specific enzyme activase
1660104	207900	99.63	270	1	0	extracellular solute-binding protein, family 3
1660179	207855	99.63	267	1	0	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
1660182	207850	99.63	267	1	0	Hydroxyethylthiazole kinase
1660642	207280	99.63	541	2	0	Cytochrome-c oxidase
1660812	207075	99.63	273	1	0	2-dehydro-3-deoxyphosphooctonate aldolase
1660885	207002	99.63	543	2	0	Radical SAM domain protein
1661131	206681	99.63	273	1	0	VacJ family lipoprotein
1661543	206171	99.63	272	1	0	ABC transporter, periplasmic substrate-binding protein
1661582	206125	99.63	819	2	1	methyl-accepting chemotaxis sensory transducer
1662129	209110	99.63	269	1	0	molybdenum ABC transporter, periplasmic molybdate-binding protein
1662212	209018	99.63	267	1	0	conserved hypothetical protein
1662226	209007	99.63	267	1	0	zinc/iron permease
1659259	208916	99.64	275	1	0	peptidase M48, Ste24p
1659270	208901	99.64	277	1	0	protein of unknown function DUF214
1659761	208329	99.64	278	1	0	amidohydrolase 2
1659950	208067	99.64	550	2	0	diguanylate cyclase
1660180	207853	99.64	274	1	0	protein of unknown function DUF1009
1660185	207847	99.64	551	2	0	transcriptional regulator, Fis family
1660277	207735	99.64	551	2	0	AMP-dependent synthetase and ligase
1660286	207724	99.64	550	2	0	Hydantoinase/oxoprolinase
1660516	207416	99.64	276	1	0	thiamine pyrophosphate enzyme domain protein TPP-binding
1660852	207034	99.64	562	2	0	Tetratricopeptide TPR_2 repeat protein
1661464	206260	99.64	275	1	0	Uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin) methyltransferase
1661626	206074	99.64	561	2	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661850	209342	99.64	280	1	0	protein of unknown function DUF6, transmembrane
1662183	209049	99.64	550	2	0	integral membrane sensor signal transduction histidine kinase
1662197	209033	99.64	277	1	0	ABC-3 protein
1662198	209032	99.64	281	1	0	ABC transporter related
1659617	208526	99.65	568	2	0	glycosyl transferase, family 2
1659677	208462	99.65	570	2	0	glutaminyl-tRNA synthetase
1660050	207960	99.65	289	1	0	flocculin repeat domain
1660083	207924	99.65	1413	5	0	diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor(s)
1660203	207826	99.65	283	1	0	ribosomal L11 methyltransferase
1660241	207784	99.65	285	1	0	Substrate-binding region of ABC-type glycine betaine transport system
1660592	207333	99.65	282	1	0	Diaminopimelate epimerase
1660646	207276	99.65	287	1	0	UbiA prenyltransferase
1660953	206876	99.65	864	3	0	Radical SAM domain protein
1661012	206807	99.65	282	1	0	anaerobic cobalt chelatase
1661322	206413	99.65	854	3	0	phosphoenolpyruvate-protein phosphotransferase
1661325	206410	99.65	284	1	0	ABC transporter, periplasmic substrate-binding protein, putative
1661396	206331	99.65	285	1	0	metal dependent phosphohydrolase
1661397	206330	99.65	285	1	0	TPR repeat-containing protein
1661434	206291	99.65	575	2	0	flagellar hook-associated 2 domain protein
1661624	206076	99.65	288	1	0	PHP C-terminal domain protein
1661676	209541	99.65	571	2	0	signal transduction histidine kinase, LytS
1662030	209213	99.65	568	2	0	sulfate transporter
1662154	209084	99.65	853	3	0	Pyruvate, water dikinase
1659477	208677	99.66	295	1	0	VacJ family lipoprotein
1659580	208568	99.66	297	1	0	protein-L-isoaspartate methyltransferase homolog
1659858	208164	99.66	294	1	0	binding-protein-dependent transport systems inner membrane component
1659968	208051	99.66	294	1	0	conserved hypothetical protein



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1660087	207917	99.66	295	1	0	RarD protein, DMT superfamily transporter
1660423	207574	99.66	293	1	0	Cobyrinic acid a,c-diamide synthase
1661114	206700	99.66	586	2	0	phage tail X family protein
1661307	206429	99.66	291	1	0	5,10-methylenetetrahydrofolate reductase
1661467	206257	99.66	590	2	0	phosphoenolpyruvate-protein phosphotransferase
1661505	206213	99.66	595	2	0	Peptidoglycan glycosyltransferase
1661519	206196	99.66	292	1	0	Phosphomethylpyrimidine kinase type-1
1662188	209044	99.66	293	1	0	ATP phosphoribosyltransferase
1662250	208983	99.66	290	1	0	hydroxymethylbutenyl pyrophosphate reductase
1659278	208891	99.67	307	1	0	conserved hypothetical protein
1659319	208842	99.67	307	1	0	dihydroorotate dehydrogenase family protein
1659554	208597	99.67	300	1	0	protein of unknown function DUF6, transmembrane
1659756	208334	99.67	307	1	0	glycyl-radical enzyme activating protein family
1659829	208249	99.67	306	1	0	inner-membrane translocator
1660088	207916	99.67	304	1	0	protein of unknown function DUF6, transmembrane
1660221	207807	99.67	612	2	0	Carboxylase-related protein
1660653	207269	99.67	609	2	0	glycosyl transferase, group 1
1661011	206808	99.67	301	1	0	lipoprotein, putative
1661353	206379	99.67	301	1	0	protein of unknown function DUF6, transmembrane
1661374	206356	99.67	302	1	0	glucose-1-phosphate thymidyltransferase
1661503	206215	99.67	304	1	0	rod shape-determining protein MreC
1661632	206066	99.67	304	1	0	periplasmic binding protein
1661757	209442	99.67	304	1	0	tRNA pseudouridine synthase B
1661957	209289	99.67	607	2	0	diguanylate cyclase with PAS/PAC sensor
1661967	209278	99.67	604	2	0	methyl-accepting chemotaxis sensory transducer
1661972	209272	99.67	301	1	0	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
1661977	209268	99.67	303	1	0	D-alanine--D-alanine ligase
1662000	209243	99.67	306	1	0	transcriptional regulator, LysR family
1662142	209097	99.67	302	1	0	cation diffusion facilitator family transporter
1662241	208992	99.67	302	1	0	conserved hypothetical protein
1659627	208516	99.68	317	1	0	Radical SAM domain protein
1659964	208055	99.68	310	1	0	biotin synthase
1660284	207726	99.68	315	1	0	peptidase T2, asparaginase 2
1660424	207573	99.68	629	2	0	carbon-monoxide dehydrogenase, catalytic subunit
1660535	207397	99.68	938	3	0	isoleucyl-tRNA synthetase
1660616	207309	99.68	317	1	0	conserved hypothetical protein
1661047	206773	99.68	308	1	0	transcriptional regulator, LysR family
1661518	206197	99.68	316	1	0	protein of unknown function DUF81
1661616	206086	99.68	308	1	0	cysteine synthases
1661627	206072	99.68	316	1	0	putative CheW protein
1661651	209573	99.68	315	1	0	Phosphate butyryltransferase
1661748	209452	99.68	310	1	0	FigA family protein
1662182	209050	99.68	312	1	0	phosphonate ABC transporter, periplasmic phosphonate-binding protein
1662249	208984	99.68	317	1	0	putative CheW protein
1662267	208966	99.68	616	2	0	phospholipid/glycerol acyltransferase
1659458	208700	99.69	321	1	0	Trans-hexaprenyltranstransferase
1659621	208522	99.69	327	1	0	Radical SAM domain protein
1659640	208503	99.69	650	2	0	molybdenum cofactor synthesis domain
1660443	207551	99.69	642	2	0	PBS lyase HEAT domain protein repeat-containing protein
1660487	207450	99.69	641	2	0	ABC transporter related
1660520	207412	99.69	637	2	0	degV family protein
1661015	206804	99.69	322	1	0	nucleoside recognition domain protein
1662063	408292	99.69	320	1	0	protein of unknown function DUF81
1662149	209089	99.69	323	1	0	thiamine-monophosphate kinase
1662155	209083	99.69	957	3	0	response regulator receiver protein
1659277	208892	99.7	330	1	0	methionyl-tRNA formyltransferase
1659285	208883	99.7	335	1	0	NAD-dependent epimerase/dehydratase
1659317	208845	99.7	1006	3	0	putative delta-1-pyrroline-5-carboxylate dehydrogenase
1659659	208482	99.7	661	2	0	acetate--CoA ligase
1659733	208407	99.7	333	1	0	conserved hypothetical protein
1659734	208406	99.7	329	1	0	protein of unknown function DUF52
1659759	208331	99.7	336	1	0	TRAP dicarboxylate transporter, DctP subunit
1659782	208304	99.7	336	1	0	ApbE family lipoprotein
1659990	208027	99.7	664	2	0	transketolase
1660048	207963	99.7	330	1	0	tetraacyldisaccharide 4'-kinase
1660475	207463	99.7	331	1	0	conserved hypothetical protein
1660578	207347	99.7	333	1	0	PhoH family protein
1660680	207237	99.7	673	2	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1660831	207056	99.7	677	2	0	excinuclease ABC, B subunit
1661017	206802	99.7	331	1	0	UDP-glucose 4-epimerase
1661174	206633	99.7	329	1	0	DNA polymerase III, delta
1661442	206283	99.7	330	1	0	Porphobilinogen synthase
1662052	209192	99.7	657	2	0	multi-sensor signal transduction histidine kinase

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1662146	209092	99.7	331	1	0	KpsF/GutQ family protein
1662164	209074	99.7	329	1	0	tryptophanyl-tRNA synthetase
1659281	208888	99.71	341	1	0	PfkB domain protein
1659367	208794	99.71	341	1	0	cytochrome d ubiquinol oxidase, subunit II
1659429	208729	99.71	698	2	0	ribonuclease II
1659625	208518	99.71	344	1	0	DegT/DnrJ/EryC1/StrS aminotransferase
1660010	208007	99.71	690	2	0	Peptidoglycan glycosyltransferase
1660081	207927	99.71	344	1	0	Mg <sup>2+</sup> transporter protein, CorA family protein
1660177	207857	99.71	344	1	0	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
1660352	207648	99.71	341	1	0	major head protein
1660386	207614	99.71	690	2	0	succinyl-CoA synthetase, alpha subunit
1660658	207264	99.71	682	2	0	translation elongation factor G
1661486	206233	99.71	346	1	0	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
1661604	206101	99.71	349	1	0	transglycosylase domain protein
1661743	209457	99.71	698	2	0	flagellar hook-associated protein FlgK
1661862	209330	99.71	339	1	0	Radical SAM domain protein
1662136	209103	99.71	689	2	0	methyl-accepting chemotaxis sensory transducer
1662206	209024	99.71	345	1	0	extracellular solute-binding protein, family 1
1659343	208826	99.72	356	1	0	protein of unknown function DUF81
1659359	208803	99.72	357	1	0	Nicotinate-nucleotide--dimethylbenzimidazolephosphoribosyltransferase
1660244	207781	99.72	359	1	0	Methicillin resistance protein
1660468	207471	99.72	714	2	0	sulphate transporter
1660501	207432	99.72	720	2	0	methyl-accepting chemotaxis sensory transducer
1660723	207122	99.72	360	1	0	permease YjgP/YjgQ family protein
1660840	207047	99.72	357	1	0	response regulator receiver modulated CheB methylesterase
1661239	206502	99.72	354	1	0	inner-membrane translocator
1661246	206495	99.72	353	1	0	glycosyl transferase, group 1
1661324	206411	99.72	354	1	0	dihydroxyacetone kinase, DhaK subunit
1661405	206322	99.72	354	1	0	Chorismate synthase
1661432	206293	99.72	354	1	0	putative membrane-associated zinc metalloprotease
1661480	206240	99.72	355	1	0	heat-inducible transcription repressor HrcA
1661517	206198	99.72	356	1	0	TOBE domain protein
1661562	206151	99.72	715	2	0	protein of unknown function DUF255
1661628	206071	99.72	362	1	0	conserved hypothetical protein
1661963	209283	99.72	352	1	0	N-acylneuraminate-9-phosphate synthase
1662150	209088	99.72	719	2	0	UvrD/REP helicase
1662178	209055	99.72	358	1	0	secretion protein HlyD family protein
1659290	208878	99.73	371	1	0	Queuosine biosynthesis protein
1659513	208639	99.73	376	1	0	Serine--pyruvate transaminase
1659661	208480	99.73	374	1	0	response regulator receiver sensor signal transduction histidine kinase
1659816	208263	99.73	375	1	0	Radical SAM domain protein
1659817	208262	99.73	372	1	0	Radical SAM domain protein
1660016	208001	99.73	365	1	0	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
1660397	207602	99.73	371	1	0	TPR repeat-containing protein
1660580	207345	99.73	366	1	0	glycosyl transferase, group 1
1660582	207343	99.73	366	1	0	polysaccharide deacetylase
1660954	206875	99.73	731	2	0	putative CheA signal transduction histidine kinases
1660956	206873	99.73	366	1	0	GTP-binding protein YchF
1661346	206387	99.73	376	1	0	alanine racemase
1661529	206186	99.73	376	1	0	Tetratricopeptide domain protein
1661550	206164	99.73	373	1	0	Extracellular ligand-binding receptor
1661561	206152	99.73	375	1	0	queuine tRNA-ribosyltransferase
1661637	209587	99.73	371	1	0	conserved hypothetical protein
1661702	209513	99.73	370	1	0	alanine dehydrogenase
1661727	209474	99.73	370	1	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1661985	209259	99.73	365	1	0	hydrogenase formation HypD protein
1662069	209178	99.73	369	1	0	dual specificity protein phosphatase
1659253	208928	99.74	384	1	0	DNA polymerase III, beta subunit
1659265	208907	99.74	777	2	0	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent
1659297	208870	99.74	389	1	0	conserved hypothetical protein
1659303	208862	99.74	379	1	0	Osmosensitive K <sup>+</sup> channel His kinase sensor
1659441	208717	99.74	383	1	0	peptidase M15B and M15C, D,D-carboxypeptidase VanY/endolysins
1659573	208576	99.74	764	2	0	signal transduction histidine kinase, nitrogen specific, NtrB
1659690	208448	99.74	390	1	0	protein of unknown function DUF39
1659897	208119	99.74	386	1	0	conserved hypothetical protein
1660181	207852	99.74	388	1	0	putative transcriptional regulator, GntR family
1660590	207335	99.74	771	2	0	methyl-accepting chemotaxis sensory transducer
1660665	207255	99.74	771	2	0	Smr protein/MutS2
1660724	207121	99.74	380	1	0	permease YjgP/YjgQ family protein
1660731	207114	99.74	388	1	0	aminotransferase, class I and II

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1660937	206895	99.74	380	1	0	response regulator receiver protein
1661033	206786	99.74	386	1	0	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
1661089	206727	99.74	387	1	0	Polysulphide reductase, NrfD
1661240	206501	99.74	382	1	0	basic membrane lipoprotein
1661290	206451	99.74	769	2	0	ABC transporter related
1661548	206166	99.74	391	1	0	major facilitator superfamily MFS_1
1661598	206108	99.74	378	1	0	HflK protein
1661785	209413	99.74	380	1	0	isocitrate/isopropylmalate dehydrogenase
1661796	209398	99.74	391	1	0	chorismate mutase
1662234	208999	99.74	386	1	0	DNA-directed DNA polymerase
1659456	208702	99.75	816	2	0	Phosphoribosylformylglycinamide synthase
1659488	208666	99.75	402	1	0	Phosphoglycerate mutase
1659563	208587	99.75	1187	3	0	FAD linked oxidase domain protein
1659601	208544	99.75	402	1	0	acetate kinase
1659812	208270	99.75	792	2	0	diguanylate cyclase
1659834	208244	99.75	801	2	0	methyl-accepting chemotaxis sensory transducer
1659971	208048	99.75	397	1	0	metal dependent phosphohydrolase
1660031	207984	99.75	395	1	0	conserved hypothetical protein
1660197	207835	99.75	399	1	0	acetylornithine and succinylornithine aminotransferases
1660951	206879	99.75	394	1	0	major facilitator superfamily MFS_1
1661091	206725	99.75	792	2	0	primosomal protein N'
1661142	206670	99.75	402	1	0	ammonium transporter
1661179	206628	99.75	399	1	0	protein of unknown function UPF0118
1661213	206530	99.75	396	1	0	Argininosuccinate synthase
1661297	206439	99.75	406	1	0	conserved hypothetical protein
1661455	206268	99.75	393	1	0	aminotransferase, class I and II
1661716	209488	99.75	407	1	0	inner-membrane translocator
1661723	209479	99.75	803	2	0	integral membrane sensor signal transduction histidine kinase
1661838	209354	99.75	396	1	0	Saccharopine dehydrogenase
1662128	209112	99.75	403	1	0	TOBE domain protein
1662135	209104	99.75	393	1	0	aminotransferase, class I and II
1662288	208950	99.75	793	2	0	diguanylate cyclase/phosphodiesterase
1659468	208688	99.76	423	1	0	glutamate-1-semialdehyde-2,1-aminomutase
1660172	207863	99.76	411	1	0	lipoprotein releasing system, transmembrane protein, LolC/E family
1660317	207689	99.76	425	1	0	aromatic amino acid transporter
1660395	207604	99.76	420	1	0	von Willebrand factor, type A
1660509	207423	99.76	419	1	0	gamma-glutamyl phosphate reductase
1660739	207105	99.76	412	1	0	diaminopimelate decarboxylase
1661172	206635	99.76	829	2	0	leucyl-tRNA synthetase
1661201	206601	99.76	424	1	0	major facilitator superfamily MFS_1
1661367	206364	99.76	414	1	0	putative PAS/PAC sensor protein
1661450	206275	99.76	412	1	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1661690	408297	99.76	423	1	0	Extracellular ligand-binding receptor
1661774	209424	99.76	424	1	0	phosphoribosylamine--glycine ligase
1661980	209264	99.76	412	1	0	response regulator receiver modulated metal dependent phosphohydrolase
1662077	209170	99.76	424	1	0	seryl-tRNA synthetase
1662220	209013	99.76	414	1	0	tryptophan synthase, beta subunit
1659366	208795	99.77	433	1	0	cytochrome bd ubiquinol oxidase, subunit I
1659474	208682	99.77	431	1	0	extracellular solute-binding protein, family 1
1659866	208154	99.77	441	1	0	Serine-type D-Ala-D-Ala carboxypeptidase
1660034	207981	99.77	430	1	0	cytochrome c family protein
1660206	207823	99.77	428	1	0	carboxyl-terminal protease
1660226	207803	99.77	862	2	0	DNA topoisomerase III
1660312	207695	99.77	872	2	0	conserved hypothetical protein
1660384	207616	99.77	439	1	0	histone deacetylase superfamily
1660459	207534	99.77	444	1	0	6-phosphofructokinase
1660488	207449	99.77	440	1	0	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaC
1660523	207409	99.77	427	1	0	Glycerol-3-phosphate dehydrogenase
1660919	206912	99.77	441	1	0	heat shock protein HslVU, ATPase subunit HslU
1660960	206869	99.77	443	1	0	Glycine dehydrogenase (decarboxylating)
1661044	206776	99.77	433	1	0	trigger factor
1661219	206524	99.77	879	2	0	alanyl-tRNA synthetase
1661292	206446	99.77	3038	7	0	putative outer membrane adhesin like protein
1661456	206267	99.77	443	1	0	signal recognition particle protein
1661643	209582	99.77	437	1	0	response regulator receiver modulated diguanylate cyclase
1661773	209425	99.77	432	1	0	Phenylacetate--CoA ligase
1661842	209350	99.77	439	1	0	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+))
1659248	208934	99.78	461	1	0	asparaginyl-tRNA synthetase
1659305	208860	99.78	449	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659338	208832	99.78	451	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659416	208744	99.78	447	1	0	Glucose-6-phosphate isomerase

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1659418	208742	99.78	459	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659694	208443	99.78	458	1	0	putative PAS/PAC sensor protein
1659855	208167	99.78	455	1	0	UDP-N-acetylglucosamine diphosphorylase
1660408	207590	99.78	462	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1660845	207041	99.78	456	1	0	DNA repair protein RadA
1660880	207007	99.78	906	2	0	aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding
1660962	206867	99.78	456	1	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1660966	206862	99.78	459	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661178	206629	99.78	926	2	0	diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor(s)
1661228	206514	99.78	457	1	0	tRNA modification GTPase TrmE
1661534	206181	99.78	455	1	0	histidine kinase
1661843	209349	99.78	445	1	0	cation transporter
1661866	209326	99.78	460	1	0	D-lactate dehydrogenase (cytochrome)
1661874	209317	99.78	463	1	0	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaC
1659478	208676	99.79	480	1	0	conserved hypothetical protein
1659611	208532	99.79	485	1	0	Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase
1659833	208245	99.79	945	2	0	Pyruvate, water dikinase
1660300	207710	99.79	471	1	0	Pyruvate carboxylase
1660400	207599	99.79	477	1	0	type II secretion system protein E
1660588	207337	99.79	468	1	0	aspartate ammonia-lyase
1660857	207029	99.79	481	1	0	peptidase M48, Ste24p
1660961	206868	99.79	481	1	0	Glycine dehydrogenase (decarboxylating)
1661152	206656	99.79	469	1	0	MATE efflux family protein
1661359	206373	99.79	964	2	0	Peptidase M16C associated domain protein
1661658	209565	99.79	479	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661675	209542	99.79	473	1	0	carbon starvation protein CstA
1662028	209215	99.79	477	1	0	Undecaprenyl-phosphate galactose phosphotransferase
1662192	209040	99.79	476	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1662225	209008	99.79	468	1	0	fumarate hydratase, class II
1662279	208955	99.79	474	1	0	conserved hypothetical protein
1659578	208570	99.8	489	1	0	ribonuclease, Rne/Rng family
1659844	208178	99.8	1005	2	0	PAS/PAC sensor hybrid histidine kinase
1660101	207903	99.8	1001	2	0	multi-sensor hybrid histidine kinase
1660171	207864	99.8	501	1	0	lysyl-tRNA synthetase
1660257	207766	99.8	502	1	0	amino acid permease-associated region
1660275	207737	99.8	491	1	0	chromosomal replication initiator protein DnaA
1660282	207728	99.8	489	1	0	glycogen/starch synthases, ADP-glucose type
1660634	207288	99.8	507	1	0	Glutamate synthase (NADPH)
1661485	206234	99.8	489	1	0	glutamyl-tRNA(Gln) amidotransferase, A subunit
1662213	209017	99.8	495	1	0	sodium/pantothenate symporter
1662243	208990	99.8	504	1	0	RND efflux system, outer membrane lipoprotein, NodT family
1659326	208836	99.81	532	1	0	DEAD/DEAH box helicase domain protein
1659517	208634	99.81	529	1	0	peptide chain release factor 3
1659978	208040	99.81	539	1	0	hybrid cluster protein
1660051	207958	99.81	527	1	0	conserved hypothetical protein
1660522	207410	99.81	516	1	0	FAD dependent oxidoreductase
1660876	207012	99.81	1039	2	0	multi-sensor hybrid histidine kinase
1660994	206829	99.81	516	1	0	membrane protein, putative
1661009	206809	99.81	540	1	0	Rhodanese domain protein
1661102	206712	99.81	524	1	0	type II and III secretion system protein
1661565	206147	99.81	518	1	0	response regulator receiver modulated metal dependent phosphohydrolase
1661611	206091	99.81	528	1	0	methyl-accepting chemotaxis sensory transducer
1661644	209581	99.81	528	1	0	dolichyl-phosphate-mannose-protein mannosyltransferase family protein
1661703	209511	99.81	526	1	0	sigma54 specific transcriptional regulator, Fis family
1661812	209382	99.81	515	1	0	SSS sodium solute transporter superfamily
1661834	209358	99.81	1065	2	0	diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor(s)
1661875	209315	99.81	520	1	0	sulfatase
1661996	209247	99.81	538	1	0	flagellar M-ring protein FlIF
1662137	209102	99.81	520	1	0	extracellular solute-binding protein, family 5
1659508	208646	99.82	543	1	0	Mammalian cell entry related domain protein
1659914	208103	99.82	569	1	0	conserved hypothetical protein
1659929	208085	99.82	560	1	0	ABC transporter related
1659993	208023	99.82	549	1	0	nickel-dependent hydrogenase, large subunit
1660064	207944	99.82	570	1	0	L-lactate transport

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1660957	206872	99.82	551	1	0	phosphoglucomutase, alpha-D-glucose phosphate-specific
1661001	206818	99.82	563	1	0	acetolactate synthase, large subunit, biosynthetic type
1661125	206687	99.82	551	1	0	arginyl-tRNA synthetase
1661205	206595	99.82	1085	2	0	multi-sensor signal transduction histidine kinase
1661395	206332	99.82	571	1	0	single-stranded-DNA-specific exonuclease RecJ
1661421	206304	99.82	554	1	0	beta-lactamase domain protein
1661726	209475	99.82	545	1	0	cytochrome c, class III
1661964	209282	99.82	563	1	0	conserved hypothetical protein
1662131	209108	99.82	543	1	0	molybdopterin binding domain
1662167	209071	99.82	570	1	0	integral membrane sensor signal transduction histidine kinase
1662277	208957	99.82	570	1	0	Hydantoinase/oxoprolinase
1659553	208598	99.83	587	1	0	methyl-accepting chemotaxis sensory transducer
1659570	208579	99.83	576	1	0	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)
1659758	208332	99.83	591	1	0	TRAP dicarboxylate transporter, DetM subunit
1660035	207980	99.83	581	1	0	cytochrome c, class III
1660099	207905	99.83	586	1	0	conserved hypothetical protein
1660225	207804	99.83	589	1	0	methyl-accepting chemotaxis sensory transducer
1660295	207715	99.83	603	1	0	GTP-binding protein TypA
1660313	207694	99.83	575	1	0	uncharacterized domain
1660389	207610	99.83	579	1	0	conserved hypothetical protein 698
1660491	207446	99.83	582	1	0	methyl-accepting chemotaxis sensory transducer
1660681	207236	99.83	606	1	0	hydrogenases, Fe-only
1660715	207130	99.83	601	1	0	ABC transporter related
1661109	206705	99.83	1145	2	0	conserved hypothetical protein
1661357	206375	99.83	579	1	0	conserved hypothetical protein 698
1661537	206177	99.83	596	1	0	polar amino acid ABC transporter, inner membrane subunit
1661579	206128	99.83	601	1	0	GTP-binding protein LepA
1661595	206111	99.83	587	1	0	Aldehyde ferredoxin oxidoreductase
1662124	209116	99.83	589	1	0	methyl-accepting chemotaxis sensory transducer
1659982	208035	99.84	644	1	0	threonyl-tRNA synthetase
1660511	207421	99.84	616	1	0	Indolepyruvate ferredoxin oxidoreductase
1660825	207062	99.84	642	1	0	molybdopterin oxidoreductase
1661243	206498	99.84	642	1	0	putative aconitate hydratase
1662246	208987	99.84	1236	2	0	acriflavin resistance protein
1659340	208830	99.85	682	1	0	response regulator receiver protein
1659455	208703	99.85	669	1	0	methyl-accepting chemotaxis sensory transducer
1661097	206718	99.85	656	1	0	ATP-dependent metalloprotease FtsH
1661451	206274	99.85	664	1	0	adenylsulfate reductase, alpha subunit
1661538	206176	99.85	669	1	0	methyl-accepting chemotaxis sensory transducer
1661540	408300	99.85	648	1	0	acetate--CoA ligase
1661601	206105	99.85	667	1	0	histidine kinase
1661666	209552	99.85	677	1	0	methyl-accepting chemotaxis sensory transducer
1659406	208754	99.86	703	1	0	flagellar biosynthesis protein FlhA
1660232	207796	99.86	695	1	0	methyl-accepting chemotaxis sensory transducer
1660437	207557	99.86	717	1	0	(p)ppGpp synthetase I, SpoT/RelA
1660842	207045	99.86	708	1	0	CheA signal transduction histidine kinases
1661078	206742	99.86	691	1	0	translation elongation factor G
1661287	206454	99.86	701	1	0	putative PAS/PAC sensor protein
1661581	206126	99.86	729	1	0	Malate synthase
1661588	206118	99.86	691	1	0	molybdopterin oxidoreductase
1662207	209023	99.86	720	1	0	methyl-accepting chemotaxis sensory transducer
1659258	208917	99.87	760	1	0	DNA topoisomerase I
1660174	207861	99.87	791	1	0	surface antigen (D15)
1660243	207782	99.87	776	1	0	methyl-accepting chemotaxis sensory transducer
1660504	207429	99.87	797	1	0	diguanylate cyclase/phosphodiesterase
1660577	207348	99.87	786	1	0	metal dependent phosphohydrolase
1660834	207053	99.87	776	1	0	ATP-dependent Clp protease, ATP-binding subunit clpA
1661121	206691	99.87	758	1	0	membrane protein, putative
1661449	206276	99.87	758	1	0	methyl-viologen-reducing hydrogenase, delta subunit
1659251	208931	99.88	856	1	0	DNA gyrase, A subunit
1660393	207606	99.88	808	1	0	signal transduction histidine kinase, nitrogen specific, NtrB
1660565	207360	99.88	806	1	0	peptidase S16, lon domain protein
1660585	207340	99.88	865	1	0	ATPase AAA-2 domain protein
1660850	207036	99.88	804	1	0	homocysteine S-methyltransferase
1661041	206779	99.88	821	1	0	ATP-dependent protease La
1661177	206630	99.88	856	1	0	ATP-dependent protease La
1661471	206252	99.88	833	1	0	preprotein translocase, SecA subunit
1659658	208483	99.89	898	1	0	GCN5-related N-acetyltransferase
1660049	207961	99.89	886	1	0	ribonuclease R
1660473	207465	99.89	917	1	0	ATPase, P-type (transporting), HAD superfamily, subfamily IC
1660737	207107	99.89	905	1	0	DNA mismatch repair protein MutS
1659391	208772	99.9	1047	1	0	transporter, hydrophobe/amphiphile efflux-1 (HAE1) family
1659588	208560	99.9	955	1	0	PAS/PAC sensor hybrid histidine kinase
1659826	208253	99.9	1014	1	0	conserved hypothetical protein

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1660969	206857	99.9	997	1	0	diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor(s)
1660435	207559	99.91	1055	1	0	SNF2-related protein
1661754	209446	99.91	1079	1	0	translation initiation factor IF-2
1660625	207299	99.92	1225	1	0	Carbamoyl-phosphate synthase L chain, ATP-binding
1659699	208438	99.93	1372	1	0	DNA-directed RNA polymerase, beta subunit
1659249	208933	100	154	0	0	UspA domain protein
1659250	208932	100	261	0	0	lipoprotein, putative
1659252	208929	100	798	0	0	DNA gyrase, B subunit
1659255	208924	100	417	0	0	peptidase M23B
1659256	208921	100	447	0	0	glutamine synthetase, type I
1659260	208915	100	337	0	0	conserved hypothetical protein
1659273	208896	100	262	0	0	Methyltransferase type 11
1659276	208893	100	171	0	0	peptide deformylase
1659280	208889	100	126	0	0	conserved hypothetical protein
1659283	208886	100	139	0	0	conserved hypothetical protein
1659284	208885	100	262	0	0	Cobyrinic acid a,c-diamide synthase
1659286	208882	100	251	0	0	band 7 protein
1659289	208879	100	189	0	0	lipoprotein, putative
1659291	208877	100	77	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659292	208876	100	357	0	0	pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
1659294	208874	100	182	0	0	pyruvate ferredoxin/flavodoxin oxidoreductase
1659298	208869	100	139	0	0	TadE family protein
1659301	208864	100	678	0	0	K <sup>+</sup> -transporting ATPase, B subunit
1659311	208852	100	106	0	0	small multidrug resistance protein
1659316	208846	100	125	0	0	conserved hypothetical protein
1659321	208840	100	658	0	0	peptidase U32
1659329	208834	100	187	0	0	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
1659341	208828	100	180	0	0	conserved hypothetical protein
1659342	208827	100	97	0	0	conserved hypothetical protein
1659344	208825	100	260	0	0	conserved hypothetical protein
1659352	208817	100	351	0	0	conserved hypothetical protein
1659354	208810	100	543	0	0	L-lactate transport
1659355	208809	100	77	0	0	conserved hypothetical protein
1659356	208807	100	299	0	0	ADP-ribosylation/Crystallin J1
1659360	208802	100	450	0	0	peptidase S1 and S6, chymotrypsin/Hap
1659361	208800	100	62	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659362	208798	100	222	0	0	protein of unknown function UPF0153
1659363	208797	100	130	0	0	conserved hypothetical protein
1659364	208796	100	207	0	0	Tetratricopeptide TPR_2 repeat protein
1659370	208791	100	157	0	0	conserved hypothetical protein
1659375	208786	100	612	0	0	succinate dehydrogenase or fumarate reductase, flavoprotein
1659376	208785	100	200	0	0	fumarate reductase, cytochrome b subunit
1659385	208777	100	421	0	0	phenylacetate-coenzyme A ligase, putative
1659388	208774	100	214	0	0	conserved hypothetical protein
1659390	208773	100	226	0	0	lipoprotein, putative
1659394	208768	100	163	0	0	transcription elongation factor GreA
1659395	208766	100	376	0	0	chaperone protein DnaJ
1659396	208765	100	77	0	0	DNA-directed RNA polymerase, omega subunit
1659397	208764	100	248	0	0	PP-loop domain protein
1659398	208763	100	301	0	0	peptidase M23B
1659399	208762	100	221	0	0	phosphoesterase, PA-phosphatase related
1659400	208761	100	134	0	0	response regulator receiver protein
1659404	208757	100	263	0	0	flagellar biosynthetic protein FliR
1659405	208755	100	357	0	0	flagellar biosynthetic protein FlhB
1659408	208752	100	271	0	0	Cobyrinic acid a,c-diamide synthase
1659409	208751	100	265	0	0	RNA polymerase, sigma 28 subunit, FliA/WhiG family
1659410	208750	100	126	0	0	response regulator receiver protein
1659412	208748	100	109	0	0	conserved hypothetical protein
1659420	208740	100	206	0	0	isochorismatase hydrolase
1659422	208738	100	565	0	0	integral membrane sensor signal transduction histidine kinase
1659423	208737	100	121	0	0	response regulator receiver protein
1659425	208735	100	72	0	0	conserved hypothetical protein
1659426	208734	100	569	0	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1659435	208723	100	278	0	0	hydrolase, TatD family
1659444	208714	100	303	0	0	DNA binding domain, excisionase family
1659447	208711	100	555	0	0	conserved hypothetical protein
1659450	208708	100	95	0	0	histone family protein DNA-binding protein
1659451	208707	100	228	0	0	conserved hypothetical protein
1659453	208705	100	52	0	0	Rubredoxin-type Fe(Cys) <sub>4</sub> protein
1659454	208704	100	126	0	0	desulfoferredoxin
1659457	208701	100	833	0	0	diguanylate cyclase with PAS/PAC sensor
1659460	208697	100	440	0	0	UDP-glucose/GDP-mannose dehydrogenase
1659461	208696	100	67	0	0	conserved hypothetical protein

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1659465	208692	100	129	0	0	cytochrome c, class III
1659469	208687	100	160	0	0	putative transcriptional regulator, AsnC family
1659471	208685	100	286	0	0	conserved hypothetical protein
1659472	208684	100	277	0	0	binding-protein-dependent transport systems inner membrane component
1659479	208675	100	607	0	0	glucosamine--fructose-6-phosphate aminotransferase, isomerizing
1659484	208670	100	429	0	0	MiaB-like tRNA modifying enzyme YliG
1659485	208669	100	577	0	0	ribosomal protein S1
1659491	208664	100	202	0	0	cytochrome B561
1659492	208663	100	542	0	0	cytochrome c family protein
1659496	208659	100	537	0	0	polysaccharide export protein
1659503	208653	100	497	0	0	glycerol kinase
1659504	208652	100	251	0	0	major intrinsic protein
1659514	208637	100	564	0	0	AMP-dependent synthetase and ligase
1659515	208636	100	101	0	0	Stress responsive alpha-beta barrel domain protein
1659516	208635	100	182	0	0	conserved hypothetical protein
1659519	208631	100	375	0	0	carbamoyl-phosphate synthase, small subunit
1659520	208630	100	267	0	0	Tetratricopeptide TPR_2 repeat protein
1659523	208627	100	66	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659524	208626	100	475	0	0	Na+/H+ antiporter NhaC
1659534	208621	100	167	0	0	OmpA/MotB domain protein
1659535	208620	100	456	0	0	WD40 domain protein beta Propeller
1659536	208619	100	195	0	0	TonB family protein
1659537	208618	100	341	0	0	TonB, C-terminal domain
1659538	208617	100	139	0	0	Biopolymer transport protein ExbD/TolR
1659539	208616	100	230	0	0	MotA/TolQ/ExbB proton channel
1659540	208614	100	439	0	0	outer membrane efflux protein
1659541	208612	100	128	0	0	ferric uptake regulator, Fur family
1659542	208611	100	191	0	0	Rubryerythrin
1659543	208610	100	75	0	0	Rubredoxin-type Fe(Cys)4 protein
1659545	208607	100	448	0	0	fumarate reductase/succinate dehydrogenase flavoprotein domain protein
1659547	208605	100	161	0	0	conserved hypothetical protein
1659548	208604	100	577	0	0	DEAD/DEAH box helicase domain protein
1659551	208601	100	81	0	0	conserved hypothetical protein
1659552	208600	100	128	0	0	transcriptional regulator, MucR family
1659555	208596	100	132	0	0	transcriptional regulator, MucR family
1659560	208590	100	287	0	0	protein of unknown function DUF6, transmembrane
1659564	208586	100	142	0	0	Holliday junction resolvase YqgF
1659568	208581	100	189	0	0	Cupin 2, conserved barrel domain protein
1659569	208580	100	550	0	0	AMP-dependent synthetase and ligase
1659582	208566	100	129	0	0	NUDIX hydrolase
1659584	208564	100	137	0	0	hemerythrin-like metal-binding protein
1659585	208563	100	349	0	0	aspartate-semialdehyde dehydrogenase
1659591	208557	100	78	0	0	protein of unknown function DUF903
1659595	208552	100	290	0	0	Rhodanese domain protein
1659599	208546	100	209	0	0	protein of unknown function DUF162
1659600	208545	100	363	0	0	DRTGG domain protein
1659602	208543	100	704	0	0	phosphate acetyltransferase
1659603	208542	100	422	0	0	protein of unknown function DUF224, cysteine-rich region domain protein
1659604	208541	100	461	0	0	FAD linked oxidase domain protein
1659605	208540	100	555	0	0	L-lactate transport
1659606	208539	100	1215	0	0	pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
1659623	208520	100	407	0	0	Tetratricopeptide TPR_2 repeat protein
1659626	208517	100	574	0	0	Radical SAM domain protein
1659641	208502	100	381	0	0	sigma54 specific transcriptional regulator, Fis family
1659643	208500	100	99	0	0	putative phage shock protein B
1659647	208496	100	167	0	0	3-isopropylmalate dehydratase, small subunit
1659649	208494	100	509	0	0	2-isopropylmalate synthase
1659650	208493	100	249	0	0	CDP-diacylglycerol--serineO-phosphatidyltransferase
1659652	208491	100	210	0	0	Haloacid dehalogenase domain protein hydrolase
1659653	208489	100	370	0	0	Protein of unknown function DUF1722
1659662	208479	100	151	0	0	response regulator receiver protein
1659663	208478	100	99	0	0	conserved hypothetical protein
1659664	208477	100	219	0	0	conserved hypothetical protein
1659665	208476	100	128	0	0	response regulator receiver protein
1659666	208475	100	577	0	0	integral membrane sensor signal transduction histidine kinase
1659667	208474	100	115	0	0	conserved hypothetical protein
1659668	208473	100	474	0	0	sigma54 specific transcriptional regulator, Fis family
1659669	208472	100	138	0	0	conserved hypothetical protein
1659670	208471	100	332	0	0	protein of unknown function DUF81
1659671	208467	100	345	0	0	sigma54 specific transcriptional regulator, Fis family
1659672	208465	100	559	0	0	diguanylate cyclase

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1659676	208463	100	345	0	0	protein of unknown function DUF6, transmembrane
1659679	208459	100	117	0	0	protein of unknown function DUF486
1659684	208454	100	429	0	0	ErkK/YbiS/YcfS/YnhG family protein
1659685	208453	100	186	0	0	orotate phosphoribosyltransferase
1659686	208452	100	430	0	0	adenylosuccinate lyase
1659687	208451	100	99	0	0	putative regulatory protein, FmdB family
1659691	208447	100	451	0	0	response regulator receiver
1659696	208441	100	733	0	0	multi-sensor signal transduction histidine kinase
1659698	208439	100	1385	0	0	DNA-directed RNA polymerase, beta' subunit
1659700	208437	100	127	0	0	ribosomal protein L7/L12
1659702	208435	100	235	0	0	ribosomal protein L1
1659703	208434	100	140	0	0	ribosomal protein L11
1659704	208433	100	183	0	0	NusG antitermination factor
1659705	208432	100	83	0	0	preprotein translocase, SecE subunit
1659707	208431	100	49	0	0	ribosomal protein L33
1659708	208430	100	397	0	0	translation elongation factor Tu
1659714	208427	100	308	0	0	UDP-3-0-acyl N-acetylglucosamine deacetylase
1659716	208424	100	357	0	0	peptide chain release factor 1
1659718	208422	100	71	0	0	ribosomal protein L31
1659719	208421	100	253	0	0	hemolysin A
1659721	208419	100	137	0	0	transcriptional regulator, MarR family
1659726	208414	100	363	0	0	radical SAM enzyme, Cfr family
1659727	208413	100	442	0	0	metal dependent phosphohydrolase
1659736	208403	100	349	0	0	sigma54 specific transcriptional regulator, Fis family
1659739	208400	100	139	0	0	putative transcriptional regulator, CopG family
1659740	208399	100	227	0	0	conserved hypothetical protein
1659744	208395	100	279	0	0	transcriptional regulator, AraC family
1659746	208393	100	467	0	0	Aspartyl aminopeptidase
1659768	208319	100	219	0	0	formate dehydrogenase, beta subunit, putative
1659769	208318	100	277	0	0	formate dehydrogenase formation protein FdhE, putative
1659772	208315	100	136	0	0	Biopolymer transport protein ExbD/TolR
1659775	208312	100	385	0	0	metallo-beta-lactamase family protein
1659776	208311	100	469	0	0	putative amino acid transporter, AAT family
1659781	208305	100	138	0	0	transcriptional regulator, MarR family
1659783	208303	100	295	0	0	electron transport complex, RnfABCDGE type, B subunit
1659784	208302	100	191	0	0	electron transport complex, RnfABCDGE type, A subunit
1659785	208301	100	223	0	0	electron transport complex, RnfABCDGE type, E subunit
1659786	208300	100	191	0	0	FMN-binding domain protein
1659787	208299	100	318	0	0	electron transport complex, RnfABCDGE type, D subunit
1659788	208298	100	401	0	0	electron transport complex protein RnfC, putative
1659789	208297	100	259	0	0	cytochrome c family protein
1659790	208295	100	183	0	0	GPR1/FUN34/yaaH family protein
1659793	208291	100	237	0	0	GntR domain protein
1659794	208290	100	341	0	0	FMN-dependent alpha-hydroxy acid dehydrogenase
1659795	208289	100	266	0	0	protein of unknown function DUF81
1659797	208286	100	290	0	0	protein of unknown function DUF161
1659800	208282	100	105	0	0	DsrC family protein
1659801	208280	100	227	0	0	CBS domain containing protein
1659802	208279	100	288	0	0	protein of unknown function DUF161
1659804	208277	100	311	0	0	import inner membrane translocase, subunit Tim44
1659805	208276	100	132	0	0	response regulator receiver protein
1659809	208272	100	55	0	0	conserved hypothetical protein
1659810	208271	100	208	0	0	beta-lactamase domain protein
1659815	208264	100	280	0	0	protein of unknown function DUF178
1659827	208252	100	314	0	0	conserved hypothetical protein
1659828	208250	100	385	0	0	Extracellular ligand-binding receptor
1659831	208247	100	255	0	0	ABC transporter related
1659832	208246	100	241	0	0	ABC transporter related
1659835	208243	100	254	0	0	tRNA/rRNA methyltransferase (SpoU)
1659836	208242	100	169	0	0	conserved hypothetical protein
1659837	208241	100	432	0	0	Phenylacetate--CoA ligase
1659840	208184	100	226	0	0	type IV pilus assembly PilZ
1659842	208181	100	213	0	0	DedA family protein
1659846	208176	100	487	0	0	response regulator receiver sensor signal transduction histidine kinase
1659847	208175	100	88	0	0	hypothetical protein
1659850	208172	100	389	0	0	FAD dependent oxidoreductase
1659852	208170	100	519	0	0	metal dependent phosphohydrolase
1659853	208169	100	87	0	0	conserved hypothetical protein
1659854	208168	100	78	0	0	conserved hypothetical protein
1659856	208166	100	292	0	0	phosphate binding protein
1659863	208158	100	242	0	0	exsB protein
1659867	208151	100	193	0	0	conserved hypothetical protein
1659870	208146	100	129	0	0	putative endoribonuclease L-PSP



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1659871	208145	100	332	0	0	pyridoxal phosphate-dependent enzymes, D-cysteine desulphydrase family
1659872	208144	100	466	0	0	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaC
1659874	208142	100	637	0	0	heat shock protein Hsp90
1659875	208141	100	147	0	0	Threonyl/alanyl tRNA synthetase, SAD
1659876	208140	100	244	0	0	lipoprotein, putative
1659877	208139	100	246	0	0	conserved hypothetical protein
1659878	208138	100	100	0	0	conserved hypothetical protein
1659884	208132	100	244	0	0	putative phage repressor
1659887	208130	100	123	0	0	conserved hypothetical protein
1659889	208129	100	291	0	0	lipoprotein, putative
1659893	208125	100	68	0	0	conserved hypothetical protein
1659895	208122	100	115	0	0	conserved hypothetical protein
1659896	208120	100	270	0	0	conserved hypothetical protein
1659898	208118	100	242	0	0	conserved hypothetical protein
1659900	208116	100	406	0	0	sodium/calcium exchanger membrane region
1659905	208112	100	188	0	0	conserved hypothetical protein
1659906	208111	100	129	0	0	conserved hypothetical protein
1659907	208110	100	519	0	0	conserved hypothetical protein
1659909	208108	100	243	0	0	OmpA/MotB domain protein
1659910	208107	100	281	0	0	chemotaxis protein MotA
1659912	208105	100	99	0	0	conserved hypothetical protein
1659919	208098	100	147	0	0	conserved hypothetical protein
1659927	208087	100	226	0	0	two component transcriptional regulator, winged helix family
1659928	208086	100	461	0	0	integral membrane sensor signal transduction histidine kinase
1659931	208082	100	310	0	0	Mg <sup>2+</sup> transporter protein, CorA family protein
1659932	208081	100	168	0	0	protein of unknown function DUF1499
1659933	208080	100	195	0	0	transcriptional regulator, TetR family
1659934	208079	100	146	0	0	response regulator receiver protein
1659936	208077	100	209	0	0	TPR repeat-containing protein
1659945	208073	100	321	0	0	oligopeptide/dipeptide ABC transporter, ATPase subunit
1659947	208071	100	78	0	0	FeoA family protein
1659948	208069	100	86	0	0	FeoA family protein
1659949	208068	100	732	0	0	ferrous iron transport protein B
1659951	208066	100	141	0	0	peptidylprolyl isomerase, FKBP-type
1659954	208064	100	234	0	0	transcriptional regulator, TrmB
1659966	208053	100	122	0	0	conserved hypothetical protein
1659969	208050	100	75	0	0	nitrogen-fixing NifU domain protein
1659973	208045	100	209	0	0	[Acyl-carrier-protein] phosphodiesterase
1659977	208041	100	271	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1659980	208037	100	380	0	0	2-hydroxyglutaryl-CoA dehydratase, D-component
1659983	208034	100	176	0	0	translation initiation factor IF-3
1659984	208033	100	65	0	0	ribosomal protein L35
1659985	208032	100	117	0	0	ribosomal protein L20
1659986	208031	100	345	0	0	phenylalanyl-tRNA synthetase, alpha subunit
1659992	208024	100	132	0	0	transcriptional regulator, MucR family
1659996	208020	100	145	0	0	lipoprotein, putative
1659998	208018	100	180	0	0	shikimate kinase
1660000	208016	100	130	0	0	ribosomal protein S9
1660001	208015	100	144	0	0	ribosomal protein L13
1660002	208014	100	413	0	0	conserved hypothetical protein
1660003	208013	100	161	0	0	putative transcriptional regulator, XRE family
1660005	208012	100	351	0	0	metal dependent phosphohydrolase
1660006	208011	100	469	0	0	Pyruvate kinase
1660007	208010	100	149	0	0	MraZ protein
1660008	208009	100	323	0	0	S-adenosyl-methyltransferase MraW
1660013	208004	100	358	0	0	phospho-N-acetylmuramoyl-pentapeptide-transferase
1660014	208003	100	433	0	0	UDP-N-acetylmuramoylalanine--D-glutamate ligase
1660015	208002	100	377	0	0	cell division protein FtsW
1660017	208000	100	454	0	0	UDP-N-acetylmuramate--alanine ligase
1660019	207998	100	278	0	0	Polypeptide-transport-associated domain protein, FtsQ-type
1660020	207997	100	408	0	0	cell division protein FtsA
1660021	408359	100	449	0	0	cell division protein FtsZ
1660033	207982	100	354	0	0	conserved hypothetical protein
1660037	207976	100	237	0	0	formate dehydrogenase, beta subunit, putative
1660039	207973	100	295	0	0	phosphate ABC transporter, inner membrane subunit PstC
1660040	207972	100	270	0	0	phosphate binding protein
1660042	207970	100	280	0	0	oxidoreductase FAD/NAD(P)-binding domain protein
1660043	207969	100	160	0	0	conserved hypothetical protein
1660047	207964	100	233	0	0	protein of unknown function UPF0005
1660052	207957	100	539	0	0	SMC domain protein
1660053	207956	100	300	0	0	binding-protein-dependent transport systems inner membrane component
1660055	207954	100	176	0	0	conserved hypothetical protein

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1660062	207948	100	316	0	0	NAD-dependent epimerase/dehydratase
1660067	207942	100	391	0	0	Methionine adenosyltransferase
1660068	207941	100	283	0	0	pantoate--beta-alanine ligase
1660070	207939	100	307	0	0	3-methyl-2-oxobutanoate hydroxymethyltransferase
1660071	207937	100	297	0	0	flagellin domain protein
1660072	207936	100	208	0	0	conserved hypothetical protein
1660073	207935	100	117	0	0	heat shock protein Hsp20
1660074	207934	100	136	0	0	heat shock protein Hsp20
1660076	207932	100	411	0	0	efflux transporter, RND family, MFP subunit
1660079	207929	100	406	0	0	protein of unknown function DUF214
1660080	207928	100	210	0	0	metal dependent phosphohydrolase
1660084	408358	100	77	0	0	RNP-1 like RNA-binding protein
1660085	207920	100	152	0	0	17 kDa surface antigen
1660086	207919	100	184	0	0	conserved hypothetical protein
1660089	207915	100	159	0	0	transcriptional regulator, HxIR family
1660090	207913	100	169	0	0	nitroreductase
1660091	207912	100	65	0	0	4-oxalocrotonate tautomerase
1660092	207911	100	109	0	0	conserved hypothetical protein
1660094	207909	100	139	0	0	VanZ family protein
1660095	207908	100	73	0	0	SlyX family protein
1660096	207907	100	160	0	0	protein of unknown function DUF55
1660098	207906	100	475	0	0	conserved hypothetical protein
1660102	207902	100	138	0	0	Calcium-binding EF-hand-containing protein
1660105	207898	100	166	0	0	conserved hypothetical protein
1660106	207896	100	393	0	0	iron-containing alcohol dehydrogenase
1660107	207895	100	186	0	0	heterodisulfide reductase, C subunit
1660108	207894	100	334	0	0	CoB--CoM heterodisulfide reductase
1660109	207893	100	652	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660113	207889	100	163	0	0	conserved hypothetical protein
1660115	207887	100	380	0	0	iron-containing alcohol dehydrogenase
1660126	207873	100	373	0	0	binding-protein-dependent transport systems inner membrane component
1660131	207868	100	301	0	0	ABC transporter related
1660173	207862	100	233	0	0	ABC transporter related
1660176	207858	100	175	0	0	outer membrane chaperone Skp (OmpH)
1660178	207856	100	154	0	0	transcriptional regulator, Fis family
1660184	207848	100	261	0	0	oxidoreductase FAD/NAD(P)-binding domain protein
1660188	207844	100	475	0	0	conserved hypothetical protein
1660195	207837	100	855	0	0	alpha-glucan phosphorylases
1660198	207833	100	106	0	0	conserved hypothetical protein
1660199	207830	100	242	0	0	ABC transporter related
1660200	207829	100	270	0	0	extracellular solute-binding protein, family 3
1660202	207827	100	230	0	0	polar amino acid ABC transporter, inner membrane subunit
1660204	207825	100	226	0	0	HhH-GPD family protein
1660205	207824	100	383	0	0	peptidase M23B
1660211	207817	100	293	0	0	Cobyrrinic acid a,c-diamide synthase
1660212	207816	100	211	0	0	hydrogenase accessory protein HypB
1660213	207815	100	117	0	0	hydrogenase expression/synthesis, HypA
1660215	207813	100	300	0	0	conserved hypothetical protein
1660218	207810	100	140	0	0	conserved hypothetical protein
1660223	207805	100	164	0	0	Rubryerythrin
1660229	207799	100	155	0	0	Tir chaperone family protein
1660231	207797	100	248	0	0	beta-lactamase domain protein
1660233	207795	100	163	0	0	conserved hypothetical protein 22
1660234	207794	100	73	0	0	transcriptional regulator, TraR/DksA family
1660235	207793	100	336	0	0	phosphate transporter
1660236	207792	100	209	0	0	protein of unknown function DUF47
1660239	207786	100	397	0	0	glycine betaine/L-proline ABC transporter, ATPase subunit
1660240	207785	100	283	0	0	binding-protein-dependent transport systems inner membrane component
1660245	207780	100	173	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660246	207779	100	120	0	0	hydrogenase nickel insertion protein HypA
1660253	207771	100	506	0	0	L-lactate transport
1660264	207755	100	37	0	0	conserved hypothetical protein
1660266	207752	100	97	0	0	conserved hypothetical protein
1660269	207745	100	204	0	0	ribosomal RNA methyltransferase RrmJ/FtsJ
1660273	207740	100	320	0	0	Holliday junction DNA helicase RuvB
1660274	207739	100	245	0	0	thymidylate synthase, flavin-dependent
1660276	207736	100	186	0	0	Cupin 2, conserved barrel domain protein
1660278	207732	100	204	0	0	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
1660281	207729	100	138	0	0	NUDIX hydrolase
1660287	207723	100	461	0	0	glycoside hydrolase, family 3 domain protein
1660297	207713	100	253	0	0	MotA/TolQ/ExbB proton channel

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1660299	207711	100	147	0	0	type IV pilus assembly PilZ
1660301	207709	100	751	0	0	Acetyl-CoA carboxylase
1660304	207706	100	176	0	0	single-strand binding protein
1660308	207700	100	87	0	0	translation initiation factor IF-1
1660309	207699	100	89	0	0	RNP-1 like RNA-binding protein
1660314	207693	100	240	0	0	methyltransferase small
1660318	207688	100	462	0	0	Tryptophanase
1660321	207685	100	385	0	0	iron-containing alcohol dehydrogenase
1660374	207629	100	120	0	0	transcriptional regulator, TraR/DksA family
1660380	207620	100	307	0	0	fructose-1,6-bisphosphate aldolase, class II
1660390	207609	100	85	0	0	conserved hypothetical protein
1660391	207608	100	159	0	0	conserved hypothetical protein
1660396	207603	100	129	0	0	TadE family protein
1660398	207601	100	284	0	0	type II secretion system protein
1660401	207598	100	404	0	0	response regulator receiver protein
1660403	207596	100	484	0	0	type II and III secretion system protein
1660406	207593	100	57	0	0	Flp/Fap pilin component
1660409	207589	100	442	0	0	Xanthine/uracil/vitamin C permease
1660414	207584	100	119	0	0	Dinitrogenase iron-molybdenum cofactor biosynthesis
1660419	207579	100	287	0	0	Cobyrinic acid a,c-diamide synthase
1660436	207558	100	565	0	0	extracellular solute-binding protein, family 5
1660438	207556	100	297	0	0	flagellin domain protein
1660444	207550	100	291	0	0	Protein-glutamate O-methyltransferase
1660445	207549	100	258	0	0	Cobyrinic acid a,c-diamide synthase
1660446	207548	100	184	0	0	putative CheW protein
1660447	207547	100	122	0	0	response regulator receiver protein
1660453	207541	100	280	0	0	metal dependent phosphohydrolase
1660456	207537	100	373	0	0	2-nitropropane dioxygenase, NPD
1660460	207532	100	330	0	0	glycosyl transferase, family 2
1660461	207531	100	187	0	0	metal dependent phosphohydrolase
1660470	207468	100	109	0	0	small multidrug resistance protein
1660471	207467	100	109	0	0	anti-sigma-factor antagonist
1660477	207462	100	215	0	0	conserved hypothetical protein
1660478	207460	100	228	0	0	protein of unknown function DUF554
1660479	207459	100	956	0	0	excinuclease ABC, A subunit
1660480	207458	100	143	0	0	conserved hypothetical protein
1660481	207456	100	418	0	0	conserved hypothetical protein
1660482	207455	100	173	0	0	peptide methionine sulfoxide reductase
1660485	207452	100	163	0	0	protein of unknown function DUF520
1660489	207448	100	95	0	0	chaperonin Cpn10
1660490	207447	100	530	0	0	chaperonin GroEL
1660493	207444	100	282	0	0	Rhodanese domain protein
1660495	207440	100	135	0	0	response regulator receiver protein
1660496	207439	100	231	0	0	protein of unknown function DUF1641
1660497	207438	100	413	0	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1660498	207437	100	173	0	0	transcriptional regulator, BadM/Rrf2 family
1660499	408342	100	170	0	0	transcriptional regulator, BadM/Rrf2 family
1660502	207431	100	167	0	0	putative CheW protein
1660512	207420	100	198	0	0	Indolepyruvate ferredoxin oxidoreductase
1660513	207419	100	529	0	0	transcriptional regulator, NifA subfamily, Fis Family
1660514	207418	100	96	0	0	conserved hypothetical protein
1660515	207417	100	207	0	0	pyruvate ferredoxin/ferredoxin oxidoreductase
1660517	207415	100	382	0	0	pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
1660518	207414	100	90	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660519	207413	100	77	0	0	conserved hypothetical protein
1660521	207411	100	255	0	0	HAD-superfamily hydrolase, subfamily IIA
1660524	207407	100	321	0	0	phosphonate ABC transporter, periplasmic phosphonate-binding protein
1660526	207405	100	265	0	0	phosphonate ABC transporter, inner membrane subunit
1660527	207404	100	266	0	0	phosphonate ABC transporter, inner membrane subunit
1660528	207403	100	173	0	0	intracellular protease, PfpI family
1660530	207401	100	147	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660531	207400	100	312	0	0	Tetratricopeptide TPR_2 repeat protein
1660534	207398	100	165	0	0	lipoprotein signal peptidase
1660538	207393	100	70	0	0	hydrogenase assembly chaperone hypC/hupF
1660539	207392	100	165	0	0	hydrogenase expression/formation protein
1660541	207390	100	317	0	0	hydrogenase (NiFe) small subunit HydA
1660543	408341	100	488	0	0	nickel-dependent hydrogenase, large subunit
1660544	207386	100	317	0	0	hydrogenase (NiFe) small subunit HydA
1660545	207383	100	538	0	0	2-isopropylmalate synthase/homocitrate synthase family protein
1660546	207382	100	408	0	0	aspartate kinase
1660548	207380	100	150	0	0	CBS domain containing protein
1660551	207377	100	241	0	0	pyridoxal phosphate biosynthetic protein PdxJ
1660552	207376	100	445	0	0	UDP-glucose 6-dehydrogenase

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1660554	207372	100	158	0	0	putative CheW protein
1660555	207371	100	1159	0	0	transcription-repair coupling factor
1660557	207369	100	343	0	0	PpiC-type peptidyl-prolyl cis-trans isomerase
1660558	207368	100	313	0	0	conserved hypothetical protein
1660559	207367	100	251	0	0	DNA repair protein RecO
1660560	207366	100	289	0	0	Glycine--tRNA ligase
1660563	207363	100	388	0	0	major facilitator superfamily MFS_1
1660571	207354	100	299	0	0	NAD(+) kinase
1660572	207353	100	580	0	0	conserved hypothetical protein
1660574	207351	100	476	0	0	glutamyl-tRNA(Gln) amidotransferase, B subunit
1660579	207346	100	213	0	0	conserved hypothetical protein
1660581	207344	100	340	0	0	Threonine aldolase
1660584	207341	100	105	0	0	DafA protein
1660586	207339	100	164	0	0	peptidyl-prolyl cis-trans isomerase, cyclophilin type
1660591	207334	100	292	0	0	dihydrodipicolinate synthase
1660594	207330	100	93	0	0	histone family protein DNA-binding protein
1660595	207329	100	272	0	0	flagellar synthesis regulator FleN, putative
1660597	207327	100	346	0	0	peptide chain release factor 2
1660598	207326	100	481	0	0	apolipoprotein N-acyltransferase
1660607	408340	100	203	0	0	conserved hypothetical protein
1660609	207316	100	142	0	0	putative signal transduction protein with CBS domains
1660610	207315	100	197	0	0	protein-L-isoaspartate O-methyltransferase
1660611	207314	100	197	0	0	conserved hypothetical protein
1660612	207313	100	288	0	0	conserved hypothetical protein
1660613	207312	100	185	0	0	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
1660614	207311	100	90	0	0	conserved hypothetical protein
1660618	207307	100	337	0	0	Inositol phosphatase/fructose-1,6-bisphosphatase
1660619	207306	100	361	0	0	putative metalloendopeptidase, glycoprotease family
1660620	207305	100	107	0	0	thioredoxin
1660621	207304	100	307	0	0	thioredoxin reductase
1660622	207303	100	243	0	0	putative lipoprotein
1660626	207298	100	1191	0	0	PEP-utilising enzyme, mobile region
1660630	207292	100	407	0	0	acetylmithine deacetylase or succinyl-diaminopimelate desuccinylase
1660631	207291	100	90	0	0	conserved hypothetical protein
1660633	207289	100	254	0	0	putative carboxylesterase
1660635	207287	100	364	0	0	glutamine amidotransferase, class-II
1660637	207285	100	121	0	0	preprotein translocase, YajC subunit
1660638	207284	100	532	0	0	protein-export membrane protein SecD
1660639	207283	100	362	0	0	protein-export membrane protein SecF
1660640	207282	100	103	0	0	cytochrome c, class I
1660643	207279	100	203	0	0	cytochrome c oxidase, subunit III
1660647	207275	100	140	0	0	conserved hypothetical protein
1660648	207274	100	528	0	0	L-aspartate oxidase
1660649	207273	100	358	0	0	quinolinate synthetase complex, A subunit
1660650	207272	100	295	0	0	nicotinate-nucleotide pyrophosphorylase
1660651	207271	100	447	0	0	magnesium transporter
1660652	207270	100	487	0	0	diguanylate cyclase
1660661	207260	100	90	0	0	histone family protein DNA-binding protein
1660662	207259	100	67	0	0	conserved hypothetical protein
1660663	207257	100	67	0	0	ribosomal protein S21
1660664	207256	100	149	0	0	GatB/Yqey domain protein
1660666	207254	100	572	0	0	DNA primase
1660667	207253	100	590	0	0	RNA polymerase, sigma 70 subunit, RpoD family
1660669	207251	100	352	0	0	diguanylate cyclase
1660670	207250	100	200	0	0	multiple antibiotic resistance (MarC)-related proteins
1660671	207249	100	253	0	0	short-chain dehydrogenase/reductase SDR
1660672	207248	100	250	0	0	protein of unknown function DUF224, cysteine-rich region domain protein
1660673	207247	100	475	0	0	iron-sulfur cluster binding protein
1660676	207243	100	481	0	0	cation diffusion facilitator family transporter
1660677	207242	100	214	0	0	Carbonate dehydratase
1660682	207235	100	123	0	0	Ferredoxin hydrogenase
1660683	207234	100	421	0	0	hydrogenases, Fe-only
1660688	207229	100	89	0	0	conserved hypothetical protein
1660689	207227	100	152	0	0	protein of unknown function DUF307
1660696	207149	100	189	0	0	transcriptional regulator, TetR family
1660697	207147	100	269	0	0	phospholipid/glycerol acyltransferase
1660699	207145	100	411	0	0	AAA ATPase, central domain protein
1660702	207142	100	578	0	0	conserved hypothetical protein
1660703	207141	100	344	0	0	putative GAF sensor protein
1660704	207140	100	340	0	0	cell shape determining protein, MreB/Mrl family
1660706	207138	100	178	0	0	NUDIX hydrolase

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1660707	207137	100	164	0	0	ribosomal-protein-alanine acetyltransferase
1660708	207136	100	251	0	0	Triose-phosphate isomerase
1660711	207134	100	54	0	0	conserved hypothetical protein
1660712	207133	100	204	0	0	putative phage repressor
1660716	207129	100	212	0	0	conserved hypothetical protein
1660718	207127	100	225	0	0	outer membrane lipoprotein carrier protein LolA
1660719	207126	100	759	0	0	cell divisionFtsK/SpoIIIE
1660720	207125	100	185	0	0	translation elongation factor P
1660729	207116	100	99	0	0	TRASH domain protein
1660730	207115	100	141	0	0	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
1660732	207113	100	294	0	0	tyrosine recombinase XerD
1660734	207111	100	174	0	0	histidine triad (HIT) protein
1660735	207110	100	123	0	0	conserved hypothetical protein
1660741	207101	100	114	0	0	regulatory protein, ArsR
1660800	207088	100	306	0	0	Inorganic diphosphatase
1660802	207085	100	153	0	0	PTS system sorbose subfamily IIB component
1660803	207084	100	145	0	0	PTS system fructose subfamily IIA component
1660804	207083	100	303	0	0	Uncharacterised P-loop ATPase protein UPF0042
1660806	207081	100	179	0	0	sigma 54 modulation protein/ribosomal protein S30EA
1660807	207080	100	476	0	0	RNA polymerase, sigma 54 subunit, RpoN
1660811	207076	100	175	0	0	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family
1660813	207074	100	547	0	0	CTP synthase
1660814	207073	100	269	0	0	phosphoribosylformylglycinamide synthase I
1660817	207071	100	80	0	0	conserved hypothetical protein
1660819	207069	100	134	0	0	iojap-like protein
1660822	207065	100	176	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1660823	207064	100	343	0	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1660824	207063	100	143	0	0	amino acid-binding ACT domain protein
1660827	207060	100	259	0	0	Dihydrodipicolinate reductase
1660830	207057	100	347	0	0	TrkA-N domain protein
1660832	207055	100	161	0	0	conserved hypothetical protein
1660833	207054	100	234	0	0	Leucyltransferase
1660835	207052	100	104	0	0	ATP-dependent Clp protease adaptor protein ClpS
1660838	207049	100	114	0	0	protein of unknown function DUF190
1660839	207048	100	218	0	0	nitrite and sulphite reductase 4Fe-4S region
1660841	207046	100	271	0	0	Protein-glutamate O-methyltransferase
1660843	207044	100	120	0	0	response regulator receiver protein
1660847	207039	100	176	0	0	hypoxanthine phosphoribosyltransferase
1660848	207038	100	154	0	0	GCN5-related N-acetyltransferase
1660851	207035	100	356	0	0	sigma-70 region 2 domain protein
1660855	207031	100	147	0	0	sugar-phosphate isomerases, RpiB/LacA/LacB family
1660858	207028	100	181	0	0	20S proteasome, A and B subunits
1660861	207025	100	312	0	0	ribose-phosphate pyrophosphokinase
1660862	207024	100	190	0	0	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5
1660863	207023	100	201	0	0	Aminoacyl-tRNA hydrolase
1660865	207021	100	416	0	0	transcription termination factor Rho
1660868	207018	100	169	0	0	Ferritin, Dps family protein
1660878	207010	100	123	0	0	putative transcriptional regulator, ModE family
1660879	207008	100	339	0	0	molybdopterin binding domain
1660884	207003	100	150	0	0	conserved hypothetical protein
1660891	206996	100	404	0	0	membrane protein involved in aromatic hydrocarbon degradation
1660895	206990	100	75	0	0	conserved hypothetical protein
1660896	206989	100	133	0	0	conserved hypothetical protein
1660897	206988	100	284	0	0	formyltetrahydrofolate deformylase
1660898	408333	100	327	0	0	fructose-1,6-bisphosphatase, class II
1660900	206985	100	174	0	0	outer membrane chaperone Skp (OmpH)
1660901	206984	100	378	0	0	Lytic transglycosylase, catalytic
1660902	206983	100	173	0	0	membrane protein, putative
1660904	206981	100	309	0	0	tRNA delta(2)-isopentenylpyrophosphate transferase
1660905	206980	100	186	0	0	pantetheine-phosphate adenyllyltransferase
1660906	206979	100	190	0	0	putative methyltransferase
1660907	206978	100	536	0	0	beta-lactamase domain protein
1660908	206977	100	218	0	0	conserved hypothetical protein 730
1660911	206921	100	225	0	0	phosphate uptake regulator, PhoU
1660914	206917	100	815	0	0	peptidase S16, lon domain protein
1660915	206916	100	122	0	0	heat shock protein Hsp20
1660916	206915	100	94	0	0	PpiC-type peptidyl-prolyl cis-trans isomerase
1660917	206914	100	487	0	0	RNA binding S1 domain protein
1660920	206911	100	308	0	0	acetylglutamate kinase
1660924	206907	100	243	0	0	cytochrome c assembly protein
1660926	206905	100	111	0	0	conserved hypothetical protein
1660929	206901	100	309	0	0	Thioredoxin-disulfide reductase

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1660934	206898	100	395	0	0	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
1660935	206897	100	564	0	0	AMP-dependent synthetase and ligase
1660939	206893	100	114	0	0	anti-sigma-factor antagonist
1660940	206892	100	378	0	0	protein of unknown function DUF342
1660943	206889	100	531	0	0	flagellar hook-length control protein
1660944	206888	100	227	0	0	flagellar hook capping protein
1660945	206887	100	564	0	0	protein of unknown function DUF1078 domain protein
1660946	206886	100	124	0	0	flagellin FlaG, putative
1660947	206885	100	298	0	0	flagellin domain protein
1660948	206884	100	228	0	0	Ribonuclease III
1660950	206882	100	354	0	0	DRTGG domain protein
1660952	206878	100	121	0	0	conserved hypothetical protein
1660958	206871	100	137	0	0	response regulator receiver protein
1660959	206870	100	127	0	0	glycine cleavage system H protein
1660963	206866	100	319	0	0	OmpA/MotB domain protein
1660964	206865	100	153	0	0	conserved hypothetical protein
1660965	206863	100	123	0	0	Hpt protein
1660967	206861	100	579	0	0	signal transduction histidine kinase, nitrogen specific, NtrB
1660971	206855	100	326	0	0	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
1660972	206854	100	429	0	0	thiamine biosynthesis protein ThiC
1660974	206851	100	154	0	0	conserved hypothetical protein
1660977	206849	100	350	0	0	phosphoribosylformylglycinamide cyclo-ligase
1660981	206845	100	331	0	0	transcriptional regulator, LysR family
1660982	206844	100	321	0	0	Auxin Efflux Carrier
1660983	206843	100	630	0	0	methyl-accepting chemotaxis sensory transducer
1660984	206840	100	179	0	0	Ferritin, Dps family protein
1660986	206838	100	73	0	0	transcriptional regulator, TraR/DksA family
1660988	206835	100	210	0	0	NLP/P60 protein
1660995	206827	100	178	0	0	Uracil phosphoribosyltransferase
1660999	206820	100	331	0	0	ketol-acid reductoisomerase
1661002	206817	100	76	0	0	conserved hypothetical protein
1661003	206816	100	106	0	0	protein of unknown function DUF167
1661004	206815	100	146	0	0	DivIVA family protein
1661005	206814	100	100	0	0	protein of unknown function YGGT
1661006	206813	100	224	0	0	HAD-superfamily hydrolase, subfamily IA, variant 1
1661008	206811	100	124	0	0	conserved hypothetical protein
1661010	206810	100	65	0	0	twin-arginine translocation protein, TatA/E family subunit
1661018	206801	100	386	0	0	conserved hypothetical protein
1661020	206799	100	208	0	0	Methyltransferase type 11
1661021	206798	100	267	0	0	metal dependent phosphohydrolase
1661022	206797	100	110	0	0	conserved hypothetical protein
1661024	206795	100	1164	0	0	DNA polymerase III, alpha subunit
1661026	206793	100	200	0	0	multiple antibiotic resistance (MarC)-related proteins
1661027	206792	100	641	0	0	deoxyxylulose-5-phosphate synthase
1661028	206791	100	287	0	0	Polyprenyl synthetase
1661036	206783	100	274	0	0	ABC-3 protein
1661037	206782	100	164	0	0	ferric uptake regulator, Fur family
1661040	206780	100	194	0	0	conserved hypothetical protein
1661042	206778	100	417	0	0	ATP-dependent Clp protease, ATP-binding subunit ClpX
1661043	206777	100	201	0	0	ATP-dependent Clp protease, proteolytic subunit ClpP
1661048	206772	100	120	0	0	ribosomal protein L17
1661049	206771	100	347	0	0	DNA-directed RNA polymerase, alpha subunit
1661051	206769	100	129	0	0	ribosomal protein S11
1661053	206767	100	37	0	0	ribosomal protein L36
1661055	206765	100	418	0	0	preprotein translocase, SecY subunit
1661056	206764	100	148	0	0	ribosomal protein L15
1661057	206763	100	56	0	0	ribosomal protein L30
1661058	206762	100	163	0	0	ribosomal protein S5
1661059	206761	100	119	0	0	ribosomal protein L18
1661060	206760	100	179	0	0	ribosomal protein L6
1661061	206759	100	126	0	0	ribosomal protein S8
1661063	206757	100	179	0	0	ribosomal protein L5
1661065	206755	100	122	0	0	ribosomal protein L14
1661066	206754	100	88	0	0	ribosomal protein S17
1661067	206753	100	61	0	0	ribosomal protein L29
1661068	206752	100	137	0	0	ribosomal protein L16
1661069	206751	100	212	0	0	ribosomal protein S3
1661070	206750	100	112	0	0	ribosomal protein L22
1661071	206749	100	83	0	0	ribosomal protein S19
1661072	206748	100	276	0	0	ribosomal protein L2
1661073	206747	100	96	0	0	Ribosomal protein L25/L23
1661074	206746	100	206	0	0	ribosomal protein L4/L1e
1661075	206745	100	209	0	0	ribosomal protein L3
1661076	206744	100	105	0	0	ribosomal protein S10

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1661079	206740	100	156	0	0	ribosomal protein S7
1661080	206739	100	123	0	0	ribosomal protein S12
1661081	206736	100	427	0	0	sulfate adenylyltransferase
1661085	408312	100	334	0	0	Nitrate reductase, gamma subunit
1661086	206730	100	536	0	0	reductase, iron-sulfur binding subunit, putative
1661087	206729	100	126	0	0	cytochrome c family protein
1661088	206728	100	261	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1661092	206724	100	290	0	0	UTP-glucose-1-phosphate uridylyltransferase GalU
1661093	206723	100	450	0	0	phosphoglucosamine mutase
1661094	206721	100	300	0	0	YbbR family protein
1661095	206720	100	248	0	0	protein of unknown function DUF147
1661100	206714	100	183	0	0	conserved hypothetical protein
1661111	206703	100	242	0	0	Lytic transglycosylase, catalytic
1661113	206701	100	369	0	0	twitching motility protein
1661116	206697	100	726	0	0	glutamine synthetase, catalytic region
1661117	206696	100	90	0	0	RNP-1 like RNA-binding protein
1661119	206694	100	210	0	0	Sua5/YciO/YrdC/YwlC family protein
1661120	206693	100	156	0	0	protein of unknown function DUF163
1661122	206690	100	72	0	0	conserved hypothetical protein
1661123	206689	100	218	0	0	glucose inhibited division protein
1661126	206686	100	273	0	0	Sporulation domain protein
1661128	206684	100	274	0	0	ABC transporter related
1661129	206683	100	148	0	0	Mammalian cell entry related domain protein
1661132	206680	100	105	0	0	Cupin 2, conserved barrel domain protein
1661134	206678	100	200	0	0	protein of unknown function DUF340, membrane
1661135	206677	100	246	0	0	extracellular solute-binding protein, family 3
1661137	206675	100	247	0	0	ABC transporter related
1661141	206671	100	112	0	0	nitrogen regulatory protein P-II
1661143	206667	100	161	0	0	Redoxin domain protein
1661149	206659	100	274	0	0	nitroreductase
1661150	206658	100	731	0	0	conserved hypothetical protein
1661153	206654	100	204	0	0	phosphoesterase, PA-phosphatase related
1661154	206653	100	667	0	0	glycosyl transferase, family 39
1661155	206652	100	311	0	0	Rhomboid family protein
1661156	206651	100	186	0	0	FxsA cytoplasmic membrane protein
1661157	206650	100	69	0	0	ribosomal protein L28
1661158	206649	100	178	0	0	protein of unknown function DUF177
1661159	206648	100	59	0	0	ribosomal protein L32
1661160	408311	100	345	0	0	fatty acid/phospholipid synthesis protein PlsX
1661161	206646	100	330	0	0	3-oxoacyl-(acyl-carrier-protein) synthase III
1661163	206644	100	76	0	0	acyl carrier protein
1661164	206643	100	415	0	0	beta-ketoacyl synthase
1661165	206642	100	412	0	0	Glycine hydroxymethyltransferase
1661169	206638	100	409	0	0	GTP cyclohydrolase II
1661170	206637	100	156	0	0	Riboflavin synthase
1661171	206636	100	153	0	0	NusB antitermination factor
1661175	206632	100	225	0	0	DNA repair protein RadC
1661176	206631	100	100	0	0	acylphosphatase
1661180	206627	100	73	0	0	conserved hypothetical protein
1661183	206624	100	159	0	0	Colicin V production protein
1661187	206620	100	74	0	0	thiamineS protein
1661188	206619	100	576	0	0	Aldehyde ferredoxin oxidoreductase
1661190	206616	100	185	0	0	conserved hypothetical protein
1661192	206614	100	125	0	0	conserved hypothetical protein
1661193	206613	100	518	0	0	integral membrane protein MviN
1661200	206602	100	334	0	0	Formamidase
1661202	206599	100	76	0	0	putative regulatory protein, FmdB family
1661203	206598	100	337	0	0	Urea transporter
1661212	206531	100	300	0	0	ornithine carbamoyltransferase
1661214	206529	100	460	0	0	argininosuccinate lyase
1661216	206527	100	453	0	0	sodium:neurotransmitter symporter
1661218	206525	100	357	0	0	recA protein
1661220	206522	100	312	0	0	protein of unknown function UPF0052 and CofD
1661223	206519	100	255	0	0	phosphate ABC transporter, ATPase subunit
1661224	206518	100	229	0	0	two component transcriptional regulator, winged helix family
1661225	206517	100	202	0	0	3'-5' exonuclease
1661229	206513	100	430	0	0	single-stranded nucleic acid binding R3H domain protein
1661230	206512	100	534	0	0	60 kDa inner membrane insertion protein
1661231	206511	100	86	0	0	protein of unknown function DUF37
1661232	206510	100	92	0	0	ribonuclease P protein component
1661233	206509	100	44	0	0	ribosomal protein L34
1661238	206503	100	306	0	0	inner-membrane translocator
1661242	206499	100	629	0	0	PpiC-type peptidyl-prolyl cis-trans isomerase
1661254	206487	100	344	0	0	protein of unknown function DUF21

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1661256	206484	100	631	0	0	cytochrome c assembly protein
1661258	206482	100	225	0	0	cytochrome c-type biogenesis protein CcmB
1661259	206481	100	224	0	0	cytochrome c assembly protein
1661260	206480	100	45	0	0	conserved hypothetical protein
1661262	206478	100	485	0	0	inosine-5'-monophosphate dehydrogenase
1661263	206477	100	515	0	0	GMP synthase, large subunit
1661264	206476	100	122	0	0	twin-arginine translocation protein, TatB subunit
1661265	206475	100	257	0	0	Sec-independent protein translocase, TatC subunit
1661276	206465	100	147	0	0	UspA domain protein
1661285	206456	100	258	0	0	ABC transporter related
1661286	206455	100	388	0	0	SufBD protein
1661289	206452	100	429	0	0	type I secretion membrane fusion protein, HlyD family
1661291	206447	100	456	0	0	type I secretion outer membrane protein, TolC family
1661294	206442	100	225	0	0	conserved hypothetical protein
1661295	206441	100	178	0	0	cobalamin biosynthesis enzyme
1661296	206440	100	149	0	0	membrane-bound metal-dependent hydrolase
1661300	206436	100	151	0	0	protein of unknown function UPF0153
1661309	206427	100	195	0	0	intracellular protease, PfpI family
1661311	206425	100	240	0	0	conserved hypothetical protein
1661312	206424	100	320	0	0	putative CheW protein
1661313	206423	100	272	0	0	conserved hypothetical protein
1661316	206420	100	308	0	0	PfkB domain protein
1661317	206418	100	67	0	0	heavy metal-binding domain protein
1661320	206415	100	181	0	0	protein of unknown function DUF151
1661321	206414	100	219	0	0	PHP C-terminal domain protein
1661323	206412	100	210	0	0	dihydroxyacetone kinase, L subunit
1661327	206408	100	387	0	0	response regulator receiver protein
1661328	206407	100	186	0	0	protein of unknown function DUF615
1661329	206406	100	112	0	0	conserved hypothetical protein
1661335	206400	100	246	0	0	ABC transporter related
1661336	206399	100	337	0	0	polar amino acid ABC transporter, inner membrane subunit
1661337	206398	100	272	0	0	extracellular solute-binding protein, family 3
1661340	206395	100	165	0	0	GTP cyclohydrolase I
1661342	206391	100	451	0	0	replicative DNA helicase
1661343	206390	100	153	0	0	ribosomal protein L9
1661344	206389	100	87	0	0	ribosomal protein S18
1661345	206388	100	101	0	0	ribosomal protein S6
1661347	206386	100	764	0	0	Organic solvent tolerance protein
1661348	206385	100	398	0	0	tyrosyl-tRNA synthetase
1661349	206384	100	290	0	0	metallophosphoesterase
1661351	206381	100	253	0	0	conserved hypothetical protein
1661352	206380	100	142	0	0	conserved hypothetical protein
1661354	206378	100	476	0	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661355	206377	100	810	0	0	multi-sensor signal transduction histidine kinase
1661356	206376	100	85	0	0	conserved hypothetical protein
1661358	206374	100	144	0	0	ferric uptake regulator, Fur family
1661360	206371	100	243	0	0	diguanylate cyclase
1661361	206370	100	249	0	0	conserved hypothetical protein
1661362	206369	100	102	0	0	isoamylase N-terminal domain protein
1661363	206368	100	128	0	0	conserved hypothetical protein
1661364	206367	100	95	0	0	DNA binding domain, excisionase family
1661365	206366	100	807	0	0	methyl-accepting chemotaxis sensory transducer
1661366	206365	100	86	0	0	conserved hypothetical protein
1661370	206361	100	380	0	0	glutamate 5-kinase
1661371	206360	100	366	0	0	GTPI/OBG sub domain protein
1661372	206359	100	87	0	0	ribosomal protein L27
1661373	206358	100	102	0	0	ribosomal protein L21
1661377	206352	100	179	0	0	cytochrome c family protein
1661381	206348	100	233	0	0	ATP synthase F0, A subunit
1661382	206347	100	82	0	0	ATP synthase F0, C subunit
1661383	206345	100	214	0	0	CoA-binding domain protein
1661386	206341	100	145	0	0	flagellar export protein FliJ
1661389	206338	100	326	0	0	flagellar motor switch protein FliM
1661390	206337	100	131	0	0	conserved hypothetical protein
1661393	206334	100	218	0	0	lipoate-protein ligase B
1661398	206329	100	235	0	0	orotidine 5'-phosphate decarboxylase
1661399	206328	100	207	0	0	Guanylate kinase
1661400	206327	100	86	0	0	protein of unknown function DUF370
1661401	206326	100	293	0	0	domain of unknown function DUF1732
1661403	206324	100	464	0	0	NLP/P60 protein
1661404	206323	100	742	0	0	helicase, RecD/TraA family
1661406	206321	100	140	0	0	UspA domain protein
1661407	206320	100	175	0	0	Shikimate kinase



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1661408	206319	100	397	0	0	aminotransferase, class I and II
1661415	206312	100	114	0	0	conserved hypothetical protein
1661416	206311	100	85	0	0	glutaredoxin
1661418	206309	100	688	0	0	small GTP-binding protein
1661423	206302	100	247	0	0	ribosomal protein S2
1661424	206301	100	279	0	0	translation elongation factor Ts
1661426	206299	100	238	0	0	uridylylate kinase
1661429	206296	100	268	0	0	phosphatidate cytidylyltransferase
1661441	206285	100	393	0	0	Radical SAM domain protein
1661443	206282	100	367	0	0	Radical SAM domain protein
1661446	206279	100	265	0	0	extracellular solute-binding protein, family 3
1661447	206278	100	248	0	0	conserved hypothetical protein
1661448	206277	100	384	0	0	heterodisulfide reductase, transmembrane subunit, putative
1661452	206272	100	167	0	0	adenylylsulfate reductase, beta subunit
1661457	206266	100	79	0	0	ribosomal protein S16
1661458	206265	100	77	0	0	conserved hypothetical protein
1661459	206264	100	176	0	0	16S rRNA processing protein RimM
1661460	206263	100	425	0	0	tRNA (guanine-N1)-methyltransferase
1661461	206262	100	115	0	0	ribosomal protein L19
1661463	408302	100	134	0	0	protein of unknown function UPF0102
1661465	206259	100	252	0	0	PTS system mannose/fructose/sorbose family IID component
1661468	206256	100	154	0	0	SsrA-binding protein
1661479	206241	100	159	0	0	Redoxin domain protein
1661481	206239	100	191	0	0	GrpE protein
1661482	206238	100	636	0	0	chaperone protein DnaK
1661483	206236	100	674	0	0	conserved hypothetical protein
1661484	206235	100	94	0	0	glutamyl-tRNA(Gln) amidotransferase, C subunit
1661487	206232	100	134	0	0	response regulator receiver protein
1661488	206231	100	98	0	0	conserved hypothetical protein
1661489	206230	100	490	0	0	two component, sigma54 specific, transcriptional regulator, Fis family
1661493	408301	100	476	0	0	conserved hypothetical protein
1661496	206221	100	254	0	0	short-chain dehydrogenase/reductase SDR
1661500	206218	100	161	0	0	methylated-DNA--protein-cysteinemethyltransferase
1661501	206217	100	351	0	0	conserved hypothetical radical SAM protein
1661502	206216	100	346	0	0	cell shape determining protein, MreB/Mrl family
1661504	206214	100	156	0	0	conserved hypothetical protein
1661506	206212	100	371	0	0	rod shape-determining protein RodA
1661508	206207	100	131	0	0	H+-transporting two-sector ATPase, B/B' subunit
1661509	206206	100	176	0	0	H+-transporting two-sector ATPase, B/B' subunit
1661511	206204	100	502	0	0	ATP synthase F1, alpha subunit
1661512	206203	100	291	0	0	ATP synthase F1, gamma subunit
1661513	206202	100	470	0	0	ATP synthase F1, beta subunit
1661514	206201	100	134	0	0	ATP synthase F1, epsilon subunit
1661515	206200	100	79	0	0	conserved hypothetical protein
1661520	206195	100	282	0	0	glutamate racemase
1661522	206193	100	176	0	0	transport-associated
1661525	206190	100	91	0	0	histone family protein DNA-binding protein
1661526	206189	100	311	0	0	diguanylate cyclase
1661527	206188	100	156	0	0	transcription activator, effector binding
1661528	206187	100	196	0	0	lipoprotein, putative
1661533	206182	100	237	0	0	Tetrapetideptide TPR_2 repeat protein
1661536	206178	100	275	0	0	extracellular solute-binding protein, family 3
1661539	206175	100	309	0	0	response regulator receiver protein
1661542	206172	100	231	0	0	binding-protein-dependent transport systems inner membrane component
1661544	206170	100	569	0	0	sigma54 specific transcriptional regulator, Fis family
1661546	206168	100	278	0	0	UspA domain protein
1661549	206165	100	190	0	0	AMMECR1 domain protein
1661551	206163	100	746	0	0	signal transduction histidine kinase, nitrogen specific, NtrB
1661552	206162	100	225	0	0	phosphoribosylglycinamide formyltransferase
1661553	206161	100	144	0	0	MOSC domain containing protein
1661554	206160	100	503	0	0	uroporphyrin-III C-methyltransferase
1661559	206155	100	151	0	0	conserved hypothetical protein
1661564	206149	100	393	0	0	phosphoribosylglycinamide formyltransferase 2
1661566	206146	100	936	0	0	multi-sensor signal transduction histidine kinase
1661568	206141	100	238	0	0	ABC transporter related
1661569	206140	100	255	0	0	ABC transporter related
1661570	206139	100	317	0	0	inner-membrane translocator
1661571	206138	100	301	0	0	inner-membrane translocator
1661576	206130	100	156	0	0	Tripartite ATP-independent periplasmic transporter, DctQ component
1661577	206131	100	427	0	0	TRAP dicarboxylate transporter, DctM subunit
1661578	206129	100	199	0	0	signal peptidase I

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1661580	206127	100	148	0	0	cytochrome c family protein
1661585	206122	100	190	0	0	dTDP-4-dehydrohamnose 3,5-epimerase
1661589	206117	100	255	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1661590	206116	100	419	0	0	molybdopterin oxidoreductase, transmembrane subunit, putative
1661591	206115	100	319	0	0	conserved hypothetical protein
1661593	206113	100	156	0	0	ribonuclease H
1661599	206107	100	283	0	0	HfC protein
1661605	206100	100	295	0	0	polar amino acid ABC transporter, inner membrane subunit
1661608	206094	100	545	0	0	ferredoxin-dependent glutamate synthase
1661610	206092	100	256	0	0	conserved hypothetical protein
1661612	206090	100	329	0	0	metal dependent phosphohydrolase
1661613	206089	100	328	0	0	metal dependent phosphohydrolase
1661614	206088	100	281	0	0	Fe-S cluster assembly protein NifU
1661622	206079	100	137	0	0	heat shock protein Hsp20
1661635	209589	100	230	0	0	UBA/THIF-type NAD/FAD binding protein
1661636	209588	100	270	0	0	alpha/beta hydrolase fold
1661638	209586	100	250	0	0	MotA/TolQ/ExbB proton channel
1661639	209585	100	257	0	0	OmpA/MotB domain protein
1661641	209584	100	288	0	0	conserved hypothetical protein
1661642	209583	100	462	0	0	FAD dependent oxidoreductase
1661645	209580	100	188	0	0	conserved hypothetical protein
1661646	209579	100	807	0	0	penicillin-binding protein, 1A family
1661652	209572	100	159	0	0	acetolactate synthase, small subunit
1661657	209566	100	127	0	0	putative endoribonuclease L-PSP
1661659	209562	100	96	0	0	conserved hypothetical protein
1661661	209558	100	93	0	0	conserved hypothetical protein
1661664	209554	100	306	0	0	Mammalian cell entry related domain protein
1661665	209553	100	211	0	0	lipoprotein, putative
1661667	209551	100	479	0	0	adenosylhomocysteinase
1661668	209550	100	307	0	0	Methyltransferase type 11
1661669	209547	100	88	0	0	conserved hypothetical protein
1661670	209546	100	120	0	0	hypothetical protein
1661672	209545	100	144	0	0	uncharacterized domain 1
1661673	209544	100	309	0	0	L-lactate dehydrogenase
1661674	209543	100	470	0	0	carbon starvation protein CstA
1661677	209540	100	257	0	0	response regulator receiver protein
1661678	209539	100	115	0	0	conserved hypothetical protein
1661679	209538	100	300	0	0	transcriptional regulator, LysR family
1661680	209537	100	206	0	0	Lysine exporter protein (LYSE/YGGA)
1661683	209534	100	102	0	0	conserved hypothetical protein
1661684	209533	100	246	0	0	molybdopterin-guanine dinucleotide biosynthesis MobB region
1661685	209532	100	236	0	0	formate dehydrogenase, beta subunit, putative
1661689	209527	100	290	0	0	transposase, putative
1661691	209525	100	672	0	0	multi-sensor signal transduction histidine kinase
1661693	209523	100	341	0	0	molybdenum cofactor biosynthesis protein A
1661695	209521	100	262	0	0	formate dehydrogenase, subunit FdhD
1661696	209520	100	293	0	0	formate dehydrogenase formation protein FdhE, putative
1661701	209514	100	112	0	0	type IV pilus assembly PilZ
1661706	209507	100	185	0	0	putative GAF sensor protein
1661714	209490	100	234	0	0	ABC transporter related
1661715	209489	100	262	0	0	ABC transporter related
1661717	209487	100	302	0	0	inner-membrane translocator
1661718	209486	100	372	0	0	Extracellular ligand-binding receptor
1661719	209484	100	141	0	0	conserved hypothetical protein
1661720	209483	100	133	0	0	conserved hypothetical protein
1661721	209482	100	369	0	0	conserved hypothetical protein 698
1661722	209481	100	140	0	0	UspA domain protein
1661728	209473	100	388	0	0	Polysulphide reductase, NrfD
1661729	209472	100	47	0	0	hmc operon protein 4
1661730	209471	100	226	0	0	hmc operon protein 5
1661731	209470	100	461	0	0	protein of unknown function DUF224, cysteine-rich region domain protein
1661732	209469	100	138	0	0	response regulator receiver protein
1661733	209468	100	150	0	0	transcriptional regulator, BadM/Rrf2 family
1661735	209466	100	210	0	0	maf protein
1661736	209465	100	467	0	0	major facilitator superfamily MFS_1
1661739	209462	100	104	0	0	anti-sigma-28 factor, FlgM
1661740	209461	100	173	0	0	protein of unknown function DUF180
1661741	209459	100	78	0	0	carbon storage regulator, CsrA
1661742	209458	100	523	0	0	flagellar hook-associated protein 3
1661744	209456	100	154	0	0	conserved hypothetical protein
1661746	209454	100	378	0	0	flagellar P-ring protein
1661747	209453	100	238	0	0	flagellar L-ring protein
1661749	209451	100	260	0	0	flagellar basal-body rod protein FlgG

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1661750	209450	100	260	0	0	protein of unknown function DUF1078 domain protein
1661751	209449	100	172	0	0	protein of unknown function DUF150
1661752	209448	100	428	0	0	NusA antitermination factor
1661755	209445	100	96	0	0	protein of unknown function DUF503
1661759	209440	100	719	0	0	Polyribonucleotide nucleotidyltransferase
1661761	209438	100	273	0	0	conserved hypothetical protein
1661762	209437	100	642	0	0	selenocysteine-specific translation elongation factor
1661765	209434	100	72	0	0	conserved hypothetical protein
1661769	209430	100	102	0	0	conserved hypothetical protein
1661770	209429	100	354	0	0	N-acetyl-gamma-glutamyl-phosphate reductase
1661771	209428	100	401	0	0	metal dependent phosphohydrolase
1661775	209423	100	166	0	0	phosphoribosylaminoimidazole carboxylase, catalytic subunit
1661776	209422	100	109	0	0	conserved hypothetical protein
1661790	209404	100	256	0	0	Indole-3-glycerol-phosphate synthase
1661792	209402	100	209	0	0	glutamine amidotransferase of anthranilate synthase
1661797	209397	100	323	0	0	3-dehydroquinate synthase
1661798	209396	100	266	0	0	predicted phospho-2-dehydro-3-deoxyheptonate aldolase
1661801	209392	100	335	0	0	phosphoesterase, RecJ domain protein
1661807	209386	100	314	0	0	riboflavin biosynthesis protein RibF
1661811	209383	100	105	0	0	protein of unknown function DUF485
1661819	209375	100	96	0	0	YCII-related
1661822	209372	100	233	0	0	transcriptional regulator, TetR family
1661823	209370	100	648	0	0	NADH dehydrogenase (quinone)
1661824	209369	100	282	0	0	respiratory-chain NADH dehydrogenase, subunit 1
1661825	209368	100	157	0	0	NADH ubiquinone oxidoreductase, 20 kDa subunit
1661826	209367	100	130	0	0	Ech hydrogenase, subunit EchD, putative
1661827	209366	100	358	0	0	NADH dehydrogenase (ubiquinone)
1661828	209365	100	113	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1661831	209361	100	268	0	0	conserved hypothetical protein
1661832	209360	100	481	0	0	phospholipase D/Transphosphatidylase
1661839	209353	100	639	0	0	arginine decarboxylase
1661840	209352	100	372	0	0	diguanylate cyclase
1661844	209348	100	221	0	0	TrkA-N domain protein
1661846	209346	100	201	0	0	conserved hypothetical protein
1661848	209344	100	715	0	0	response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)
1661849	209343	100	214	0	0	rare lipoprotein A
1661852	209340	100	78	0	0	dissimilatory sulfite reductase B
1661853	209339	100	381	0	0	sulfite reductase, dissimilatory-type beta subunit
1661854	209338	100	437	0	0	sulfite reductase, dissimilatory-type alpha subunit
1661857	209335	100	262	0	0	conserved hypothetical protein
1661858	209334	100	608	0	0	pyruvate carboxyltransferase
1661859	209333	100	243	0	0	rare lipoprotein A
1661860	209332	100	95	0	0	histone family protein DNA-binding protein
1661861	209331	100	139	0	0	histidine triad (HIT) protein
1661864	209328	100	399	0	0	aminotransferase, class I and II
1661869	209323	100	225	0	0	polar amino acid ABC transporter, inner membrane subunit
1661870	209322	100	249	0	0	extracellular solute-binding protein, family 3
1661871	209320	100	190	0	0	flavin reductase domain protein, FMN-binding
1661876	209314	100	225	0	0	cyclic nucleotide-binding protein
1661877	209313	100	104	0	0	glutaredoxin
1661878	209312	100	305	0	0	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1661879	209311	100	88	0	0	conserved hypothetical protein
1661880	209310	100	409	0	0	Glu/Leu/Phe/Val dehydrogenase, C terminal
1661884	209306	100	474	0	0	conserved hypothetical protein
1661933	207509	100	79	0	0	transcriptional regulator, CopG family
1661947	209298	100	184	0	0	glutamine amidotransferase class-I
1661951	209294	100	563	0	0	acetolactate synthase, large subunit, biosynthetic type
1661952	209293	100	95	0	0	HesB/YadR/YfhF-family protein
1661959	209287	100	357	0	0	iron-containing alcohol dehydrogenase
1661960	209286	100	393	0	0	DegT/DnrJ/EryC1/StrS aminotransferase
1661961	209285	100	544	0	0	cytidine 5' monophosphate N-acetylneuraminic acid synthetase
1661965	209281	100	223	0	0	transferase hexapeptide repeat containing protein
1661968	209277	100	260	0	0	2-dehydro-3-deoxyglucarate aldolase
1661969	209276	100	304	0	0	NAD-dependent epimerase/dehydratase
1661970	209275	100	256	0	0	3-deoxy-manno-octulosonate cytidyltransferase
1661971	209274	100	197	0	0	transferase hexapeptide repeat containing protein
1661978	209267	100	218	0	0	metal dependent phosphohydrolase
1661982	209262	100	381	0	0	glycosyl transferase, group 1
1661983	209261	100	421	0	0	sugar transferase
1661984	209260	100	341	0	0	hydrogenase expression/formation protein HypE
1661986	209257	100	286	0	0	Methylenetetrahydrofolate dehydrogenase (NADP(+))
1661987	209256	100	437	0	0	Phosphopyruvate hydratase
1661988	209255	100	262	0	0	putative transcriptional acitvator, Baf family

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1661989	209254	100	86	0	0	conserved hypothetical protein
1661990	209253	100	341	0	0	NAD-dependent epimerase/dehydratase
1661994	209249	100	145	0	0	flagellar basal-body rod protein FlgC
1661995	209248	100	111	0	0	flagellar hook-basal body complex subunit FlhE
1661999	209244	100	437	0	0	flagellar protein export ATPase FlhI
1662001	209242	100	144	0	0	transmembrane pair domain protein
1662002	209241	100	498	0	0	protein of unknown function DUF1078 domain protein
1662005	209238	100	93	0	0	conserved hypothetical protein
1662006	209237	100	105	0	0	Tetratricopeptide TPR_2 repeat protein
1662007	209236	100	155	0	0	chemotaxis protein CheX, putative
1662008	209234	100	245	0	0	anaerobic ribonucleoside-triphosphate reductase activating protein
1662012	209230	100	356	0	0	peptidase M24
1662015	209226	100	113	0	0	transcriptional regulator, TraR/DksA family
1662023	209220	100	259	0	0	imidazoleglycerol phosphate synthase, cyclase subunit
1662029	209214	100	379	0	0	glycosyl transferase, group 1
1662033	209210	100	132	0	0	protein of unknown function DUF302
1662037	209209	100	231	0	0	polysaccharide deacetylase
1662038	209208	100	123	0	0	conserved hypothetical protein
1662042	209204	100	756	0	0	multi-sensor signal transduction histidine kinase
1662043	209203	100	165	0	0	transcriptional regulator, BadM/Rrf2 family
1662046	209198	100	439	0	0	protein of unknown function DUF224, cysteine-rich region domain protein
1662047	209197	100	126	0	0	acidic cytochrome c3
1662049	209195	100	308	0	0	UspA domain protein
1662050	209194	100	133	0	0	response regulator receiver protein
1662051	209193	100	129	0	0	response regulator receiver protein
1662061	209188	100	184	0	0	conserved hypothetical protein
1662065	209182	100	320	0	0	phosphonate ABC transporter, periplasmic phosphonate-binding protein
1662067	209180	100	119	0	0	response regulator receiver protein
1662071	209176	100	222	0	0	lipoprotein, putative
1662073	209175	100	162	0	0	SEC-C motif domain protein
1662074	209174	100	113	0	0	Dinitrogenase iron-molybdenum cofactor biosynthesis
1662075	209173	100	135	0	0	type IV pilus assembly PilZ
1662076	209171	100	129	0	0	conserved hypothetical protein
1662122	209119	100	259	0	0	protein of unknown function DUF169
1662125	209115	100	307	0	0	Radical SAM domain protein
1662133	209105	100	333	0	0	4Fe-4S ferredoxin, iron-sulfur binding domain protein
1662138	209101	100	325	0	0	binding-protein-dependent transport systems inner membrane component
1662139	209100	100	306	0	0	binding-protein-dependent transport systems inner membrane component
1662140	209099	100	328	0	0	oligopeptide/dipeptide ABC transporter, ATPase subunit
1662141	209098	100	337	0	0	oligopeptide/dipeptide ABC transporter, ATPase subunit
1662144	209094	100	1077	0	0	carbamoyl-phosphate synthase, large subunit
1662145	209093	100	462	0	0	amidophosphoribosyltransferase
1662147	209091	100	173	0	0	thioesterase superfamily protein
1662148	209090	100	332	0	0	class II aldolase/adducin family protein
1662152	209085	100	127	0	0	conserved hypothetical protein
1662156	209082	100	98	0	0	conserved hypothetical protein
1662157	209081	100	350	0	0	protein of unknown function DUF81
1662158	209080	100	203	0	0	lipoprotein, putative
1662159	209079	100	86	0	0	lipoprotein, putative
1662160	209078	100	269	0	0	conserved hypothetical protein
1662161	209077	100	135	0	0	response regulator receiver protein
1662163	209075	100	258	0	0	protein of unknown function UPF0153
1662165	209073	100	224	0	0	peptidase M50
1662166	209072	100	137	0	0	response regulator receiver protein
1662168	209070	100	126	0	0	response regulator receiver protein
1662169	209068	100	303	0	0	PP-loop domain protein
1662171	209065	100	240	0	0	conserved hypothetical protein
1662172	209063	100	374	0	0	protein of unknown function DUF81
1662175	209058	100	352	0	0	protein of unknown function UPF0118
1662179	209053	100	360	0	0	conserved hypothetical protein 698
1662180	209052	100	32	0	0	conserved hypothetical protein
1662181	209051	100	147	0	0	conserved hypothetical protein
1662184	209048	100	454	0	0	two component, sigma54 specific, transcriptional regulator, Fis family
1662189	209043	100	126	0	0	Phosphoribosyl-AMP cyclohydrolase
1662191	209041	100	268	0	0	response regulator receiver protein
1662193	209039	100	368	0	0	integral membrane sensor signal transduction histidine kinase
1662194	209037	100	249	0	0	extracellular solute-binding protein, family 3
1662195	209036	100	223	0	0	polar amino acid ABC transporter, inner membrane subunit
1662203	209027	100	368	0	0	spermidine/putrescine ABC transporter ATPase subunit

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1662204	209026	100	295	0	0	binding-protein-dependent transport systems inner membrane component
1662205	209025	100	257	0	0	binding-protein-dependent transport systems inner membrane component
1662210	209020	100	240	0	0	conserved hypothetical protein
1662221	209012	100	350	0	0	eIF-2B alpha/beta/delta-related uncharacterized proteins
1662223	209010	100	530	0	0	NAD-dependent epimerase/dehydratase
1662224	209009	100	576	0	0	multi-sensor signal transduction histidine kinase
1662227	209006	100	113	0	0	conserved hypothetical protein
1662231	209002	100	147	0	0	polysaccharide biosynthesis domain protein
1662233	209000	100	259	0	0	glucose-1-phosphate cytidyltransferase
1662239	208994	100	189	0	0	CMP/dCMP deaminase, zinc-binding
1662242	208991	100	146	0	0	transcriptional regulator, TrmB
1662244	208989	100	1046	0	0	transporter, hydrophobe/amphiphile efflux-1 (HAE1) family
1662245	208988	100	376	0	0	efflux transporter, RND family, MFP subunit
1662252	208981	100	590	0	0	sulfate transporter
1662253	208980	100	308	0	0	GTP-binding protein Era
1662254	208979	100	237	0	0	alanine racemase domain protein
1662257	208976	100	246	0	0	OmpA/MotB domain protein
1662258	208975	100	169	0	0	flagellar basal body-associated protein FliL
1662259	208974	100	170	0	0	flagellar motor switch protein FliN
1662262	208971	100	89	0	0	flagellar biosynthetic protein FliQ
1662264	208969	100	587	0	0	Lytic transglycosylase, catalytic
1662266	208967	100	151	0	0	transcriptional regulator, TraR/DksA family
1662268	208965	100	138	0	0	protein of unknown function DUF523
1662270	208963	100	57	0	0	conserved hypothetical protein
1662272	208961	100	204	0	0	isochorismatase hydrolase
1662274	208959	100	245	0	0	AzIc family protein
1662275	408289	100	500	0	0	putative transcriptional regulator, GntR family
1662278	208956	100	119	0	0	export-related chaperone CsaA
1662287	208952	100	56	0	0	conserved hypothetical protein
1662290	208949	100	325	0	0	conserved hypothetical protein
1662291	208946	100	202	0	0	Ruberythrin
1662295	208941	100	72	0	0	translation initiation factor IF-1
1662296	208940	100	602	0	0	multi-sensor signal transduction histidine kinase
1662300	208936	100	426	0	0	TRAP dicarboxylate transporter, DetM subunit

PLASMID

locusId_1VIMSS	locusId_2VIMSS	ident	align_len	mismatches	gaps	Description
1659119	209594	75.77	619	123	7	CRISPR-associated protein, Csd1 family
1659128	209604	86.91	489	45	3	type III secretion system apparatus protein YscQ/HrcQ
1659241	209716	89.29	504	13	2	Radical SAM domain protein
1659159	209624	89.67	513	7	1	Radical SAM domain protein
1659107	209728	89.74	156	13	1	Tir chaperone family protein
1659124	209600	90.07	453	27	4	Lytic transglycosylase, catalytic
1659155	209621	90.72	614	18	4	sigma54 specific transcriptional regulator, Fis family
1659198	209669	91.63	466	12	1	glycosyl transferase, group 1
1659145	209614	92.9	169	12	0	conserved hypothetical protein
1659207	209678	92.96	554	23	2	DegT/DnrJ/EryC1/StrS aminotransferase
1659206	209677	93.19	426	13	1	glycosyl transferase, family 2
1659122	209597	93.48	844	53	1	conserved hypothetical protein
1659139	209610	93.85	602	33	2	type III secretion apparatus protein, YscD/HrpQ family
1659104	209725	93.94	594	20	3	conserved hypothetical protein
1659239	408369	94	550	15	1	nitrogenase MoFe cofactor biosynthesis protein NifE
1659105	209726	94.14	1006	32	6	major facilitator superfamily MFS_1
1659098	209719	94.43	1131	47	3	conserved hypothetical protein
1659240	209715	94.96	516	10	2	Nitrogenase
1659201	209672	95.02	462	14	2	glycosyl transferase, group 1
1659192	209662	95.23	461	7	1	conserved hypothetical protein
1659221	209692	95.37	216	10	0	conserved hypothetical protein
1659129	408385	96	225	8	1	type III secretion system needle length determinant
1659117	408387	96.23	212	8	0	CRISPR-associated protein Cas4
1659190	209660	96.36	439	8	1	protein of unknown function DUF201
1659184	209654	96.52	374	13	0	conserved hypothetical protein
1659185	209656	96.63	475	11	1	Patatin
1659197	209668	96.64	298	10	0	eight transmembrane protein EpsH
1659115	209737	96.88	96	3	0	CRISPR-associated protein Cas2
1659121	209595	97.15	702	20	0	metal dependent phosphohydrolase
1659101	209722	97.22	431	12	0	HipA domain protein
1659157	209622	97.39	727	15	1	Stage II sporulation E family protein
1659212	209682	97.64	297	7	0	polysaccharide biosynthesis protein, putative
1659194	209665	97.81	913	5	3	glycosyl hydrolase, BNR repeat-containing protein

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1659191	209661	97.83	415	9	0	conserved hypothetical protein
1659143	408383	97.91	335	7	0	type III secretion system target, YopB family
1659116	209738	97.96	343	7	0	CRISPR-associated protein Cas1
1659238	209713	98	100	2	0	ferredoxin, 2fe-2s
1659108	408391	98.31	1241	21	0	conserved hypothetical protein
1659136	209607	98.35	121	2	0	conserved hypothetical protein
1659215	209685	98.35	484	8	0	sugar transferase
1659199	408375	98.46	195	3	0	transferase hexapeptide repeat containing protein
1659147	209616	98.66	374	5	0	type III secretion regulator YopN/LcrE/InvE/MxiC
1659246	408368	98.69	306	4	0	UspA domain protein
1659123	209599	98.71	155	2	0	Tir chaperone family protein
1659168	209635	98.72	1176	15	0	conserved hypothetical protein
1659178	209647	98.76	889	4	1	asparagine synthase (glutamine-hydrolyzing)
1659106	209727	98.79	413	4	1	conserved hypothetical protein
1659142	209612	98.92	277	3	0	type III secretion system protein, IpaC family, putative
1659118	209592	98.97	290	3	0	CRISPR-associated protein, Csd2 family
1659162	209630	98.97	290	3	0	protein of unknown function DUF554
1659112	209735	98.99	694	7	0	integral membrane sensor signal transduction histidine kinase
1659189	209659	98.99	495	5	0	Orn/DAP/Arg decarboxylase 2
1659165	209633	99.04	1037	10	0	multi-sensor signal transduction histidine kinase
1659202	408373	99.04	416	4	0	glycosyl transferase, group 1
1659181	209650	99.07	643	6	0	Methyltransferase type 11
1659111	209734	99.09	659	6	0	outer membrane autotransporter barrel domain
1659200	408374	99.1	222	2	0	Acetyltransferase (isoleucine patch superfamily)-like
1659164	408380	99.12	339	3	0	conserved hypothetical protein
1659158	209623	99.14	349	3	0	Glycerol-1-phosphate dehydrogenase (NAD(P)(+))
1659247	209718	99.15	117	1	0	histone family protein DNA-binding protein
1659232	408370	99.17	362	3	0	pyruvate carboxyltransferase
1659214	209684	99.25	268	2	0	polysaccharide export protein
1659186	209657	99.26	678	5	0	integral membrane sensor signal transduction histidine kinase
1659125	209601	99.28	138	1	0	putative anti-sigma regulatory factor, serine/threonine protein kinase
1659171	209639	99.29	704	5	0	glycosyl transferase, family 2
1659187	209658	99.3	573	4	0	conserved hypothetical protein
1659220	209691	99.31	288	2	0	conserved hypothetical protein
1659179	209648	99.33	445	3	0	glycosyl transferase, group 1
1659193	209664	99.34	457	3	0	conserved hypothetical protein
1659204	209674	99.35	465	3	0	O-antigen polymerase
1659160	209628	99.37	159	1	0	conserved hypothetical protein
1659144	209613	99.4	166	1	0	type III secretion low calcium response chaperone LcrH/SycD
1659228	209702	99.43	353	2	0	secretion protein HlyD family protein
1659132	408384	99.51	205	1	0	type III secretion apparatus protein, HrpE/YscL family
1659113	408388	99.53	215	1	0	two component transcriptional regulator, LuxR family
1659127	209603	99.54	216	1	0	Yop virulence translocation R
1659216	209686	99.55	886	4	0	Tetrapeptide TPR_2 repeat protein
1659120	408386	99.56	227	1	0	CRISPR-associated protein Cas5 family
1659173	209640	99.56	228	1	0	Adenylyl-sulfate kinase
1659227	209701	99.56	228	1	0	ABC transporter related
1659176	209644	99.57	468	2	0	Radical SAM domain protein
1659103	408392	99.59	245	1	0	extracellular solute-binding protein, family 3
1659161	209629	99.59	485	2	0	Catalase
1659203	408372	99.59	489	2	0	polysaccharide biosynthesis protein
1659134	209606	99.63	271	1	0	type III secretion apparatus lipoprotein, YscJ/HrcJ family
1659153	209619	99.63	271	1	0	type III secretion protein SpaR/YscT/HrcT
1659114	209736	99.64	277	1	0	zinc/iron permease
1659174	408377	99.66	294	1	0	ABC-2 type transporter
1659208	408371	99.69	325	1	0	conserved hypothetical protein
1659183	209653	99.7	660	2	0	conserved hypothetical protein
1659218	209688	99.7	989	3	0	UBA/THIF-type NAD/FAD binding protein
1659154	209620	99.71	346	1	0	type III secretion protein, YscU/HrpY family
1659170	209638	99.71	343	1	0	phage integrase family protein
1659167	209634	99.72	363	1	0	response regulator receiver modulated metal dependent phosphohydrolase
1659205	209676	99.77	438	1	0	conserved hypothetical protein
1659211	209681	99.77	439	1	0	AAA ATPase
1659237	209712	99.78	461	1	0	nitrogenase molybdenum-iron protein beta chain
1659195	209666	99.79	476	1	0	two component, sigma54 specific, transcriptional regulator, Fis family
1659213	209683	99.8	500	1	0	lipopolysaccharide biosynthesis
1659109	209730	99.81	515	1	0	transcriptional regulator, NifA, Fis Family
1659236	209711	99.82	542	1	0	nitrogenase molybdenum-iron protein alpha chain
1659140	209611	99.84	624	1	0	type III secretion outer membrane pore, YscC/HrcC family
1659180	408376	99.86	718	1	0	glycosyl transferase, family 2
1659099	209720	100	272	0	0	Cobyrinic acid a,c-diamide synthase
1659102	209723	100	130	0	0	DNA-binding protein, putative

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1659126	209602	100	111	0	0	anti-sigma-factor antagonist
1659131	209605	100	438	0	0	type III secretion apparatus H <sup>+</sup> -transporting two-sector ATPase
1659137	209608	100	83	0	0	type III secretion system needle protein
1659138	209609	100	69	0	0	conserved hypothetical protein
1659148	408382	100	124	0	0	type III secretion chaperone SycN
1659151	209617	100	697	0	0	type III secretion protein, HrcV family
1659152	209618	100	86	0	0	type III secretion protein, HrpO family
1659163	209631	100	205	0	0	conserved hypothetical protein
1659172	408379	100	293	0	0	glycosyl transferase, family 2
1659175	209643	100	464	0	0	ABC transporter related
1659177	209646	100	229	0	0	sulfotransferase family protein
1659196	209667	100	195	0	0	conserved hypothetical protein
1659209	209679	100	283	0	0	polysaccharide deacetylase
1659210	209680	100	440	0	0	lipoprotein, putative
1659219	209690	100	286	0	0	conserved hypothetical protein
1659224	209694	100	136	0	0	conserved hypothetical protein
1659226	209700	100	376	0	0	protein of unknown function DUF214
1659233	209708	100	277	0	0	nitrogenase iron protein
1659234	209709	100	108	0	0	nitrogen regulatory protein P-II
1659235	209710	100	131	0	0	nitrogen regulatory protein P-II
1659245	209717	100	331	0	0	CBS domain containing protein

**Supplemental Table 2: ORFs present in strain DePue and not strain Hildenborough**

HP – hypothetical protein; CHP – conserved hypothetical protein

**CHROMOSOME**

ORF	Strand	Left bp	Right bp	Length (bp)	Best BLAST hit
Dvul_0010	+	15,142	15,996	854	HP
Dvul_0040	-	55,963	56,880	917	HP
Dvul_0065	+	79,754	80,026	272	HP
Dvul_0077	-	93,604	95,058	1,454	putative GntR-family transcriptional regulator
Dvul_0078	+	95,240	95,716	476	pyridoxamine 5'-phosphate oxidase-related , FMN-binding
Dvul_0083	-	101,089	101,370	281	HP
Dvul_0084	-	101,367	101,684	317	HP
Dvul_0085	-	101,700	101,921	221	DNA binding domain, excisionase family
Dvul_0086	-	102,296	102,829	533	HP
Dvul_0087	-	102,826	105,174	2,348	toprim sub domain protein
Dvul_0088	-	105,174	105,422	248	HP
Dvul_0089	-	105,895	107,097	1,202	phage integrase family protein
Dvul_0091	-	109,337	110,797	1,460	integral membrane sensor signal transduction histidine kinase
Dvul_0110	-	135,660	136,646	986	oligopeptide/dipeptide ABC transporter, ATPase subunit
Dvul_0117	-	141,912	142,202	290	HP
Dvul_0181	+	221,783	222,148	365	HP
Dvul_0231	+	284,226	284,489	263	HP
Dvul_0240	+	295,791	296,162	371	HP
Dvul_0248	+	306,376	306,786	410	HP
Dvul_0258	-	317,775	318,413	638	paraquat-inducible protein A
Dvul_0259	-	318,410	319,006	596	paraquat-inducible protein A
Dvul_0276	-	345,969	346,259	290	HP
Dvul_0356	-	459,734	460,615	881	methyltransferase
Dvul_0418	+	535,525	537,243	1,718	diguanylate cyclase with PAS/PAC sensor
Dvul_0467	-	595,144	594,524	-620	HP
Dvul_0484	-	614,617	614,883	266	HP
Dvul_0486	-	618,361	619,206	845	HP
Dvul_0494	-	631,550	631,813	263	HP
Dvul_0500	-	640,246	640,662	416	HP
Dvul_0511	-	652,896	653,117	221	HP
Dvul_0572	-	722,598	723,668	1,070	HP
Dvul_0618	+	774,601	774,930	329	HP
Dvul_0621	+	775,819	776,115	296	HP
Dvul_0679	+	842,511	842,861	350	HP
Dvul_0684	-	847,146	847,739	593	HP
Dvul_0729	-	893,941	894,180	239	HP
Dvul_0770	-	944,002	944,538	536	Fe-S oxidoreductase
Dvul_0783	-	965,962	966,333	371	HP
Dvul_0785	-	968,972	969,178	206	HP
Dvul_0796	+	979,041	979,940	899	ABC transporter, ATP-binding component
Dvul_0797	+	979,937	981,403	1,466	ABC transporter, permease component
Dvul_0816	-	999,073	999,330	257	HP
Dvul_0837	-	1,026,884	1,028,980	2,096	HP
Dvul_0854	+	1,053,152	1,054,939	1,787	restriction modification system, DNA specificity domain
Dvul_0855	+	1,054,943	1,056,613	1,670	SMC domain protein
Dvul_0856	+	1,056,620	1,057,432	812	HP
Dvul_0857	+	1,057,445	1,058,932	1,487	N-6 DNA methylase
Dvul_0858	+	1,058,935	1,059,288	353	CHP
Dvul_0860	-	1,060,902	1,061,855	953	CHP
Dvul_0861	-	1,062,386	1,068,262	5,876	CHP



*DePue Genome - Supplemental Table 2*

Dvul_0862	-	1,068,859	1,069,581	722	HP
Dvul_0863	-	1,069,931	1,070,302	371	HP
Dvul_0864	-	1,070,308	1,070,682	374	HP
Dvul_0868	-	1,073,342	1,074,094	752	phage prohead protease, HK97 family
Dvul_0874	+	1,080,327	1,080,734	407	transcriptional regulator, putative
Dvul_0875	+	1,080,777	1,081,310	533	putative cold-shock DNA-binding domain protein
Dvul_0876	+	1,081,307	1,081,963	656	HP
Dvul_0880	-	1,086,250	1,086,936	686	sigma-24, FecI-like
Dvul_0881	-	1,086,990	1,087,301	311	HP
Dvul_0882	-	1,087,511	1,088,551	1,040	HP
Dvul_0883	-	1,088,529	1,089,719	1,190	HP
Dvul_0884	+	1,089,927	1,090,280	353	DsrE family protein
Dvul_0885	-	1,090,343	1,090,768	425	HP
Dvul_0886	-	1,090,779	1,092,314	1,535	resolvase, N-terminal domain
Dvul_0887	-	1,092,311	1,092,838	527	putative bacteriophage-related protein
Dvul_0904	+	1,113,473	1,113,721	248	HP
Dvul_0931	+	1,143,887	1,144,648	761	tetratricopeptide TPR_2 repeat protein
Dvul_0937	-	1,151,172	1,151,480	308	HP
Dvul_0941	+	1,154,896	1,155,147	251	HP
Dvul_0947	-	1,162,599	1,163,858	1,259	HP
Dvul_0996	+	1,225,218	1,225,454	236	HP
Dvul_1006	-	1,237,641	1,237,964	323	HP
Dvul_1039	-	1,274,404	1,275,249	845	HP
Dvul_1041	-	1,277,948	1,278,781	833	HP
Dvul_1043	-	1,279,434	1,279,748	314	HP
Dvul_1045	-	1,280,720	1,282,762	2,042	DNA-ligase, NAD-dependent
Dvul_1049	-	1,285,042	1,285,815	773	peptidase S24, S26A and S26B
Dvul_1051	+	1,286,671	1,287,243	572	HP
Dvul_1054	+	1,290,579	1,290,953	374	HP
Dvul_1058	-	1,293,871	1,294,170	299	HP
Dvul_1060	-	1,295,303	1,295,836	533	lipoprotein, putative
Dvul_1077	+	1,308,539	1,309,492	953	HP
Dvul_1078	+	1,309,494	1,310,537	1,043	HP
Dvul_1079	+	1,310,539	1,312,224	1,685	HP
Dvul_1080	+	1,312,221	1,313,018	797	HP
Dvul_1081	+	1,313,026	1,313,301	275	HP
Dvul_1082	+	1,313,567	1,315,732	2,165	HP
Dvul_1116	-	1,354,721	1,354,897	176	pilin, putative
Dvul_1148	-	1,399,817	1,400,155	338	HP
Dvul_1160	+	1,416,789	1,417,121	332	HP
Dvul_1173	-	1,436,434	1,436,694	260	HP
Dvul_1176	+	1,441,088	1,442,659	1,571	putative anti-sigma regulatory factor, serine/threonine protein kinase
Dvul_1179	-	1,444,009	1,444,479	470	HP
Dvul_1206	-	1,478,763	1,479,014	251	HP
Dvul_1238	-	1,516,776	1,516,934	158	HP
Dvul_1274	-	1,557,826	1,558,083	257	HP
Dvul_1292	-	1,580,173	1,580,790	617	HP
Dvul_1306	-	1,596,891	1,597,271	380	HP
Dvul_1307	-	1,597,396	1,597,536	140	HP
Dvul_1330	-	1,622,718	1,623,545	827	CBS domain containing protein
Dvul_1360	+	1,657,534	1,658,532	998	HP
Dvul_1443	-	1,745,393	1,745,686	293	putative transcriptional regulator
Dvul_1444	-	1,745,670	1,745,984	314	HP
Dvul_1445	-	1,746,207	1,746,446	239	HP
Dvul_1447	-	1,748,490	1,749,176	686	HP
Dvul_1448	-	1,749,173	1,749,733	560	nucleoid DNA-binding protein

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Dvul_1449	-	1,749,730	1,750,665	935	HP
Dvul_1452	-	1,752,615	1,753,226	611	HP
Dvul_1457	-	1,755,471	1,757,267	1,796	phage tail tape measure protein, TP901 family
Dvul_1458	-	1,757,288	1,757,428	140	HP
Dvul_1459	-	1,757,473	1,757,733	260	putative phage protein
Dvul_1460	-	1,757,743	1,758,057	314	HP
Dvul_1461	-	1,758,253	1,758,603	350	HP
Dvul_1463	-	1,759,025	1,759,231	206	transcriptional regulator, TraR/DksA family
Dvul_1464	-	1,759,240	1,759,728	488	putative tail tube protein, prophage PSPPH06
Dvul_1466	-	1,760,856	1,761,542	686	phage virion morphogenesis protein
Dvul_1467	-	1,761,535	1,761,999	464	HP
Dvul_1468	-	1,762,002	1,762,493	491	putative head completion/stabilization protein, prophage PSPPH06
Dvul_1469	-	1,762,562	1,763,296	734	phage small terminase subunit
Dvul_1470	-	1,763,299	1,764,324	1,025	phage major capsid protein, P2 family
Dvul_1471	-	1,764,333	1,765,193	860	phage capsid scaffolding
Dvul_1472	+	1,765,341	1,767,140	1,799	HP
Dvul_1473	+	1,767,151	1,768,194	1,043	phage portal protein, PBSX family
Dvul_1474	+	1,768,313	1,769,038	725	lipoprotein
Dvul_1475	+	1,769,160	1,769,399	239	phage transcriptional activator Ogr/delta
Dvul_1476	-	1,769,419	1,770,390	971	HP
Dvul_1477	-	1,770,586	1,770,843	257	HP
Dvul_1478	-	1,770,833	1,771,099	266	HP
Dvul_1479	-	1,771,096	1,771,524	428	HP
Dvul_1480	-	1,772,196	1,773,077	881	D12 class N6 adenine-specific DNA methyltransferase
Dvul_1481	-	1,773,104	1,774,453	1,349	HP
Dvul_1483	-	1,774,788	1,775,192	404	HP
Dvul_1484	-	1,775,767	1,776,366	599	HP
Dvul_1485	-	1,779,304	1,779,744	440	HP
Dvul_1486	-	1,779,764	1,780,090	326	HP
Dvul_1487	+	1,780,775	1,781,803	1,028	phage integrase family protein
Dvul_1488	-	1,782,643	1,782,906	263	putative transcriptional regulator
Dvul_1489	-	1,782,963	1,783,544	581	HP
Dvul_1493	-	1,784,534	1,784,856	322	HP
Dvul_1494	+	1,784,900	1,785,172	272	HP
Dvul_1495	+	1,785,150	1,785,392	242	helix-turn-helix protein, CopG family
Dvul_1496	-	1,785,488	1,786,192	704	phage tail tape measure protein, TP901 family
Dvul_1507	-	1,794,874	1,795,464	590	HP
Dvul_1513	+	1,800,285	1,800,758	473	HP
Dvul_1568	+	1,857,469	1,857,906	437	pyridoxamine 5'-phosphate oxidase-related , FMN-binding
Dvul_1569	-	1,858,350	1,858,697	347	HP
Dvul_1605	+	1,903,681	1,904,100	419	HP
Dvul_1640	-	1,941,966	1,942,211	245	HP
Dvul_1687	+	2,001,362	2,001,664	302	HesB-like domain
Dvul_1730	+	2,040,875	2,041,162	287	HP
Dvul_1773	+	2,070,872	2,071,819	947	HP
Dvul_1794	+	2,096,585	2,097,076	491	HP
Dvul_1886	+	2,197,110	2,197,304	194	HP
Dvul_1893	+	2,204,799	2,205,311	512	HP
Dvul_1896	-	2,210,380	2,210,713	333	HP
Dvul_1961	+	2,279,937	2,280,215	278	HP
Dvul_1971	+	2,289,531	2,289,962	431	HP
Dvul_2003	+	2,334,394	2,334,639	245	HP
Dvul_2011	+	2,343,012	2,343,419	407	HP
Dvul_2122	+	2,464,362	2,465,621	1,259	HP
Dvul_2124	+	2,466,993	2,467,328	335	HP
Dvul_2206	+	2,560,290	2,560,556	266	putative mytomycin resistance protein

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Dvul_2265	-	2,638,895	2,640,574	1,679	histidine kinase
Dvul_2268	+	2,643,252	2,643,884	632	HP
Dvul_2378	-	2,774,612	2,775,370	758	HP
Dvul_2387	+	2,784,782	2,785,498	716	methyltransferase
Dvul_2388	-	2,785,592	2,786,590	998	glycosyl transferase, family 2
Dvul_2389	-	2,786,614	2,787,621	1,007	glycosyl transferase, family 8
Dvul_2390	-	2,787,618	2,788,814	1,196	HP
Dvul_2391	-	2,788,854	2,789,840	986	HP
Dvul_2451	+	2,853,598	2,854,869	1,271	diguanylate phosphodiesterase
Dvul_2478	-	2,884,974	2,885,267	293	HP
Dvul_2551	+	2,978,503	2,978,844	341	HP
Dvul_2563	+	2,993,664	2,993,972	308	HP
Dvul_2564	+	2,994,488	2,995,741	1,253	site-specific recombinase, XerD family
Dvul_2565	+	2,995,738	2,996,763	1,025	HP
Dvul_2566	-	2,996,915	2,997,211	296	HP
Dvul_2567	-	2,997,138	2,997,890	752	CHP
Dvul_2568	+	2,998,737	2,999,012	275	HP
Dvul_2569	+	2,999,489	3,000,421	932	diguanylate cyclase with PAS/PAC sensor
Dvul_2570	+	3,000,502	3,001,008	506	HP
Dvul_2571	+	3,001,226	3,002,035	809	extracellular solute-binding protein, HisJ family
Dvul_2572	-	3,002,296	3,004,383	2,087	methyl-accepting chemotaxis protein
Dvul_2573	+	3,004,804	3,005,646	842	extracellular solute-binding protein, HisJ family
Dvul_2574	-	3,005,719	3,006,189	470	nucleoside 2-deoxyribosyltransferase
Dvul_2575	-	3,006,170	3,006,868	698	nuclease family protein
Dvul_2576	+	3,007,289	3,007,885	596	HP
Dvul_2577	-	3,008,033	3,009,148	1,115	radical SAM domain protein
Dvul_2578	-	3,009,145	3,010,024	879	HP
Dvul_2579	+	3,010,027	3,010,293	266	transposase IS3/IS911 family protein
Dvul_2580	+	3,010,767	3,011,786	1,019	KpsF, predicted sugar phosphate isomerase involved in capsule formation
Dvul_2581	+	3,012,106	3,012,942	836	KpsM, ABC-type polysaccharide transport system, permease component
Dvul_2582	+	3,012,939	3,013,604	665	KpsT, ABC-type polysaccharide transport system, ATPase component
Dvul_2583	+	3,013,591	3,014,901	1,310	KpsE, capsule polysaccharide export protein
Dvul_2584	+	3,014,906	3,016,723	1,817	KpsD, capsule polysaccharide export protein, periplasmic component
Dvul_2585	+	3,017,332	3,018,435	1,103	nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis
Dvul_2586	+	3,018,411	3,019,415	1,004	NAD-dependent epimerase/dehydratase
Dvul_2587	+	3,019,422	3,020,573	1,151	pyridoxal phosphate-dependent enzyme involved in cell wall biogenesis regulation
Dvul_2588	+	3,020,659	3,021,360	701	N-acylneuraminate cytidylyltransferase
Dvul_2589	+	3,021,377	3,025,759	4,382	HP with capsule polysaccharide export domain
Dvul_2590	+	3,025,814	3,026,830	1,016	N-acylneuraminate-9-phosphate synthase
Dvul_2591	+	3,026,827	3,027,990	1,163	UDP-N-acetylglucosamine 2-epimerase
Dvul_2592	+	3,028,032	3,028,688	656	UDP-3-O-(3-hydroxymyristoyl)-like protein
Dvul_2593	+	3,028,700	3,029,095	395	lactoylglutathione lyase
Dvul_2594	+	3,029,359	3,031,008	1,649	FkbH, capsule polysaccharide modification protein
Dvul_2595	+	3,031,005	3,033,056	2,051	KpsC, capsule polysaccharide export protein
Dvul_2596	+	3,033,053	3,034,294	1,241	KpsS, capsule polysaccharide export protein
Dvul_2597	-	3,034,336	3,034,590	254	HP
Dvul_2598	-	3,034,596	3,035,549	953	HP
Dvul_2616	-	3,048,006	3,050,030	2,024	HP
Dvul_2663	-	3,106,288	3,106,566	278	HP
Dvul_2693	-	3,134,903	3,135,673	770	HP
Dvul_2708	+	3,153,586	3,153,855	269	HP

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Dvul_2722	+	3,167,819	3,168,223	404	HP
Dvul_2729	+	3,185,169	3,187,277	2,108	multi-sensor signal transduction histidine kinase
Dvul_2735	-	3,193,173	3,193,826	653	HP
Dvul_2744	-	3,200,607	3,201,293	686	HP
Dvul_2745	-	3,201,290	3,201,850	560	nucleoid DNA-binding protein
Dvul_2746	-	3,201,847	3,202,785	938	HP
Dvul_2749	-	3,204,815	3,205,426	611	HP
Dvul_2752	-	3,206,963	3,208,759	1,796	phage tail tape measure protein, TP901 family
Dvul_2753	-	3,208,780	3,208,920	140	HP
Dvul_2754	-	3,208,965	3,209,225	260	putative phage protein
Dvul_2755	-	3,209,235	3,209,549	314	HP
Dvul_2756	-	3,209,745	3,210,095	350	HP
Dvul_2757	-	3,210,092	3,210,520	428	HP
Dvul_2758	-	3,210,517	3,210,723	206	transcriptional regulator, TraR/DksA family
Dvul_2759	-	3,210,732	3,211,220	488	putative tail tube protein, prophage PSPPH06
Dvul_2760	-	3,211,228	3,212,337	1,109	HP
Dvul_2761	-	3,212,348	3,213,034	686	phage virion morphogenesis protein
Dvul_2762	-	3,213,027	3,213,491	464	HP
Dvul_2763	-	3,213,494	3,213,949	455	putative head completion/stabilization protein, prophage PSPPH06
Dvul_2764	-	3,214,054	3,214,788	734	phage small terminase subunit
Dvul_2765	-	3,214,791	3,215,816	1,025	phage major capsid protein, P2 family
Dvul_2766	-	3,215,825	3,216,673	848	phage capsid scaffolding
Dvul_2767	+	3,216,821	3,218,620	1,799	HP
Dvul_2768	+	3,218,631	3,219,674	1,043	phage portal protein, PBSX family
Dvul_2769	+	3,219,743	3,219,985	242	phage transcriptional activator Ogr/delta
Dvul_2770	-	3,220,041	3,220,478	437	HP
Dvul_2771	-	3,220,575	3,220,781	206	HP
Dvul_2772	-	3,220,999	3,221,244	245	HP
Dvul_2773	-	3,221,234	3,221,500	266	HP
Dvul_2774	-	3,221,497	3,221,925	428	HP
Dvul_2775	+	3,222,228	3,223,205	977	AAA ATPase, central domain protein
Dvul_2776	+	3,223,218	3,225,710	2,492	subtilisin-like serine protease
Dvul_2777	-	3,227,345	3,230,068	2,723	HP
Dvul_2778	-	3,230,245	3,230,703	458	HP
Dvul_2779	-	3,230,696	3,231,049	353	HP
Dvul_2780	+	3,231,137	3,231,403	266	HP
Dvul_2781	+	3,231,475	3,231,735	260	HP
Dvul_2782	+	3,231,739	3,232,809	1,070	phage integrase family protein
Dvul_2796	-	3,250,774	3,251,031	257	HP
Dvul_2932	-	3,430,043	3,430,447	404	HP
Dvul_2936	+	3,435,271	3,437,304	2,033	HP
Dvul_2937	+	3,437,317	3,438,096	779	OmpA/MotB domain protein
Dvul_2938	+	3,438,093	3,439,460	1,367	HP
Dvul_2939	+	3,439,486	3,442,881	3,395	SNF2-related protein
Dvul_2944	+	3,449,340	3,449,582	242	HP

**MEGAPLASMID**

<b>ORF</b>	<b>Strand</b>	<b>Left bp</b>	<b>Right bp</b>	<b>Length (bp)</b>	<b>Best BLAST hit</b>
Dvul_2957	+	4,936	5,196	260	HP
Dvul_2987	-	48,948	49,442	494	type III secretion YscO family protein
Dvul_2990	-	51,686	52,582	896	HP
Dvul_2992	-	53,429	54,289	860	HP
Dvul_2998	-	59,350	59,805	455	Tir chaperone family protein
Dvul_3003	-	62,761	63,063	302	HP
Dvul_3006	+	65,273	65,641	368	HP
Dvul_3007	+	65,644	66,003	359	tetratricopeptide TPR_4
Dvul_3013	+	72,379	72,753	374	HP
Dvul_3023	+	87,387	87,779	392	response regulator receiver domain protein, CheY-like
Dvul_3045	-	122,769	123,776	1,007	methicillin reistance protein, putative
Dvul_3074	-	162,649	163,212	563	HP
Dvul_3079	-	169,754	170,455	701	HP
Dvul_3086	+	177,382	178,206	824	abortive infection protein
Dvul_3087	+	178,500	179,087	587	HP
Dvul_3088	-	179,176	179,532	356	HP
Dvul_3099	+	192,492	193,775	1,283	HP
Dvul_3100	-	193,834	194,190	356	HP
Dvul_3101	+	194,287	194,961	674	HP

**Supplemental Table 3: ORFs within the strain DePue unique exopolysaccharide coding region****Cluster 1**

Coding percentage: 81.0%

Number	ORF	Left bp	Right bp	Strand	Length	Annotation
1	Dvul_2564	2,994,488	2,995,741	+	1253	site-specific recombinase, XerD family
	Dvul_2565	2,995,738	2,996,763	+	1025	hypothetical protein
	Dvul_2566	2,996,915	2,997,211	-	296	hypothetical protein
	Dvul_2567	2,997,138	2,997,890	-	752	conserved hypothetical protein
	Dvul_2568	2,998,737	2,999,012	+	275	hypothetical protein
2	Dvul_2569	2,999,489	3,000,421	+	932	diguanylate cyclase with PAS/PAC sensor
	Dvul_2570	3,000,502	3,001,008	+	506	hypothetical protein
3	Dvul_2571	3,001,226	3,002,035	+	809	extracellular solute-binding protein, HisJ family
4	Dvul_2572	3,002,296	3,004,383	-	2087	methyl-accepting chemotaxis protein
5	Dvul_2573	3,004,804	3,005,646	+	842	extracellular solute-binding protein, HisJ family
6	Dvul_2574	3,005,719	3,006,189	-	470	nucleoside 2-deoxyribosyltransferase
7	Dvul_2575	3,006,170	3,006,868	-	698	nuclease family protein
	Dvul_2576	3,007,289	3,007,885	+	596	hypothetical protein
8	Dvul_2577	3,008,033	3,009,148	-	1115	radical SAM domain protein
	Dvul_2578	3,009,145	3,010,024	-	879	hypothetical protein
9	Dvul_2579	3,010,027	3,010,293	+	266	transposase IS3/IS911 family protein

**Cluster 2**

Coding percentage: 94.2%

Number	ORF	Left bp	Right bp	Strand	Length	Annotation
10	Dvul_2580	3,010,767	3,011,786	+	1019	KpsF, predicted sugar phosphate isomerase involved in capsule formation
11	Dvul_2581	3,012,106	3,012,942	+	836	KpsM, ABC-type polysaccharide transport system, permease component
12	Dvul_2582	3,012,939	3,013,604	+	665	KpsT, ABC-type polysaccharide transport system, ATPase component
13	Dvul_2583	3,013,591	3,014,901	+	1310	KpsE, capsule polysaccharide export protein
14	Dvul_2584	3,014,906	3,016,723	+	1817	KpsD, capsule polysaccharide export protein, periplasmic component
15	Dvul_2585	3,017,332	3,018,435	+	1103	nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis
16	Dvul_2586	3,018,411	3,019,415	+	1004	NAD-dependent epimerase/dehydratase
17	Dvul_2587	3,019,422	3,020,573	+	1151	pyridoxal phosphate-dependent enzyme involved in cell wall biogenesis regulation
18	Dvul_2588	3,020,659	3,021,360	+	701	N-acylneuraminate cytidyltransferase
19	Dvul_2589	3,021,377	3,025,759	+	4382	hypothetical protein with capsule polysaccharide export domain
20	Dvul_2590	3,025,814	3,026,830	+	1016	N-acylneuraminate-9-phosphate synthase
21	Dvul_2591	3,026,827	3,027,990	+	1163	UDP-N-acetylglucosamine 2-epimerase
22	Dvul_2592	3,028,032	3,028,688	+	656	UDP-3-O-(3-hydroxymyristoyl)-like protein
23	Dvul_2593	3,028,700	3,029,095	+	395	lactoylglutathione lyase
24	Dvul_2594	3,029,359	3,031,008	+	1649	FkbH, capsule polysaccharide modification protein
25	Dvul_2595	3,031,005	3,033,056	+	2051	KpsC, capsule polysaccharide export protein
26	Dvul_2596	3,033,053	3,034,294	+	1241	KpsS, capsule polysaccharide export protein

**Supplemental Table 4: CRISPR spacer sequences for strains DePue and Hildenborough***Strain DePue CRISPR spacer sequences*

Spacer	Length (bp)	Sequence
Leader sequence	178	CGCGAACCCCAAGCGACCCTGTTTTACCTGGCAGGTTTCGTGAATATGGCAATA TCCTGTTTTTCATTGAATGGTGTAACCTTTAATACAGGCCAGTCACACATTTTGG CGGTGCTTCTGACCCGGTTCGCGGAACCGACGTCGCAAAGGCACTACTGCCA ACGAGTTTGATGGCTGACA
1	29	CACCGCCTCCGTCTTGATGCCCACATAAA
2	34	CCCAGCATTGGCCACCGTTCGAGCAGGTGAGAT
3	33	TCCAACAAGTGCGATGCCAGCATGTACGCGAAC
4	35	ATCATGCGCACATCGATGTCGTGGCGGACGCGGAT
5	33	CAAGATGGTCGATAACTTCGGCAAGGCGAACCA
6	35	CCCACGAAGCTTGATTGCCCTGACCCGACGCTTGT
7	36	CTCAACGACTCCGTAGCAATTGGTGGGCAAGGGAAT
8	35	ACCCAAAGATGGATTGGTGATGATGGGAAGGAATA
9	35	CCCTTTGCCGCCTGCTGTTGCGGAGCGGGCGGGCA
10	34	TTTTTGTCAAGTGGTGGGTTGTGGCTTCTTTGCAT
11	35	TCGTCGTTGAACAGCGCCTTGAGCGGGATGACCGG
12	35	AACTTGTCGTTGAGCATCTTTGTCAACCGCACGTC
13	34	GCGGAGGCCGTGCATGTCATGAGCGGCGACATCA
14	35	CCAGATATCCCGCAATGCCCGTGGTGGGGCAGCA
15	33	CTGAACCCGGAGGCCAGTACCGATGACATGGAA
16	35	CGACCGAATGCCAACTTGCCGAATGCTGTGTCAGG
17	34	GATGTCTCCTATCGCGTCGACTAGACCTGCGGTG
18	35	AGCCCCTGCATTCTGGATGTCTGCCGAACCGTCGT
19	34	CTGCCGACGCCGCGGCCACATCGACCGCGAGA
20	33	GTGGTGCAAATACGCAAAACATGTTGACCGATG
21	34	CGGACTAATACGATACGTCCCTTCCGTCCGGGGT
22	35	TCGAGATACTCCGTGCGGTGGTACGCAGCCCGCAC
23	35	CGAAACTGACCATAGAGCGCATGCCTGCACGCCTC
24	34	GCCCCACTGTTGCCCGGACGCCGTGGCCTGCCGC
25	35	CGGTATGGATACCTCAGGGTACCTCTCAGCCGTAT
26	34	CGTAAGGTAGGCGTACGGCCCCGCGTCGTCGACG
27	35	AGCATATGGATATGGAAGTGCTGATAGATGGACAA
28	33	TTGTCGAACACCACCAACTGAATATTGGGGGAA
29	34	TCGCGCCTCCTCGTCCGATACGGCGGCGATATCC
30	34	TCCTACATGGCCGCTGACGACCGCGACCGCTCCA
31	34	AGATAGAAGGCGAATTGTGCAAAACCCCGGCATTT
32	34	CACGAAGGCATCCAGCGGCAATTGGCCGTTGGCG
33	34	ACAACCGCCGGCGTGGACTCCACGGCCAACCTTCT
34	34	ACACTCGTGGGCTTCTCGCCGCCCTTGAGCAGGG
35	33	GCGAAGGGCGCGGGCGTCATGGGCGAGGCCGGT
36	36	GAGCAAATGTGAAGTCGTCCAGTGTGTCTTGGGTGA
37	35	GTTTTTTCGGCCCAGTAGGGGAAATGCTTGGCGCA
38	34	ACGGGGTTCGTACGCGCCCTCGTCGGGGCGGAATA
39	34	ACGTAATCACTCATTTTTCCACCTCCGGCCCCGAG
40	35	ACGGGGGCCAGCAACATCGACGCGCTGAACGAGAA
41	34	CCTATGATGTCCCCAAGGAACCTTGAAGCCTTGG
42	34	ACCTGCAGGACGGGACCACGCCTATTTTGAGCAG
43	35	GGCAGCGTCGAAGTCTCAACGCGGTGCTCATCCT
44	35	GTCACCTTGATGGCGGGCTTGATGTCAGCGGCTAT

**Strain Hildenborough CRISPR spacer sequences**

Spacer	Length (bp)	Sequence	Location of matches in strain DePue
Leader sequence	178	CGCGAACCCCAAGCGACCCTGTTTTTCCCGGCAGGTT	
		CGCGAACATGACAATGACCTGTTTTTCATTGAATTGCGT	
		AACCTTTAATGCAGGCTGGTCACACATCTTGGCGGTG	
		CTGCTGGCCCGGTTTCGCGGAACCCCTCGTCGCAAGGTC	
		AATACTGCCAACGTGTTTGATGGCCGACA	
1	33	CAGTCTCGTTACCCTGTCGCGGAGGGCGTCGAT	
2	35	GCCATGCTCAGGCTGGCGAGTGCGCCACTCATCAA	
3	36	CTTGTTTGGAGGCACCAAGAATCAATCAGGCATCGC	
4	33	TTGAGCGCGGCGAGTGCCTGGACATCGTGGCGA	
5	34	ATCACACACCTCGCTTGCTCTACGTTCCCTGCATC	
6	32	CAGTTGGAGGAAGACCATCAACAGTTCATAG	
7	34	ACGCCGCCGGTTCGCGCCGTGCTCAAGTGCATTTG	Intergenic region between Dvul_1048-9
8	35	TGCGATGCACTGCACCGCCATGCCAGCCTGCGCCG	
9	35	CGCGCCGCAGGGTTTCAAGCCGCCACGCTGGACGG	
10	35	TCAACGCCACGCCCTCCGCGATGCACAAGTGGCG	
11	35	GCCCCGACCGACATGGTGCAGCGTGCCATCACGGG	
12	33	GGCAGAAGGCGCGTGAGGTCGCAGCCGAACTTG	
13	33	CGAAGAATTACGCGCAGTACGAAATTGACGAGC	
14	36	ATGGCGGTTGCTGACGTTGCGATGATGCAGCGGCAC	
15	33	AAGTCGCAGGCTTGCGAAGCCTACACGCGCAAG	
16	34	ACGGTGATGCCAAGAAGTGCACAAGCTCGTAGT	
17	33	AGCCTCAACGCGCACGGGGCAGTGTACTCCGCG	
18	33	TCCCTGGCGGCGCAGAGCGTACTGTTTCAGGGAT	Dvul_1039
19	33	GATCTCATAGGCGTTATGGAGCGTGGCTCGTGA	Dvul_1045
20	34	ATCCAGATACCGCAGGATGATGACAACCTACCTGT	Dvul_1049
21	33	AACATCGGAACGGATGTTGACCGTGTGGTGGA	
22	34	GACCTGCCGGTGGTGACAACGGCAATCCTGTTGC	
23	34	TACTATCCCCAAGCCGCCGTCTCGAATCGGCAG	
24	35	CTGTGCATCGGTTGTGGCAGGCGTTGCAGCCTGAA	
25	35	ACCTGATCGATACGGTTATGCCCGTAACGCTGCGC	
26	33	GCGGGCGGGGCGGTGCATCGCTCGGCATCGAG	
27	35	AGCGAAAGTGCCACGCATCAGTCACCTTGGCTAT	



**Supplemental Table 5: Prophage density in select microbial genome sequences**

Organism	Phage	Size (Mb)	Prophage/Mb	Type	Disease	Oxygen Requirement	Temperature range
<i>Bacillus</i> species	1 - 9	3.9 - 5.3	0.26 - 1.72	FIRMICUTES		Aerobe	Mesophile
<i>Clostridium</i> species	1 - 6	2.9 - 4.3	0.31 - 1.54	FIRMICUTES	Y	Obligate anaerobe	Mesophile
<i>Dehalococcoides ethenogenes</i> 195	5	1,500	3.33	CHLOROFLEXI		Anaerobe	Mesophile
<i>Desulfobacterium hafniense</i> Y51	5	5,727	0.87	FIRMICUTES		Anaerobe	Mesophile
<i>Desulfotalea psychrophila</i> LSv54	2	3,523	0.57	PROTEOBACTERIA-DELTA		Anaerobe	Psychrophile
<i>Desulfotomaculum reducens</i> MI-1	5	3,608	1.39	FIRMICUTES		Anaerobe	Mesophile
<b><i>Desulfovibrio desulfuricans</i> G20</b>	<b>6</b>	<b>3,730</b>	<b>1.61</b>	<b>PROTEOBACTERIA-DELTA</b>		<b>Anaerobe</b>	<b>Mesophile</b>
<b><i>Desulfovibrio vulgaris</i> strain DePue</b>	<b>4</b>	<b>3,462</b>	<b>1.16</b>	<b>PROTEOBACTERIA-DELTA</b>		<b>Anaerobe</b>	<b>Mesophile</b>
<b><i>Desulfovibrio vulgaris</i> strain Hildenborough</b>	<b>7</b>	<b>3,570</b>	<b>1.96</b>	<b>PROTEOBACTERIA-DELTA</b>		<b>Anaerobe</b>	<b>Mesophile</b>
<i>Escherichia coli</i> strains	1 - 17	4.6 - 5.6	0.20 - 3.04	PROTEOBACTERIA-GAMMA	Y	Facultative	Mesophile
<i>Haemophilus influenzae</i> strains	1 - 3	1.8 - 1.9	0.53 - 1.57	PROTEOBACTERIA-GAMMA	Y	Facultative	Mesophile
<i>Lactobacillus</i> species	2 - 4	1.8 - 3.3	0.69 - 2.11	FIRMICUTES		Aerobe	Mesophile
<i>Lactococcus lactis</i> strains	4 - 6	2.4 - 2.5	1.64 - 2.37	FIRMICUTES		Facultative	Mesophile
<i>Listeria innocua</i> Clip11262	12	3,011	3.99	FIRMICUTES		Facultative	Mesophile
<i>Mycobacterium</i> species	1 - 2	4.4 - 7.0	0.14 - 0.45	ACTINOBACTERIA	Y	Aerobe	Mesophile
<i>Mycococcus xanthus</i> DK 1622	3	9,139	0.33	PROTEOBACTERIA-DELTA		Obligate aerobe	Mesophile
<i>Neisseria meningitidis</i> strains	1 - 2	2	0.44 - 0.92	PROTEOBACTERIA-BETA	Y	Aerobe	Mesophile
<i>Nitrobacter hamburgensis</i> X14	6	4,406	1.36	PROTEOBACTERIA-ALPHA		Aerobe	Mesophile
<i>Nitrobacter winogradskyi</i> Nb-255	6	3,402	1.76	PROTEOBACTERIA-ALPHA		Facultative	Mesophile
<i>Nitrosomonas eutropha</i> C91	2	2,661	0.75	PROTEOBACTERIA-BETA		Aerobe	Mesophile
<i>Nitrospira multififormis</i> ATCC 25196	1	3,184	0.31	PROTEOBACTERIA-BETA		Aerobe	Mesophile
<i>Pseudomonas</i> species	1 - 6	5.0 - 7.1	0.16 - 0.97	PROTEOBACTERIA-GAMMA	Y	Aerobe	Mesophile
<i>Salmonella</i> species	2 - 6	4.6 - 4.9	0.43 - 1.26	PROTEOBACTERIA-GAMMA	Y	Facultative	Mesophile
<i>Shewanella</i> species	1 - 6	4.5 - 5.3	0.19 - 1.17	PROTEOBACTERIA-GAMMA		Facultative	Mesophile
<i>Shigella</i> species	8 - 16	4.4 - 5.0	1.83 - 3.06	PROTEOBACTERIA-GAMMA	Y	Facultative	Mesophile
<i>Staphylococcus aureus</i> strains	1 - 4	2.5 - 3.0	0.36 - 1.39	FIRMICUTES	Y	Facultative	Mesophile
<i>Streptococcus pyogenes</i> strains	3 - 10	1.8 - 1.9	1.08 - 5.28	FIRMICUTES	Y	Facultative	Mesophile
<i>Synechococcus</i> species	1 - 2	2.2 - 2.7	0.37 - 0.45	CYANOBACTERIA		Aerobe	Mesophile
<i>Syntrophobacter fumaroxidans</i> MPOB	2	4,990	0.40	PROTEOBACTERIA-DELTA		Anaerobe	Mesophile
<i>Syntrophus aciditrophicus</i> SB	2	3,179	0.63	PROTEOBACTERIA-DELTA		Anaerobe	Mesophile
<i>Yersinia pestis</i> strains	2 - 4	4.5 - 4.7	0.44 - 0.85	PROTEOBACTERIA-GAMMA	Y	Aerobe	Mesophile

**Supplemental Table 5: Signal intensity ratios of gDNA from *Desulfovibrio vulgaris* strains hybridized against a strain Hildenborough complete genome microarray**

Boxes indicate phage regions in strain Hildenborough

Refer to Supplemental Figure 1 for COG descriptions

GeneID refers to ORFs in strain Hildenborough

***D. vulgaris* NCIMB 8306 (Brockhurst Hill)**

Gene ID	Ratio to DvH	Predicted function	COG
ORF00120	0.35	sensory transduction histidine kinase, putative	T
ORF00290	0.23	hypothetical protein	
ORF00291	0.48	Nodulation protein A (NodA) family	R
ORF00293	0.13	hypothetical protein	
ORF00295	0.06	conserved hypothetical protein	
ORF00297	0.13	hypothetical protein	
ORF00358	0.17	lipoprotein, putative	
ORF00470	0.48	endoribonuclease L-PSP, putative	J
ORF00491	0.20	Methyl-accepting chemotaxis protein (MCP) signaling domain protein	N
ORF00563	0.48	hypothetical protein	
ORF00765	0.32	tail fiber assembly protein, putative	
ORF00766	0.16	tail fiber protein, putative	
ORF00786	0.29	ATPase domain protein	D
ORF00788	0.49	hypothetical protein	
ORF00823	0.00	conserved domain protein	
ORF00837	0.11	transcriptional regulator, Cro/CI family	K
ORF00850	0.18	protein kinase C inhibitor, putative	
ORF00851	0.14	hypothetical protein	
ORF00852	0.08	hypothetical protein	
ORF00860	0.10	hypothetical protein	
ORF00871	0.44	hypothetical protein	
ORF00873	0.36	hypothetical protein	
ORF00875	0.20	hypothetical protein	
ORF00880	0.35	hypothetical protein	
ORF01265	0.48	thiamine biosynthesis protein ThiC (thiC)	H
ORF01345	0.36	cell cycle protein MesJ	D
ORF01386	0.13	conserved hypothetical protein	
ORF01388	0.06	conserved domain protein	
ORF01389	0.17	nuclease domain protein	
ORF01392	0.26	tail fiber assembly protein, putative	
ORF01426	0.11	conserved hypothetical protein	
ORF01439	0.00	transcriptional regulator cI, truncation	
ORF01445	0.00	hypothetical protein	
ORF01447	0.11	hypothetical protein	
ORF01486	0.12	Hemolysin-type calcium-binding proteins domain protein	
ORF01487	0.25	hypothetical protein	
ORF01508	0.08	conserved domain protein	
ORF01528	0.23	ferritin	P
ORF01573	0.34	chemotaxis protein CheY (cheY-4)	T
ORF01725	0.48	inositol monophosphatase family protein	G
ORF01747	0.00	C4-type zinc finger protein, DksA/TraR family	
ORF01750	0.00	hypothetical protein	
ORF01754	0.10	hypothetical protein	
ORF01758	0.00	hypothetical protein	
ORF01759	0.00	metallo-beta-lactamase superfamily domain protein	J

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ORF01762	0.00	hypothetical protein	
ORF01764	0.00	conserved hypothetical protein	
ORF01766	0.11	type I restriction-modification enzyme, R subunit	V
ORF01769	0.07	hypothetical protein	
ORF01770	0.24	type I restriction-modification enzyme, S subunit	V
ORF01772	0.00	hypothetical protein	
ORF01773	0.00	conserved hypothetical protein	
ORF01775	0.09	type I restriction-modification system, M subunit (hsdM)	V
ORF01777	0.00	conserved hypothetical protein	
ORF01780	0.07	hypothetical protein	
ORF01782	0.00	hypothetical protein	
ORF01783	0.00	hypothetical protein	
ORF01785	0.16	conserved hypothetical protein	
ORF01786	0.19	hypothetical protein	
ORF01788	0.22	hypothetical protein	
ORF01789	0.00	hypothetical protein	
ORF01790	0.00	hypothetical protein	
ORF01792	0.20	conserved domain protein	
ORF01793	0.00	hypothetical protein	
ORF01797	0.12	hypothetical protein	
ORF01798	0.00	hypothetical protein	
ORF01799	0.00	hypothetical protein	
ORF01800	0.00	phage uncharacterized protein, putative	R
ORF01801	0.19	conserved hypothetical protein	
ORF01802	0.10	hypothetical protein	
ORF01805	0.00	killer protein, putative	R
ORF01806	0.09	helix-turn-helix domain protein	R
ORF01808	0.07	hypothetical protein	
ORF01809	0.09	hypothetical protein	
ORF01810	0.00	hypothetical protein	
ORF01811	0.18	hypothetical protein	
ORF01812	0.07	hypothetical protein	
ORF01815	0.00	hypothetical protein	
ORF01816	0.19	conserved hypothetical protein	
ORF01818	0.00	site-specific recombinase, phage integrase family	
ORF01819	0.41	hypothetical protein	
ORF01821	0.00	hypothetical protein	
ORF01822	0.17	hypothetical protein	
ORF01823	0.10	prevent-host-death family protein	D
ORF01824	0.13	hypothetical protein	
ORF01825	0.09	helix-turn-helix domain protein	R
ORF01827	0.43	helix-turn-helix domain protein	R
ORF01830	0.17	C-5 cytosine-specific DNA methylase family protein	L
ORF01831	0.00	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein	T
ORF01833	0.00	hypothetical protein	
ORF01837	0.32	hypothetical protein	
ORF01838	0.16	hypothetical protein	
ORF01840	0.00	hypothetical protein	
ORF01842	0.35	hypothetical protein	
ORF01843	0.15	hypothetical protein	
ORF01844	0.10	hypothetical protein	
ORF01845	0.14	hypothetical protein	
ORF01846	0.14	hypothetical protein	
ORF01848	0.13	hypothetical protein	
ORF01849	0.27	hypothetical protein	

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ORF01850	0.34	site-specific recombinase, phage integrase family	L
ORF01862	0.41	aspartate ammonia-lyase, putative	E
ORF02015	0.43	hypothetical protein	
ORF02268	0.21	hypothetical protein	
ORF02271	0.16	hypothetical protein	
ORF02273	0.00	transposase, IS5 family, truncation	L
ORF02275	0.46	ISDvu4, transposase	
ORF02278	0.27	hypothetical protein	
ORF02280	0.22	parb protein	L
ORF02379	0.40	HD domain protein	T
ORF02413	0.00	GTP pyrophosphokinase (relA)	T
ORF02442	0.27	hypothetical protein	
ORF02445	0.13	conserved hypothetical protein	
ORF02446	0.00	lipoprotein, putative	
ORF02447	0.06	ParA family protein	C
ORF02448	0.00	ParA family protein	C
ORF02450	0.21	hypothetical protein	
ORF02451	0.21	flagellar regulatory protein C (flrC)	K/T
ORF02452	0.23	hypothetical protein	
ORF02569	0.39	hypothetical protein	
ORF02581	0.12	hypothetical protein	
ORF02584	0.07	ISDvu2, transposase OrfB	
ORF02585	0.37	ISDvu2, transposase OrfA	
ORF02593	0.20	hypothetical protein	
ORF02594	0.30	hypothetical protein	
ORF02615	0.00	hypothetical protein	
ORF02617	0.41	hypothetical protein	
ORF02618	0.09	hypothetical protein	
ORF02733	0.00	hypothetical protein	
ORF02735	0.25	Major Outer Sheath Protein C-terminal region family	
ORF02736	0.32	hypothetical protein	
ORF02737	0.25	hypothetical protein	
ORF02738	0.22	hypothetical protein	
ORF02745	0.30	pyruvate formate-lyase activating enzyme, putative	O
ORF02756	0.36	hypothetical protein	
ORF02817	0.47	hypothetical protein	
ORF02870	0.49	hypothetical protein	
ORF02953	0.26	hypothetical protein	
ORF03120	0.23	N-(5'-phosphoribosyl)anthranilate isomerase (trpF)	E
ORF03124	0.21	thioesterase family protein	Q
ORF03128	0.41	lipoprotein, putative	
ORF03129	0.18	hypothetical protein	
ORF03170	0.11	cytochrome c3, putative	
ORF03171	0.22	periplasmic [NiFe] hydrogenase, small subunit, isozyme 2 (hynB)	C
ORF03173	0.25	periplasmic [NiFe] hydrogenase, large subunit, isozyme 2 (hynA)	C
ORF03238	0.29	8-amino-7-oxononanoate synthase, putative	H
ORF03240	0.37	dethiobiotin synthetase (bioD)	H
ORF03374	0.23	hypothetical protein	
ORF03434	0.19	peptidase, S24 family	K
ORF03463	0.13	hypothetical protein	
ORF03478	0.14	hypothetical protein	
ORF03494	0.16	membrane protein, putative	
ORF03543	0.42	C_GCAxxG_C_C family protein	
ORF03668	0.00	site-specific recombinase, phage integrase family	L

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ORF03670	0.09	hypothetical protein	
ORF03671	0.19	hypothetical protein	
ORF03674	0.14	hypothetical protein	
ORF03675	0.00	transcriptional regulator cII, putative	
ORF03676	0.13	hypothetical protein	
ORF03677	0.10	hypothetical protein	
ORF03679	0.09	transcriptional regulator, putative	
ORF03680	0.09	hypothetical protein	
ORF03682	0.00	conserved hypothetical protein	
ORF03685	0.07	conserved hypothetical protein	
ORF03687	0.00	conserved hypothetical protein	
ORF03689	0.17	conserved hypothetical protein	
ORF03692	0.12	type II restriction endonuclease, putative	L
ORF03693	0.08	type II DNA modification methyltransferase, putative	L
ORF03694	0.00	DNA mismatch endonuclease Vsr, putative	L
ORF03695	0.08	hypothetical protein	
ORF03697	0.10	HIT family protein	F/G/R
ORF03698	0.13	hypothetical protein	
ORF03700	0.00	hypothetical protein	
ORF03702	0.34	tail fiber assembly protein, putative	
ORF03703	0.12	tail fiber protein, putative	
ORF03704	0.00	tail protein, putative	S
ORF03706	0.09	tail protein, putative	S
ORF03708	0.21	tail protein, putative	S
ORF03709	0.00	phage baseplate assembly protein V, putative	S
ORF03711	0.11	tail protein, putative	R
ORF03712	0.09	tail/DNA circulation protein, putative	R
ORF03714	0.16	conserved domain protein	
ORF03717	0.00	tail tube protein, putative	
ORF03718	0.08	conserved hypothetical protein	
ORF03720	0.00	tail sheath protein, putative	R
ORF03721	0.00	conserved hypothetical protein	
ORF03723	0.12	hypothetical protein	
ORF03724	0.07	hypothetical protein	
ORF03725	0.04	hypothetical protein	
ORF03726	0.00	hypothetical protein	
ORF03727	0.00	lipoprotein, putative	
ORF03730	0.09	conserved hypothetical protein	
ORF03732	0.20	hypothetical protein	
ORF03733	0.08	major head protein	
ORF03734	0.00	conserved hypothetical protein	
ORF03736	0.16	minor capsid protein C	O/U
ORF03738	0.17	phage portal protein, lambda family	R
ORF03739	0.00	hypothetical protein	
ORF03740	0.08	hypothetical protein	
ORF03741	0.16	DNA binding domain, excisionase family	
ORF03742	0.17	terminase, large subunit, putative	R
ORF03744	0.12	hypothetical protein	
ORF03745	0.09	adenine specific DNA methyltransferase, putative	L
ORF03747	0.12	conserved hypothetical protein	
ORF03748	0.00	hypothetical protein	
ORF03750	0.00	phage/plasmid primase, P4 family	R
ORF03792	0.23	UmuC protein (umuC)	L
ORF03804	0.20	hypothetical protein	

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ORF03934	0.39	NAD-dependent epimerase/dehydratase family protein, putative	M
ORF03978	0.24	HDIG domain protein	T
ORF04060	0.24	hydrogenase maturation protein HypF (hypF)	O
ORF04191	0.10	hypothetical protein	
ORF04227	0.47	glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)	C
ORF04228	0.21	hypothetical protein	
ORF04294	0.26	branched-chain amino acid aminotransferase (ilvE)	E
ORF04468	0.16	hypothetical protein	
ORF04470	0.35	membrane protein, putative	G
ORF04472	0.15	hypothetical protein	
ORF04473	0.24	hypothetical protein	
ORF04474	0.13	hypothetical protein	
ORF04476	0.00	ATP-dependent protease La (lon)	T
ORF04477	0.14	sensor kinase homolog	
ORF04479	0.10	acetoacetate metabolism regulatory protein atoc (atoC)	T
ORF04480	0.22	conserved hypothetical protein	
ORF04489	0.28	conserved hypothetical protein	
ORF04514	0.11	hypothetical protein	
ORF04517	0.43	hypothetical protein	
ORF04520	0.43	hypothetical protein	
ORF04588	0.38	hypothetical protein	
ORF04623	0.49	hypothetical protein	
ORF04801	0.19	TonB domain protein	M
ORF04817	0.46	hypothetical protein	
ORF04873	0.00	chemotaxis protein CheYI (cheYI)	T
ORF04958	0.07	phage/plasmid primase, P4 family	R
ORF04960	0.00	hypothetical protein	
ORF04961	0.00	conserved hypothetical protein	
ORF04963	0.00	adenine specific DNA methyltransferase, putative	L
ORF04964	0.19	hypothetical protein	
ORF04966	0.06	terminase, large subunit, putative	R
ORF04967	0.10	hypothetical protein	
ORF04968	0.12	hypothetical protein	
ORF04969	0.00	phage portal protein, lambda family	R
ORF04971	0.12	minor capsid protein C	O
ORF04973	0.08	conserved hypothetical protein	
ORF04974	0.07	major head protein	
ORF04975	0.13	hypothetical protein	
ORF04976	0.00	holin	R
ORF04977	0.06	conserved hypothetical protein	
ORF04979	0.00	lipoprotein, putative	
ORF04981	0.11	hypothetical protein	
ORF04982	0.00	hypothetical protein	
ORF04983	0.14	hypothetical protein	
ORF04984	0.12	hypothetical protein	
ORF04985	0.00	conserved hypothetical protein	
ORF04987	0.00	tail sheath protein, putative	R
ORF04988	0.00	tail tube protein, putative	
ORF04991	0.11	conserved hypothetical protein	
ORF04994	0.20	conserved domain protein	
ORF04996	0.00	tail/DNA circulation protein, putative	R
ORF04997	0.25	tail protein, putative	R
ORF04999	0.15	phage baseplate assembly protein V, putative	S
ORF05000	0.00	tail protein, putative	S

*DePue Genome - Supplemental Table 6*

ORF05002	0.13	tail protein, putative	S
ORF05003	0.09	tail protein, putative	S
ORF05008	0.07	hypothetical protein	
ORF05010	0.11	conserved hypothetical protein	
ORF05011	0.09	conserved hypothetical protein	
ORF05012	0.14	hypothetical protein	
ORF05014	0.13	hypothetical protein	
ORF05016	0.10	conserved hypothetical protein	
ORF05017	0.09	hypothetical protein	
ORF05020	0.42	hypothetical protein	
ORF05021	0.26	transcriptional regulator cII, putative	
ORF05022	0.14	hypothetical protein	
ORF05023	0.12	hypothetical protein	
ORF05025	0.16	hypothetical protein	
ORF05027	0.27	hypothetical protein	
ORF05028	0.20	hypothetical protein	
ORF05031	0.14	site-specific recombinase, phage integrase family	L
ORF05057	0.37	membrane protein, putative	
ORF05063	0.48	ATP-dependent RNA helicase, DEAD/DEAH box family	R
ORF05067	0.49	acetyltransferase, GNAT family	R
ORF05253	0.37	conserved hypothetical protein	
ORF05356	0.00	chromate transport family protein	P
ORF05362	0.00	Ech hydrogenase, subunit EchE, putative	C
ORF05389	0.24	DNA polymerase III, epsilon subunit, putative	L
ORF05440	0.43	hypothetical protein	
ORF05446	0.37	hypothetical protein	
ORF05576	0.21	hypothetical protein	
ORF05577	0.00	hypothetical protein	
ORF05580	0.00	hypothetical protein	
ORF05581	0.12	hypothetical protein	
ORF05582	0.35	NAD-dependent epimerase/dehydratase family protein	M
ORF05583	0.00	hypothetical protein	
ORF05589	0.18	hypothetical protein	
ORF05590	0.00	lipoprotein, putative	
ORF05593	0.06	glycosyl transferase, group 1 family protein, putative	M
ORF05598	0.16	ISDvu4, transposase, truncation	
ORF05705	0.43	sigma-54 dependent response regulator	T
ORF05707	0.35	sensor histidine kinase/response regulator	T
ORF05709	0.14	hypothetical protein	
ORF05751	0.15	hypothetical protein	
ORF05752	0.14	hypothetical protein	
ORF05753	0.45	tail fiber protein, truncation	
ORF05754	0.09	hypothetical protein	
ORF05755	0.00	hypothetical protein	
ORF05761	0.10	hypothetical protein	
ORF05762	0.00	hypothetical protein	
ORF05763	0.00	transcriptional regulator, putative	
ORF05766	0.26	hypothetical protein	
ORF05770	0.08	hypothetical protein	

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*D. vulgaris* NCIMB 8457 (Woolwich)

Gene ID	Ratio to DvH	Predicted function	COG
ORF00050	0.41	hypothetical protein	
ORF00258	0.44	conserved hypothetical protein	
ORF00290	0.21	hypothetical protein	
ORF00293	0.17	hypothetical protein	
ORF00295	0.07	conserved hypothetical protein	
ORF00297	0.17	hypothetical protein	
ORF00347	0.43	hypothetical protein	
ORF00358	0.20	lipoprotein, putative	
ORF00470	0.44	endoribonuclease L-PSP, putative	J
ORF00523	0.36	organic solvent tolerance protein, putative	M
ORF00763	0.19	adenine specific DNA methyltransferase, putative	L
ORF00765	0.39	tail fiber assembly protein, putative	
ORF00766	0.23	tail fiber protein, putative	
ORF00771	0.20	hypothetical protein	
ORF00774	0.17	baseplate assembly protein, putative	
ORF00777	0.18	baseplate assembly protein, putative	
ORF00778	0.17	hypothetical protein	
ORF00779	0.29	hypothetical protein	
ORF00781	0.00	tail tape measure protein, FRAMESHIFT	
ORF00784	0.15	hypothetical protein	
ORF00786	0.17	ATPase domain protein	D
ORF00788	0.14	hypothetical protein	
ORF00790	0.18	hypothetical protein	
ORF00794	0.12	hypothetical protein	
ORF00795	0.19	virion morphogenesis protein	R
ORF00796	0.00	conserved hypothetical protein	
ORF00797	0.00	hypothetical protein	
ORF00798	0.00	hypothetical protein	
ORF00800	0.00	conserved hypothetical protein	
ORF00802	0.00	conserved hypothetical protein	
ORF00803	0.08	hypothetical protein	
ORF00805	0.00	portal protein, putative	R
ORF00807	0.00	conserved domain protein	
ORF00810	0.00	hypothetical protein	
ORF00811	0.00	hypothetical protein	
ORF00812	0.15	lipoprotein, putative	
ORF00816	0.09	conserved hypothetical protein	
ORF00817	0.00	DNA-binding domain protein	
ORF00818	0.07	hypothetical protein	
ORF00819	0.00	conserved hypothetical protein	
ORF00820	0.29	hypothetical protein	
ORF00822	0.14	DNA-binding protein HU, beta subunit (hupB)	L
ORF00823	0.00	conserved domain protein	
ORF00824	0.10	host-nuclease inhibitor protein Gam, putative	R
ORF00826	0.33	hypothetical protein	
ORF00827	0.00	hypothetical protein	
ORF00829	0.15	bacteriophage DNA transposition B protein, putative	R
ORF00830	0.00	bacteriophage transposase A protein, putative	
ORF00832	0.09	hypothetical protein	
ORF00833	0.09	transcriptional regulator, putative	
ORF00836	0.25	hypothetical protein	



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ORF00837	0.00	transcriptional regulator, Cro/CI family	K
ORF00839	0.30	hypothetical protein	
ORF00840	0.18	transposase, degenerate	
ORF00842	0.19	AlfI	M
ORF00843	0.09	hypothetical protein	
ORF00845	0.23	conserved hypothetical protein	
ORF00860	0.32	hypothetical protein	
ORF00872	0.28	hypothetical protein	
ORF00873	0.09	hypothetical protein	
ORF00936	0.00	fatty acid/phospholipid synthesis protein PlsX (plsX)	
ORF01032	0.28	hypothetical protein	
ORF01064	0.48	primosomal protein N (priA)	L
ORF01345	0.35	cell cycle protein MesJ	D
ORF01376	0.44	hypothetical protein	
ORF01386	0.15	conserved hypothetical protein	
ORF01388	0.08	conserved domain protein	
ORF01389	0.13	nuclease domain protein	
ORF01392	0.22	tail fiber assembly protein, putative	
ORF01426	0.14	conserved hypothetical protein	
ORF01439	0.00	transcriptional regulator cI, truncation	
ORF01445	0.00	hypothetical protein	
ORF01447	0.11	hypothetical protein	
ORF01486	0.14	Hemolysin-type calcium-binding proteins domain protein	
ORF01487	0.29	hypothetical protein	
ORF01508	0.00	conserved domain protein	
ORF01691	0.31	hypothetical protein	
ORF01750	0.00	hypothetical protein	
ORF01758	0.23	hypothetical protein	
ORF01759	0.00	metallo-beta-lactamase superfamily domain protein	J
ORF01762	0.00	hypothetical protein	
ORF01764	0.00	conserved hypothetical protein	
ORF01766	0.18	type I restriction-modification enzyme, R subunit	V
ORF01769	0.07	hypothetical protein	
ORF01770	0.31	type I restriction-modification enzyme, S subunit	V
ORF01772	0.00	hypothetical protein	
ORF01773	0.11	conserved hypothetical protein	
ORF01775	0.12	type I restriction-modification system, M subunit (hsdM)	V
ORF01777	0.00	conserved hypothetical protein	
ORF01780	0.18	hypothetical protein	
ORF01809	0.11	hypothetical protein	
ORF01810	0.00	hypothetical protein	
ORF01811	0.20	hypothetical protein	
ORF01812	0.12	hypothetical protein	
ORF01815	0.15	hypothetical protein	
ORF01819	0.49	hypothetical protein	
ORF01823	0.27	prevent-host-death family protein	D
ORF01825	0.11	helix-turn-helix domain protein	R
ORF01827	0.37	helix-turn-helix domain protein	R
ORF01830	0.20	C-5 cytosine-specific DNA methylase family protein	L
ORF01831	0.00	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein	T
ORF01833	0.00	hypothetical protein	
ORF01834	0.00	hypothetical protein	
ORF01837	0.43	hypothetical protein	
ORF01838	0.24	hypothetical protein	

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ORF01840	0.17	hypothetical protein	
ORF01842	0.40	hypothetical protein	
ORF01848	0.15	hypothetical protein	
ORF01862	0.39	aspartate ammonia-lyase, putative	E
ORF02256	0.30	hypothetical protein	
ORF02259	0.00	quatarnary ammonium compound-resistance protein QacC, putative	P
ORF02261	0.00	hypothetical protein	
ORF02275	0.00	ISDvu4, transposase	
ORF02413	0.00	GTP pyrophosphokinase (relA)	T
ORF02433	0.33	thiamine biosynthesis protein, thiazole moiety	H
ORF02452	0.24	hypothetical protein	
ORF02527	0.00	hypothetical protein	
ORF02536	0.13	conserved hypothetical protein	
ORF02537	0.00	hypothetical protein	
ORF02540	0.23	tail assembly protein, putative	
ORF02542	0.18	hypothetical protein	
ORF02543	0.00	hypothetical protein	
ORF02544	0.00	tail tape measure protein, putative	*
ORF02549	0.00	hypothetical protein	
ORF02550	0.00	hypothetical protein	
ORF02552	0.31	hypothetical protein	
ORF02553	0.38	hypothetical protein	
ORF02554	0.00	hypothetical protein	
ORF02557	0.00	lipoprotein, putative	
ORF02558	0.00	lysozyme, putative	
ORF02559	0.14	holin	
ORF02560	0.28	hypothetical protein	
ORF02561	0.15	major head protein	
ORF02563	0.35	conserved hypothetical protein	
ORF02565	0.21	minor capsid protein C	
ORF02567	0.20	portal protein	
ORF02568	0.22	hypothetical protein	
ORF02569	0.00	hypothetical protein	
ORF02578	0.17	adenine specific DNA methyltransferase, putative	
ORF02580	0.13	hypothetical protein	
ORF02581	0.12	hypothetical protein	
ORF02584	0.00	ISDvu2, transposase OrfB	
ORF02585	0.00	ISDvu2, transposase OrfA	
ORF02586	0.29	hypothetical protein	
ORF02589	0.11	antirepressor, putative	
ORF02593	0.00	hypothetical protein	
ORF02594	0.00	hypothetical protein	
ORF02595	0.11	DNA-binding domain protein, excisionase family	
ORF02596	0.12	terminase, large subunit, putative	
ORF02597	0.00	hypothetical protein	
ORF02598	0.17	hypothetical protein	
ORF02601	0.20	primase, putative	
ORF02602	0.32	transcriptional regulator cII, putative	
ORF02604	0.19	transcriptional regulator, putative	
ORF02606	0.24	hypothetical protein	
ORF02607	0.21	hypothetical protein	
ORF02609	0.15	hypothetical protein	
ORF02610	0.16	hypothetical protein	
ORF02612	0.39	hypothetical protein	

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ORF02613	0.21	hypothetical protein	
ORF02614	0.16	site-specific recombinase, phage integrase family	
ORF02733	0.00	hypothetical protein	
ORF02735	0.22	Major Outer Sheath Protein C-terminal region family	
ORF02736	0.40	hypothetical protein	
ORF02737	0.17	hypothetical protein	
ORF02738	0.00	hypothetical protein	
ORF02886	0.39	glycosyl transferase family protein	
ORF02934	0.41	tonB dependent receptor domain protein	
ORF03120	0.24	N-(5'-phosphoribosyl)anthranilate isomerase (trpF)	E
ORF03124	0.20	thioesterase family protein	Q
ORF03128	0.42	lipoprotein, putative	
ORF03129	0.21	hypothetical protein	
ORF03434	0.23	peptidase, S24 family	K
ORF03444	0.18	hypothetical protein	
ORF03451	0.09	transglycosylase SLT domain protein	
ORF03460	0.25	virion morphogenesis protein	
ORF03462	0.39	virion morphogenesis protein	
ORF03463	0.19	hypothetical protein	
ORF03476	0.26	hypothetical protein	
ORF03478	0.14	hypothetical protein	
ORF03494	0.25	membrane protein, putative	
ORF03496	0.37	hypothetical protein	
ORF03503	0.07	tail fiber protein, putative	
ORF03504	0.16	tail fiber assembly protein, putative	
ORF03543	0.37	C_GCAxxG_C_C family protein	
ORF03655	0.00	Amidohydrolase family superfamily	
ORF03668	0.00	site-specific recombinase, phage integrase family	L
ORF03670	0.09	hypothetical protein	
ORF03671	0.20	hypothetical protein	
ORF03674	0.00	hypothetical protein	
ORF03675	0.00	transcriptional regulator cII, putative	
ORF03676	0.14	hypothetical protein	
ORF03677	0.10	hypothetical protein	
ORF03679	0.10	transcriptional regulator, putative	
ORF03680	0.08	hypothetical protein	
ORF03682	0.00	conserved hypothetical protein	
ORF03685	0.09	conserved hypothetical protein	
ORF03687	0.00	conserved hypothetical protein	
ORF03689	0.17	conserved hypothetical protein	
ORF03692	0.15	type II restriction endonuclease, putative	L
ORF03693	0.08	type II DNA modification methyltransferase, putative	L
ORF03694	0.07	DNA mismatch endonuclease Vsr, putative	L
ORF03695	0.08	hypothetical protein	
ORF03697	0.12	HIT family protein	F/G/R
ORF03698	0.17	hypothetical protein	
ORF03700	0.00	hypothetical protein	
ORF03702	0.29	tail fiber assembly protein, putative	
ORF03703	0.17	tail fiber protein, putative	
ORF03704	0.00	tail protein, putative	S
ORF03706	0.10	tail protein, putative	S
ORF03708	0.20	tail protein, putative	S
ORF03709	0.00	phage baseplate assembly protein V, putative	S
ORF03711	0.10	tail protein, putative	R

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ORF03712	0.09	tail/DNA circulation protein, putative	R
ORF03714	0.16	conserved domain protein	
ORF03717	0.10	tail tube protein, putative	
ORF03718	0.00	conserved hypothetical protein	
ORF03720	0.00	tail sheath protein, putative	R
ORF03721	0.00	conserved hypothetical protein	
ORF03723	0.13	hypothetical protein	
ORF03724	0.07	hypothetical protein	
ORF03725	0.05	hypothetical protein	
ORF03726	0.00	hypothetical protein	
ORF03727	0.00	lipoprotein, putative	
ORF03730	0.11	conserved hypothetical protein	
ORF03732	0.23	hypothetical protein	
ORF03733	0.09	major head protein	
ORF03734	0.10	conserved hypothetical protein	
ORF03736	0.17	minor capsid protein C	O
ORF03738	0.19	phage portal protein, lambda family	R
ORF03739	0.00	hypothetical protein	
ORF03740	0.12	hypothetical protein	
ORF03741	0.16	DNA binding domain, excisionase family	
ORF03742	0.21	terminase, large subunit, putative	R
ORF03744	0.12	hypothetical protein	
ORF03745	0.11	adenine specific DNA methyltransferase, putative	L
ORF03747	0.13	conserved hypothetical protein	
ORF03748	0.00	hypothetical protein	
ORF03750	0.15	phage/plasmid primase, P4 family	R
ORF03804	0.21	hypothetical protein	
ORF03969	0.08	Mg-protoporphyrin IX monomethyl ester oxidative cyclase, putative	C
ORF04004	0.00	methyl-accepting chemotaxis protein, putative	N/T
ORF04060	0.24	hydrogenase maturation protein HypF (hypF)	O
ORF04191	0.11	hypothetical protein	
ORF04294	0.24	branched-chain amino acid aminotransferase (ilvE)	E/H
ORF04334	0.38	hypothetical protein	
ORF04379	0.00	lipoprotein, putative	
ORF04588	0.45	hypothetical protein	
ORF04627	0.00	hypothetical protein	
ORF04759	0.40	conserved hypothetical protein	S
ORF04760	0.39	ZIP zinc transporter family protein	P
ORF04801	0.18	TonB domain protein	M
ORF04828	0.46	shikimate 5-dehydrogenase (aroE)	E
ORF04873	0.00	chemotaxis protein CheYI (cheYI)	T
ORF04958	0.07	phage/plasmid primase, P4 family	R
ORF04960	0.00	hypothetical protein	
ORF04961	0.00	conserved hypothetical protein	
ORF04963	0.00	adenine specific DNA methyltransferase, putative	L
ORF04964	0.16	hypothetical protein	
ORF04966	0.08	terminase, large subunit, putative	R
ORF04967	0.08	hypothetical protein	
ORF04968	0.15	hypothetical protein	
ORF04969	0.00	phage portal protein, lambda family	R
ORF04971	0.11	minor capsid protein C	O/U
ORF04973	0.10	conserved hypothetical protein	
ORF04974	0.08	major head protein	
ORF04975	0.14	hypothetical protein	

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ORF04976	0.06	holin	R
ORF04977	0.09	conserved hypothetical protein	
ORF04979	0.00	lipoprotein, putative	
ORF04981	0.13	hypothetical protein	
ORF04982	0.00	hypothetical protein	
ORF04983	0.15	hypothetical protein	
ORF04984	0.13	hypothetical protein	
ORF04985	0.00	conserved hypothetical protein	
ORF04987	0.00	tail sheath protein, putative	R
ORF04988	0.00	tail tube protein, putative	
ORF04991	0.11	conserved hypothetical protein	
ORF04994	0.16	conserved domain protein	
ORF04996	0.00	tail/DNA circulation protein, putative	R
ORF04997	0.00	tail protein, putative	R
ORF04999	0.16	phage baseplate assembly protein V, putative	S
ORF05000	0.08	tail protein, putative	S
ORF05002	0.12	tail protein, putative	S
ORF05003	0.00	tail protein, putative	S
ORF05006	0.31	tail fiber assembly protein, putative	
ORF05008	0.08	hypothetical protein	
ORF05010	0.11	conserved hypothetical protein	
ORF05011	0.09	conserved hypothetical protein	
ORF05012	0.14	hypothetical protein	
ORF05014	0.12	hypothetical protein	

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ORF05016	0.00	conserved hypothetical protein	
ORF05017	0.09	hypothetical protein	
ORF05020	0.36	hypothetical protein	
ORF05021	0.26	transcriptional regulator cII, putative	
ORF05022	0.19	hypothetical protein	
ORF05023	0.12	hypothetical protein	
ORF05025	0.13	hypothetical protein	
ORF05027	0.27	hypothetical protein	
ORF05028	0.21	hypothetical protein	
ORF05031	0.15	site-specific recombinase, phage integrase family	L
ORF05057	0.39	membrane protein, putative	
ORF05063	0.49	ATP-dependent RNA helicase, DEAD/DEAH box family	R
ORF05356	0.00	chromate transport family protein	P
ORF05362	0.00	Ech hydrogenase, subunit EchE, putative	C
ORF05439	0.13	hypothetical protein	
ORF05440	0.13	hypothetical protein	
ORF05445	0.00	membrane protein, putative	
ORF05446	0.00	hypothetical protein	
ORF05576	0.24	hypothetical protein	
ORF05577	0.00	hypothetical protein	
ORF05580	0.00	hypothetical protein	
ORF05581	0.15	hypothetical protein	
ORF05582	0.48	NAD-dependent epimerase/dehydratase family protein	M/G
ORF05583	0.18	hypothetical protein	
ORF05589	0.27	hypothetical protein	
ORF05590	0.00	lipoprotein, putative	
ORF05593	0.00	glycosyl transferase, group 1 family protein, putative	M
ORF05594	0.45	ISD1, transposase OrfA	
ORF05597	0.10	ISD1, transposase OrfB	
ORF05598	0.34	ISDvu4, transposase, truncation	
ORF05638	0.47	hypothetical protein	
ORF05685	0.32	ABC transporter, ATP-binding protein	Q
ORF05705	0.44	sigma-54 dependent response regulator	T
ORF05707	0.33	sensor histidine kinase/response regulator	T
ORF05709	0.11	hypothetical protein	
ORF05749	0.17	hypothetical protein	
ORF05750	0.00	hypothetical protein	
ORF05751	0.18	hypothetical protein	
ORF05752	0.00	hypothetical protein	
ORF05753	0.48	tail fiber protein, truncation	
ORF05755	0.00	hypothetical protein	
ORF05761	0.15	hypothetical protein	
ORF05762	0.00	hypothetical protein	
ORF05763	0.00	transcriptional regulator, putative	
ORF05766	0.00	hypothetical protein	
ORF05769	0.00	tail fiber protein, putative	
ORF05770	0.00	hypothetical protein	

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*D. vulgaris* ATCC 35115 (Marburg)

Gene ID	Ratio to DvH	Predicted function	COG
ORF00024	0.00	HspA protein, putative	
ORF00044	0.00	hypothetical protein	
ORF00045	0.13	exopolysaccharide production protein, putative	*
ORF00050	0.47	hypothetical protein	*
ORF00120	0.48	sensory transduction histidine kinase, putative	*
ORF00256	0.25	hypothetical protein	*
ORF00290	0.19	hypothetical protein	*
ORF00358	0.24	lipoprotein, putative	*
ORF00523	0.39	organic solvent tolerance protein, putative	*
ORF00618	0.37	hypothetical protein	*
ORF00620	0.25	hypothetical protein	*
ORF00621	0.09	hypothetical protein	*
ORF00622	0.14	Hemolysin-type calcium-binding proteins domain protein	*
ORF00704	0.00	flagellar regulatory protein C (flrC)	*
ORF00763	0.21	adenine specific DNA methyltransferase, putative	L
ORF00765	0.42	tail fiber assembly protein, putative	
ORF00766	0.17	tail fiber protein, putative	
ORF00771	0.15	hypothetical protein	
ORF00774	0.18	baseplate assembly protein, putative	
ORF00777	0.13	baseplate assembly protein, putative	
ORF00778	0.16	hypothetical protein	
ORF00779	0.33	hypothetical protein	
ORF00781	0.00	tail tape measure protein, FRAMESHIFT	
ORF00784	0.14	hypothetical protein	
ORF00786	0.17	ATPase domain protein	D
ORF00788	0.00	hypothetical protein	
ORF00790	0.12	hypothetical protein	
ORF00794	0.11	hypothetical protein	
ORF00795	0.22	virion morphogenesis protein	R
ORF00796	0.00	conserved hypothetical protein	
ORF00797	0.00	hypothetical protein	
ORF00798	0.00	hypothetical protein	
ORF00800	0.00	conserved hypothetical protein	
ORF00802	0.00	conserved hypothetical protein	
ORF00803	0.00	hypothetical protein	
ORF00805	0.00	portal protein, putative	R
ORF00807	0.00	conserved domain protein	
ORF00810	0.00	hypothetical protein	
ORF00811	0.00	hypothetical protein	
ORF00812	0.11	lipoprotein, putative	
ORF00815	0.14	lysozyme, putative	
ORF00816	0.10	conserved hypothetical protein	
ORF00817	0.00	DNA-binding domain protein	
ORF00818	0.00	hypothetical protein	
ORF00819	0.00	conserved hypothetical protein	
ORF00820	0.27	hypothetical protein	
ORF00822	0.12	DNA-binding protein HU, beta subunit (hupB)	L
ORF00823	0.00	conserved domain protein	
ORF00824	0.00	host-nuclease inhibitor protein Gam, putative	R
ORF00826	0.00	hypothetical protein	
ORF00827	0.00	hypothetical protein	

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ORF00829	0.00	bacteriophage DNA transposition B protein, putative	R
ORF00830	0.00	bacteriophage transposase A protein, putative	
ORF00832	0.07	hypothetical protein	
ORF00833	0.00	transcriptional regulator, putative	
ORF00836	0.00	hypothetical protein	
ORF00837	0.00	transcriptional regulator, Cro/CI family	K
ORF00839	0.27	hypothetical protein	
ORF00840	0.00	transposase, degenerate	
ORF00842	0.20	AlgI	M
ORF00843	0.00	hypothetical protein	
ORF00845	0.26	conserved hypothetical protein	
ORF00846	0.00	hypothetical protein	
ORF00847	0.00	hypothetical protein	
ORF00850	0.25	protein kinase C inhibitor, putative	
ORF00851	0.13	hypothetical protein	
ORF00852	0.00	hypothetical protein	
ORF00854	0.13	nitrogen regulation protein NR(I) (ntrC)	
ORF00856	0.17	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family	
ORF00857	0.14	hypothetical protein	
ORF00860	0.19	hypothetical protein	
ORF00862	0.17	urea transporter, putative	
ORF00865	0.00	hypothetical protein	
ORF00867	0.38	hypothetical protein	
ORF00868	0.00	major facilitator superfamily protein	
ORF00869	0.00	aliphatic amidase (amiE)	
ORF00871	0.21	hypothetical protein	
ORF00872	0.47	hypothetical protein	
ORF00875	0.21	hypothetical protein	
ORF00936	0.00	fatty acid/phospholipid synthesis protein PlsX (plsX)	
ORF00938	0.00	conserved hypothetical protein	
ORF01024	0.36	outer membrane protein P1, putative	
ORF01032	0.00	hypothetical protein	
ORF01033	0.40	hypothetical protein	
ORF01035	0.00	hypothetical protein	
ORF01037	0.48	twitching motility protein PilT (pilT-1)	
ORF01050	0.36	hypothetical protein	
ORF01305	0.37	membrane protein, putative	
ORF01376	0.00	hypothetical protein	
ORF01386	0.12	conserved hypothetical protein	
ORF01388	0.07	conserved domain protein	
ORF01389	0.00	nuclease domain protein	
ORF01392	0.28	tail fiber assembly protein, putative	
ORF01398	0.30	minor tail protein, putative	
ORF01399	0.00	hypothetical protein	
ORF01401	0.00	tail tape measure protein, putative	
ORF01402	0.00	conserved hypothetical protein	
ORF01404	0.00	hypothetical protein	
ORF01406	0.00	hypothetical protein	
ORF01410	0.15	conserved hypothetical protein	
ORF01411	0.15	hypothetical protein	
ORF01412	0.00	major capsid protein, HK97 family	
ORF01415	0.12	ClpP protease family protein	
ORF01416	0.16	portal protein, HK97 family	
ORF01417	0.00	terminase, large subunit	



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ORF01420	0.20	terminase, small subunit
ORF01421	0.00	holin, putative
ORF01422	0.00	hypothetical protein
ORF01423	0.13	hypothetical protein
ORF01426	0.00	conserved hypothetical protein
ORF01431	0.08	hypothetical protein
ORF01432	0.41	conserved hypothetical protein
ORF01434	0.16	hypothetical protein
ORF01436	0.22	type II DNA modification methyltransferase, putative
ORF01437	0.11	hypothetical protein
ORF01438	0.00	transcriptional regulator cII, putative
ORF01439	0.00	transcriptional regulator cI, truncation
ORF01445	0.00	hypothetical protein
ORF01447	0.00	hypothetical protein
ORF01448	0.00	hypothetical protein
ORF01449	0.13	hypothetical protein
ORF01450	0.00	conserved hypothetical protein
ORF01452	0.24	conserved domain protein
ORF01454	0.00	site-specific recombinase, phage integrase family
ORF01486	0.00	Hemolysin-type calcium-binding proteins domain protein
ORF01487	0.34	hypothetical protein
ORF01488	0.31	PAS domain S-box protein
ORF01508	0.00	conserved domain protein
ORF01645	0.11	hypothetical protein
ORF01660	0.38	conserved hypothetical protein, degenerate, POINT MUTATION
ORF01681	0.00	tRNA nucleotidyl transferase-related protein
ORF01691	0.16	hypothetical protein
ORF01747	0.00	C4-type zinc finger protein, DksA/TraR family
ORF01750	0.00	hypothetical protein
ORF01754	0.00	hypothetical protein
ORF01758	0.00	hypothetical protein
ORF01759	0.00	metallo-beta-lactamase superfamily domain protein
ORF01762	0.00	hypothetical protein
ORF01764	0.00	conserved hypothetical protein
ORF01766	0.17	type I restriction-modification enzyme, R subunit
ORF01769	0.07	hypothetical protein
ORF01770	0.27	type I restriction-modification enzyme, S subunit
ORF01772	0.00	hypothetical protein
ORF01773	0.00	conserved hypothetical protein
ORF01775	0.00	type I restriction-modification system, M subunit (hsdM)
ORF01777	0.00	conserved hypothetical protein
ORF01780	0.18	hypothetical protein
ORF01782	0.00	hypothetical protein
ORF01783	0.00	hypothetical protein
ORF01785	0.27	conserved hypothetical protein
ORF01786	0.26	hypothetical protein
ORF01788	0.00	hypothetical protein
ORF01789	0.00	hypothetical protein
ORF01790	0.00	hypothetical protein
ORF01792	0.21	conserved domain protein
ORF01793	0.00	hypothetical protein
ORF01797	0.17	hypothetical protein
ORF01798	0.00	hypothetical protein
ORF01799	0.00	hypothetical protein

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ORF01800	0.00	phage uncharacterized protein, putative
ORF01801	0.28	conserved hypothetical protein
ORF01802	0.11	hypothetical protein
ORF01803	0.10	hypothetical protein
ORF01808	0.00	hypothetical protein
ORF01809	0.10	hypothetical protein
ORF01810	0.00	hypothetical protein
ORF01811	0.29	hypothetical protein
ORF01812	0.10	hypothetical protein
ORF01815	0.00	hypothetical protein
ORF01816	0.21	conserved hypothetical protein
ORF01818	0.00	site-specific recombinase, phage integrase family
ORF01819	0.38	hypothetical protein
ORF01821	0.00	hypothetical protein
ORF01822	0.00	hypothetical protein
ORF01823	0.16	prevent-host-death family protein
ORF01824	0.15	hypothetical protein
ORF01825	0.12	helix-turn-helix domain protein
ORF01830	0.22	C-5 cytosine-specific DNA methylase family protein
ORF01831	0.00	ATPase, histidine kinase-, DNA gyrase B-like domain protein
ORF01833	0.00	hypothetical protein
ORF01837	0.43	hypothetical protein
ORF01838	0.18	hypothetical protein
ORF01840	0.25	hypothetical protein
ORF01842	0.43	hypothetical protein
ORF01843	0.23	hypothetical protein
ORF01844	0.00	hypothetical protein
ORF01845	0.19	hypothetical protein
ORF01846	0.16	hypothetical protein
ORF01848	0.16	hypothetical protein
ORF01849	0.31	hypothetical protein
ORF01968	0.21	succinyl-diaminopimelate desuccinylase (dapE-2)
ORF01970	0.16	glucose inhibited division protein A (gidA)
ORF01971	0.00	hypothetical protein
ORF01975	0.00	hypothetical protein
ORF02015	0.48	hypothetical protein
ORF02019	0.00	cold shock domain family protein
ORF02236	0.00	conserved domain protein
ORF02244	0.00	hypothetical protein
ORF02259	0.00	quaternary ammonium compound-resistance protein QacC, putative
ORF02261	0.00	hypothetical protein
ORF02264	0.00	hypothetical protein
ORF02266	0.24	sulfate transporter family protein
ORF02270	0.00	site-specific recombinase, phage integrase family, FRAMESHIFT
ORF02271	0.46	hypothetical protein
ORF02273	0.00	transposase, IS5 family, truncation
ORF02275	0.00	ISDvu4, transposase
ORF02276	0.00	hypothetical protein
ORF02278	0.34	hypothetical protein
ORF02347	0.00	transposase OrfA, IS3 family, degenerate
ORF02379	0.35	HD domain protein
ORF02413	0.00	GTP pyrophosphokinase (relA)
ORF02438	0.00	carbon monoxide dehydrogenase accessory protein CooC
ORF02440	0.00	universal stress protein family, putative

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ORF02447	0.00	ParA family protein
ORF02448	0.00	ParA family protein
ORF02450	0.26	hypothetical protein
ORF02452	0.25	hypothetical protein
ORF02461	0.46	hypothetical protein
ORF02536	0.00	conserved hypothetical protein
ORF02537	0.00	hypothetical protein
ORF02540	0.00	tail assembly protein, putative
ORF02542	0.00	hypothetical protein
ORF02543	0.00	hypothetical protein
ORF02544	0.00	tail tape measure protein, putative
ORF02548	0.00	hypothetical protein
ORF02549	0.00	hypothetical protein
ORF02550	0.00	hypothetical protein
ORF02552	0.00	hypothetical protein
ORF02554	0.00	hypothetical protein
ORF02557	0.00	lipoprotein, putative
ORF02558	0.00	lysozyme, putative
ORF02559	0.18	holin
ORF02560	0.31	hypothetical protein
ORF02561	0.18	major head protein
ORF02563	0.42	conserved hypothetical protein
ORF02565	0.00	minor capsid protein C
ORF02567	0.21	portal protein
ORF02568	0.26	hypothetical protein
ORF02569	0.00	hypothetical protein
ORF02578	0.17	adenine specific DNA methyltransferase, putative
ORF02580	0.19	hypothetical protein
ORF02581	0.13	hypothetical protein
ORF02584	0.00	ISDvu2, transposase OrfB
ORF02585	0.35	ISDvu2, transposase OrfA
ORF02586	0.26	hypothetical protein
ORF02589	0.00	antirepressor, putative
ORF02593	0.00	hypothetical protein
ORF02594	0.00	hypothetical protein
ORF02595	0.11	DNA-binding domain protein, excisionase family
ORF02596	0.00	terminase, large subunit, putative
ORF02597	0.00	hypothetical protein
ORF02598	0.00	hypothetical protein
ORF02601	0.20	primase, putative
ORF02602	0.29	transcriptional regulator cII, putative
ORF02604	0.18	transcriptional regulator, putative
ORF02606	0.29	hypothetical protein
ORF02607	0.24	hypothetical protein
ORF02609	0.19	hypothetical protein
ORF02610	0.00	hypothetical protein
ORF02612	0.42	hypothetical protein
ORF02613	0.21	hypothetical protein
ORF02614	0.13	site-specific recombinase, phage integrase family
ORF02703	0.32	MutT/nudix family protein family
ORF02733	0.00	hypothetical protein
ORF02735	0.19	Major Outer Sheath Protein C-terminal region family
ORF02736	0.33	hypothetical protein
ORF02737	0.23	hypothetical protein

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ORF02738	0.00	hypothetical protein
ORF02745	0.48	pyruvate formate-lyase activating enzyme, putative
ORF02756	0.38	hypothetical protein
ORF02923	0.35	hypothetical protein
ORF02925	0.22	Bacterial regulatory helix-turn-helix proteins, araC family protein
ORF02927	0.23	peptidase, M16 family, putative
ORF02928	0.14	ABC transporter, ATP-binding protein
ORF02930	0.15	hypothetical protein
ORF02932	0.34	hypothetical protein
ORF02934	0.23	tonB dependent receptor domain protein
ORF02936	0.00	ABC transporter, periplasmic substrate-binding protein
ORF02937	0.24	ABC transporter, permease protein
ORF02940	0.12	ABC transporter, permease protein
ORF02942	0.21	ABC transporter, ATP-binding protein
ORF02945	0.44	tolQ protein (tolQ)
ORF02947	0.21	ExbD/TolR family protein (tolR)
ORF02953	0.18	hypothetical protein
ORF03120	0.27	N-(5'-phosphoribosyl)anthranilate isomerase (trpF)
ORF03124	0.21	thioesterase family protein
ORF03128	0.42	lipoprotein, putative
ORF03129	0.20	hypothetical protein
ORF03240	0.31	dethiobiotin synthetase (bioD)
ORF03321	0.00	TPR Domain domain protein
ORF03434	0.22	peptidase, S24 family
ORF03449	0.28	hypothetical protein
ORF03453	0.38	hypothetical protein
ORF03460	0.29	virion morphogenesis protein
ORF03463	0.20	hypothetical protein
ORF03478	0.13	hypothetical protein
ORF03494	0.16	membrane protein, putative
ORF03496	0.40	hypothetical protein
ORF03543	0.40	C_GCAXxG_C_C family protein
ORF03644	0.35	hypothetical protein
ORF03662	0.38	formate acetyltransferase
ORF03668	0.00	site-specific recombinase, phage integrase family
ORF03670	0.00	hypothetical protein
ORF03671	0.24	hypothetical protein
ORF03674	0.00	hypothetical protein
ORF03675	0.00	transcriptional regulator cII, putative
ORF03676	0.16	hypothetical protein
ORF03677	0.12	hypothetical protein
ORF03679	0.11	transcriptional regulator, putative
ORF03680	0.10	hypothetical protein
ORF03682	0.00	conserved hypothetical protein
ORF03685	0.00	conserved hypothetical protein
ORF03687	0.00	conserved hypothetical protein
ORF03689	0.16	conserved hypothetical protein
ORF03692	0.22	type II restriction endonuclease, putative
ORF03693	0.11	type II DNA modification methyltransferase, putative
ORF03694	0.00	DNA mismatch endonuclease Vsr, putative
ORF03695	0.00	hypothetical protein
ORF03697	0.13	HIT family protein
ORF03698	0.16	hypothetical protein
ORF03700	0.00	hypothetical protein

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ORF03702	0.23	tail fiber assembly protein, putative
ORF03703	0.22	tail fiber protein, putative
ORF03704	0.00	tail protein, putative
ORF03706	0.00	tail protein, putative
ORF03708	0.21	tail protein, putative
ORF03709	0.00	phage baseplate assembly protein V, putative
ORF03711	0.00	tail protein, putative
ORF03712	0.00	tail/DNA circulation protein, putative
ORF03714	0.00	conserved domain protein
ORF03717	0.11	tail tube protein, putative
ORF03718	0.00	conserved hypothetical protein
ORF03720	0.00	tail sheath protein, putative
ORF03721	0.00	conserved hypothetical protein
ORF03723	0.16	hypothetical protein
ORF03724	0.00	hypothetical protein
ORF03725	0.07	hypothetical protein
ORF03726	0.00	hypothetical protein
ORF03727	0.00	lipoprotein, putative
ORF03730	0.14	conserved hypothetical protein
ORF03732	0.27	hypothetical protein
ORF03733	0.00	major head protein
ORF03734	0.00	conserved hypothetical protein
ORF03736	0.15	minor capsid protein C
ORF03738	0.18	phage portal protein, lambda family
ORF03739	0.00	hypothetical protein
ORF03740	0.10	hypothetical protein
ORF03741	0.20	DNA binding domain, excisionase family
ORF03742	0.29	terminase, large subunit, putative
ORF03744	0.16	hypothetical protein
ORF03745	0.11	adenine specific DNA methyltransferase, putative
ORF03747	0.15	conserved hypothetical protein
ORF03748	0.00	hypothetical protein
ORF03750	0.00	phage/plasmid primase, P4 family
ORF03804	0.26	hypothetical protein
ORF03927	0.27	glycosyl transferase, group 2 family protein domain protein
ORF03929	0.22	glycosyl transferase, group 2 family protein domain protein
ORF03932	0.15	glycosyl transferase, group 1 family protein domain protein
ORF03934	0.15	NAD-dependent epimerase/dehydratase family protein, putative
ORF03936	0.00	hypothetical protein
ORF03937	0.17	hypothetical protein
ORF03938	0.49	methionyl-tRNA formyltransferase, putative
ORF03940	0.30	hypothetical protein
ORF03941	0.00	conserved domain protein
ORF03943	0.34	conserved hypothetical protein
ORF03945	0.00	hypothetical protein
ORF03947	0.18	moaA / nifB / pqqE family family
ORF03948	0.00	perosamine synthase (rfbE)
ORF03950	0.24	Cytidylyltransferase family (spsF)
ORF03951	0.00	hypothetical protein
ORF03953	0.24	neuB protein, putative
ORF03955	0.16	hypothetical protein
ORF03957	0.00	perosamine synthetase (lpsC)
ORF03958	0.23	conserved hypothetical protein
ORF03960	0.22	membrane protein, putative

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ORF03962	0.17	dolichol-phosphate mannosyltransferase (dmt)
ORF03966	0.00	conserved domain protein
ORF03969	0.10	Mg-protoporphyrin IX monomethyl ester oxidative cyclase, putative
ORF03970	0.26	hypothetical protein
ORF03972	0.00	moaA / nifB / pqqE family family
ORF03973	0.16	oxidative cyclase, putative
ORF04060	0.24	hydrogenase maturation protein HypF (hypF)
ORF04068	0.46	oxidoreductase, putative
ORF04191	0.14	hypothetical protein
ORF04220	0.00	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)
ORF04294	0.29	branched-chain amino acid aminotransferase (ilvE)
ORF04379	0.00	lipoprotein, putative
ORF04503	0.24	hypothetical protein
ORF04517	0.46	hypothetical protein
ORF04627	0.00	hypothetical protein
ORF04801	0.19	TonB domain protein
ORF04873	0.00	chemotaxis protein CheYI (cheYI)
ORF04958	0.08	phage/plasmid primase, P4 family
ORF04960	0.00	hypothetical protein
ORF04961	0.00	conserved hypothetical protein
ORF04963	0.00	adenine specific DNA methyltransferase, putative
ORF04964	0.18	hypothetical protein
ORF04966	0.08	terminase, large subunit, putative
ORF04967	0.09	hypothetical protein
ORF04968	0.17	hypothetical protein
ORF04969	0.00	phage portal protein, lambda family
ORF04971	0.14	minor capsid protein C
ORF04973	0.00	conserved hypothetical protein
ORF04974	0.08	major head protein
ORF04975	0.14	hypothetical protein
ORF04976	0.00	holin
ORF04977	0.08	conserved hypothetical protein
ORF04979	0.00	lipoprotein, putative
ORF04981	0.14	hypothetical protein
ORF04982	0.00	hypothetical protein
ORF04983	0.17	hypothetical protein
ORF04984	0.14	hypothetical protein
ORF04985	0.00	conserved hypothetical protein
ORF04987	0.00	tail sheath protein, putative
ORF04988	0.00	tail tube protein, putative
ORF04991	0.12	conserved hypothetical protein
ORF04994	0.17	conserved domain protein
ORF04996	0.00	tail/DNA circulation protein, putative
ORF04997	0.00	tail protein, putative
ORF04999	0.18	phage baseplate assembly protein V, putative
ORF05000	0.00	tail protein, putative
ORF05002	0.15	tail protein, putative
ORF05003	0.00	tail protein, putative
ORF05004	0.49	tail fiber protein, putative
ORF05006	0.50	tail fiber assembly protein, putative
ORF05008	0.10	hypothetical protein
ORF05010	0.00	conserved hypothetical protein
ORF05011	0.11	conserved hypothetical protein
ORF05012	0.16	hypothetical protein

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ORF05014	0.15	hypothetical protein
ORF05016	0.00	conserved hypothetical protein
ORF05017	0.16	hypothetical protein
ORF05021	0.26	transcriptional regulator cII, putative
ORF05022	0.20	hypothetical protein
ORF05023	0.14	hypothetical protein
ORF05025	0.18	hypothetical protein
ORF05027	0.35	hypothetical protein
ORF05028	0.25	hypothetical protein
ORF05031	0.16	site-specific recombinase, phage integrase family
ORF05063	0.49	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF05125	0.19	hypothetical protein
ORF05127	0.18	hypothetical protein
ORF05140	0.36	hypothetical protein
ORF05258	0.39	hypothetical protein
ORF05260	0.00	hypothetical protein
ORF05261	0.31	hypothetical protein
ORF05264	0.31	hypothetical protein
ORF05265	0.00	conserved hypothetical protein
ORF05267	0.09	membrane protein, putative
ORF05268	0.00	CoA-binding domain protein
ORF05269	0.18	pyruvate ferredoxin/ferredoxin oxidoreductase family
ORF05271	0.00	glutamate dehydrogenase, putative
ORF05272	0.27	hypothetical protein
ORF05273	0.22	thioredoxin reductase (trxB)
ORF05274	0.14	thioredoxin, putative
ORF05277	0.31	DNR protein, putative
ORF05279	0.18	sulfatase family protein [imported], putative
ORF05280	0.27	hypothetical protein
ORF05281	0.09	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaC (nhaC)
ORF05282	0.00	hypothetical protein
ORF05292	0.00	amino acid ABC transporter, permease protein
ORF05312	0.00	hypothetical protein
ORF05356	0.00	chromate transport family protein
ORF05362	0.00	Ech hydrogenase, subunit EchE, putative
ORF05389	0.20	DNA polymerase III, epsilon subunit, putative
ORF05430	0.00	anthranilate phosphoribosyltransferase (trpD)
ORF05439	0.15	hypothetical protein
ORF05440	0.19	hypothetical protein
ORF05445	0.00	membrane protein, putative
ORF05446	0.00	hypothetical protein
ORF05576	0.26	hypothetical protein
ORF05577	0.00	hypothetical protein
ORF05580	0.00	hypothetical protein
ORF05581	0.17	hypothetical protein
ORF05582	0.39	NAD-dependent epimerase/dehydratase family protein
ORF05583	0.00	hypothetical protein
ORF05586	0.00	ISDvu3, transposase OrfB POINT MUTATION
ORF05589	0.26	hypothetical protein
ORF05590	0.00	lipoprotein, putative
ORF05593	0.00	glycosyl transferase, group 1 family protein, putative
ORF05598	0.38	ISDvu4, transposase, truncation
ORF05691	0.00	hypothetical protein
ORF05693	0.35	hypothetical protein

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ORF05705	0.41	sigma-54 dependent response regulator
ORF05707	0.45	sensor histidine kinase/response regulator
ORF05709	0.17	hypothetical protein
ORF05749	0.22	hypothetical protein
ORF05750	0.00	hypothetical protein
ORF05751	0.00	hypothetical protein
ORF05752	0.00	hypothetical protein
ORF05753	0.00	tail fiber protein, truncation
ORF05754	0.09	hypothetical protein
ORF05755	0.00	hypothetical protein
ORF05756	0.00	conserved domain protein
ORF05757	0.00	hypothetical protein
ORF05758	0.00	hypothetical protein
ORF05759	0.14	hypothetical protein
ORF05760	0.00	head-tail adaptor, putative
ORF05761	0.00	hypothetical protein
ORF05762	0.00	hypothetical protein
ORF05763	0.00	transcriptional regulator, putative
ORF05764	0.13	hypothetical protein
ORF05765	0.00	hypothetical protein
ORF05766	0.00	hypothetical protein
ORF05767	0.19	hypothetical protein
ORF05769	0.00	tail fiber protein, putative
ORF05770	0.00	hypothetical protein

*D. vulgaris* NCIMB 8446 (Llanelly)

Gene ID	Ratio to DvH	Predicted function	COG
ORF00024	0.00	HspA protein, putative	O
ORF00936	0.00	fatty acid/phospholipid synthesis protein PlsX (plsX)	
ORF02259	0.00	quaternary ammonium compound-resistance protein QacC, putative	P
ORF02261	0.00	hypothetical protein	
ORF02270	0.00	site-specific recombinase, phage integrase family, FRAMESHIFT	
ORF02413	0.00	GTP pyrophosphokinase (relA)	T
ORF02584	0.49	ISDvu2, transposase OrfB	
ORF03682	0.41	conserved hypothetical protein	S
ORF04873	0.00	chemotaxis protein CheYI (cheYI)	T
ORF05292	0.00	amino acid ABC transporter, permease protein, His/Glu/Gln/Arg/opine family	E
ORF05312	0.00	hypothetical protein	
ORF05356	0.00	chromate transport family protein	P
ORF05362	0.00	Ech hydrogenase, subunit EchE, putative	C
ORF05446	0.37	hypothetical protein	
ORF05584	0.00	ISDvu3, transposase OrfA	



**Supplemental Table 7: 16S rRNA nucleotide identity of *D. vulgaris* strains**

*Nucleotide percent identity of D. vulgaris strains*

	<b>Marburg</b>	<b>Brockhurst Hill</b>	<b>Llanelly</b>	<b>Woolwich</b>	<b>DePue</b>	<b>Hildenborough</b>
<b>Marburg</b>		99.25%	99.46%	99.52%	99.66%	99.66%
<b>Brockhurst Hill</b>	99.25%		99.66%	99.32%	99.46%	99.46%
<b>Llanelly</b>	99.46%	99.66%		99.66%	99.80%	99.80%
<b>Woolwich</b>	99.52%	99.32%	99.66%		99.86%	99.59%
<b>DePue</b>	99.66%	99.46%	99.80%	99.86%		99.73%
<b>Hildenborough</b>	99.66%	99.46%	99.80%	99.59%	99.73%	

*Nucleotide identities of D. vulgaris strains*

	<b>Marburg</b>	<b>Brockhurst Hill</b>	<b>Llanelly</b>	<b>Woolwich</b>	<b>DePue</b>	<b>Hildenborough</b>
<b>Marburg</b>		1460/1471	1463/1471	1464/1471	1466/1471	1466/1471
<b>Brockhurst Hill</b>	1460/1471		1465/1470	1461/4171	1463/1471	1463/1471
<b>Llanelly</b>	1463/1471	1465/1470		1466/1471	1468/1471	1468/1471
<b>Woolwich</b>	1464/1471	1461/4171	1466/1471		1469/1471	1465/1471
<b>DePue</b>	1466/1471	1463/1471	1468/1471	1469/1471		1467/1471
<b>Hildenborough</b>	1466/1471	1463/1471	1468/1471	1465/1471	1467/1471	