

ORF	ORF start	ORF end	ORF fr	Length	ACCESSION	Gene Product	Score	E-Value	COG No.	Func. Cat.
ZMO0001	147	2516	3	2370	NP_792808	TonB-dependent sideophore rec	407	1.00E-112	COG1629	P
ZMO0002	2538	3653	3	1116	ZP_0005890	histidinol-phosphate/aromatic ar	133	5.00E-30	COG0079	E
ZMO0003	4326	3700	-1	627	NP_457322	adenosine 5-phosphosulfate kin	310	1.00E-83	COG0529	P
ZMO0004	5767	4343	-2	1425	AAG42464	ATP sulfurylase N subunit	751	0	COG2895	P
ZMO0005	6686	5784	-3	903	AAG42465	ATP sulfurylase D subunit	573	1.00E-162	COG0175	EH
ZMO0006	8112	6703	-1	1410	NP_406830	siroheme synthase	588	1.00E-166	COG0007	H
ZMO0007	9117	8389	-1	729	NP_461867	3'-phosphoadenosine 5'-phosph	390	1.00E-107	COG0175	EH
ZMO0008	10840	9134	-2	1707	NP_406833	sulfite reductase [NADPH] hemo	884	0	COG0155	P
ZMO0009	12660	10846	-1	1815	P38038	CYS, sulfite reductase [NADPH] flavop	804	0	COG0369	P
ZMO0010	13006	13716	1	711	NP_634315	zinc metalloprotease	182	6.00E-45	COG1451	R
ZMO0011	14470	13760	-2	711	NP_296224	conserved hypothetical protein	100	2.00E-20	-	-
ZMO0012	15726	14551	-1	1176	ZP_0009491	coproporphyrinogen III oxidase a	468	1.00E-131	COG0635	H
ZMO0013	16362	15739	-1	624	ZP_0005559	xanthosine triphosphate pyropho	237	1.00E-61	COG0127	F
ZMO0014	17077	16370	-2	708	ZP_0009491	RNase PH	362	5.00E-99	COG0689	J
ZMO0015	17333	18370	2	1038	ZP_0009491	transcriptional regulator of heat s	357	2.00E-97	COG1420	K
ZMO0016	18367	18939	1	573	ZP_0009491	heat shock protein, molecular ch	178	6.00E-44	COG0576	O
ZMO0017	18995	20401	2	1407	ZP_0009451	tRNA and rRNA cytosine-C5-met	395	1.00E-108	COG0144	J
ZMO0018	20553	21215	3	663	ZP_0009603	pentose-5-phosphate-3-epimera	315	4.00E-85	COG0036	G
ZMO0019	21212	22978	2	1767	ZP_0009603	conserved hypothetical protein	373	1.00E-102	COG5360	S
ZMO0020	23827	23207	-2	621	ZP_0003468	conserved hypothetical protein	153	2.00E-36	COG1556	S
ZMO0021	25236	23800	-1	1437	ZP_0003468	electron transport protein ykgF, p	606	1.00E-172	COG1139	C
ZMO0022	25979	25242	-3	738	ZP_0003468	Fe-S oxidoreductase, putative gl	347	1.00E-94	COG0247	C
ZMO0023	26826	26356	-1	471	NP_108143	transcriptional regulator	156	1.00E-37	COG1522	K
ZMO0024	26925	27104	3	180	NP_641244	integral membrane protein	58.9	2.00E-08	COG0697	GER
ZMO0025	27151	27855	1	705	NP_532127	conserved hypothetical protein	241	1.00E-62	COG0697	GER
ZMO0026	28030	28977	1	948	ZP_0004325	FOG: TPR repeat, SEL1 subfam	227	3.00E-58	COG0790	R
ZMO0027	29294	30898	2	1605	NP_945384	bifunctional purine biosynthesis p	648	0	COG0138	F
ZMO0028	31084	32007	1	924	NP_490238	mrr restriction system protein	275	8.00E-73	COG1715	V
ZMO0029	33932	32040	-3	1893	ZP_0004325	FOG: TPR repeat, SEL1 subfam	316	9.00E-85	COG0790	R
ZMO0030	34225	34632	1	408	ZP_000255	lactoylglutathione lyase and relat	133	7.00E-31	COG0346	E
ZMO0031	37053	34639	-1	2415	ZP_0009617	outer membrane receptor protein	241	6.00E-62	COG1629	P
ZMO0032	37273	37392	1	120		hypothetical protein				
ZMO0033	37835	37407	-3	429	ZP_0009641	conserved hypothetical protein	201	2.00E-51	COG2983	S
ZMO0034	37994	37842	-3	153		hypothetical protein				
ZMO0035	38018	38620	2	603	ZP_0009641	FOG: Ankyrin repeat	123	2.00E-27	COG0666	R
ZMO0036	38959	38627	-2	333	ZP_0001412	conserved hypothetical protein	73.2	1.00E-12	COG5447	S
ZMO0037	39420	38965	-1	456	ZP_0001311	PTS system, mannitol/fructose-s	139	2.00E-32	COG1762	GT
ZMO0038	40223	39627	-3	597	ZP_0009602	ribosome-associated protein Y (F	199	3.00E-50	COG1544	J
ZMO0039	41040	40342	-1	699	ZP_0009602	DNA polymerase III, epsilon sub	293	3.00E-78	COG0847	L
ZMO0040	41641	41054	-2	588	ZP_0009602	dephospho-CoA kinase	174	1.00E-42	COG0237	H
ZMO0041	42436	41660	-2	777	ZP_0009602	shikimate 5-dehydrogenase	202	7.00E-51	COG0169	E
ZMO0042	42449	42568	2	120		hypothetical protein				
ZMO0043	43128	42538	-1	591	ZP_0005453	nucleotide-binding protein implic	167	8.00E-41	COG0424	D
ZMO0044	43595	45352	2	1758	ZP_0004325	FOG: TPR repeat, SEL1 subfam	289	1.00E-76	COG0790	R
ZMO0045	45537	45394	-1	144		hypothetical protein				
ZMO0046	45925	46092	1	168		hypothetical protein				
ZMO0047	45833	45402	-3	432	NP_250996	conserved hypothetical protein, t	114	4.00E-25	COG1280	E
ZMO0048	46104	45934	-1	171		hypothetical protein				
ZMO0049	45956	46150	2	195		hypothetical protein				
ZMO0050	46172	47083	2	912	NP_947114	transcriptional regulator, LysR fa	267	2.00E-70	COG0583	K
ZMO0051	47080	47202	1	123		hypothetical protein				
ZMO0052	48423	47278	-1	1146	ZP_0008551	cyanate permease (MFS)	308	2.00E-82	COG2807	P
ZMO0053	49226	48426	-3	801	NP_230173	beta-ketoacid enol-lactone hy	95.9	7.00E-19	COG0596	R
ZMO0054	49349	49858	2	510	NP_798142	transcriptional regulator, MarR fa	149	2.00E-35	COG1846	K
ZMO0055	50783	49998	-3	786	ZP_0003132	permeases, predicted	306	2.00E-82	COG0730	R
ZMO0056	52790	50973	-3	1818	ZP_0009382	glucosamine 6-phosphate synthe	924	0	COG0449	M
ZMO0057	53436	52882	-1	555	AAS11297	conserved hypothetical protein, p	107	1.00E-22	-	-
ZMO0058	53444	53647	2	204		hypothetical protein				
ZMO0059	53616	54764	3	1149	ZP_0006974	glycerate kinase	450	1.00E-125	COG1929	G
ZMO0060	55111	54815	-2	297		hypothetical protein				
ZMO0061	56422	55127	-2	1296	CAE01322	phytase	375	1.00E-103	-	-
ZMO0062	57527	56565	-3	963	NP_104615	conserved hypothetical protein, s	363	2.00E-99	COG0667	C
ZMO0063	57575	57706	2	132		hypothetical protein				
ZMO0064	59452	57800	-2	1653	ZP_0003410	carbohydrate-selective porin	375	1.00E-102	COG3659	M
ZMO0065	59429	59530	2	102		hypothetical protein				
ZMO0066	59628	59897	3	270		hypothetical protein				
ZMO0067	59966	60067	2	102		hypothetical protein				
ZMO0068	60238	61365	1	1128	ZP_0004325	FOG: TPR repeat, SEL1 subfam	266	7.00E-70	COG0790	R
ZMO0069	61631	62068	2	438		hypothetical protein				
ZMO0070	62194	62865	1	672	NP_455658	glutaredoxin 2	211	7.00E-54	COG2999	O
ZMO0071	63051	62920	-1	132		hypothetical protein				
ZMO0072	64484	63129	-3	1356	ZP_0009234	glucose/sorbose dehydrogena	346	5.00E-94	COG2133	G
ZMO0073	65377	64499	-2	879	ZP_0009591	hemolysins and related proteins	317	2.00E-85	COG1253	R
ZMO0074	65962	65438	-2	525	ZP_0009591	predicted metal-dependent hydr	154	1.00E-36	COG0319	R
ZMO0075	67028	65955	-3	1074	ZP_0009591	phosphate starvation-inducible p	450	1.00E-125	COG1702	T

ZMO0076	67143	67012	-1	132	hypothetical protein				-	-
ZMO0077	68486	67155	-3	1332	ZP_00095912: 2-methylthioadenine synthetase	584	1.00E-165	COG0621		J
ZMO0078	69093	68590	-1	504	NP_419253 chemotaxis protein CheW	150	1.00E-35	COG0835		NT
ZMO0079	69629	69270	-3	360	NP_419251 chemotaxis protein CheYI	154	3.00E-37	COG0784		T
ZMO0080	70310	69780	-3	531	NP_419257 chemotaxis protein CheD	149	3.00E-35	COG1871		NT
ZMO0081	71405	70353	-3	1053	O85128 CHE chemotaxis response regulator p	368	1.00E-101	COG2201		NT
ZMO0082	72274	71408	-2	867	NP_531220 chemotaxis methyltransferase Cl	235	7.00E-61	COG1352		NT
ZMO0083	74601	72277	-1	2325	NP_419252 chemotaxis protein CheA	624	1.00E-177	COG0643		NT
ZMO0084	74881	74618	-2	264	hypothetical protein					-
ZMO0085	76368	75061	-1	1308	NP_421939 chemotaxis methyl-accepting prc	285	1.00E-75	COG0840		NT
ZMO0086	78966	76807	-1	2160	ZP_00095961: guanosine polyphosphate pyropt	877	0	COG0317		TK
ZMO0087	79591	79115	-2	477	hypothetical protein					-
ZMO0088	80421	79723	-1	699	hypothetical protein					-
ZMO0089	81322	80636	-2	687	hypothetical protein					-
ZMO0090	82556	81765	-3	792	ZP_0002294: dehydrogenases with different sp	343	2.00E-93	COG1028		IQR
ZMO0091	82626	82781	3	156	hypothetical protein					-
ZMO0092	82882	83646	1	765	hypothetical protein					-
ZMO0093	83741	83941	2	201	hypothetical protein					-
ZMO0094	83922	84869	3	948	NP_897026 biotin synthase	378	1.00E-104	COG0502		H
ZMO0095	85170	84955	-1	216	hypothetical protein					-
ZMO0096	86167	85622	-2	546	ZP_0005647: phosphatidylglycerophosphate s	177	1.00E-43	COG0558		I
ZMO0097	86169	86315	3	147	hypothetical protein					-
ZMO0098	86443	86649	1	207	hypothetical protein					-
ZMO0099	86672	87940	2	1269	ZP_0005487: 1-acyl-sn-glycerol-3-phosphate a	288	2.00E-76	COG0477		GEPR
ZMO0100	88382	88008	-3	375	NP_420643 conserved hypothetical protein	78.6	2.00E-14	COG1733		K
ZMO0101	88492	89556	1	1065	ZP_0012689: nucleoside-diphosphate-sugar e	392	1.00E-108			-
ZMO0102	89568	89774	3	207	hypothetical protein					-
ZMO0103	90130	91548	1	1419	NP_420514 conserved hypothetical protein, t	316	9.00E-85	COG1680		V
ZMO0104	91568	91681	2	114	hypothetical protein					-
ZMO0105	91653	93107	3	1455	ZP_0009483: 3-isopropylmalate dehydratase l	748	0	COG0065		E
ZMO0106	93104	93682	2	579	ZP_0009483: 3-isopropylmalate dehydratase s	263	1.00E-69	COG0066		E
ZMO0107	94553	93750	-3	804	NP_840874 conserved hypothetical protein	120	2.00E-26			-
ZMO0108	94937	94617	-3	321	ZP_0001356: membrane transporters of cation	87	7.00E-17	COG2076		P
ZMO0109	95278	96717	1	1440	hypothetical protein					-
ZMO0110	96714	97703	3	990	NP_484086 conserved hypothetical protein	306	5.00E-82	COG0463		M
ZMO0111	99643	97853	-2	1791	ZP_0009492: ATPase components of ABC trar	789	0	COG0488		R
ZMO0112	99833	100192	2	360	ZP_0009492: conserved hypothetical protein	67.4	5.00E-11			-
ZMO0113	100982	102388	2	1407	NP_768732 para-aminobenzoate synthase $\alpha$	427	1.00E-118	COG0147		EH
ZMO0114	102405	103016	3	612	NP_953428 anthranilate synthase componen	218	5.00E-56	COG0512		EH
ZMO0115	102961	103818	1	858	ZP_0005021: branched-chain amino acid amin	205	7.00E-52	COG0115		EH
ZMO0116	104018	104455	2	438	NP_638113 conserved hypothetical protein	80.1	1.00E-14	COG1959		K
ZMO0117	104522	106159	2	1638	ZP_0001378: 6Fe-6S prismane cluster-contain	560	1.00E-158	COG1151		C
ZMO0118	106299	106436	3	138	hypothetical protein					-
ZMO0119	106417	107484	1	1068	NP_419269 Na <sup>+</sup> /H <sup>+</sup> antiporter	296	3.00E-79	COG3004		P
ZMO0120	107594	108712	2	1119	NP_696430 conserved hypothetical protein w	343	3.00E-93	COG0167		F
ZMO0121	108980	110329	2	1350	ZP_0009597: ATPase related to the helicase s	572	1.00E-162	COG2256		L
ZMO0122	110510	110851	2	342	hypothetical protein					-
ZMO0123	110972	111115	2	144	hypothetical protein					-
ZMO0124	112698	111121	-1	1578	ZP_0009620: ATPase, predicted	542	1.00E-153	COG0433		R
ZMO0125	113184	112717	-1	468	NP_384411 conserved hypothetical protein	192	1.00E-48	COG2606		S
ZMO0126	114284	114433	2	150	hypothetical protein					-
ZMO0127	115550	114597	-3	954	NP_712431 nuclease S1	116	7.00E-25			-
ZMO0128	117958	115574	-2	2385	NP_902858 TonB-dependent receptor, proba	352	1.00E-95	COG1629		P
ZMO0129	117948	118127	3	180	hypothetical protein					-
ZMO0130	119177	118389	-3	789	P14924 PPA acid phosphatase precursor	536	1.00E-151	COG0671		I
ZMO0131	120360	119341	-1	1020	NP_809361 conserved hypothetical protein	86.3	9.00E-16	COG1409		R
ZMO0132	120850	121608	1	759	ZP_0004325: FOG: TPR repeat, SEL1 subfam	162	6.00E-39	COG0790		R
ZMO0133	121929	122669	3	741	ZP_0004325: FOG: TPR repeat, SEL1 subfam	228	1.00E-58	COG0790		R
ZMO0134	122852	123352	2	501	ZP_0004325: FOG: TPR repeat, SEL1 subfam	122	2.00E-27	COG0790		R
ZMO0135	123511	124161	1	651	ZP_0004325: FOG: TPR repeat, SEL1 subfam	182	4.00E-45	COG0790		R
ZMO0136	124255	124971	1	717	ZP_0004325: FOG: TPR repeat, SEL1 subfam	157	2.00E-37	COG0790		R
ZMO0137	125171	126427	2	1257	ZP_0004325: FOG: TPR repeat, SEL1 subfam	157	1.00E-93	COG0790		R
ZMO0138	126496	126618	1	123	hypothetical protein					-
ZMO0139	127415	126528	-3	888	ZP_0004965: fructosamine-3-kinase	164	3.00E-39	COG3001		G
ZMO0140	127960	127487	-2	474	ZP_0000556: protein-tyrosine-phosphatase	180	1.00E-44	COG0394		T
ZMO0141	128159	128305	2	147	hypothetical protein					-
ZMO0142	128320	129000	1	681	ZP_0009653: predicted enzyme with a TIM-bar	262	3.00E-69	COG0325		R
ZMO0143	129000	129977	3	978	ZP_0001305: ABC-type multidrug transport sy	362	4.00E-99	COG1131		V
ZMO0144	130042	131634	1	1593	ZP_0009656: aspartate oxidase	687	0	COG0029		H
ZMO0145	131657	133330	2	1674	NP_639261 peptidase	481	1.00E-134	COG2234		R
ZMO0146	133455	133273	-1	183	hypothetical protein					-
ZMO0147	133858	133754	-2	105	hypothetical protein					-
ZMO0148	134798	133998	-3	801	hypothetical protein					-
ZMO0149	135678	134989	-1	690	ZP_0009683: S-adenosylmethionine-depender	282	3.00E-75	COG0220		R
ZMO0150	136384	135764	-2	621	ZP_0000810: conserved hypothetical protein	116	3.00E-25	COG0454		KR
ZMO0151	136673	136395	-3	279	hypothetical protein					-
ZMO0152	138078	136657	-1	1422	NP_773778 pyruvate kinase	473	1.00E-132	COG0469		G

ZMO0153	139093	139842	1	750	NP_539238	glucose-1-phosphate adenylyl tr	317	1.00E-85	COG0217	S
ZMO0154	139877	140380	2	504	ZP_0009654	Holliday junction resolvosome, e	186	2.00E-46	COG0817	L
ZMO0155	140422	141063	1	642	ZP_0009654	Holliday junction resolvosome, D	181	7.00E-45	COG0632	L
ZMO0156	141482	141126	-3	357		hypothetical protein				-
ZMO0157	142620	141697	-1	924	NP_535169	2-hydroxyacid dehydrogenase	254	1.00E-66	COG1052	CHR
ZMO0158	142769	143812	2	1044	ZP_0009654	Holliday junction resolvosome, h	505	1.00E-142	COG2255	L
ZMO0159	143992	144120	1	129		hypothetical protein				-
ZMO0160	144121	144492	1	372	ZP_0009594	thioesterase, predicted	106	1.00E-22	COG0824	R
ZMO0161	144500	145054	2	555	ZP_0009594	biopolymer transport proteins, Tc	95.1	6.00E-19	COG0811	U
ZMO0162	145216	145743	1	528	ZP_0009657	biopolymer transport protein, Toll	132	4.00E-30	COG0848	U
ZMO0163	145771	146178	1	408	EAA53379	conserved hypothetical protein	56.2	1.00E-07	COG0810	M
ZMO0164	146153	146833	2	681	ZP_0009594	periplasmic protein TonB, links in	100	2.00E-20	-	-
ZMO0165	146887	148263	1	1377	ZP_0009594	periplasmic component of the To	546	1.00E-154	COG0823	U
ZMO0166	148390	148920	1	531	ZP_0009658	outer membrane protein and rela	166	2.00E-40	COG2885	M
ZMO0167	149071	148928	-2	144		hypothetical protein				-
ZMO0168	149502	149101	-1	402	NP_518623	glycerophosphoryl diester phosp	164	2.00E-40	COG0584	C
ZMO0169	151579	150842	-2	738	NP_103600	short chain oxidoreductase, puta	176	5.00E-43	COG1028	IQR
ZMO0170	152619	152074	-1	546	NP_644661	glycerophosphoryl diester phosp	132	4.00E-30	COG0584	C
ZMO0171	155028	153520	-1	1509	NP_419539	TonB-dependent receptor	436	1.00E-121	COG1629	P
ZMO0172	155420	157234	2	1815	ZP_0009344	thiamine biosynthesis protein thi	938	0	COG0422	H
ZMO0173	158150	157755	-3	396	NP_422041	conserved hypothetical protein	64.3	4.00E-10	COG3027	S
ZMO0174	158735	158349	-3	387	NP_903384	conserved hypothetical protein	80	6.00E-15	-	-
ZMO0175	159227	158952	-3	276		hypothetical protein				-
ZMO0176	159445	161436	1	1992	ZP_0009550	transketolase	790	0	COG0021	G
ZMO0177	161486	162499	2	1014	P09316	G3P_glyceraldehyde 3-phosphate deh	661	0	COG0057	G
ZMO0178	162722	163915	2	1194	P09404	PGK_phosphoglycerate kinase	772	0	COG0126	G
ZMO0179	164684	165598	2	915	AAS14884	fructose-bisphosphate aldolase	357	2.00E-97	COG1830	G
ZMO0180	166885	165758	-2	1128	ZP_0009655	enzyme involved in the deoxyxyl	621	1.00E-177	COG0821	I
ZMO0181	166940	167068	2	129		hypothetical protein				-
ZMO0182	167266	168660	1	1395	ZP_0009509	S-adenosylhomocysteine hydroly	717	0	COG0499	H
ZMO0183	170633	168957	-3	1677	ZP_0009426	ABC transporters with duplicated	883	0	COG0488	R
ZMO0184	171345	171584	3	240		hypothetical protein				-
ZMO0185	171287	171162	-3	126		hypothetical protein				-
ZMO0186	171805	173355	1	1551	ZP_0009526	cysteinyI-tRNA synthetase	558	1.00E-157	COG0215	J
ZMO0187	173448	174776	3	1329	ZP_0009592	3-deoxy-D-arabino-heptulosonat	492	1.00E-138	COG3200	E
ZMO0188	175355	177721	2	2367	Q08017	PBU_ferric-pseudobactin M114 recept	401	1.00E-110	COG4773	P
ZMO0189	179105	177750	-3	1356	NP_421902	L-serine dehydratase	501	1.00E-140	COG1760	E
ZMO0190	180113	179202	-3	912	NP_104268	transcriptional regulator, hypothe	152	1.00E-35	COG1737	K
ZMO0191	181226	180453	-3	774	ZP_0005390	protein-disulfide isomerase	135	1.00E-30	COG1651	O
ZMO0192	182579	181263	-3	1317	ZP_0009676	Zn-dependent protease contains	386	1.00E-106	COG4783	R
ZMO0193	185689	182957	-2	2733	NP_420684	ribonuclease, Rne/Rng family pr	679	0	COG1530	J
ZMO0194	186017	186274	2	258		hypothetical protein				-
ZMO0195	186454	187242	1	789	ZP_0009571	N-acetylmuramoyl-L-alanine ami	204	1.00E-51	COG0860	M
ZMO0196	187309	187461	1	153		hypothetical protein				-
ZMO0197	187454	190033	2	2580	ZP_0009571	membrane carboxypeptidase/pe	804	0	COG5009	M
ZMO0198	190144	191271	1	1128	ZP_0009572	protein chain release factor B	553	1.00E-156	COG1186	J
ZMO0199	191974	191327	-2	648	ZP_0009512	SOS-response transcriptional re	276	3.00E-73	COG1974	KT
ZMO0200	193165	192146	-2	1020	ZP_0009511	anthranilate phosphoribosyltrans	321	1.00E-86	COG0547	E
ZMO0201	193821	193198	-1	624	ZP_0009511	anthranilate/para-aminobenzoate	265	4.00E-70	COG0512	EH
ZMO0202	194772	196664	3	1893	NP_419249	chemotaxis methyl-accepting prc	348	2.00E-94	COG0840	NT
ZMO0203	197152	196709	-2	444	NP_948600	heavy metal resistance transcrip	135	1.00E-31	COG0789	K
ZMO0204	197207	197854	2	648	ZP_0008878	Co/Zn/Cd efflux system compon	168	8.00E-41	COG1230	P
ZMO0205	198778	197861	-2	918	ZP_0009485	nucleoside-diphosphate-sugar e	285	8.00E-76	COG0702	MG
ZMO0206	199968	198781	-1	1188	ZP_0009485	glutamate 5-kinase	384	1.00E-105	COG0263	E
ZMO0207	200996	199959	-3	1038	ZP_0009485	GTPase, predicted	475	1.00E-133	COG0536	R
ZMO0208	201696	201094	-1	603		hypothetical protein				-
ZMO0209	202158	201895	-1	264	ZP_0009375	ribosomal protein L27	153	8.00E-37	COG0211	J
ZMO0210	202206	202328	3	123		hypothetical protein				-
ZMO0211	202665	202297	-1	369	ZP_0009375	ribosomal protein L21	152	2.00E-36	COG0261	J
ZMO0212	202781	202900	2	120		hypothetical protein				-
ZMO0213	205377	202909	-1	2469	NP_887465	autotransporter	295	3.00E-78	COG4625	S
ZMO0214	208043	206595	-3	1449	NP_946153	cation efflux pump, DNA-damage	246	7.00E-64	COG0534	V
ZMO0215	208259	208921	2	663	NP_422039	5-formyltetrahydrofolate cyclo-lig	113	3.00E-24	COG0212	H
ZMO0216	210407	209004	-3	1404	ZP_0009606	membrane proteins related to me	211	2.00E-53	COG0739	M
ZMO0217	210618	210421	-1	198		hypothetical protein				-
ZMO0218	210739	210858	1	120		hypothetical protein				-
ZMO0219	210925	213756	1	2832	NP_766799	helicase, ATP-dependent	640	0	COG0513	LKJ
ZMO0220	213988	214326	1	339	ZP_0009642	ferredoxin	205	1.00E-52	COG1146	C
ZMO0221	214655	215209	2	555	ZP_0009642	transcriptional regulators, similar	265	4.00E-70	COG1329	K
ZMO0222	215423	215722	2	300	NP_108090	conserved hypothetical protein	110	8.00E-24	COG5470	S
ZMO0223	215802	216563	3	762	ZP_0001805	conserved hypothetical protein	74.3	2.00E-12	-	-
ZMO0224	217216	216575	-2	642	NP_104622	conserved hypothetical protein	194	1.00E-48	COG0500	QR
ZMO0225	218337	217222	-1	1116	ZP_0005595	homoserine acetyltransferase	489	1.00E-137	COG2021	E
ZMO0226	218719	219468	1	750	NP_534594	serine dehydrogenase	328	1.00E-88	COG4221	R
ZMO0227	219484	222249	1	2766	ZP_0009680	DNA polymerase I - 3'-5' exonucl	1055	0	COG0749	L
ZMO0228	222231	223634	3	1404	ZP_0009385	membrane protein involved in the	389	1.00E-110	COG2244	R
ZMO0229	223778	224824	2	1047	ZP_0000559	ABC-type Fe3+-siderophore tran	267	3.00E-70	COG0609	P

ZMO0230	224821	225606	1	786	ZP_0001651f	ABC-type cobalamin/Fe3+-sidero	195	7.00E-49	COG1120	PH
ZMO0231	225865	226380	1	516	ZP_0009656f	conserved hypothetical protein	199	4.00E-50	-	-
ZMO0232	227243	226500	-3	744	ZP_0009464f	rRNA methylases	290	2.00E-77	COG0566	J
ZMO0233	228202	227822	-2	381	NP_355784	conserved hypothetical protein	77	6.00E-14	COG3631	R
ZMO0234	229956	228301	-1	1656	ZP_0009668f	trypsin-like serine proteases, typ	544	1.00E-153	COG0265	O
ZMO0235	230425	230306	-2	120	-	hypothetical protein	-	-	-	-
ZMO0236	230409	231437	3	1029	ZP_0009668f	ATPases involved in chromosom	276	6.00E-73	COG0489	D
ZMO0237	231554	231453	-3	102	-	hypothetical protein	-	-	-	-
ZMO0238	231871	232425	1	555	ZP_0009524f	ATP synthase, delta subunit	149	3.00E-35	COG0712	C
ZMO0239	232428	233957	3	1530	ZP_0009524f	ATP synthase, alpha subunit	808	0	COG0056	C
ZMO0240	233991	234887	3	897	ZP_0005046f	ATP synthase, gamma subunit	289	5.00E-77	COG0224	C
ZMO0241	234916	236370	1	1455	ZP_0005525f	ATP synthase, beta subunit	746	0	COG0055	C
ZMO0242	236430	236696	3	267	ZP_0009325f	ATP synthase, epsilon subunit	92	2.00E-18	COG0355	C
ZMO0243	237895	237098	-2	798	ZP_0009518f	conserved hypothetical protein	186	4.00E-46	-	-
ZMO0244	238465	238196	-2	270	ZP_0009351f	DNA-binding protein (HU)	116	1.00E-25	COG0776	L
ZMO0245	238673	238810	2	138	-	hypothetical protein	-	-	-	-
ZMO0246	239003	239557	2	555	ZP_0009482f	heat shock protein, ATP-depend	288	3.00E-77	COG5405	O
ZMO0247	239582	240874	2	1293	ZP_0009416f	heat shock protein, ATP-depend	622	1.00E-177	COG1220	O
ZMO0248	240896	241090	2	195	-	hypothetical protein	-	-	-	-
ZMO0249	241160	241327	2	168	ZP_0009582f	ribosomal protein L33	105	3.00E-22	COG0267	J
ZMO0250	241802	241446	-3	357	ZP_0009450f	two-component CheY-like receiv	144	3.00E-34	COG0784	T
ZMO0251	241977	242435	3	459	ZP_0009450f	translation initiation inhibitor yjgF	199	3.00E-50	COG0251	J
ZMO0252	242784	251738	3	8955	NP_286230	RTX family exoprotein, autotrans	608	1.00E-172	-	-
ZMO0253	251743	253218	1	1476	NP_742966	outer membrane efflux protein	237	5.00E-61	COG1538	MU
ZMO0254	253215	255362	3	2148	NP_286231	cytoplasmic membrane export pr	762	0	COG2274	V
ZMO0255	255355	256536	1	1182	NP_286232	membrane spanning export prot	468	1.00E-130	COG0845	M
ZMO0256	256658	258382	2	1725	ZP_0003403f	FAD/FMN-containing dehydroge	739	0	COG0277	C
ZMO0257	258605	259282	2	678	ZP_0009492f	two-component transcriptional re	392	1.00E-108	COG0745	TK
ZMO0258	259285	260742	1	1458	ZP_0009491f	two-component sensor histidine l	509	1.00E-143	COG0642	T
ZMO0259	260986	260876	-2	111	-	hypothetical protein	-	-	-	-
ZMO0260	260993	261604	2	612	ZP_0009436f	ABC-type transport system invol	185	4.00E-46	COG4133	O
ZMO0261	261573	261722	3	150	-	hypothetical protein	-	-	-	-
ZMO0262	261712	262248	1	537	ZP_0009436f	ABC-type transport system invol	204	8.00E-52	COG2386	O
ZMO0263	263654	262257	-3	1398	-	hypothetical protein	-	-	-	-
ZMO0264	265163	263715	-3	1449	-	hypothetical protein	-	-	-	-
ZMO0265	266627	265203	-3	1425	-	hypothetical protein	-	-	-	-
ZMO0266	268109	266688	-3	1422	-	hypothetical protein	-	-	-	-
ZMO0267	269612	268170	-3	1443	-	hypothetical protein	-	-	-	-
ZMO0268	271070	269652	-3	1419	-	hypothetical protein	-	-	-	-
ZMO0269	272546	271131	-3	1416	-	hypothetical protein	-	-	-	-
ZMO0270	274082	272607	-3	1476	-	hypothetical protein	-	-	-	-
ZMO0271	275186	276472	2	1287	ZP_0009681f	apolipoprotein N-acyltransferase	290	5.00E-77	COG0815	M
ZMO0272	276672	276472	-1	201	-	hypothetical protein	-	-	-	-
ZMO0273	276665	277840	2	1176	ZP_0009681f	S-adenosylmethionine synthetas	570	1.00E-161	COG0192	H
ZMO0274	279411	277918	-1	1494	ZP_0009682f	DNA-directed RNA polymerase s	471	1.00E-131	COG1508	K
ZMO0275	280253	279465	-3	789	ZP_0009682f	ABC-type (unclassified) transpor	376	1.00E-103	COG1137	R
ZMO0276	281052	280462	-1	591	ZP_0009558f	conserved hypothetical protein	120	2.00E-26	COG1934	S
ZMO0277	281696	281064	-3	633	ZP_0009558f	conserved hypothetical protein	131	8.00E-30	COG5375	S
ZMO0278	282346	281735	-2	612	ZP_0009558f	ribonuclease D, 3'-5' exonucleas	313	1.00E-84	COG0349	J
ZMO0279	282879	283409	3	531	ZP_0009352f	cold shock proteins	242	8.00E-63	COG1278	K
ZMO0280	283440	283595	3	156	-	hypothetical protein	-	-	-	-
ZMO0281	284446	283805	-2	642	ZP_0000551f	transcriptional regulator, tetR far	79.7	4.00E-14	COG1309	K
ZMO0282	284674	285843	1	1170	NP_286204	acridine efflux pump	351	1.00E-95	COG0845	M
ZMO0283	285847	288990	1	3144	NP_249117	RND multidrug efflux transporter	1242	0	COG0841	V
ZMO0284	288990	289589	3	600	ZP_0008101f	outer membrane protein	126	2.00E-28	COG1538	MU
ZMO0285	289769	290524	2	756	NP_518130	probable drug efflux lipoprotein	204	1.00E-51	COG1538	MU
ZMO0286	291368	290574	-3	795	AAG02145	outer membrane protein	350	1.00E-95	COG2968	S
ZMO0287	291695	292843	2	1149	NP_386567	transport transmembrane protein	132	2.00E-29	COG0845	M
ZMO0288	292989	292870	-1	120	-	hypothetical protein	-	-	-	-
ZMO0289	292976	292827	-3	150	-	hypothetical protein	-	-	-	-
ZMO0290	292972	294228	1	1257	ZP_0009664f	membrane protein, predicted	258	2.00E-67	COG2733	S
ZMO0291	295048	294221	-2	828	AA053572	prolipoprotein diacylglycerol tran	253	4.00E-66	COG0682	M
ZMO0292	295207	295317	1	111	-	hypothetical protein	-	-	-	-
ZMO0293	296775	295339	-1	1437	NP_391860	metabolite (sugar) transport prot	276	5.00E-73	COG0477	GEPR
ZMO0294	297636	297466	-1	171	NP_945846	ribosomal protein L28	64.7	4.00E-10	COG0227	J
ZMO0295	297686	297799	2	114	-	hypothetical protein	-	-	-	-
ZMO0296	298056	298538	3	483	NP_946515	cytidine and deoxycytidylate dea	171	3.00E-42	COG0590	FJ
ZMO0297	298787	300112	2	1326	ZP_0009552f	hemolysins and related proteins	429	1.00E-119	COG1253	R
ZMO0298	300905	300213	-3	693	NP_104209	conserved hypothetical protein, s	101	1.00E-20	COG3743	S
ZMO0299	302317	301070	-2	1248	Q9FDL5 PUF	phosphoribosylamine-glycine lig	733	0	COG0151	F
ZMO0300	302319	303953	3	1635	Q9FDL4 EX7	exodeoxyribonuclease VII large s	1061	0	COG1570	L
ZMO0301	304099	304851	1	753	NP_643253	conserved hypothetical protein	152	4.00E-36	COG3295	S
ZMO0302	305116	304826	-2	291	NP_948839	conserved hypothetical protein	59.3	2.00E-08	COG4321	R
ZMO0303	306078	305128	-1	951	P57779 HEM	ferrochelatase (protoheme ferro-	620	1.00E-176	COG0276	H
ZMO0304	306071	306262	2	192	-	hypothetical protein	-	-	-	-
ZMO0305	306747	306280	-1	468	EAA54023	conserved hypothetical protein	59.3	2.00E-08	-	-
ZMO0306	308109	306847	-1	1263	AAK26455	putative glycosyltransferase Wct	150	4.00E-35	COG0438	M

ZMO0307	309870	308143	-1	1728	P42217 KSC	capsule polysaccharide export p	252	2.00E-65	COG3563	M
ZMO0308	310007	310144	2	138		hypothetical protein			-	-
ZMO0309	310425	311222	3	798	NP_636454	oxidoreductase	364	1.00E-99	COG1028	IQR
ZMO0310	311204	311308	2	105		hypothetical protein			-	-
ZMO0311	312100	311291	-2	810	NP_622979	pyrroline-5-carboxylate reductas	154	1.00E-36	COG0345	E
ZMO0312	312306	313448	3	1143	NP_833392	N-acyl-L-amino acid amidohydro	370	1.00E-101	COG1473	R
ZMO0313	313478	313960	2	483	BAB15928	L-2-Amino-thiazoline-4-carboxyli	179	2.00E-44	-	-
ZMO0314	315414	314002	-1	1413	NP_639367	cardiolipin synthase	331	2.00E-89	COG1502	I
ZMO0315	315670	315485	-2	186		hypothetical protein			-	-
ZMO0316	315707	315895	2	189		hypothetical protein			-	-
ZMO0317	316217	316014	-3	204		hypothetical protein			-	-
ZMO0318	316209	316964	3	756	NP_231231	oxidoreductase, short-chain dehy	307	1.00E-82	COG1028	IQR
ZMO0319	317282	317040	-3	243	NP_085648	conserved hypothetical protein	56.2	1.00E-07	COG3831	S
ZMO0320	317573	317752	2	180		hypothetical protein			-	-
ZMO0321	317899	318396	1	498	NP_539526	dihydrofolate reductase	125	5.00E-28	COG0262	H
ZMO0322	318735	319679	3	945	NP_419520	riboflavin biosynthesis protein Ri	251	1.00E-65	COG0196	H
ZMO0323	319798	322623	1	2826	NP_419518	isoleucyl-tRNA synthetase	874	0	COG0060	J
ZMO0324	322627	323151	1	525	ZP_0009559	lipoprotein signal peptidase	133	1.00E-30	COG0597	MU
ZMO0325	323236	323748	1	513	ZP_0009559	conserved hypothetical protein	103	2.00E-21	-	-
ZMO0326	324205	323768	-2	438	ZP_0009598	enzyme related to GTP cyclohyd	242	8.00E-64	COG0780	R
ZMO0327	324392	326440	2	2049	NP_717789	cystathionine beta-lyase	436	1.00E-121	COG0626	E
ZMO0328	326596	327159	1	564	NP_698695	translation elongation factor P	251	1.00E-65	COG0231	J
ZMO0329	327159	327974	3	816	ZP_0009549	archaeal fructose-1,6-bisphosph	372	1.00E-102	COG0483	G
ZMO0330	328139	327963	-3	177		hypothetical protein			-	-
ZMO0331	328420	329016	1	597	NP_706845	conserved hypothetical protein	126	3.00E-28	COG3108	S
ZMO0332	329794	329084	-2	711	NP_422058	thiamine-phosphate pyrophosph	195	7.00E-49	COG0352	H
ZMO0333	330146	329976	-3	171		hypothetical protein			-	-
ZMO0334	330029	330196	2	168		hypothetical protein			-	-
ZMO0335	330186	330971	3	786	ZP_0009670	ATPases involved in chromosom	289	3.00E-77	COG1192	D
ZMO0336	331068	331742	3	675	AAS14729	DnaJ domain protein	61.6	1.00E-08	COG2214	O
ZMO0337	331732	331845	1	114		hypothetical protein			-	-
ZMO0338	331849	331742	-2	108		hypothetical protein			-	-
ZMO0339	331883	333262	2	1380	AAF19992	phosphoglucosyltransferase	660	0	COG1109	G
ZMO0340	333237	333389	3	153		hypothetical protein			-	-
ZMO0341	333449	334228	2	780	NP_952627	oxidoreductase, short chain dehy	339	4.00E-92	COG1028	IQR
ZMO0342	335489	334293	-3	1197	AAR38379	aspartate aminotransferase	503	1.00E-141	COG0436	E
ZMO0343	336283	335618	-2	666	ZP_0009652	anthranilate/para-aminobenzoate	130	2.00E-29	COG0115	EH
ZMO0344	336589	338031	1	1443	ZP_0009655	Zn-dependent proteases and the	716	0	COG0312	R
ZMO0345	338326	339039	1	714	ZP_0009475	hydrolase, metal-dependent	208	8.00E-53	COG3568	R
ZMO0346	339240	340589	3	1350	ZP_0009475	ammonia permease	505	1.00E-142	COG0004	P
ZMO0347	340984	341469	1	486	ZP_0009320	host factor I protein, uncharacter	190	9.00E-48	COG1923	R
ZMO0348	341466	342848	3	1383	ZP_0009320	GTPases. GTP binding protein	492	1.00E-138	COG2262	R
ZMO0349	342869	343435	2	567	ZP_0009474	transcriptional regulator, putative	174	8.00E-43	COG1678	K
ZMO0350	343575	344201	3	627	NP_947369	conserved hypothetical protein	242	4.00E-63	COG4318	S
ZMO0351	344424	349625	3	5202	ZP_0012374	superfamily I DNA and RNA helic	1710	0	COG1112	L
ZMO0352	349727	351358	2	1632	NP_811791	conserved hypothetical protein	119	2.00E-25	-	-
ZMO0353	351403	352746	1	1344	NP_810564	pyrophosphorylase	300	4.00E-80	COG1211	I
ZMO0354	354773	352887	-3	1887	ZP_0009534	DNA mismatch repair enzyme (p	664	0	COG0323	L
ZMO0355	354983	356029	2	1047	ZP_0009534	ATPase involved in cell morphog	546	1.00E-154	COG1077	D
ZMO0356	356060	357079	2	1020	ZP_0009534	cell (rod) shape-determining prot	209	7.00E-53	COG1792	M
ZMO0357	357093	357644	3	552	ZP_0009534	conserved hypothetical protein	117	1.00E-25	-	-
ZMO0358	357798	357688	-1	111		hypothetical protein			-	-
ZMO0359	357835	359703	1	1869	ZP_0009533	cell division protein FtsI/penicillin	700	0	COG0768	M
ZMO0360	359715	360821	3	1107	NP_716792	rod shape-determining protein R	316	6.00E-85	COG0772	D
ZMO0361	361428	362420	3	993		hypothetical protein			-	-
ZMO0362	362518	364740	1	2223	NP_386007	excinuclease ABC subunit B	949	0	COG0556	L
ZMO0363	364874	366073	2	1200	AAA27705	tRNA guanine transglycosylase (	791	0	COG0343	J
ZMO0364	366120	368315	3	2196	P28719 DNL	DNA ligase (polydeoxyribonuclec	1431	0	COG0272	L
ZMO0365	368372	368473	2	102		hypothetical protein			-	-
ZMO0366	368688	370109	3	1422	P21906 GLF	glucose facilitated diffusion prote	933	0	COG0477	GEPR
ZMO0367	370255	371712	1	1458	P21907 G6P	glucose-6-phosphate 1-dehydroc	971	0	COG0364	G
ZMO0368	371705	373528	2	1824	P21909 EDD	phosphoglucosyltransferase (	1163	0	COG0129	EG
ZMO0369	373661	374635	2	975	P21908 GLK	glucokinase (glucose kinase)	617	1.00E-176	COG0837	G
ZMO0370	374727	374608	-1	120		hypothetical protein			-	-
ZMO0371	375824	375141	-3	684	NP_534566	aspartate racemase	350	2.00E-95	COG1794	M
ZMO0372	375999	376460	3	462	Q57001 ZRP	global regulatory protein	299	1.00E-80	COG1522	K
ZMO0373	376810	376460	-2	351		hypothetical protein			-	-
ZMO0374	377648	378919	2	1272	Q60114 SAC	levansucrase (beta-D-fructofurar	893	0	-	-
ZMO0375	379075	380316	1	1242	Q60115 INVE	extracellular sucrose (beta-fructo	868	0	-	-
ZMO0376	383030	380610	-3	2421	ZP_0009465	ATP-dependent Lon protease, ba	1122	0	COG0466	O
ZMO0377	383220	383849	3	630	ZP_0009436	3-methyladenine DNA glycosylas	153	2.00E-36	COG0122	L
ZMO0378	383933	384439	2	507	NP_881914	conserved hypothetical protein, f	109	2.00E-23	-	-
ZMO0379	384439	385725	1	1287	NP_958178	gene 2 protein, terminase [Enter	134	5.00E-30	COG1783	R
ZMO0380	385768	387957	1	2190	NP_775254	putative portal protein [P. aerugir	285	3.00E-75	-	-
ZMO0381	387957	388256	3	300		hypothetical protein			-	-
ZMO0382	388306	388476	1	171		hypothetical protein			-	-
ZMO0383	388445	389230	2	786		hypothetical protein			-	-

ZMO0384	389256	389363	3	108	hypothetical protein								
ZMO0385	389548	389667	1	120	hypothetical protein								
ZMO0386	389715	389602	-1	114	hypothetical protein								
ZMO0387	389894	390610	2	717	NP_775251	major head protein [P. aeruginos	102	8.00E-21	-	-			
ZMO0388	390746	391090	2	345	hypothetical protein								
ZMO0389	391100	391759	2	660	NP_775249	constituent protein [P. aeruginos	61.6	1.00E-08	-	-			
ZMO0390	391753	393174	1	1422	hypothetical protein								
ZMO0391	393144	393419	3	276	hypothetical protein								
ZMO0392	393398	393901	2	504	hypothetical protein								
ZMO0393	393902	394573	2	672	hypothetical protein								
ZMO0394	394586	395260	2	675	hypothetical protein								
ZMO0395	395440	395808	1	369	ZP_0009496	conserved hypothetical protein	60.8	5.00E-09	-	-			
ZMO0396	395754	395410	-1	345	hypothetical protein								
ZMO0397	395805	396251	3	447	hypothetical protein								
ZMO0398	396205	396657	1	453	ZP_0009495	RTX toxins and related Ca2+-bin	64.3	4.00E-10	-	-			
ZMO0399	396662	397663	2	1002	NP_073695	neck appendage protein precurs	122	1.00E-26	-	-			
ZMO0400	397668	400322	3	2655	hypothetical protein								
ZMO0401	402380	400335	-3	2046	ZP_0012410	signal transduction protein conta	327	7.00E-88	COG5001		T		
ZMO0402	403265	402606	-3	660	ZP_0009554	23S rRNA methylase (cell divisio	306	1.00E-82	COG0293		J		
ZMO0403	404365	403268	-2	1098	ZP_0009554	exopolyphosphatase	380	1.00E-104	COG0248		FP		
ZMO0404	405047	405211	2	165	hypothetical protein								
ZMO0405	405319	407640	1	2322	ZP_0009607	ATPases with chaperone activity	1158	0	COG0542		O		
ZMO0406	408548	407733	-3	816	ZP_0009477	ABC-type multidrug transport sys	294	1.00E-78	COG0842		V		
ZMO0407	408703	409395	1	693	ZP_0009477	conserved hypothetical protein	282	4.00E-75	COG5352		S		
ZMO0408	409612	410820	1	1209	ZP_0009352	ornithine/acetylornithine aminotr	542	1.00E-153	COG4992		E		
ZMO0409	410842	411792	1	951	ZP_0009352	ornithine carbamoyltransferase	445	1.00E-124	COG0078		E		
ZMO0410	411921	412844	3	924	ZP_0009352	heat shock protein, chaperone pr	276	3.00E-73	COG1281		O		
ZMO0411	412919	414901	2	1983	ZP_0009494	topoisomerase (DNA gyrase/topo	977	0	COG0187		L		
ZMO0412	415720	415100	-2	621	ZP_0009679	multiple antibiotic transporter	218	8.00E-56	COG2095		U		
ZMO0413	416235	415915	-1	321	NP_387192	conserved hypothetical transmer	97.1	7.00E-20	COG0762		S		
ZMO0414	417299	416265	-3	1035	NP_768029	conserved hypothetical protein	73.9	4.00E-12	-		-		
ZMO0415	417409	417302	-2	108	hypothetical protein								
ZMO0416	417463	418209	1	747	ZP_0009387	cell division involved ATPase Fts	236	2.00E-61	COG2884		D		
ZMO0417	418191	419081	3	891	ZP_0009387	cell division protein FtsX	135	1.00E-30	COG2177		S		
ZMO0418	419113	419724	1	612	ZP_0009386	conserved hypothetical protein	157	1.00E-37	COG1434		D		
ZMO0419	419773	420525	1	753	ZP_0009386	1-acyl-sn-glycerol-3-phosphate a	145	1.00E-33	COG0204		I		
ZMO0420	421452	420577	-1	876	Q04983 TYR	protein tyrC [includes: Cyclohex	573	1.00E-162	COG0287		E		
ZMO0421	422562	421459	-1	1104	P34037 HIS8	histidinol-phosphate aminotransf	717	0	COG0079		E		
ZMO0422	423132	423539	3	408	ZP_0009649	predicted transcriptional regulato	119	8.00E-27	COG1959		K		
ZMO0423	423539	425011	2	1473	ZP_0009649	ABC-type transport system invol	797	0	COG0719		O		
ZMO0424	425035	425184	1	150	NP_904582	ABC transporter, ATP-binding pr	73.9	7.00E-13	COG0396		O		
ZMO0425	425168	425779	2	612	ZP_0009649	ABC-type transport system invol	285	5.00E-76	COG0396		O		
ZMO0426	425776	426891	1	1116	NP_947808	ABC-type transport system invol	135	1.00E-30	COG0719		O		
ZMO0427	426888	428111	3	1224	ZP_0009649	selenocysteine lyase	505	1.00E-142	COG0520		E		
ZMO0428	428108	428542	2	435	ZP_0009650	metal-sulfur cluster biosynthetic	151	2.00E-36	COG2151		R		
ZMO0429	428581	428922	1	342	ZP_0009650	conserved hypothetical protein	147	5.00E-35	COG0316		S		
ZMO0430	429047	429715	2	669	ZP_0005422	predicted hydrolase (HAD superf	177	1.00E-43	COG1011		R		
ZMO0431	429749	430579	2	831	ZP_0009342	tetrahydrodipicolinate N-succinyl	399	1.00E-110	COG2171		E		
ZMO0432	431522	430650	-3	873	ZP_0012405	arginase/agmatinase/formimiono	327	1.00E-88	COG0010		E		
ZMO0433	432514	431870	-2	645	ZP_0009593	guanylate kinase	272	3.00E-72	COG0194		F		
ZMO0434	432696	432559	-1	138	hypothetical protein								
ZMO0435	433075	432674	-2	402	ZP_0009388	conserved hypothetical protein	105	3.00E-22	-		-		
ZMO0436	433638	433246	-1	393	NP_539060	conserved hypothetical membrar	100	5.00E-21	COG3686		S		
ZMO0437	433799	434020	2	222	NP_644340	conserved hypothetical protein	54.7	4.00E-07	-		-		
ZMO0438	434159	434278	2	120	hypothetical protein								
ZMO0439	434275	435399	1	1125	ZP_0009311	pseudouridylyl synthases, 23S	312	8.00E-84	COG0564		J		
ZMO0440	435509	435799	2	291	hypothetical protein								
ZMO0441	435826	436530	1	705	ZP_0000447	chaperone required for the asser	209	5.00E-53	COG5387		O		
ZMO0442	436559	437203	2	645	NP_863883	phosphatase, putative	127	2.00E-28	COG0637		R		
ZMO0443	438321	437290	-1	1032	ZP_0009679	ribonucleotide reductase, beta su	576	1.00E-163	COG0208		F		
ZMO0444	438653	439699	2	1047	NP_903735	conserved hypothetical protein	80.9	4.00E-14	COG2845		S		
ZMO0445	439696	441261	1	1566	NP_927853	conserved hypothetical protein	84	8.00E-15	-		-		
ZMO0446	441293	442699	2	1407	NP_905383	alginate O-acetyltransferase, put	363	6.00E-99	COG1696		M		
ZMO0447	442717	443028	1	312	hypothetical protein								
ZMO0448	443730	443047	-1	684	ZP_0009603	cell wall hydrolyses involved in s	78.2	1.00E-13	COG3773		M		
ZMO0449	444524	445291	2	768	ZP_0009389	conserved hypothetical protein	100	3.00E-20	COG4649		S		
ZMO0450	445314	446558	3	1245	ZP_0009389	FOG: WD40-like repeat (PQQ er	319	8.00E-86	COG1520		S		
ZMO0451	446644	446540	-2	105	hypothetical protein								
ZMO0452	446661	446798	3	138	hypothetical protein								
ZMO0453	446865	448229	3	1365	ZP_0009624	GTPases, predicted	610	1.00E-173	COG1160		R		
ZMO0454	449968	449330	-3	639	NP_386496	formate-tetrahydrofolate ligase	429	1.00E-119	COG2759		F		
ZMO0455	450261	450157	-1	105	hypothetical protein								
ZMO0456	450398	450715	2	318	NP_640666	vanillate O-demethylase oxidore	110	6.00E-24	COG1018		C		
ZMO0457	450841	451335	1	495	P74996 GRP	glutamate uptake regulatory prot	295	2.00E-79	COG1522		K		
ZMO0458	452027	451335	-3	693	NP_697838	lipoprotein releasing system ATP	238	7.00E-62	COG1136		V		
ZMO0459	453270	452026	-1	1245	ZP_0009345	ABC-type transport system, invol	503	1.00E-141	COG4591		M		
ZMO0460	454602	453475	-1	1128	NP_420738	prolyl-tRNA synthetase (proline--	498	1.00E-140	COG0442		J		

ZMO0461	454718	454575	-3	144	hypothetical protein			-	-		
ZMO0462	456723	455095	-1	1629	NP_539766	CTP synthase	794	0	COG0504	F	
ZMO0463	456735	456881	3	147	hypothetical protein			-	-	-	
ZMO0464	457290	456868	-1	423	ZP_00095111	preprotein translocase subunit S	100	5.00E-21	COG1314	U	
ZMO0465	458219	457476	-3	744	ZP_00006314	triosephosphate isomerase	227	1.00E-58	COG0149	G	
ZMO0466	458401	458282	-2	120	hypothetical protein			-	-	-	
ZMO0467	458508	460466	3	1959	ZP_00095111	peptidyl-prolyl isomerase	305	2.00E-81	COG0760	O	
ZMO0468	460463	462013	2	1551	ZP_00095114	anthranilate/para-aminobenzoate	639	0	COG0147	EH	
ZMO0469	462480	462055	-1	426	hypothetical protein			-	-	-	
ZMO0470	462735	462595	-1	141	hypothetical protein			-	-	-	
ZMO0471	462737	463696	2	960	ZP_00033891	transcriptional regulator	342	8.00E-93	COG0583	K	
ZMO0472	464412	463738	-1	675	ZP_00096411	conserved hypothetical protein	184	1.00E-45	COG5590	S	
ZMO0473	465041	464628	-3	414	ZP_00094031	riboflavin synthase beta-chain	209	1.00E-53	COG0054	H	
ZMO0474	466182	465049	-1	1134	ZP_00095221	GTP cyclohydrolase II	441	1.00E-122	COG0108	H	
ZMO0475	466799	466185	-3	615	ZP_00096401	riboflavin synthase alpha chain	228	4.00E-59	COG0307	H	
ZMO0476	467859	466894	-1	966	ZP_00096401	riboflavin-specific deaminase/rec	320	3.00E-86	COG0117	H	
ZMO0477	468240	467896	-1	345	hypothetical protein			-	-	-	
ZMO0478	468425	469144	2	720	ZP_00029851	response regulators consisting o	229	5.00E-59	COG0745	TK	
ZMO0479	469148	470500	2	1353	NP_422120	peptidoglycan binding domain pr	167	6.00E-40	COG4254	S	
ZMO0480	470493	472784	3	2292	NP_422121	two-component sensory box hist	391	1.00E-107	COG4252	T	
ZMO0481	473325	472750	-1	576	hypothetical protein			-	-	-	
ZMO0482	474335	473343	-3	993	ZP_00006121	fructose-1,6-bisphosphatase/sed	336	3.00E-91	COG1494	G	
ZMO0483	475749	474463	-1	1287	ZP_00096661	homoserine dehydrogenase	454	1.00E-126	COG0460	E	
ZMO0484	475910	476620	2	711	NP_946216	magnesium transport MgtC, prec	187	1.00E-46	COG1285	S	
ZMO0485	476871	478049	3	1179	NP_946958	acyl-CoA dehydrogenase	591	1.00E-168	COG1960	I	
ZMO0486	478113	478988	3	876	NP_699369	conserved hypothetical protein	288	7.00E-77	COG3777	S	
ZMO0487	478981	479793	1	813	NP_542052	citrate lyase beta chain	300	2.00E-80	COG2301	G	
ZMO0488	480912	479914	-1	999	NP_102733	GTP binding protein, probable	70.5	5.00E-11	-	-	-
ZMO0489	481247	481477	2	231	hypothetical protein			-	-	-	
ZMO0490	483547	481487	-2	2061	ZP_00096531	protease II	756	0	COG1770	E	
ZMO0491	483675	485474	3	1800	ZP_00096531	aminopeptidase P (Xaa-pro)	676	0	COG0006	E	
ZMO0492	485584	485946	1	363	ZP_00056441	nitrogen regulatory protein PII	166	8.00E-41	COG0347	E	
ZMO0493	486040	487452	1	1413	ZP_00094351	glutamine synthetase	781	0	COG0174	E	
ZMO0494	487648	488898	1	1251	NP_772234	MFS permease	303	6.00E-81	COG0477	GEPR	
ZMO0495	493166	488895	-3	4272	ZP_00094351	conserved hypothetical protein	669	0	COG2911	S	
ZMO0496	495058	493172	-2	1887	NP_103198	conserved hypothetical protein	208	4.00E-52	COG0729	M	
ZMO0497	495939	495244	-1	696	ZP_00093821	phosphatases, predicted	169	5.00E-41	COG0546	R	
ZMO0498	496114	497499	1	1386	ZP_00093821	N-acetylglucosamine-1-phospha	525	1.00E-148	COG1207	M	
ZMO0499	499786	497684	-2	2103	ZP_00096681	membrane carboxypeptidase (pe	724	0	COG0744	M	
ZMO0500	501757	499823	-2	1935	NP_105540	conserved hypothetical protein	200	7.00E-50	-	-	-
ZMO0501	502012	502464	1	453	ZP_00025731	conserved hypothetical membrar	60.1	7.00E-09	COG2246	S	
ZMO0502	504134	502479	-3	1656	ZP_00096721	conserved hypothetical protein	193	7.00E-48	-	-	-
ZMO0503	504300	505469	3	1170	NP_949121	dolichol-phosphate mannosyltr	315	1.00E-84	COG0463	M	
ZMO0504	505552	505355	-2	198	hypothetical protein			-	-	-	
ZMO0505	505576	506235	1	660	ZP_00096521	pseudouridylyl synthases, 23S	225	6.00E-58	COG0564	J	
ZMO0506	506901	506488	-1	414	ZP_00083731	protein chain release factor B	134	3.00E-31	COG1186	J	
ZMO0507	507018	507503	3	486	ZP_00096431	GAF domain-containing protein	172	2.00E-42	COG1956	T	
ZMO0508	507527	507958	2	432	CAE77991	acetyltransferase	94	5.00E-19	COG0454	KR	
ZMO0509	508043	508762	2	720	CAA63807	conserved hypothetical protein	516	1.00E-145	-	-	-
ZMO0510	509042	510364	2	1323	O66119 ODP	dihydrolipoamide acetyltransfera	826	0	COG0508	C	
ZMO0511	510361	510810	1	450	ZP_00051841	acyl-CoA hydrolase	139	7.00E-33	COG1607	I	
ZMO0512	510856	512256	1	1401	P50970 DLDI	dihydrolipoyl dehydrogenase (E3	912	0	COG1249	C	
ZMO0513	512268	512975	3	708	NP_105411	conserved hypothetical protein, f	102	8.00E-21	COG0671	I	
ZMO0514	513761	514231	2	471	ZP_00094601	ribosomal protein S7	251	3.00E-66	COG0049	J	
ZMO0515	514290	516362	3	2073	ZP_00094611	translation elongation factors (G	1139	0	COG0480	J	
ZMO0516	516466	517659	1	1194	ZP_00094611	GTPases - translation elongation	697	0	COG0050	J	
ZMO0517	518391	519119	3	729	ZP_00094611	ribosomal protein L3	367	1.00E-100	COG0087	J	
ZMO0518	519122	519745	2	624	ZP_00094611	ribosomal protein L4	302	3.00E-81	COG0088	J	
ZMO0519	519738	520049	3	312	ZP_00094611	ribosomal protein L23	141	3.00E-33	COG0089	J	
ZMO0520	520054	520890	1	837	ZP_00094611	ribosomal protein L2	494	1.00E-139	COG0090	J	
ZMO0521	521168	521548	2	381	ZP_00094611	ribosomal protein L22	195	2.00E-49	COG0091	J	
ZMO0522	521550	522245	3	696	ZP_00094611	ribosomal protein S3	403	1.00E-111	COG0092	J	
ZMO0523	522309	522740	3	432	ZP_00094621	ribosomal protein L16/L10E	235	1.00E-61	COG0197	J	
ZMO0524	522743	522946	2	204	ZP_00094621	ribosomal protein L29	101	4.00E-21	COG0255	J	
ZMO0525	522958	523209	1	252	ZP_00094621	ribosomal protein S17	130	6.00E-30	COG0186	J	
ZMO0526	523337	523648	2	312	NP_948579	ribosomal protein L14, 50S	159	1.00E-38	COG0093	J	
ZMO0527	523648	523965	1	318	ZP_00094621	ribosomal protein L24	145	2.00E-34	COG0198	J	
ZMO0528	523958	524536	2	579	ZP_00094621	ribosomal protein L5	306	1.00E-82	COG0094	J	
ZMO0529	524580	524885	3	306	ZP_00094621	ribosomal protein S14	175	1.00E-43	COG0199	J	
ZMO0530	524899	525294	1	396	ZP_00094621	ribosomal protein S8	210	4.00E-54	COG0096	J	
ZMO0531	525294	525827	3	534	ZP_00094621	ribosomal protein L6P/L9E	283	1.00E-75	COG0097	J	
ZMO0532	525827	526183	2	357	ZP_00094621	ribosomal protein L18	159	8.00E-39	COG0256	J	
ZMO0533	526184	526885	2	702	ZP_00094631	ribosomal protein S5	339	3.00E-92	COG0098	J	
ZMO0534	526893	527069	3	177	ZP_00013701	ribosomal protein L30/L7E	87.4	6.00E-17	COG1841	J	
ZMO0535	527193	527056	-1	138	hypothetical protein			-	-	-	
ZMO0536	527220	527711	3	492	ZP_00094631	ribosomal protein L15	229	2.00E-59	COG0200	J	
ZMO0537	527997	529385	3	1389	NP_385482	preprotein translocase, transmer	544	1.00E-153	COG0201	U	

ZMO0538	529418	530089	2	672	ZP_0009463	adenylate kinase and related kin	262	3.00E-69	COG0563	F
ZMO0539	530403	530792	3	390	ZP_0009596	ribosomal protein S13	211	2.00E-54	COG0099	J
ZMO0540	530857	531246	1	390	ZP_0009596	ribosomal protein S11	246	8.00E-65	COG0100	J
ZMO0541	531339	532400	3	1062	ZP_0009595	DNA-directed RNA polymerase, $\sigma$	557	1.00E-157	COG0202	K
ZMO0542	532520	532942	2	423	ZP_0009595	ribosomal protein L17	210	4.00E-54	COG0203	J
ZMO0543	533710	535980	1	2271	NP_810985	aconitate hydratase	1073	0	COG1048	C
ZMO0544	536046	537308	3	1263	NP_810984	isocitrate dehydrogenase [NADP	562	1.00E-159	COG0538	C
ZMO0545	538208	537420	-3	789	Q9XBM3 TRF	indole-3-glycerol phosphate synt	506	1.00E-142	COG0134	E
ZMO0546	538609	540051	1	1443	NP_638866	sulfate permease	577	1.00E-163	COG0659	P
ZMO0547	542067	540559	-1	1509	NP_561506	conserved hypothetical protein	343	7.00E-93	COG0038	P
ZMO0548	543223	542216	-2	1008	ZP_0000449	two-component signal transducti	152	1.00E-35	COG3920	T
ZMO0549	545622	543382	-1	2241	ZP_0009477	polyribonucleotide nucleotidyltra	1062	0	COG1185	J
ZMO0550	546005	545742	-3	264	NP_540879	ribosomal protein S15P, SSU	136	1.00E-31	COG0184	J
ZMO0551	546934	546029	-2	906	ZP_0009476	tRNA pseudouridine synthase	321	1.00E-86	COG0130	J
ZMO0552	547512	546937	-1	576	ZP_0009476	thymidine kinase, zeocin resistar	255	4.00E-67	COG1435	F
ZMO0553	547961	547542	-3	420	ZP_0009476	ribosome-binding factor A	139	1.00E-32	COG0858	J
ZMO0554	551077	548114	-2	2964	ZP_0009476	translation initiation factor 2 (IF-2	983	0	COG0532	J
ZMO0555	551815	551087	-2	729	ZP_0009476	transcription termination involvec	184	1.00E-45	COG2740	K
ZMO0556	553507	551888	-2	1620	NP_767425	N-utilization substance protein A	629	1.00E-179	COG0195	K
ZMO0557	554058	553510	-1	549	ZP_0009690	conserved hypothetical protein	168	4.00E-41	COG0779	S
ZMO0558	554462	555790	2	1329	NP_644174	dehydrogenase	315	2.00E-84	COG2133	G
ZMO0559	555866	556693	2	828	ZP_0009642	ATPase (AAA+ superfamily), pre	236	5.00E-61	COG2607	R
ZMO0560	556860	558008	3	1149	NP_419887	histidinol-phosphate aminotransf	277	2.00E-73	COG0079	E
ZMO0561	560558	559101	-3	1458	ZP_0002744	outer membrane receptor proteir	396	1.00E-109	COG1629	P
ZMO0562	560726	561883	2	1158	NP_419887	histidinol-phosphate aminotransf	275	2.00E-72	COG0079	E
ZMO0563	562325	562029	-3	297	NP_387347	putative chorismate mutase prot	97.8	4.00E-20	COG1605	E
ZMO0564	562444	563457	1	1014	ZP_0009466	geranylgeranyl pyrophosphate sy	393	1.00E-108	COG0142	H
ZMO0565	563499	566012	3	2514	ZP_0009465	helicases, HrpA-like, ATP-depen	724	0	COG1643	L
ZMO0566	567455	566208	-3	1248	NP_640673	MFS transporter	373	1.00E-102	COG0477	GEPR
ZMO0567	568602	567682	-1	921	ZP_0009369	succinyl-CoA synthetase, alpha s	437	1.00E-121	COG0074	C
ZMO0568	569042	568665	-3	378	ZP_0009316	succinate dehydrogenase, hydro	53.5	7.00E-07	-	-
ZMO0569	569470	569051	-2	420	ZP_0009316	succinate dehydrogenase/fumar	57	6.00E-08	-	-
ZMO0570	569630	570577	2	948	ZP_0009316	ribosomal protein L11 methylase	261	2.00E-68	COG2264	J
ZMO0571	571449	573218	3	1770	ZP_0010345	ABC-type anion transport system	742	0	COG4986	P
ZMO0572	573245	574564	2	1320	ZP_0004000	ABC-type nitrate/sulfonate/bicart	598	1.00E-169	COG3842	E
ZMO0573	574746	575393	3	648	NP_455658	glutaredoxin 2	211	8.00E-54	COG2999	O
ZMO0574	577749	575449	-1	2301	ZP_0009469	DNA and RNA helicases	906	0	COG0210	L
ZMO0575	578364	577819	-1	546	ZP_0009470	N6-adenine-specific methylase	191	5.00E-48	COG0742	L
ZMO0576	579395	578997	-2	399	ZP_0009470	16S rRNA uridine-516 pseudouri	258	5.00E-68	COG1187	J
ZMO0577	579778	579981	1	204		hypothetical protein	-	-	-	-
ZMO0578	581333	580059	-3	1275	ZP_0002477	Na <sup>+</sup> /H <sup>+</sup> -dicarboxylate symporter	433	1.00E-120	COG1301	C
ZMO0579	581479	581661	1	183		hypothetical protein	-	-	-	-
ZMO0580	581696	581541	-3	156		hypothetical protein	-	-	-	-
ZMO0581	581710	583014	1	1305	ZP_0009470	permeases of the major facilitato	375	1.00E-102	COG0477	GEPR
ZMO0582	584363	583038	-3	1326	NP_945428	putative poly(oligo)glutamate synth	336	7.00E-91	COG0285	H
ZMO0583	585246	584398	-1	849	ZP_0009470	acetyl-CoA carboxylase beta sub	400	1.00E-110	COG0777	I
ZMO0584	586067	585249	-3	819	P34816 TRP	tryptophan synthase alpha chain	263	2.00E-69	COG0159	E
ZMO0585	587290	586070	-2	1221	P56929 TRP	tryptophan synthase beta chain	592	1.00E-168	COG0133	E
ZMO0586	587922	587293	-1	630	Q9S3U4 TRF	N-(5'-phosphoribosyl)anthranilate	415	1.00E-115	COG0135	E
ZMO0587	588745	588041	-2	705	ZP_0009471	orotidine-5'-phosphate decarbox	259	4.00E-68	COG0284	F
ZMO0588	589073	588765	-3	309	ZP_0009471	conserved hypothetical protein	52.8	1.00E-06	-	-
ZMO0589	589166	590533	2	1368	ZP_0009549	ATP-dependent serine protease,	603	1.00E-171	COG1066	O
ZMO0590	590533	591258	1	726	ZP_0009548	uncharacterized membrane prot	74.7	2.00E-12	COG1286	R
ZMO0591	591473	591922	2	450	ZP_0000783	NifU homolog involved in Fe-S cl	89	1.00E-17	COG0822	C
ZMO0592	591952	592326	1	375	NP_439229	conserved hypothetical protein	79.7	1.00E-14	COG2363	S
ZMO0593	593505	592372	-1	1134	ZP_0009453	3-dehydroquinase synthetase	433	1.00E-120	COG0337	E
ZMO0594	594032	593508	-3	525	NP_421802	shikimate kinase	176	2.00E-43	COG0703	E
ZMO0595	594116	594265	2	150		hypothetical protein	-	-	-	-
ZMO0596	594307	594155	-2	153		hypothetical protein	-	-	-	-
ZMO0597	594369	596009	3	1641	ZP_0009453	conserved hypothetical protein	245	2.00E-63	-	-
ZMO0598	596051	596974	2	924	NP_421800	integrase/recombinase XerD	241	2.00E-62	COG4974	L
ZMO0599	596985	597926	3	942	ZP_0009453	acetyl-CoA carboxylase alpha su	424	1.00E-117	COG0825	I
ZMO0600	598197	598033	-1	165		hypothetical protein	-	-	-	-
ZMO0601	598187	600622	2	2436	AAP46184	two component sensor kinase/re	662	0	COG0642	T
ZMO0602	602653	601679	-2	975	ZP_0003214	flagellar motor protein, MotB	193	4.00E-48	COG1360	N
ZMO0603	603568	602711	-2	858	NP_419567	flagellar motor component, chem	264	2.00E-69	COG1291	N
ZMO0604	604628	603777	-3	852	NP_455677	flagellar hook-associated protein	94.7	2.00E-18	COG1344	N
ZMO0605	606019	604649	-2	1371	AAG31286	flagellar hook-associated protein	149	2.00E-34	COG1256	N
ZMO0606	606572	606186	-3	387	NP_746496	peptidoglycan hydrolase FlgJ	55.1	3.00E-07	COG3951	MNO
ZMO0607	607720	606575	-2	1146	Q9Z5T9 FLG	flagellar P-ring protein precursor	686	0	COG1706	N
ZMO0608	608409	607741	-1	669	Q9Z5T8 FLG	flagellar L-ring protein precursor	415	1.00E-116	COG2063	N
ZMO0609	609214	608429	-2	786	NP_791763	flagellar basal-body rod protein F	282	4.00E-75	COG4786	N
ZMO0610	610016	609273	-3	744	NP_718799	flagellar basal-body rod protein F	174	1.00E-42	COG4787	N
ZMO0611	611291	610062	-3	1230	NP_637314	flagellar biosynthesis, hook prote	209	1.00E-52	COG1749	N
ZMO0612	612024	611338	-1	687	AAF14369	flagellar scaffolding protein FlgD	115	9.00E-25	COG1843	N
ZMO0613	612490	612092	-2	399	NP_642311	flagellar biosynthesis cell-proxim	121	2.00E-27	COG1558	N
ZMO0614	612852	612505	-1	348	AAF14367	flagellar proximal rod protein FlgI	104	4.00E-22	COG1815	N



ZMO0615	612887	613090	2	204	hypothetical protein			-	-
ZMO0616	613068	613763	3	696 NP_759315	flagellar motor component MotA	102	6.00E-21	COG1291	N
ZMO0617	613820	614425	2	606 NP_901484	chemotaxis motB protein	52.8	5.00E-06	COG1360	N
ZMO0618	614621	614779	2	159	hypothetical protein			-	-
ZMO0619	614991	615557	3	567 NP_797151	flagellar FlgA, polar	55.1	7.00E-07	-	-
ZMO0620	615923	615624	-3	300	hypothetical protein			-	-
ZMO0621	615649	616083	1	435 AAL13053	platelet binding protein GspB (ce	65.1	2.00E-10	-	-
ZMO0622	616076	616393	2	318	hypothetical protein			-	-
ZMO0623	616667	616807	2	141	hypothetical protein			-	-
ZMO0624	616807	618930	1	2124 NP_231701	flagellar biosynthetic protein FlhA	624	1.00E-177	COG1298	NU
ZMO0625	618931	619752	1	822 NP_791801	flagellar synthesis regulator FleN	191	1.00E-47	COG0455	D
ZMO0626	619742	620485	2	744 NP_798611	flagellar-specific RNA polymerase	162	4.00E-39	COG1191	R
ZMO0627	620618	621304	2	687	hypothetical protein			COG1216	K
ZMO0628	621363	621989	3	627	hypothetical protein			-	-
ZMO0629	622931	622083	-3	849 ZP_00094271	flagellin and related hook-associated	279	4.00E-74	COG1344	N
ZMO0630	623618	624001	2	384	hypothetical protein			-	-
ZMO0631	624040	624942	1	903 NP_746485	two component response regulator	278	1.00E-73	COG2204	T
ZMO0632	625049	625390	2	342 NP_798629	flagellar hook-basal body complex	66.6	9.00E-11	COG1677	NU
ZMO0633	625394	627049	2	1656 Q53151 FLIF	flagellar M-Ring protein; FliF	279	1.00E-73	COG1766	NU
ZMO0634	627114	627254	3	141	hypothetical protein			-	-
ZMO0635	627247	628281	1	1035 ZP_00006051	flagellar motor switch protein	281	1.00E-74	COG1536	N
ZMO0636	628268	629035	2	768 ZP_00084951	flagellar biosynthesis/type III secretion	53.5	4.00E-06	-	-
ZMO0637	629032	629925	1	894 CAA65834	flagellum-specific ATP synthase subunit	263	3.00E-69	COG1157	NU
ZMO0638	630361	630786	1	426	hypothetical protein			-	-
ZMO0639	630783	631331	3	549 NP_870028	conserved hypothetical protein-s	52	6.00E-06	-	-
ZMO0640	631386	632666	3	1281 NP_647392	conserved hypothetical protein, s	77.4	5.00E-13	-	-
ZMO0641	632782	633186	1	405 NP_531272	chemotaxis MotD protein	53.1	1.00E-06	-	-
ZMO0642	633199	633768	1	570 ZP_00004601	conserved hypothetical protein	101	9.00E-21	COG1580	N
ZMO0643	633765	634763	3	999 AAC32319	flagellar switch protein; FliM	150	5.00E-35	COG1868	N
ZMO0644	634760	635071	2	312 ZP_00065091	flagellar motor switch/type III secretion	95.1	3.00E-19	COG1886	NU
ZMO0645	635064	635228	3	165	hypothetical protein			-	-
ZMO0646	635068	635388	1	321 NP_791794	flagellar protein FliO	52.8	1.00E-06	-	-
ZMO0647	635393	636343	2	951 NP_840547	flagellar transport protein FljP	255	9.00E-67	COG1338	NU
ZMO0648	636340	636615	1	276 NP_660435	flagellar biosynthetic protein FliQ	81.6	3.00E-15	COG1987	NU
ZMO0649	636629	637426	2	798 ZP_00089071	flagellar biosynthesis pathway, c	162	8.00E-39	COG1684	NU
ZMO0650	637416	638558	3	1143 NP_231751	flagellar biosynthetic protein FlhE	226	8.00E-58	COG1377	NU
ZMO0651	638660	640354	2	1695 NP_945994	flagellar hook-associated protein	200	8.00E-50	COG1345	N
ZMO0652	640395	640784	3	390 NP_521945	flagellar protein FliS, probable	75.1	2.00E-13	COG1516	NUO
ZMO0653	641944	640880	-2	1065 ZP_00029761	permease, predicted	249	5.00E-65	COG0628	R
ZMO0654	645373	641999	-2	3375 NP_845761	glycosyl transferase, protein/poly	718	0	COG1215	M
ZMO0655	645528	647108	3	1581 ZP_00110911	adenosine deaminase	323	4.00E-87	COG1816	F
ZMO0656	647754	647239	-1	516 NP_940382	purine phosphoribosyltransferase	73.6	2.00E-12	COG2236	R
ZMO0657	648860	647838	-3	1023 ZP_00094391	arginine/ornithine N-succinyltransferase	377	1.00E-103	COG3138	E
ZMO0658	650011	648863	-2	1149 ZP_00094391	acetylornithine deacetylase/succinyltransferase	387	1.00E-106	COG0624	E
ZMO0659	650527	651072	1	546 NP_249834	conserved hypothetical protein	82	9.00E-15	COG0560	E
ZMO0660	651304	653211	1	1908 ZP_00094901	heat shock protein dnaK, hsp70,	998	0	COG0443	O
ZMO0661	653331	654458	3	1128 ZP_00094901	heat shock protein DnaJ, molecular chaperone	485	1.00E-136	COG0484	O
ZMO0662	655861	654572	-2	1290 NP_101953	adenylosuccinate lyase	650	0	COG0015	F
ZMO0663	656684	656007	-3	678 ZP_00094711	DNA repair proteins, RadC	234	1.00E-60	COG2003	L
ZMO0664	656842	659982	1	3141 ZP_00094711	exoproteins involved in heme utilization	365	4.00E-99	-	-
ZMO0665	660037	660237	1	201 ZP_00094721	conserved hypothetical protein	70.5	8.00E-12	-	-
ZMO0666	660234	660632	3	399 ZP_00094721	conserved hypothetical protein	95.1	2.00E-19	COG3784	S
ZMO0667	661242	662042	3	801 ZP_00094721	ATP synthase A chain	298	6.00E-80	COG0356	C
ZMO0668	662078	662317	2	240 ZP_00094721	ATP synthase C chain, archaeal/	114	3.00E-25	COG0636	C
ZMO0669	662439	662939	3	501 ZP_00094721	ATP synthase B chain	139	2.00E-32	COG0711	C
ZMO0670	662953	663210	1	258	hypothetical protein			-	-
ZMO0671	663245	663592	2	348 ZP_00094721	ATP synthase, subunit b	89.4	1.00E-17	COG0711	C
ZMO0672	663747	665741	3	1995 ZP_00095031	nuclease subunit of the excinuclease	728	0	COG0322	L
ZMO0673	665783	666541	2	759 ZP_00054201	recombinational DNA repair protein	122	7.00E-27	COG1381	L
ZMO0674	666579	667103	3	525 ZP_00050361	conserved hypothetical protein	113	2.00E-24	-	-
ZMO0675	667910	667107	-3	804 ZP_00094791	transcriptional regulator, LysR family	293	3.00E-78	COG0583	K
ZMO0676	669185	667983	-3	1203 ZP_00055521	cystathionine beta-lyases/cystathionase	431	1.00E-119	COG0626	E
ZMO0677	670301	669258	-3	1044 Q845W3 LEL	3-isopropylmalate dehydrogenase	432	1.00E-120	COG0473	CE
ZMO0678	671057	670440	-3	618 ZP_00034391	nitroreductase	179	4.00E-44	COG0778	C
ZMO0679	671150	671251	2	102	hypothetical protein			-	-
ZMO0680	671414	672451	2	1038 NP_901426	conserved hypothetical protein	462	1.00E-129	COG1518	L
ZMO0681	672448	674391	1	1944 NP_901425	conserved hypothetical protein	639	0	COG1203	R
ZMO0682	675915	677234	3	1320 NP_901424	conserved hypothetical protein	296	5.00E-79	-	-
ZMO0683	677276	678259	2	984 NP_901423	conserved hypothetical protein	262	7.00E-69	-	-
ZMO0684	678308	679348	2	1041 NP_901422	conserved hypothetical protein	431	1.00E-119	-	-
ZMO0685	679332	679919	3	588 NP_405996	conserved hypothetical protein	139	4.00E-32	-	-
ZMO0686	680361	680783	3	423 ZP_00093711	conserved hypothetical protein	62.4	2.00E-09	-	-
ZMO0687	682528	680873	-2	1656 ZP_00079041	acetolactate synthase, pyruvate-dependent	709	0	COG0028	EH
ZMO0688	683098	682598	-2	501 ZP_00070291	permeases, predicted	107	9.00E-23	COG0679	R
ZMO0689	685049	683754	-3	1296 1H6DJA	glucose-fructose oxidoreductase	864	0	COG0673	R
ZMO0690	685597	685472	-2	126	hypothetical protein			-	-
ZMO0691	687017	685683	-3	1335 ZP_00093711	NAD(FAD)-utilizing enzyme possessing	558	1.00E-157	COG1206	J

ZMO0692	689843	687072	-3	2772	ZP_0009371	type IIA topoisomerase (DNA gyr	1208	0	COG0188	L
ZMO0693	690337	689918	-2	420	NP_767375	organic hydroperoxide resistance	187	2.00E-47	COG1764	O
ZMO0694	691344	690625	-1	720		hypothetical protein			-	-
ZMO0695	695630	692061	-3	3570	NP_637005	conserved hypothetical protein	622	1.00E-176	COG1112	L
ZMO0696	695798	695697	-3	102		hypothetical protein			-	-
ZMO0697	696419	696102	-3	318	NP_697794	sugE protein:multi-drug resistant	133	8.00E-31	COG2076	P
ZMO0698	696992	696492	-3	501		hypothetical protein			-	-
ZMO0699	697132	697323	1	192		hypothetical protein			-	-
ZMO0700	698364	697333	-1	1032	ZP_0010248	dipeptidyl aminopeptidases/acyl	216	6.00E-55	COG1506	E
ZMO0701	699476	699330	-3	147		hypothetical protein			-	-
ZMO0702	699638	699513	-3	126		hypothetical protein			-	-
ZMO0703	699343	698225	-2	1119	NP_874138	colicin tolerance protein	55.1	2.00E-06	-	-
ZMO0704	701431	699983	-2	1449	ZP_0009628	acyl-CoA synthetases (AMP-form	602	1.00E-174	COG0318	IQ
ZMO0705	701467	702075	1	609	ZP_0009628	conserved hypothetical protein	107	1.00E-22	-	-
ZMO0706	702728	702087	-3	642	ZP_0001405	endonuclease III, predicted	270	1.00E-71	COG0177	L
ZMO0707	703489	702731	-2	759	ZP_0009667	dihydrodipicolinate reductase	260	2.00E-68	COG0289	E
ZMO0708	704120	703500	-3	621	ZP_0005370	folate-dependent phosphoribosyl	210	1.00E-53	COG0299	F
ZMO0709	705213	704119	-1	1095	ZP_0009438	phosphoribosylaminoimidazole (	514	1.00E-144	COG0150	F
ZMO0710	705271	706368	1	1098	ZP_0009438	conserved hypothetical protein	227	3.00E-58	-	-
ZMO0711	706372	707016	1	645	ZP_0009438	ATPase involved in DNA replicati	139	4.00E-32	COG0593	L
ZMO0712	707198	709351	2	2154	ZP_0001580	polyphosphate kinase	828	0	COG0855	P
ZMO0713	709518	711044	3	1527	ZP_0001580	exopolyphosphatase	298	1.00E-79	COG0248	FP
ZMO0714	712291	711125	-2	1167	ZP_0009467	ribonuclease D	512	1.00E-144	COG0349	J
ZMO0715	712396	714186	1	1791	ZP_0001552	aspartyl-tRNA synthetase	817	0	COG0173	J
ZMO0716	714219	715004	3	786	NP_617297	conserved hypothetical protein	194	2.00E-48	COG2326	S
ZMO0717	715077	714973	-1	105		hypothetical protein			-	-
ZMO0718	715546	715055	-2	492	ZP_0009505	transcription elongation factor	228	4.00E-59	COG0782	K
ZMO0719	717714	715627	-1	2088	ZP_0009505	transglycosylase and related reg	390	1.00E-107	COG0741	M
ZMO0720	717739	718614	1	876	ZP_0009505	dihydrodipicolinate synthase/N-a	352	6.00E-96	COG0329	EM
ZMO0721	718618	719100	1	483	AAP46182	small protein B	246	1.00E-64	COG0691	O
ZMO0722	719295	721340	3	2046	NP_639017	metallopeptidase	632	1.00E-180	COG3590	O
ZMO0723	722321	721770	-3	552	ZP_0009627	transcription antiterminator, NusC	169	3.00E-41	COG0250	K
ZMO0724	722013	722552	3	540	ZP_0009627	transcription antiterminator, NusC	256	2.00E-67	COG0250	K
ZMO0725	722639	723070	2	432	ZP_0009627	ribosomal protein L11	218	1.00E-56	COG0080	J
ZMO0726	723075	723776	3	702	NP_385451	ribosomal protein L1	327	1.00E-88	COG0081	J
ZMO0727	724041	724556	3	516	ZP_0009664	ribosomal protein L10	219	2.00E-56	COG0244	J
ZMO0728	724614	724985	3	372	ZP_0009664	ribosomal protein L7/L12	186	8.00E-47	COG0222	J
ZMO0729	724903	724556	-2	348	ZP_0009664	ribosomal protein L7/L12	153	7.00E-37	COG0222	J
ZMO0730	725416	725222	-2	195		hypothetical protein			-	-
ZMO0731	725449	729654	1	4206	ZP_0009665	DNA-directed RNA polymerase, I	2280	0	COG0085	K
ZMO0732	729737	733912	2	4176	ZP_0009665	DNA-directed RNA polymerase, I	2211	0	COG0086	K
ZMO0733	734532	734044	-1	489	NP_888193	acetyltransferase, putative	141	4.00E-33	COG0454	KR
ZMO0734	734709	735527	3	819	NP_107864	pssB protein, exopolysaccharide	212	6.00E-54	COG1218	P
ZMO0735	736870	735590	-2	1281	ZP_0009493	acetyl-CoA carboxylase, biotin ca	650	0	COG0439	I
ZMO0736	737429	736953	-3	477	ZP_0009493	acetyl-CoA carboxylase, biotin ca	165	3.00E-40	COG0511	I
ZMO0737	737965	737531	-2	435	ZP_0009493	3-dehydroquinone dehydratase II	206	1.00E-52	COG0757	E
ZMO0738	738047	739042	2	996	ZP_0009672	uncharacterized enzyme of thiaz	479	1.00E-134	COG2022	H
ZMO0739	739402	739112	-2	291	NP_880694	conserved hypothetical protein	80.5	7.00E-15	COG2329	R
ZMO0740	739626	739898	3	273	ZP_0008385	conserved hypothetical protein	62.8	1.00E-09	COG3237	S
ZMO0741	740077	739976	-2	102		hypothetical protein			-	-
ZMO0742	740102	740218	2	117		hypothetical protein			-	-
ZMO0743	740230	741819	1	1590	ZP_0009475	peptide chain release factor RF-1	699	0	COG4108	J
ZMO0744	741978	742778	3	801	NP_641539	conserved hypothetical protein	242	5.00E-63	-	-
ZMO0745	742896	743369	3	474	ZP_0014021	conserved hypothetical protein	231	3.00E-60	COG3558	S
ZMO0746	743990	744523	2	534	ZP_0009572	conserved hypothetical protein	115	3.00E-25	COG3807	S
ZMO0747	744627	745046	3	420	ZP_0009352	conserved hypothetical protein	62.4	2.00E-09	-	-
ZMO0748	746009	745092	-3	918	ZP_0009392	cysteine synthase	447	1.00E-124	COG0031	E
ZMO0749	747127	746225	-2	903	P50512 RP3	RNA polymerase sigma-32 facto	593	1.00E-168	COG0568	K
ZMO0750	748133	747186	-3	948	P50513 RLUI	ribosomal large subunit pseudou	629	1.00E-179	COG0564	J
ZMO0751	748181	748636	2	456	ZP_0009333	metal-dependent protease, predi	85.9	1.00E-16	COG1310	R
ZMO0752	748754	749380	2	627	ZP_0009333	conserved hypothetical protein	200	2.00E-50	COG5385	S
ZMO0753	749552	749806	2	255	NP_290193	glutaredoxin 3	114	6.00E-25	COG0695	O
ZMO0754	749844	750146	3	303	NP_104186	conserved hypothetical protein	69.7	1.00E-11	COG3255	I
ZMO0755	751249	750224	-2	1026	NP_634744	conserved hypothetical protein	74.3	3.00E-12	COG0457	R
ZMO0756	751640	751230	-3	411		hypothetical protein			-	-
ZMO0757	752881	751757	-2	1125	NP_617725	conserved hypothetical protein	60.1	8.00E-08	COG0457	R
ZMO0758	753515	752871	-3	645	NP_822563	isochorismatase, putative	204	1.00E-51	COG1335	Q
ZMO0759	754278	753559	-1	720	ZP_0001493	Zn-dependent hydrolases, includ	247	2.00E-64	COG0491	R
ZMO0760	754714	754325	-2	390	ZP_0009398	lactoylglutathione lyase and relat	171	2.00E-42	COG0346	E
ZMO0761	754406	754819	2	414	ZP_0009398	lactoylglutathione lyase and relat	146	8.00E-35	COG0346	E
ZMO0762	754850	754698	-3	153		hypothetical protein			-	-
ZMO0763	755960	754941	-3	1020	ZP_0009650	FOG: TPR repeat	144	3.00E-33	COG0457	R
ZMO0764	756729	755992	-1	738	ZP_0005619	hydrolases or acyltransferases, p	209	3.00E-53	COG0596	R
ZMO0765	756996	758975	3	1980	ZP_0009650	threonyl-tRNA synthetase	964	0	COG0441	J
ZMO0766	758989	761769	1	2781	ZP_0009474	UTP:glnB (protein PII) uridylyltra	819	0	COG2844	O
ZMO0767	761963	764182	2	2220	NP_717031	conserved hypothetical protein	59.3	3.00E-07	-	-
ZMO0768	764459	764211	-3	249		hypothetical protein			-	-

ZMO0769	764537	765688	2	1152	ZP_0009663	tRNA (5-methylaminomethyl-2-th	465	1.00E-130	COG0482	J
ZMO0770	767243	765774	-3	1470	ZP_0009589	Mg/Co/Ni transporter MgtE (cont	534	1.00E-150	COG2239	P
ZMO0771	767231	767422	2	192		hypothetical protein	-	-	-	-
ZMO0772	767352	767486	3	135		hypothetical protein	-	-	-	-
ZMO0773	767459	767926	2	468	NP_420395	peptidyl-prolyl cis-trans isomeras	250	5.00E-66	COG0652	O
ZMO0774	768833	767940	-3	894	ZP_0009591	transcriptional regulator	255	7.00E-67	COG0583	K
ZMO0775	768868	769032	1	165		hypothetical protein	-	-	-	-
ZMO0776	769365	769991	3	627	ZP_0009604	phospholipid N-methyltransferas	238	4.00E-62	COG3963	I
ZMO0777	770701	770024	-2	678	NP_718619	metallo-beta-lactamase family pr	268	5.00E-71	COG0491	R
ZMO0778	770972	771373	3	402	ZP_0003210	cation/multidrug efflux pump	1133	0	COG0841	V
ZMO0779	774196	775434	1	1239	ZP_0003437	membrane-fusion protein	338	1.00E-91	COG0845	M
ZMO0780	775412	776914	2	1503	ZP_0003437	outer membrane protein	409	1.00E-113	COG1538	MU
ZMO0781	777103	778050	1	948	CAE78845	transcriptional regulator, LysR fa	241	1.00E-62	COG0583	K
ZMO0782	779658	778129	-1	1530	NP_539985	glutamyl-tRNA(gln) amidotransfe	621	1.00E-176	COG0064	J
ZMO0783	781075	779603	-2	1473	ZP_0009311	glutamyl-tRNA(gln) amidotransfe	700	0	COG0154	J
ZMO0784	781365	781081	-1	285	ZP_0009311	glutamyl-tRNA(gln) amidotransfe	105	3.00E-22	COG0721	J
ZMO0785	781602	782141	3	540	ZP_0009437	endonuclease involved in recomb	166	3.00E-40	COG0816	L
ZMO0786	782345	782905	2	561	ZP_0008419	conserved hypothetical protein	68.6	6.00E-11	-	-
ZMO0787	782963	784549	2	1587	ZP_0008419	choline dehydrogenase and relat	502	1.00E-141	COG2303	E
ZMO0788	784559	786076	2	1518	BAA92379	sorbitol dehydrogenase cytochro	397	1.00E-109	COG2010	C
ZMO0789	786394	788919	1	2526	NP_902858	TonB-dependent receptor, proba	358	4.00E-97	COG1629	P
ZMO0790	789561	789689	3	129		hypothetical protein	-	-	-	-
ZMO0791	789730	790689	1	960	ZP_0009431	aspartate carbamoyltransferase,	414	1.00E-114	COG0540	F
ZMO0792	790686	791912	3	1227	ZP_0009431	dihydroorotase and related cyclic	426	1.00E-118	COG0044	F
ZMO0793	792024	792644	3	621		hypothetical protein	-	-	-	-
ZMO0794	794736	792694	-1	2043	NP_422482	prolyl oligopeptidase family prote	712	0	COG1505	E
ZMO0795	797029	794855	-2	2175	NP_950091	outer membrane receptor for iron	454	1.00E-126	COG1629	P
ZMO0796	797343	797185	-1	159		hypothetical protein	-	-	-	-
ZMO0797	798384	797605	-1	780	ZP_0010856	dehydrogenases with different sp	284	1.00E-75	COG1028	IQR
ZMO0798	800027	798618	-3	1410	ZP_0003009	outer membrane protein	189	9.00E-47	COG1538	MU
ZMO0799	801154	800033	-2	1122	NP_246920	conserved hypothetical protein	347	3.00E-94	COG0842	V
ZMO0800	803986	801164	-2	2823	NP_246921	conserved hypothetical protein	995	0	COG1131	V
ZMO0801	804977	803937	-3	1041	ZP_0008358	membrane-fusion protein	226	7.00E-58	COG0845	M
ZMO0802	805321	805130	-2	192		hypothetical protein	-	-	-	-
ZMO0803	806998	805406	-2	1593	ZP_0009431	FOG: TPR repeat	120	1.00E-25	-	-
ZMO0804	808107	807175	-1	933	NP_420191	N-acetyl-gamma-glutamyl-phosp	303	4.00E-81	COG0002	E
ZMO0805	809012	808116	-3	897	NP_384257	conserved hypothetical protein	167	3.00E-40	COG0791	M
ZMO0806	810490	809102	-2	1389	ZP_0009436	leucyl aminopeptidase	468	1.00E-131	COG0260	E
ZMO0807	811929	810640	-1	1290	NP_879393	conserved hypothetical protein	567	1.00E-160	COG0621	J
ZMO0808	812068	811898	-2	171		hypothetical protein	-	-	-	-
ZMO0809	812551	812216	-2	336	ZP_0005174	conserved hypothetical protein	79.3	1.00E-14	COG1872	S
ZMO0810	813303	812572	-1	732	Q9REQJ TR	tRNA pseudouridine synthase A	499	1.00E-140	COG0101	J
ZMO0811	814205	813306	-3	900	ZP_0009637	methionyl-tRNA formyltransferas	365	1.00E-100	COG0223	J
ZMO0812	814355	814951	2	597	ZP_0009637	recombinational DNA repair prot	275	4.00E-73	COG0353	L
ZMO0813	814974	815507	3	534	NP_384525	polypeptide deformylase	193	1.00E-48	COG0242	J
ZMO0814	815592	816938	3	1347	Q9REQ3 RM	DNA recombination protein rmuC	869	0	COG1322	S
ZMO0815	817211	816978	-3	234		hypothetical protein	-	-	-	-
ZMO0816	817388	817254	-3	135		hypothetical protein	-	-	-	-
ZMO0817	817623	817429	-1	195		hypothetical protein	-	-	-	-
ZMO0818	817881	818237	3	357	NP_947004	6-pyruvyl tetrahydrobiopterin syn	189	7.00E-48	COG0720	H
ZMO0819	818450	819763	2	1314	ZP_0005212	UDP-glucose 6-dehydrogenase	616	1.00E-175	COG1004	M
ZMO0820	822041	819843	-3	2199	Q9REQ6 PUI	phosphoribosylformylglycinamidi	1459	0	COG0046	F
ZMO0821	822192	823205	3	1014	ZP_0009436	cysteine synthase, cysZ	442	1.00E-123	COG0031	E
ZMO0822	823275	823637	3	363		hypothetical protein	-	-	-	-
ZMO0823	824847	825845	3	999	Q9REQ9 MR	S-adenosyl-methyltransferase m	630	1.00E-179	COG0275	M
ZMO0824	825842	826432	2	591		hypothetical protein	-	-	-	-
ZMO0825	826510	828144	1	1635	AAS14917	penicillin-binding protein	332	2.00E-89	COG0768	M
ZMO0826	828144	829520	3	1377	ZP_0009348	UDP-N-acetylmuramyl tripeptide	483	1.00E-135	COG0769	M
ZMO0827	829602	830993	3	1392	AAD53940	UDP-N-acetylmuramyl pentapep	445	1.00E-124	COG0770	M
ZMO0828	830981	832051	2	1071	P56834 MRA	phospho-N-acetylmuramoyl-pent	721	0	COG0472	M
ZMO0829	832048	833373	1	1326	ZP_0009348	UDP-N-acetylmuramoylalanine-[	466	1.00E-130	COG0771	M
ZMO0830	833373	834608	3	1236	NP_103116	cell division protein	313	3.00E-84	COG0772	D
ZMO0831	834605	835768	2	1164	ZP_0009349	UDP-N-acetylglucosamine:LPS f	438	1.00E-121	COG0707	M
ZMO0832	835765	837195	1	1431	ZP_0009349	UDP-N-acetylmuramate-alanine	719	0.00E+00	COG0773	M
ZMO0833	837192	838124	3	933	Q9RNM8 MU	UDP-N-acetylenolpyruvoylglucos	617	1.00E-175	COG0812	M
ZMO0834	838121	839086	2	966	NP_103112	D-alanyl-D-alanine ligase	289	6.00E-77	COG1181	M
ZMO0835	839250	840029	3	780	NP_421345	cell division protein FtsQ	121	2.00E-26	COG1589	M
ZMO0836	840047	841309	2	1263	NP_539501	cell division protein FtsA	301	2.00E-80	COG0849	D
ZMO0837	841526	842935	2	1410	NP_386274	cell division protein FtsZ	441	1.00E-122	COG0206	D
ZMO0838	843134	843871	2	738		hypothetical protein	-	-	-	-
ZMO0839	843855	844517	3	663		hypothetical protein	-	-	-	-
ZMO0840	844676	845080	2	405	ZP_0009486	conserved hypothetical protein	85.9	1.00E-16	-	-
ZMO0841	845077	846354	1	1278	NP_274019	chloride channel protein-related	303	4.00E-81	COG0038	P
ZMO0842	846462	847622	3	1161	Q9RNN5 DG	deoxyguanosinetriphosphate trip	786	0	COG0232	F
ZMO0843	847823	849319	2	1497	ZP_0009410	arginyl-tRNA synthetase	695	0.00E+00	COG0018	J
ZMO0844	849582	850679	3	1098	ZP_0009410	conserved hypothetical protein	70.5	5.00E-11	-	-
ZMO0845	850820	851548	3	729	Q9RNN8 SY	alanyl-tRNA synthetase (Alanine	1238	0	COG0013	J

ZMO0846	855338	853572	-3	1767 NP_949181	glutathione-regulated potassium-	354	3.00E-96	COG0475	P
ZMO0847	856042	857928	1	1887 NP_523191	outer membrane porin OprB prec	202	2.00E-50	COG3659	M
ZMO0848	858586	858218	-2	369	hypothetical protein	-	-	-	-
ZMO0849	859741	858707	-2	1035 ZP_00093571	conserved hypothetical protein	179	6.00E-44	-	-
ZMO0850	860529	861647	3	1119 NP_798632	polar flagellar protein FlaK (sigm	316	6.00E-85	COG2204	T
ZMO0851	862262	861690	-3	573 NP_946547	pyridoxamine 5'-phosphate oxidase	218	5.00E-56	COG0259	H
ZMO0852	863356	862334	-2	1023 ZP_00094551	S-adenosylmethionine:tRNA-ribc	442	1.00E-123	COG0809	J
ZMO0853	864037	863399	-2	639 NP_420395	peptidyl-prolyl cis-trans isomeras	171	1.00E-41	COG0652	O
ZMO0854	864999	864469	-1	531 ZP_00094561	phosphopantetheine adenylyltras	186	2.00E-46	COG0669	H
ZMO0855	865979	865089	-3	891 NP_945877	geranyltransterferase (farnesy	281	1.00E-74	COG0142	H
ZMO0856	866234	865995	-3	240 Q92R19 EX7C	exodeoxyribonuclease VII small	88	4.00E-17	COG1722	L
ZMO0857	866982	866317	-1	666 ZP_00096071	conserved hypothetical protein	255	5.00E-67	COG3820	S
ZMO0858	867407	868036	2	630 ZP_0005299	cysteine sulfinate desulfinate/cy	173	2.00E-42	COG1104	E
ZMO0859	868116	868523	3	408 NP_220863	NifS protein homolog (spl1)	89	2.00E-17	COG1104	E
ZMO0860	868533	868847	3	315 ZP_00093861	ferredoxin	94	4.00E-19	COG0633	C
ZMO0861	869297	871090	2	1794 NP_945968	DNA polymerase III tau subunit	404	1.00E-111	COG2812	L
ZMO0862	871249	871581	1	333 ZP_0009465	conserved hypothetical protein	128	3.00E-29	COG0718	S
ZMO0863	872133	871636	-1	498 ZP_00096441	deoxycytidine deaminase	324	6.00E-88	COG0717	F
ZMO0864	872723	872244	-3	480 ZP_00096441	cytidine deaminase	131	4.00E-30	COG0295	F
ZMO0865	872822	874357	2	1536 NP_948423	replicative DNA helicase (dnaB)	449	1.00E-125	COG0305	L
ZMO0866	874473	875441	3	969 NP_945573	cation efflux system protein	295	8.00E-79	COG1230	P
ZMO0867	875696	876733	2	1038 ZP_00030951	nucleoside-diphosphate-sugar ep	415	1.00E-115	COG0451	MG
ZMO0868	876733	877872	1	1140 ZP_00030951	glycosyltransferases involved in	354	2.00E-96	COG0463	M
ZMO0869	877836	878729	3	894 NP_949080	phytoene synthase-related prote	257	2.00E-67	COG1562	I
ZMO0870	878729	879604	2	876 ZP_00030941	phytoene/squalene synthetase	271	1.00E-71	COG1562	I
ZMO0871	879601	880845	1	1245 NP_949078	oxidoreductase, putative	372	1.00E-102	COG2907	R
ZMO0872	880860	882836	3	1977 P33990 SQH	squalene--hopene cyclase	1360	0	COG1657	I
ZMO0873	882977	883654	2	678 NP_841224	purine and other phosphorylases	99	9.00E-20	COG0775	F
ZMO0874	884740	883601	-2	1140 ZP_00051291	predicted Fe-S oxidoreductases	513	1.00E-144	COG0535	R
ZMO0875	885766	884750	-2	1017 ZP_00030951	penicillin tolerance protein	438	1.00E-122	COG0761	IM
ZMO0876	886265	886855	2	591 ZP_00013071	ABC-type transport system invol	100	1.00E-20	COG2854	Q
ZMO0877	887254	886928	-2	327	hypothetical protein	-	-	-	-
ZMO0878	888267	887248	-1	1020 S61837	protein-glutamate methylesteras	272	7.00E-72	COG2201	NT
ZMO0879	888437	888592	2	156	hypothetical protein	-	-	-	-
ZMO0880	890297	888630	-3	1668 NP_384745	chemotaxis sensor histidine kina	177	7.00E-43	COG0643	NT
ZMO0881	890349	890513	3	165	hypothetical protein	-	-	-	-
ZMO0882	891922	890525	-2	1398 ZP_00095061	methyl-accepting chemotaxis prc	277	3.00E-73	COG0840	NT
ZMO0883	892676	892134	-3	543 ZP_00096731	ribosomal protein S9	254	7.00E-67	COG0103	J
ZMO0884	893155	892682	-2	474 ZP_00096731	ribosomal protein L13	254	5.00E-67	COG0102	J
ZMO0885	893488	893871	1	384 ZP_00096721	conserved hypothetical protein	90.1	7.00E-18	-	-
ZMO0886	894464	893937	-3	528 NP_444537	conserved hypothetical protein	90.1	2.00E-17	COG1430	S
ZMO0887	894621	894496	-1	126	hypothetical protein	-	-	-	-
ZMO0888	895247	894699	-3	549 AAF23988	transposase, putative	194	7.00E-49	COG1961	L
ZMO0889	896626	895478	-2	1149 P05149 GALI	aldose 1-epimerase precursor (M	386	1.00E-106	COG2017	G
ZMO0890	898749	897160	-1	1590 ZP_00094261	lysyl-tRNA synthetase (class I)	675	0	COG1384	J
ZMO0891	899145	899041	-1	105	hypothetical protein	-	-	-	-
ZMO0892	899175	901826	3	2652 ZP_00094271	Rad3-related DNA helicases	922	0	COG1199	KL
ZMO0893	902870	901830	-3	1041 NP_107604	esterase	328	8.00E-89	COG1680	V
ZMO0894	903820	902912	-2	909 NP_840920	conserved hypothetical protein	65.1	2.00E-09	-	-
ZMO0895	904228	903989	-2	240	hypothetical protein	-	-	-	-
ZMO0896	904858	905676	1	819 ZP_00096761	conserved hypothetical protein	108	1.00E-22	-	-
ZMO0897	905703	905858	3	156	hypothetical protein	-	-	-	-
ZMO0898	905907	905755	-1	153	hypothetical protein	-	-	-	-
ZMO0899	905909	907579	2	1671 ZP_00095901	amidohydrolase (NAD+ syntheta	716	0	COG0171	H
ZMO0900	907592	908926	2	1335 ZP_00095891	glutamyl-tRNA synthetase	531	1.00E-149	COG0008	J
ZMO0901	909147	908950	-1	198 NP_348535	phage related protein, uncharact	65.5	2.00E-10	-	-
ZMO0902	911472	909220	-1	2253 ZP_00032641	outer membrane receptor proteir	573	1.00E-162	COG1629	P
ZMO0903	913360	911666	-2	1695 ZP_00094571	Isopropylmalate/homocitrate/citr	752	0	COG0119	E
ZMO0904	916781	913686	-3	3096 NP_826933	beta-galactosidase	660	0	COG1874	G
ZMO0905	917079	918650	3	1572 ZP_00014801	glucans biosynthesis protein, per	390	1.00E-107	COG3131	P
ZMO0906	918767	920308	2	1542 NP_420825	glycosyl transferase family protei	394	1.00E-108	COG2943	M
ZMO0907	920280	920726	3	447 ZP_00050971	membrane glycosyltransferase	66.6	1.00E-10	COG2943	M
ZMO0908	922354	921182	-2	1173 ZP_00094451	capsule polysaccharide export pi	171	2.00E-41	COG3524	M
ZMO0909	923688	922396	-1	1293 ZP_00050341	glycosyltransferase	209	9.00E-53	COG0438	M
ZMO0910	924304	923651	-2	654 emb CAB621	polysaccharide export protein, pi	224	9.00E-58	COG1134	GM
ZMO0911	924590	925852	2	1263 ZP_00094461	polysaccharide export periplasmi	202	8.00E-51	COG1596	M
ZMO0912	926037	927917	3	1881 NP_420821	conserved hypothetical protein	436	1.00E-121	COG4805	S
ZMO0913	929063	927969	-3	1095 NP_949706	branched-chain amino acid amin	438	1.00E-122	COG0115	EH
ZMO0914	930006	929119	-1	888 ZP_00096711	5,10-methylene-tetrahydrofolate	355	8.00E-97	COG0190	H
ZMO0915	930236	932458	2	2223 NP_841092	copper-transporting ATPase, cop	687	0	COG2217	P
ZMO0916	932455	932664	1	210	hypothetical protein	-	-	COG2608	P
ZMO0917	933263	934669	2	1407 ZP_00095721	dioxygenases related to 2-nitropr	704	0	COG2070	R
ZMO0918	934833	936278	3	1446 ZP_00125961	catalase	605	1.00E-172	COG0753	P
ZMO0919	937704	939461	3	1758 NP_813574	two-component system sensor h	155	3.00E-36	COG2199	T
ZMO0920	939866	939483	-3	384 NP_295541	conserved hypothetical protein	72.4	2.00E-12	-	-
ZMO0921	940012	941145	1	1134	hypothetical protein	-	-	-	-
ZMO0922	941194	941640	1	447 NP_540143	transcriptional regulator	80.1	7.00E-15	COG4933	S

ZMO0923	942907	941684	-2	1224	ZP_0009361f	N-acetylglutamate synthase (N-a	487	1.00E-136	COG1364	E
ZMO0924	943263	946040	3	2778	ZP_0009361f	preprotein translocase subunit S	1246	0	COG0653	U
ZMO0925	946264	946788	1	525	NP_102024	cold shock protein	108	6.00E-23	COG1278	K
ZMO0926	946933	947442	1	510	NP_422488	ABC transporter, substrate-bindir	116	2.00E-25	COG1463	Q
ZMO0927	948748	947948	-2	801	ZP_0009628f	leu/phe-tRNA-protein transferase	221	2.00E-56	COG2360	O
ZMO0928	948904	949464	1	561	NP_420990	conserved hypothetical protein	201	5.00E-51	COG3191	EQ
ZMO0929	950043	949924	-1	120		hypothetical protein			-	-
ZMO0930	950488	950054	-2	435		hypothetical protein			-	-
ZMO0931	950690	950475	-3	216		hypothetical protein			-	-
ZMO0932	951276	950731	-1	546	NP_539912	secretion activator protein	56.2	2.00E-07	COG3926	R
ZMO0933	951241	951375	1	135		hypothetical protein			-	-
ZMO0934	951743	951423	-3	321		hypothetical protein			-	-
ZMO0935	952601	951975	-3	627	ZP_0003337f	glutathione S-transferase	215	5.00E-55	COG0625	O
ZMO0936	952890	953780	3	891	NP_949636	permeases of the drug/metabolit	186	7.00E-46	COG0697	GER
ZMO0937	955038	953821	-1	1218	ZP_0006752f	aspartate/tyrosine/aromatic amin	340	4.00E-92	COG1448	E
ZMO0938	955358	957088	2	1731	AAA74034	alkaline phosphatase	1151	0	COG1524	R
ZMO0939	958390	957095	-2	1296	ZP_0008379f	cytosine deaminase and related	398	1.00E-109	COG0402	FR
ZMO0940	958903	958409	-2	495	ZP_0001574f	transcriptional regulators	124	9.00E-28	COG1846	K
ZMO0941	960018	959023	-1	996	AAO38864	nucleotide sugar epimerase	629	0	COG0451	MG
ZMO0942	961759	960227	-2	1533	AAO38865	invertase A	1060	0	COG1621	G
ZMO0943	961871	961746	-3	126		hypothetical protein			-	-
ZMO0944	961914	961795	-1	120		hypothetical protein			-	-
ZMO0945	962985	962104	-1	882	NP_102213	conserved hypothetical protein	190	3.00E-47	COG2017	G
ZMO0946	963329	964807	2	1479	ZP_0009431f	peptidyl-prolyl cis-trans isomeras	541	1.00E-154	COG0544	O
ZMO0947	964825	965790	1	966	NP_484086	conserved hypothetical protein	310	2.00E-83	COG0463	M
ZMO0948	965869	966501	1	633	ZP_0009432f	heat shock protein, protease sub	321	7.00E-87	COG0740	OU
ZMO0949	966651	967919	3	1269	ZP_0009432f	heat shock protein, ATP-dependt	684	0	COG1219	O
ZMO0950	968584	967979	-2	606	ZP_0009596f	acetyltransferase	162	4.00E-39	COG0454	KR
ZMO0951	969430	968594	-2	837	ZP_0009596f	coproporphyrinogen III oxidase	343	2.00E-93	COG0408	H
ZMO0952	969890	969438	-3	453	NP_103994	RNA methyltransferase	162	2.00E-39	COG0219	J
ZMO0953	969917	970036	2	120		hypothetical protein			-	-
ZMO0954	970108	970004	-2	105		hypothetical protein			-	-
ZMO0955	971080	970811	-2	270	NP_659770	conserved hypothetical protein	110	8.00E-24	COG3293	L
ZMO0956	972065	972697	2	633	ZP_0009474f	ubiquinol-cytochrome-c reductas	222	4.00E-57	COG0723	C
ZMO0957	972705	973961	3	1257	ZP_0009474f	cytochrome b subunit of the bc c	538	1.00E-151	COG1290	C
ZMO0958	973963	974802	1	840	ZP_0009474f	cytochrome c1	239	6.00E-62	COG2857	C
ZMO0959	975295	974735	-2	561	ZP_0009333f	membrane carboxypeptidase (pe	204	7.00E-52	COG0744	M
ZMO0960	975503	975318	-3	186		hypothetical protein			-	-
ZMO0961	975661	976110	1	450	P04164 C552	cytochrome c-552 precursor (C5-	94.7	6.00E-19	COG2010	C
ZMO0962	977260	976121	-2	1140	NP_419353	N-acetylglucosamine-6-phospha	328	1.00E-88	COG1820	G
ZMO0963	977956	977342	-2	615	NP_900381	transcriptional regulator, tetR fan	118	7.00E-26	COG1309	K
ZMO0964	978061	979494	1	1434	NP_900380	outer membrane multidrug resist	398	1.00E-109	COG1538	MU
ZMO0965	979516	980721	1	1206	NP_049065	aromatic efflux pump membrane	389	1.00E-107	COG1566	V
ZMO0966	980699	981712	2	1014	NP_900378	multidrug resistance protein	341	2.00E-95	COG0477	GEPR
ZMO0967	982393	983589	1	1197	ZP_0009672f	nucleoside permease	442	1.00E-123	COG1972	F
ZMO0968	983593	983820	1	228		hypothetical protein			-	-
ZMO0969	983792	985129	2	1338	NP_419005	xanthine/uracil permease family	526	1.00E-148	COG2252	R
ZMO0970	985203	986255	3	1053	NP_419006	purine nucleoside permease, put	261	2.00E-68	COG5042	F
ZMO0971	986292	987305	3	1014	NP_421974	adenosine deaminase	401	1.00E-110	COG1816	F
ZMO0972	987394	988548	1	1155	ZP_0002810f	glycosyltransferases, probably in	290	5.00E-77	COG1215	M
ZMO0973	988566	989993	3	1428	ZP_0002810f	Fe-S oxidoreductase	655	0	COG1032	C
ZMO0974	990009	990854	3	846	ZP_0009245f	conserved hypothetical protein	254	1.00E-66	COG3394	S
ZMO0975	991056	992045	3	990	ZP_0005433f	conserved hypothetical integral r	154	4.00E-36	-	-
ZMO0976	993258	992242	-1	1017	NP_249818	oxidoreductase, putative	447	1.00E-124	COG0667	C
ZMO0977	993254	993400	2	147		hypothetical protein			-	-
ZMO0978	994583	993405	-3	1179	NP_947426	Fe ABC transporter, probable	164	4.00E-39	COG0614	P
ZMO0979	994636	996747	1	2112	NP_420558	TonB-dependent receptor	507	1.00E-142	COG4206	H
ZMO0980	997920	996817	-1	1104	NP_945358	DNA polymerase III beta subunit	413	1.00E-114	COG0592	L
ZMO0981	999617	998031	-3	1587	ZP_0002836f	ABC-type uncharacterized transp	320	5.00E-86	COG1123	R
ZMO0982	1000432	999620	-2	813	NP_102837	permease protein of oligopeptide	199	5.00E-50	COG1173	EP
ZMO0983	1002911	1002417	-1	495	NP_102835	ABC transporter, dipeptide-bindir	210	8.00E-53	COG0747	E
ZMO0984	1003914	1003045	-1	870	ZP_0005407f	membrane proteins related to me	165	9.00E-40	COG0739	M
ZMO0985	1004678	1003917	-3	762	NP_771386	stationary-phase survival protein	218	1.00E-55	COG0496	R
ZMO0986	1005955	1004684	-2	1272	ZP_0009625f	seryl-tRNA synthetase	567	1.00E-160	COG0172	J
ZMO0987	1006255	1006740	1	486	ZP_0009451f	DnaK suppressor protein	196	2.00E-49	COG1734	T
ZMO0988	1007148	1007345	3	198	ZP_0009605f	conserved hypothetical protein	73.6	9.00E-13	COG5481	S
ZMO0989	1007926	1007444	-2	483	ZP_0001435f	heat shock protein, molecular ch	160	8.00E-39	COG0071	O
ZMO0990	1008202	1008086	-2	117		hypothetical protein			-	-
ZMO0991	1008117	1008257	3	141		hypothetical protein			-	-
ZMO0992	1009867	1008341	-2	1527	ZP_0003469f	carboxypeptidase C (cathepsin A	466	1.00E-130	COG2939	E
ZMO0993	1010071	1010184	1	114		hypothetical protein			-	-
ZMO0994	1010835	1010311	-1	525		hypothetical protein			-	-
ZMO0995	1011023	1011127	2	105		hypothetical protein			-	-
ZMO0996	1011165	1012262	3	1098	ZP_0002858f	small-conductance mechanosen:	213	7.00E-54	COG0668	M
ZMO0997	1012264	1012890	1	627	S18559	2-dehydro-3-deoxy-phosphoglu	405	1.00E-112	COG0800	G
ZMO0998	1013229	1013771	3	543	ZP_0009451f	peptide methionine sulfoxide red	227	1.00E-58	COG0225	O
ZMO0999	1014786	1013803	-1	984	ZP_0000809f	translation factor (SUA5), putativ	314	2.00E-84	COG0009	J

ZMO1000	1015219	1017498	1	2280	NP_419301	5-methyltetrahydropteroyltriglu	981	0	COG0620	E
ZMO1001	1017751	1019244	1	1494	NP_388249	similar to di-tripeptide ABC trans	336	8.00E-91	COG3104	E
ZMO1002	1019317	1020654	1	1338	ZP_0009555	phosphomannomutase	615	1.00E-175	COG1109	G
ZMO1003	1020617	1021495	2	879	ZP_0009555	hydroxymethylpyrimidine/phosph	275	1.00E-72	COG0351	H
ZMO1004	1021495	1022142	1	648	ZP_0005590	ribonuclease HII	189	2.00E-47	COG0164	L
ZMO1005	1022339	1023460	2	1122	O30570	MTB modification methylase BabI (ad	469	1.00E-131	COG0863	L
ZMO1006	1023496	1024566	1	1071	ZP_0009328	dihydropteroate synthase and re	272	7.00E-72	COG0294	H
ZMO1007	1024688	1025551	2	864	NP_795226	conserved hypothetical protein	221	1.00E-56	COG3781	S
ZMO1008	1025677	1027122	1	1446	ZP_0009362	FAD/FMN-containing dehydroge	426	1.00E-118	COG0277	C
ZMO1009	1027261	1028049	1	789	ZP_0009362	conserved hypothetical protein	284	1.00E-75	-	-
ZMO1010	1028150	1028605	2	456	NP_753841	conserved hypothetical protein	160	1.00E-38	-	-
ZMO1011	1029009	1028830	-1	180	ZP_0000822	conserved hypothetical protein	56.2	1.00E-07	COG3024	S
ZMO1012	1030045	1029038	-2	1008	ZP_0009502	ribonucleases G and E	201	1.00E-50	-	-
ZMO1013	1030654	1030052	-2	603	ZP_0009502	nucleotide-binding protein implic	204	9.00E-52	COG0424	D
ZMO1014	1030923	1030666	-1	258	ZP_0009502	translation initiation factor 1 (IF-1	138	3.00E-32	COG0361	J
ZMO1015	1031722	1031102	-2	621	ZP_0009335	conserved hypothetical protein	103	2.00E-21	-	-
ZMO1016	1032675	1031734	-1	942	ZP_0009335	ABC-type transport system invol	262	6.00E-69	COG1463	Q
ZMO1017	1033477	1032692	-2	786	ZP_0009335	ABC-type transport system invol	317	2.00E-85	COG1127	Q
ZMO1018	1034574	1033480	-1	1095	ZP_0009335	ABC-type transport system invol	359	4.00E-98	COG0767	Q
ZMO1019	1035809	1034763	-3	1047	NP_819749	deoxyhypusine synthase, putativ	484	1.00E-135	COG1899	O
ZMO1020	1037072	1035897	-3	1176	ZP_0009489	diaminopimelate (ornithine) deca	521	5.00E-163	COG0019	E
ZMO1021	1038045	1037398	-1	648	ZP_0009307	predicted hydrolase of the alpha/	365	1.00E-100	COG2945	R
ZMO1022	1038181	1039227	1	1047	ZP_0009307	cysteine sulfinate desulfinase/cy	298	1.00E-79	COG1104	E
ZMO1023	1039279	1040043	1	765	ZP_0002816	ATPase, predicted PP-loop supe	342	4.00E-93	COG0603	R
ZMO1024	1040429	1040328	-3	102	-	hypothetical protein	-	-	-	-
ZMO1025	1040392	1042410	1	2019	NP_942878	anaerobic class III ribonucleotide	929	0	COG1328	F
ZMO1026	1042447	1042635	1	189	NP_942877	conserved hypothetical protein	80.1	1.00E-14	-	-
ZMO1027	1042622	1043224	2	603	ZP_0001531	pyruvate-formate lyase-activatin	227	1.00E-58	COG1180	O
ZMO1028	1043328	1043224	-1	105	-	hypothetical protein	-	-	-	-
ZMO1029	1043305	1044222	1	918	ZP_0009961	ABC-type multidrug transport sys	208	1.00E-52	COG1131	V
ZMO1030	1044231	1045031	3	801	NP_241313	conserved hypothetical protein	61.2	2.00E-08	COG4200	S
ZMO1031	1045052	1045213	2	162	-	hypothetical protein	-	-	-	-
ZMO1032	1045191	1046366	3	1176	ZP_0009505	predicted Fe-S-cluster redox enz	568	1.00E-161	COG0820	R
ZMO1033	1046422	1047669	1	1248	ZP_0009602	cyclopropane fatty acid synthase	411	1.00E-113	COG2230	M
ZMO1034	1048401	1047793	-1	609	ZP_0009653	conserved hypothetical protein	66.2	4.00E-10	-	-
ZMO1035	1048662	1048516	-1	147	-	hypothetical protein	-	-	-	-
ZMO1036	1048664	1049890	2	1227	ZP_0009382	argininosuccinate synthase	677	0	COG0137	E
ZMO1037	1050125	1050235	2	111	-	hypothetical protein	-	-	-	-
ZMO1038	1050196	1050324	1	129	-	hypothetical protein	-	-	-	-
ZMO1039	1052248	1051409	-1	840	ZP_0009680	ribonucleotide reductase, alpha s	523	1.00E-148	COG0209	F
ZMO1040	1052996	1056211	2	3216	NP_779782	TonB-dependent receptor	398	1.00E-109	COG1629	P
ZMO1041	1057006	1056455	-2	552	ZP_0009623	NTP pyrophosphohydrolases inc	173	2.00E-42	COG0494	LR
ZMO1042	1058221	1057097	-2	1125	NP_422250	conserved hypothetical protein	125	2.00E-27	COG1512	R
ZMO1043	1058777	1058157	-3	621	ZP_0009622	conserved hypothetical protein	231	1.00E-59	COG1704	S
ZMO1044	1059012	1059476	3	465	ZP_0002901	mechanosensitive channel	156	2.00E-37	COG1970	M
ZMO1045	1061145	1059565	-1	1581	-	hypothetical protein	-	-	-	-
ZMO1046	1061127	1061354	3	228	-	hypothetical protein	-	-	-	-
ZMO1047	1061414	1062454	2	1041	NP_519650	ABC transporter phosphate-bind	390	1.00E-107	COG0226	P
ZMO1048	1062549	1063508	3	960	ZP_0014542	conserved hypothetical protein	316	4.00E-85	COG0573	P
ZMO1049	1063517	1064353	2	837	NP_104767	phosphate transport system perr	295	7.00E-79	COG0581	P
ZMO1050	1064269	1065225	1	957	Q9AML4	IPST phosphate import ATP-binding pr	329	5.00E-89	COG1117	P
ZMO1051	1065330	1065208	-1	123	-	hypothetical protein	-	-	-	-
ZMO1052	1065560	1066339	2	780	NP_697856	phosphoribosylaminoimidazole-s	373	1.00E-102	COG0152	F
ZMO1053	1066567	1066439	-2	129	-	hypothetical protein	-	-	-	-
ZMO1054	1066743	1068989	3	2247	NP_108473	DNA topoisomerase IV subunitA	819	0	COG0188	L
ZMO1055	1069238	1070977	2	1740	ZP_0011121	FOG: PAS/PAC domain	326	8.00E-88	COG5001	T
ZMO1056	1072191	1070977	-1	1215	ZP_0009595	tRNA nucleotidyltransferase/poly	330	5.00E-89	COG0617	J
ZMO1057	1072729	1072202	-2	528	ZP_0009595	acetyltransferase, putative	155	4.00E-37	COG3153	R
ZMO1058	1072752	1072910	3	159	-	hypothetical protein	-	-	-	-
ZMO1059	1073129	1073551	2	423	NP_518278	conserved hypothetical protein	68.2	3.00E-11	COG1539	H
ZMO1060	1074237	1073617	-1	621	ZP_0009555	superoxide dismutase	213	2.00E-54	COG0605	P
ZMO1061	1075528	1074458	-2	1071	ZP_0009485	transcriptional regulators contain	420	1.00E-116	COG1221	KT
ZMO1062	1075707	1076225	3	519	-	hypothetical protein	-	-	-	-
ZMO1063	1076228	1076896	2	669	ZP_0009484	phage shock protein A (IM30), su	233	3.00E-60	COG1842	KT
ZMO1064	1076896	1077168	1	273	ZP_0009484	conserved hypothetical protein	77.4	6.00E-14	-	-
ZMO1065	1077186	1077569	3	384	ZP_0009484	stress-responsive transcriptional	106	8.00E-23	COG1983	KT
ZMO1066	1077706	1077894	1	189	-	hypothetical protein	-	-	-	-
ZMO1067	1078027	1078431	1	405	ZP_0009484	SufE protein probably involved ir	187	3.00E-47	COG2166	R
ZMO1068	1078428	1078862	3	435	-	hypothetical protein	-	-	-	-
ZMO1069	1079426	1078908	-3	519	ZP_0009594	heat shock protein, DnaJ-class n	204	8.00E-52	COG2214	O
ZMO1070	1080932	1080006	-3	927	ZP_0009318	signal recognition particle GTPa	426	1.00E-118	COG0552	U
ZMO1071	1082188	1080935	-2	1254	NP_422478	conserved hypothetical protein	398	1.00E-109	COG0621	J
ZMO1072	1082994	1082191	-1	804	ZP_0009318	diaminopimelate epimerase	323	2.00E-87	COG0253	E
ZMO1073	1082971	1083150	1	180	-	hypothetical protein	-	-	-	-
ZMO1074	1083340	1083230	-2	111	-	hypothetical protein	-	-	-	-
ZMO1075	1083359	1084783	2	1425	ZP_0009318	signal recognition particle GTPa	635	0	COG0541	U
ZMO1076	1084814	1085245	2	432	ZP_0009508	ribosomal protein S16	191	3.00E-48	COG0228	J

ZMO1077	1085249	1085740	2	492	ZP_0009508	16S rRNA processing RimM prot	137	7.00E-32	COG0806	J
ZMO1078	1085737	1086486	1	750	ZP_0009508	tRNA-(guanine-N1)-methyltransf	342	5.00E-93	COG0336	J
ZMO1079	1086483	1086857	3	375	ZP_0009508	ribosomal protein L19	194	2.00E-49	COG0335	J
ZMO1080	1087000	1087185	1	186		hypothetical protein	-	-	-	-
ZMO1081	1087238	1087858	2	621		hypothetical protein	-	-	-	-
ZMO1082	1087830	1088051	3	222		hypothetical protein	-	-	-	-
ZMO1083	1088029	1090026	1	1998	ZP_0008972	glycosyltransferases involved in	659	0	COG1215	M
ZMO1084	1090023	1092338	3	2316	NP_643824	conserved hypothetical protein	395	1.00E-108	-	-
ZMO1085	1092335	1096345	2	4011	NP_643822	cellulose synthase subunit C	208	8.00E-52	COG0457	R
ZMO1086	1096501	1097520	1	1020	ZP_0008972	endoglucanase Y	306	5.00E-82	COG3405	G
ZMO1087	1097599	1098684	1	1086	ZP_0013743	membrane-bound lytic murein tra	222	8.00E-57	COG2951	M
ZMO1088	1098641	1099141	2	501	AAS14213	rare lipoprotein A, putative	142	3.00E-33	COG0797	M
ZMO1089	1099193	1100395	2	1203	ZP_0009547	D-alanyl-D-alanine carboxypeptid	352	1.00E-95	COG1686	M
ZMO1090	1100374	1101024	1	651	NP_385710	thymidylate kinase (dTMP kinase	188	6.00E-47	COG0125	F
ZMO1091	1101024	1102016	3	993	AAF06832	DNA polymerase III delta prime ε	159	1.00E-37	COG0470	L
ZMO1092	1102034	1103599	2	1566	NP_948120	methionyl-tRNA synthetase	640	0	COG0143	J
ZMO1093	1103599	1104375	1	777	ZP_0009305	Mg-dependent DNase	323	2.00E-87	COG0084	L
ZMO1094	1104372	1105136	3	765	ZP_0009305	metal-dependent hydrolases of tl	253	3.00E-66	COG1235	R
ZMO1095	1105488	1106309	3	822	ZP_0009320	pyrophosphatase, predicted	250	2.00E-65	COG1694	R
ZMO1096	1109035	1109753	-2	2283	ZP_0009548	exoribonuclease R	822	0	COG0557	K
ZMO1097	1109457	1109143	-1	315	ZP_0005549	thiol-disulfide isomerase and thic	141	3.00E-33	COG0526	OC
ZMO1098	1113030	1109548	-1	3483	ZP_0009509	ATP-dependent exoDNase (exor	622	1.00E-176	COG1074	L
ZMO1099	1116021	1113046	-1	2976	ZP_0009509	helicase, inactivated superfamily	714	0	COG3893	L
ZMO1100	1116791	1116036	-3	756	ZP_0009509	nucleotidyl pyrophosphorylase in	258	1.00E-67	COG1208	MJ
ZMO1101	1117391	1116873	-3	519	ZP_0009509	ATPase or kinase, predicted	127	7.00E-29	COG0802	R
ZMO1102	1119384	1117381	-1	2004	ZP_0009509	two-component sensor signal tra	521	5.00E-163	COG2202	T
ZMO1103	1119793	1119617	-2	177		hypothetical protein	-	-	-	-
ZMO1104	1119940	1119824	-2	117		hypothetical protein	-	-	-	-
ZMO1105	1122374	1120065	-3	2310	ZP_0009466	two-component sensor signal tra	119	3.00E-25	COG0642	T
ZMO1106	1122400	1122531	1	132		hypothetical protein	-	-	-	-
ZMO1107	1122623	1123105	2	483	ZP_0009466	transcriptional regulators	225	2.00E-58	COG1522	K
ZMO1108	1123326	1123177	-1	150		hypothetical protein	-	-	-	-
ZMO1109	1124658	1123342	-1	1317	ZP_0009371	conserved hypothetical protein	150	7.00E-35	-	-
ZMO1110	1124977	1124873	-2	105		hypothetical protein	-	-	-	-
ZMO1111	1124998	1126245	1	1248	NP_346805	ABC transporter (permease)	190	6.00E-47	COG2807	P
ZMO1112	1126849	1126253	-2	597	ZP_0009318	intracellular septation protein A	172	4.00E-42	COG2917	D
ZMO1113	1127117	1128442	2	1326	NP_753292	NADH dehydrogenase	405	1.00E-112	COG1252	C
ZMO1114	1128573	1129193	3	621	NP_947144	uracil-DNA glycosylase:Phage S	162	4.00E-39	COG1573	L
ZMO1115	1129615	1130418	1	804	Q9RNL1 JUP	putative undecaprenol kinase (B	520	5.00E-163	COG1968	V
ZMO1116	1130576	1132048	2	1473	AAD56915	glutamate synthase [NADPH] sr	932	0	COG0493	ER
ZMO1117	1132150	1136745	1	4596	Q05755 GLT	glutamate synthase [NADPH] lar	1901	0	COG0069	E
ZMO1118	1136825	1137496	2	672	AAS14715	glutathione S-transferase family	194	1.00E-48	COG0625	O
ZMO1119	1137540	1137644	3	105		hypothetical protein	-	-	-	-
ZMO1120	1137718	1137554	-2	165		hypothetical protein	-	-	-	-
ZMO1121	1138219	1137749	-2	471	ZP_0005447	transcriptional regulators, predict	100	9.00E-21	COG0789	K
ZMO1122	1138562	1138227	-3	336	Q9RNZ5 JHF	integration host factor alpha-sub	197	5.00E-50	COG0776	L
ZMO1123	1138742	1138629	-3	114		hypothetical protein	-	-	-	-
ZMO1124	1140802	1139381	-2	1422	NP_771130	two-component response regulat	521	5.00E-163	COG2204	T
ZMO1125	1143108	1140808	-1	2301	ZP_0009320	two-component signal transducti	577	1.00E-163	COG5000	T
ZMO1126	1143553	1143245	-2	309	AAB35496	nitrogen assimilation regulatory p	80.5	6.00E-15	COG2204	T
ZMO1127	1144591	1143572	-2	1020	P45672 DUS	tRNA-dihydrouridine synthase	413	1.00E-114	COG0042	J
ZMO1128	1144746	1145906	3	1161	Q9RNR2 JSD	IspD/IspF bifunctional enzyme	655	0	COG0245	I
ZMO1129	1145918	1146457	2	540	ZP_0009372	conserved hypothetical protein	80.9	1.00E-14	-	-
ZMO1130	1146408	1147148	3	741	NP_947931	possible competence-damaged p	139	7.00E-32	COG1546	R
ZMO1131	1147775	1147338	-3	438	ZP_0005329	Oligoketide cyclase/lipid transpo	166	1.00E-40	COG2867	I
ZMO1132	1148746	1147781	-2	966	Q9RNY7 LIP	lipoic acid synthetase (Lip-syn) (l	646	0	COG0320	H
ZMO1133	1148850	1149479	3	630	ZP_0009371	carbonic anhydrase	222	4.00E-57	COG0288	P
ZMO1134	1149495	1150391	3	897		hypothetical protein	-	-	-	-
ZMO1135	1151789	1150449	-3	1341	ZP_0009682	Zn-dependent proteases, predict	483	1.00E-135	COG0312	R
ZMO1136	1153359	1151920	-1	1440	AAF14629	cytochrome c peroxidase	400	1.00E-110	COG1858	P
ZMO1137	1154700	1153789	-1	912	NP_698389	phosphoserine phosphatase	223	4.00E-57	COG0560	E
ZMO1138	1154660	1155598	2	939	Q9X5G1 JMA	tRNA delta(2)-isopentenylpyroph	613	1.00E-174	COG0324	J
ZMO1139	1155752	1157539	2	1788	NP_773143	acetolactate synthase large subu	723	0	COG0028	EH
ZMO1140	1157561	1158073	2	513	NP_947377	acetolactate synthase small subu	192	2.00E-48	COG0440	E
ZMO1141	1158119	1159138	2	1020	Q9X5F8 JLVC	ketol-acyl reductoisomerase (act	669	0	COG0059	EH
ZMO1142	1160805	1159855	-1	951	NP_774020	thioredoxin reductase	397	1.00E-109	COG0492	O
ZMO1143	1161770	1161123	-3	648	NP_346876	chloramphenicol acetyltransferas	114	2.00E-24	COG4845	V
ZMO1144	1162199	1161852	-3	348	ZP_0009434	conserved hypothetical protein	83.2	9.00E-16	-	-
ZMO1145	1162486	1162265	-2	222	ZP_0009406	ribosomal protein L31	118	2.00E-26	COG0254	J
ZMO1146	1163091	1162621	-1	471	Q9X5F5 FAB	(3R)-hydroxymyristoyl-[acyl carri	307	4.00E-83	COG0764	I
ZMO1147	1163769	1163104	-1	666	ZP_0009406	conserved hypothetical protein	105	7.00E-22	COG2825	M
ZMO1148	1166939	1163775	-3	3165	ZP_0009406	outer membrane protein	968	0	COG4775	M
ZMO1149	1168021	1167131	-2	891	ZP_0009405	predicted membrane-associated	355	9.00E-97	COG0750	M
ZMO1150	1169418	1168258	-1	1161	AAD29659	1-deoxy-D-xylulose 5-phosphate	756	0	COG0743	I
ZMO1151	1170047	1169424	-3	624	ZP_0005334	CDP-diglyceride synthetase	169	3.00E-41	COG0575	I
ZMO1152	1170712	1170050	-2	663	NP_948259	undecaprenyl pyrophosphate syr	268	6.00E-71	COG0020	I
ZMO1153	1171344	1170793	-1	552	Q9X5F0 RRF	ribosome recycling factor (riboso	358	2.00E-98	COG0233	J

ZMO1154	1172078	1171350	-3	729	Q9X5E9 PYF	uridylylate kinase (UK) (uridine m	475	1.00E-133	COG0528	F
ZMO1155	1173132	1172215	-1	918	Q9X5E8 EFT	translation elongation factor Ts (t	575	1.00E-163	COG0264	J
ZMO1156	1173992	1173246	-3	747	Q9X5E7 RS2	ribosomal protein S2	498	1.00E-140	COG0052	J
ZMO1157	1174250	1174597	2	348		hypothetical protein	-	-	-	-
ZMO1158	1174638	1175336	3	699	AAD29652	aspartate racemase	454	1.00E-127	COG1794	M
ZMO1159	1176288	1175494	-1	795	NP_770437	phosphatidylserine synthase	206	3.00E-52	COG1183	I
ZMO1160	1177025	1176291	-3	735	Q9X5E3 PSC	phosphatidylserine decarboxylas	464	1.00E-130	COG0688	I
ZMO1161	1177223	1177080	-3	144		hypothetical protein	-	-	-	-
ZMO1162	1177232	1178497	2	1266	NP_767730	two-component sensor histidine l	210	4.00E-53	COG0642	T
ZMO1163	1178704	1179417	1	714	Q9X5E1 PHC	phosphate transport system prot	457	1.00E-128	COG0704	P
ZMO1164	1179417	1180112	3	696	AAD29647	phosphate regulon response reg	459	1.00E-128	COG0745	TK
ZMO1165	1181040	1180201	-1	840	ZP_0009393	amidophosphoribosyltransferase	166	5.00E-40	COG1040	R
ZMO1166	1182137	1181124	-3	1014	AAM50050	RecA/RadA recombinase A	652	0	COG0468	L
ZMO1167	1184355	1182406	-1	1950	NP_642657	glutaryl-7-ACA acylase precursor	792	0	COG2936	R
ZMO1168	1184519	1184418	-3	102		hypothetical protein	-	-	-	-
ZMO1169	1184558	1185418	2	861	NP_107610	conserved hypothetical protein	249	3.00E-65	COG2971	G
ZMO1170	1185465	1185773	3	309		hypothetical protein	-	-	-	-
ZMO1171	1186801	1185773	-2	1029	NP_420813	glycosyl hydrolase	283	5.00E-75	COG1472	G
ZMO1172	1186930	1188204	1	1275	NP_419401	succinylarginine dihydrolase	439	1.00E-122	COG3724	E
ZMO1173	1192367	1188204	-3	4164	ZP_0009435	conserved hypothetical protein	363	2.00E-98	COG2911	S
ZMO1174	1194583	1192373	-2	2211	ZP_0009435	outer membrane protein	414	1.00E-114	COG0729	M
ZMO1175	1195605	1194589	-1	1017	ZP_0008808	two-component signal transducti	221	2.00E-56	COG0642	T
ZMO1176	1195921	1195664	-2	258		hypothetical protein	-	-	-	-
ZMO1177	1196721	1196002	-1	720	NP_948908	two-component transcriptional re	213	2.00E-54	COG0745	TK
ZMO1178	1197123	1196755	-1	369	Q9X3W1 HIS	phosphoribosyl-AMP cyclohydrol	259	9.00E-69	COG0139	E
ZMO1179	1198371	1197184	-1	1188	NP_697466	RNA methyltransferase, putative	228	2.00E-58	COG2265	J
ZMO1180	1199822	1198374	-3	1449	ZP_0009488	sugar kinase	319	8.00E-86	COG0063	G
ZMO1181	1200918	1200187	-1	732	ZP_0009488	N-formylglutamate amidohydrola	188	7.00E-47	COG3931	E
ZMO1182	1201927	1201085	-2	843	NP_769166	4-diphosphocytidyl-2-C-methyl-D	181	1.00E-44	COG1947	I
ZMO1183	1203865	1202228	-2	1638	NP_420148	TPR domain protein	148	3.00E-34	COG0457	R
ZMO1184	1205638	1203989	-2	1650	NP_420147	electrotransfer ubiquinone oxidor	668	0	COG0644	C
ZMO1185	1205936	1206730	2	795	NP_420146	phage SPO1 DNA polymerase-rt	68	2.00E-10	COG1573	L
ZMO1186	1207593	1208645	3	1053	ZP_0009487	soluble lytic murein transglycosyl	407	1.00E-112	COG0741	M
ZMO1187	1209466	1208660	-2	807	Q9X3X1 FPC	formamidopyrimidine-DNA glyco:	542	1.00E-153	COG0266	L
ZMO1188	1209779	1210507	2	729	AAD21548	ubiquinone methyltransferase	486	1.00E-136	COG2226	H
ZMO1189	1210511	1212049	2	1539	NP_700227	ubiquinone biosynthesis protein l	382	1.00E-104	COG0661	R
ZMO1190	1212076	1213329	1	1254	NP_700226	phosphopantothenoylecysteine sy	397	1.00E-109	COG0452	H
ZMO1191	1213361	1213801	2	441	Q9X3X5 DUT	deoxyuridine 5'-triphosphate nuc	290	7.00E-78	COG0756	F
ZMO1192	1213798	1214556	1	759	AAD21552	molybdopterin biosynthesis prote	484	1.00E-136	COG0476	H
ZMO1193	1218615	1214968	-1	3648	NP_421254	DNA topoisomerase I	768	0	COG0550	L
ZMO1194	1219909	1218758	-2	1152	ZP_0009490	nucleotide-binding protein involv	339	5.00E-92	COG0758	LU
ZMO1195	1220615	1219965	-3	651	NP_699785	membrane protein, putative	191	1.00E-47	COG0344	S
ZMO1196	1220894	1222306	2	1413	ZP_0003377	permease, multidrug resistance p	426	1.00E-118	COG0477	GEPR
ZMO1197	1222331	1223161	2	831	AAD21556	glutamate racemase	392	1.00E-108	COG0796	M
ZMO1198	1223471	1224511	2	1041	P18079 HEM	aminolevulinic acid synthase	499	1.00E-140	COG0156	H
ZMO1199	1224533	1224694	2	162		hypothetical protein	-	-	-	-
ZMO1200	1224730	1225203	1	474	ZP_0009302	ribose 5-phosphate isomerase	198	2.00E-50	COG0698	G
ZMO1201	1225223	1226512	2	1290	ZP_0000698	glycine/serine hydroxymethyltran	580	1.00E-164	COG0112	E
ZMO1202	1226466	1226987	3	522	ZP_0001609	transcriptional regulator, predicte	197	9.00E-50	COG1327	K
ZMO1203	1226984	1227715	2	732	ZP_0009455	rRNA methylase	337	2.00E-91	COG0565	J
ZMO1204	1228034	1227846	-3	189		hypothetical protein	-	-	-	-
ZMO1205	1228405	1228094	-2	312		hypothetical protein	-	-	-	-
ZMO1206	1229845	1228901	-2	945	ZP_0008821	transcriptional regulator	200	4.00E-50	COG0583	K
ZMO1207	1229918	1230907	2	990	NP_887662	nitrilase	339	4.00E-92	COG0388	R
ZMO1208	1231577	1231257	-3	321		hypothetical protein	-	-	-	-
ZMO1209	1233793	1231841	-2	1953	ZP_0009407	K+ transporter	740	0	COG3158	P
ZMO1210	1234087	1233848	-2	240		hypothetical protein	-	-	-	-
ZMO1211	1235606	1234266	-3	1341	ZP_0009417	pyruvate/2-oxoglutarate dehydro	507	1.00E-142	COG1249	C
ZMO1212	1237292	1235775	-3	1518	P28718 G6PI	glucose-6-phosphate isomerase	1003	0	COG0166	G
ZMO1213	1237660	1238052	1	393	ZP_0009363	conserved hypothetical protein	75.5	6.00E-13	-	-
ZMO1214	1238222	1239700	2	1479	ZP_0009363	DNA and RNA helicases superfa	548	1.00E-154	COG0513	LKJ
ZMO1215	1240045	1240257	1	213		hypothetical protein	-	-	-	-
ZMO1216	1240284	1241936	3	1653	ZP_0000794	two-component signal transducti	99	2.00E-19	COG3920	T
ZMO1217	1242626	1242243	-3	384		hypothetical protein	-	-	-	-
ZMO1218	1244383	1243601	-2	783	ZP_0009409	Sec-independent protein secretic	289	3.00E-77	COG0805	U
ZMO1219	1244838	1244386	-1	453	ZP_0009409	Sec-independent protein secretic	113	1.00E-24	COG1826	U
ZMO1220	1245186	1244929	-1	258	ZP_0009409	Sec-independent protein secretic	84	6.00E-16	COG1826	U
ZMO1221	1246040	1245345	-3	696	ZP_0009410	conserved hypothetical protein	160	3.00E-38	-	-
ZMO1222	1246890	1246159	-1	732	ZP_0001429	dehydrogenases with different sp	310	1.00E-83	COG1028	IQR
ZMO1223	1247895	1246966	-1	930	ZP_0009506	(acyl-carrier-protein) S-malonyltr	374	1.00E-102	COG0331	I
ZMO1224	1247925	1248059	3	135		hypothetical protein	-	-	-	-
ZMO1225	1248419	1248793	2	375	ZP_0009507	ribosomal protein S6	169	1.00E-41	COG0360	J
ZMO1226	1248814	1249038	1	225	ZP_0009507	ribosomal protein S18	137	4.00E-32	COG0238	J
ZMO1227	1249053	1249682	3	630	ZP_0009508	ribosomal protein L9	248	7.00E-65	COG0359	J
ZMO1228	1250754	1249765	-1	990	NP_421907	mandelate racemase/muconate l	301	1.00E-80	COG4948	MR
ZMO1229	1251504	1250848	-1	657	ZP_0009509	GTP cyclohydrolase I	275	4.00E-73	COG0302	H
ZMO1230	1251496	1251678	1	183		hypothetical protein	-	-	-	-



ZMO1231	1251782	1253359	2	1578	ZP_0009458	single-stranded DNA-specific ex	608	1.00E-173	COG0608	L
ZMO1232	1253711	1255036	2	1326	ZP_0009459	glycosyltransferase	278	1.00E-73	COG0438	M
ZMO1233	1256495	1255089	-3	1407	ZP_0005580	mannose-6-phosphate isomeras	496	1.00E-139	COG0836	M
ZMO1234	1258496	1256553	-3	1944	ZP_0009646	deoxyxylulose-5-phosphate synt	894	0	COG1154	HI
ZMO1235	1259159	1258680	-3	480	ZP_0009645	transcriptional regulator, Fe2+/Zr	187	6.00E-47	COG0735	P
ZMO1236	1260419	1259412	-3	1008	P20368 ADH	alcohol dehydrogenase I (ADH I)	673	0	COG1064	R
ZMO1237	1262116	1261127	-2	990	ZP_0010650	D-lactate dehydrogenase	346	3.00E-94	COG1052	CHR
ZMO1238	1262094	1262210	3	117		hypothetical protein				
ZMO1239	1262273	1262383	2	111		hypothetical protein				
ZMO1240	1263272	1262592	-3	681	P30798 GPM	phosphoglycerate mutase	470	1.00E-131	COG0588	G
ZMO1241	1263379	1263516	1	138		hypothetical protein				
ZMO1242	1264664	1263528	-3	1137	ZP_0009674	carboxypeptidase, predicted	466	1.00E-130	COG2866	E
ZMO1243	1265473	1264667	-2	807	A40649	conserved hypothetical protein	538	1.00E-152	-	-
ZMO1244	1265495	1265620	2	126		hypothetical protein				
ZMO1245	1265601	1265738	3	138		hypothetical protein				
ZMO1246	1265756	1265881	2	126	ZP_0009674	ribosomal protein L36	75.9	2.00E-13	COG0257	J
ZMO1247	1266432	1266554	3	123		hypothetical protein				
ZMO1248	1267076	1266594	-3	483		hypothetical protein				
ZMO1249	1267617	1267372	-1	246		hypothetical protein				
ZMO1250	1267942	1267760	-2	183		hypothetical protein				
ZMO1251	1268527	1268045	-2	483		hypothetical protein				
ZMO1252	1269200	1268565	-3	636	ZP_0009407	cytochrome c biogenesis factor	124	1.00E-27	COG4235	O
ZMO1253	1269625	1269203	-2	423	ZP_0009407	cytochrome c biogenesis protein	116	9.00E-26	COG3088	O
ZMO1254	1270062	1269628	-1	435	NP_642006	cytochrome c biogenesis protein	110	5.00E-24	COG0526	OC
ZMO1255	1272095	1270155	-3	1941	ZP_0009407	cytochrome c biogenesis factor	651	0	COG1138	O
ZMO1256	1272537	1272103	-1	435	ZP_0009407	cytochrome c biogenesis protein	134	2.00E-31	COG2332	O
ZMO1257	1272725	1272567	-3	159		hypothetical protein				
ZMO1258	1273438	1272728	-2	711	ZP_0009407	ABC-type transport system invol	294	1.00E-78	COG0755	O
ZMO1259	1273598	1273726	2	129		hypothetical protein				
ZMO1260	1274039	1276291	2	2253	ZP_0008646	TonB-dependent receptor, outer	609	1.00E-173	COG1629	P
ZMO1261	1276477	1277535	1	1059	ZP_0008991	ABC-type nitrate/sulfonate/bicart	205	1.00E-51	COG0715	P
ZMO1262	1277480	1278313	2	834	ZP_0011122	ABC-type nitrate/sulfonate/bicart	268	7.00E-71	COG0600	P
ZMO1263	1278314	1279036	2	723	ZP_0012667	ABC-type nitrate/sulfonate/bicart	270	2.00E-71	COG1116	P
ZMO1264	1279074	1280255	3	1182	NP_462733	putative mandelate racemase	446	1.00E-124	COG4948	MR
ZMO1265	1280266	1280922	1	657	ZP_0009814	metal-binding protein conserved	247	1.00E-64	COG4887	R
ZMO1266	1280950	1281168	1	219		hypothetical protein				
ZMO1267	1281143	1282723	2	1581	ZP_0009515	GMP synthase - glutamine amid	852	0	COG0519	F
ZMO1268	1283840	1282803	-3	1038	ZP_0009358	conserved hypothetical protein	152	1.00E-35	-	-
ZMO1269	1284416	1284045	-3	372	ZP_0009450	conserved hypothetical protein	92.8	1.00E-18	-	-
ZMO1270	1284395	1285606	2	1212	BAB56013	serine palmitoyltransferase	599	1.00E-170	COG0156	H
ZMO1271	1286600	1285740	-3	861	ZP_0009598	siroheme synthase (precorrin-2 c	210	3.00E-53	COG0007	H
ZMO1272	1286815	1288245	1	1431	ZP_0009388	NAD-dependent aldehyde dehyd	560	1.00E-158	COG1012	C
ZMO1273	1289875	1288298	-2	1578	ZP_0009409	metal-dependent hydrolase, prec	381	1.00E-104	COG1574	R
ZMO1274	1290066	1289965	-1	102		hypothetical protein				
ZMO1275	1290233	1291471	2	1239	ZP_0009434	threonine dehydratase	473	1.00E-132	COG1171	E
ZMO1276	1291504	1291743	1	240		hypothetical protein				
ZMO1277	1292945	1291950	-3	996	NP_420489	conserved hypothetical protein	234	1.00E-60	COG1559	R
ZMO1278	1294247	1292955	-3	1293	ZP_0009467	3-oxoacyl-(acyl-carrier-protein) s	615	1.00E-175	COG0304	IQ
ZMO1279	1294637	1294407	-3	231	ZP_0009467	acyl carrier protein	130	5.00E-30	COG0236	IQ
ZMO1280	1294413	1294688	3	276	ZP_0009467	acyl carrier protein	129	2.00E-29	COG0236	IQ
ZMO1281	1294828	1294977	1	150		hypothetical protein				
ZMO1282	1295081	1295200	2	120		hypothetical protein				
ZMO1283	1295281	1296321	1	1041	NP_420858	transcriptional regulator, Lacl fan	296	6.00E-79	COG1609	K
ZMO1284	1297783	1296347	-2	1437	BAA92379	sorbitol dehydrogenase cytochro	492	1.00E-138	COG2010	C
ZMO1285	1299413	1297782	-3	1632	BAA92378	sorbitol dehydrogenase large su	909	0	COG2303	E
ZMO1286	1300025	1299438	-3	588	BAA92377	sorbitol dehydrogenase small su	121	9.00E-27	-	-
ZMO1287	1301565	1300477	-1	1089	NP_279218	LPS glycosyltransferase; Lpg	108	2.00E-22	COG0438	M
ZMO1288	1301964	1303085	3	1122	ZP_0012750	permeases of the major facilitato	347	2.00E-94	COG0477	GEPR
ZMO1289	1303438	1303196	-2	243	NP_639383	transglycosylase associated prot	85.1	3.00E-16	COG2261	S
ZMO1290	1303544	1303660	2	117		hypothetical protein				
ZMO1291	1305242	1303638	-3	1605	NP_294688	carboxypeptidase-related protein	331	3.00E-89	COG2939	E
ZMO1292	1305858	1305700	-1	159		hypothetical protein				
ZMO1293	1305786	1305932	3	147		hypothetical protein				
ZMO1294	1305913	1306866	1	954	ZP_0005200	sugar phosphate isomerase, put	290	3.00E-77	COG2103	R
ZMO1295	1306863	1307516	3	654	ZP_0002310	organic radical activating enzym	243	2.00E-63	COG0602	O
ZMO1296	1310084	1309335	-3	750		hypothetical protein				
ZMO1297	1310218	1310544	1	327		hypothetical protein				
ZMO1298	1310721	1313138	3	2418	ZP_0002744	outer membrane receptor protein	666	0	COG1629	P
ZMO1299	1314028	1315653	1	1626	BAB72034	capsular polysaccharide biosynt	358	1.00E-97	-	-
ZMO1300	1315650	1316372	3	723	BAB72033	capsular polysaccharide biosynt	240	2.00E-62	-	-
ZMO1301	1317488	1316406	-3	1083	NP_229885	conserved hypothetical protein	65.5	2.00E-09	-	-
ZMO1302	1317728	1318378	2	651	NP_541656	lipote-protein ligase B	240	1.00E-62	COG0321	H
ZMO1303	1319356	1318508	-2	849	ZP_0009486	pyrroline-5-carboxylate reductas	216	3.00E-55	COG0345	E
ZMO1304	1319916	1319413	-1	504	ZP_0009486	conserved hypothetical protein	190	8.00E-48	COG5465	S
ZMO1305	1320260	1320051	-3	210	ZP_0009395	conserved hypothetical protein	72.8	2.00E-12	COG2960	S
ZMO1306	1321215	1320472	-1	744	ZP_0009394	rRNA methylase, predicted	300	2.00E-80	COG1189	J
ZMO1307	1321511	1323034	2	1524	NP_641794	fumarate hydratase	687	0	COG1951	C

ZMO1308	1323570	1323130	-1	441	ZP_0009439	DNA polymerase III, chi subunit	110	5.00E-24	COG2927	L
ZMO1309	1325081	1323588	-3	1494	ZP_0009439	leucyl aminopeptidase	533	1.00E-150	COG0260	E
ZMO1310	1325287	1325186	-2	102		hypothetical protein				
ZMO1311	1325487	1327778	3	2292	ZP_0009439	organic solvent tolerance protein	656	0	COG1452	M
ZMO1312	1327897	1329312	1	1416	ZP_0009439	peptidyl-prolyl isomerase	414	1.00E-114	COG0760	O
ZMO1313	1329354	1330361	3	1008	ZP_0009439	pyridoxal phosphate biosynthesis	323	2.00E-87	COG1995	H
ZMO1314	1330372	1331208	1	837	ZP_0009439	dimethyladenosine transferase (r	330	1.00E-89	COG0030	J
ZMO1315	1332086	1331223	-3	864	NP_708800	conserved hypothetical protein	136	4.00E-31	-	-
ZMO1316	1333437	1332109	-1	1329	NP_755591	conserved hypothetical protein	366	1.00E-100	COG2244	R
ZMO1317	1334293	1333529	-2	765	NP_417458	conserved hypothetical protein	185	1.00E-45	-	-
ZMO1318	1335020	1334304	-3	717	NP_417460	conserved hypothetical protein	185	8.00E-46	-	-
ZMO1319	1336153	1335530	-2	624	ZP_0009334	FOG: TPR repeat	106	4.00E-22	-	-
ZMO1320	1337555	1336329	-3	1227	ZP_0009334	tRNA and rRNA cytosine-C5-met	351	2.00E-95	COG0144	J
ZMO1321	1339042	1337591	-2	1452	ZP_0009334	IMP dehydrogenase/GMP reduct	757	0	COG0516	F
ZMO1322	1339322	1340029	2	708	NP_105817	two-component system response	302	4.00E-81	COG0745	TK
ZMO1323	1339998	1341635	3	1638	ZP_0009636	two-component signal transducti	429	1.00E-119	COG0642	T
ZMO1324	1341778	1342269	1	492	ZP_0005483	Serine kinase of the HPr protein,	110	1.00E-23	COG1493	T
ZMO1325	1342292	1343263	2	972	ZP_0009636	predicted P-loop-containing kina	310	3.00E-83	COG1660	R
ZMO1326	1343271	1343675	3	405	ZP_0009636	PTS system, mannose/fructose-	187	3.00E-47	COG2893	G
ZMO1327	1343672	1343944	2	273	NP_945707	PTS system phosphocarrier prot	92.4	2.00E-18	COG1925	G
ZMO1328	1343962	1344768	1	807	ZP_0009636	tRNA methylases	327	1.00E-88	COG0566	J
ZMO1329	1344821	1345597	2	777	ZP_0009551	sugar kinase, predicted	282	5.00E-75	COG0061	G
ZMO1330	1345840	1345703	-2	138		hypothetical protein				-
ZMO1331	1345922	1348732	2	2811	ZP_0003468	small-conductance mechanosen:	355	3.00E-96	COG0668	M
ZMO1332	1348878	1348991	3	114		hypothetical protein				-
ZMO1333	1349451	1349335	-1	117		hypothetical protein				-
ZMO1334	1349455	1350069	1	615	ZP_0005101	conserved hypothetical protein	148	6.00E-35	COG2353	S
ZMO1335	1350349	1350951	1	603	ZP_0010091	flavodoxin WrbA, multimeric	282	3.00E-75	COG0655	R
ZMO1336	1352000	1351095	-3	906	NP_900952	transcriptional regulator	275	6.00E-73	COG0583	K
ZMO1337	1352135	1352842	2	708	NP_420285	conserved hypothetical protein	294	9.00E-79	COG1741	R
ZMO1338	1353457	1352849	-2	609	NP_883746	efflux protein, LysE family	210	2.00E-53	COG1280	E
ZMO1339	1353459	1353569	3	111		hypothetical protein				-
ZMO1340	1354842	1354639	-3	204	ZP_0003122	permeases of the major facilitato	438	1.00E-121	COG0477	GEPR
ZMO1341	1356088	1355504	-2	585	ZP_0009334	metalloprotease	134	1.00E-30	COG2321	R
ZMO1342	1356194	1356081	-3	114		hypothetical protein				-
ZMO1343	1356815	1356714	-3	102		hypothetical protein				-
ZMO1344	1356974	1357822	2	849	NP_691310	2,5-diketo-D-gluconate reductase	371	1.00E-102	COG0656	R
ZMO1345	1360546	1357949	-2	2598	NP_251773	aminopeptidase N	803	0	COG0308	E
ZMO1346	1361570	1360620	-3	951	ZP_0009560	permeases of the drug/metabolit	209	8.00E-53	COG0697	GER
ZMO1347	1362621	1361614	-1	1008	AAD42401	threonine aldolase	670	0	COG2008	E
ZMO1348	1363517	1362693	-3	825	AAD42400	methionine aminopeptidase	565	1.00E-160	COG0024	J
ZMO1349	1363639	1363532	-2	108		hypothetical protein				-
ZMO1350	1363633	1364394	1	762	ZP_0009627	nucleotide-utilizing enzyme (rela	309	4.00E-83	COG1058	R
ZMO1351	1364407	1365411	1	1005	NP_103069	carboxymethylenebutenolidase,	166	8.00E-40	COG0412	Q
ZMO1352	1366204	1365506	-2	699	ZP_0009486	integral membrane protein	300	2.00E-80	COG0670	R
ZMO1353	1367020	1366466	-2	555	ZP_0003156	conserved hypothetical protein	162	2.00E-39	COG4702	S
ZMO1354	1367980	1367210	-2	771	ZP_0005639	outer membrane protein and rela	206	6.00E-52	COG2885	M
ZMO1355	1370585	1368726	-3	1860	ZP_0009466	ABC transporters with duplicated	750	0	COG0488	R
ZMO1356	1372134	1370686	-1	1449	ZP_0000456	chromosomal replication initiator	400	1.00E-110	COG0593	L
ZMO1357	1372549	1372800	1	252		hypothetical protein				-
ZMO1358	1373064	1372807	-1	258	Q9Z5V0 RS2	ribosomal protein S20	167	6.00E-41	COG0268	J
ZMO1359	1373148	1373264	3	117		hypothetical protein				-
ZMO1360	1375108	1373408	-2	1701	P06672 DCP	pyruvate decarboxylase (PDC)	1135	0	COG3961	GHR
ZMO1361	1375371	1375189	-1	183		hypothetical protein				-
ZMO1362	1375645	1375361	-2	285		hypothetical protein				-
ZMO1363	1375810	1376031	1	222		hypothetical protein				-
ZMO1364	1376059	1377420	1	1362	AAD19712	oxygen-independent (anaerobic)	846	0	COG0635	H
ZMO1365	1379200	1380891	1	1692	NP_638679	conserved hypothetical protein	233	2.00E-59	COG2199	T
ZMO1366	1381072	1381686	1	615	Q9Z5U7 RS4	ribosomal protein S4	411	1.00E-114	COG0522	J
ZMO1367	1381820	1382059	2	240		hypothetical protein				-
ZMO1368	1382061	1381954	-1	108		hypothetical protein				-
ZMO1369	1382194	1383174	1	981	ZP_0009468	peptidylarginine deiminase and r	323	4.00E-87	COG2957	E
ZMO1370	1383186	1384034	3	849	NP_924628	hydrolase, hydratase	371	1.00E-102	COG0388	R
ZMO1371	1384172	1384008	-3	165		hypothetical protein				-
ZMO1372	1385464	1384625	-2	840	NP_250021	probable short-chain dehydroger	255	7.00E-67	COG1028	IQR
ZMO1373	1385910	1386422	3	513		hypothetical protein				-
ZMO1374	1387535	1386588	-3	948	NP_107357	conserved hypothetical protein	374	1.00E-102	COG0451	MG
ZMO1375	1388338	1387673	-2	666	Q9Z5U2 RNC	ribonuclease III (RNase III)	430	1.00E-119	COG0571	K
ZMO1376	1388469	1388585	3	117		hypothetical protein				-
ZMO1377	1389883	1388711	-2	1173		hypothetical protein				-
ZMO1378	1391592	1390189	-1	1404	AAK51697	permease (ethanolamin), amino	574	1.00E-162	COG0531	E
ZMO1379	1391782	1391561	-2	222		hypothetical protein				-
ZMO1380	1392982	1391918	-2	1065	ZP_0001439	transcriptional regulatory protein,	256	5.00E-67	COG2207	K
ZMO1381	1394370	1393192	-1	1179	NP_535625	conserved hypothetical protein, t	249	9.00E-65	COG2334	R
ZMO1382	1394440	1395759	1	1320	NP_436219	putative aminotransferase	458	1.00E-127	COG0160	E
ZMO1383	1395857	1395958	2	102		hypothetical protein				-
ZMO1384	1395955	1396875	1	921	ZP_0009416	GTPase	370	1.00E-101	COG1159	R

ZMO1385	1396959	1398233	3	1275	ZP_0009421:	conserved hypothetical protein	496	1.00E-139	COG3853	P
ZMO1386	1398243	1398938	3	696	ZP_0009421:	conserved hypothetical protein	93.2	4.00E-18	-	-
ZMO1387	1399125	1399829	3	705	ZP_0009683:	two-component response regulat	376	1.00E-103	COG0745	TK
ZMO1388	1401727	1399967	-2	1761	NP_419350	gamma-glutamyltransferase	625	1.00E-177	COG0405	E
ZMO1389	1401890	1404070	2	2181	ZP_0009385:	thiol:disulfide interchange protein	512	1.00E-143	COG4232	OC
ZMO1390	1405027	1404128	-2	900	NP_840879	conserved hypothetical protein	171	2.00E-41	-	-
ZMO1391	1406078	1405107	-3	972	ZP_0009043:	sphingosine kinase	94.7	2.00E-18	-	-
ZMO1392	1406578	1406081	-2	498	ZP_0009603:	conserved hypothetical protein	52	4.00E-06	-	-
ZMO1393	1407222	1407956	3	735	ZP_0009365:	permeases, predicted	213	6.00E-54	COG0795	R
ZMO1394	1407953	1409047	2	1095	ZP_0009364:	permeases, predicted	335	7.00E-91	COG0795	R
ZMO1395	1409909	1409052	-3	858	ZP_0009362:	N-formylglutamate amidohydrola	171	1.00E-41	COG3741	E
ZMO1396	1410568	1409900	-2	669		hypothetical protein			-	-
ZMO1397	1410688	1410795	1	108		hypothetical protein			-	-
ZMO1398	1411145	1410903	-3	243		hypothetical protein			-	-
ZMO1399	1411450	1412124	1	675	NP_655509	conserved hypothetical protein	78.2	2.00E-13	COG3000	I
ZMO1400	1412260	1413417	1	1158	ZP_0009556:	conserved hypothetical protein	457	1.00E-127	-	-
ZMO1401	1414278	1413499	-1	780	NP_252861	nuclease, probable	288	6.00E-77	COG0708	L
ZMO1402	1414625	1414284	-3	342	ZP_0009645:	conserved hypothetical protein	123	8.00E-28	COG0316	S
ZMO1403	1415730	1414723	-1	1008	ZP_0009468:	membrane proteins related to me	164	2.00E-39	COG0739	M
ZMO1404	1416642	1415950	-1	693	ZP_0009555:	RNA polymerase sigma-24 facto	202	6.00E-51	COG1595	K
ZMO1405	1417504	1416716	-2	789	NP_422271	two component response regulat	283	2.00E-75	COG0784	T
ZMO1406	1418486	1417740	-3	747	ZP_0009508:	hydrolases or acyltransferases	166	4.00E-40	COG0596	R
ZMO1407	1419729	1418710	-1	1020	ZP_0009508:	aspartate-semialdehyde dehydr	574	1.00E-163	COG0136	E
ZMO1408	1421998	1419842	-2	2157	ZP_0009508:	dipeptidyl aminopeptidases/acyl	791	0	COG1506	E
ZMO1409	1423039	1422227	-2	813	ZP_0009361:	archaeal fructose-1,6-bisphosph	233	4.00E-60	COG0483	G
ZMO1410	1423567	1424058	1	492	NP_903069	bacterioferritin	178	3.00E-44	COG2193	P
ZMO1411	1424606	1424181	-3	426	ZP_0009591:	Fe2+/Zn2+ uptake regulation prc	216	5.00E-56	COG0735	P
ZMO1412	1425267	1424860	-1	408	ZP_0009591:	transcriptional regulator, predicte	188	1.00E-47	COG4957	K
ZMO1413	1425919	1425449	-2	471	ZP_0001316:	acetyltransferases	75.5	3.00E-13	COG0456	R
ZMO1414	1426542	1425922	-1	621	ZP_0009591:	metal-dependent proteases, put	154	1.00E-36	COG1214	O
ZMO1415	1427045	1426548	-3	498	ZP_0009591:	thioredoxin-like proteins and don	171	7.00E-42	COG0694	O
ZMO1416	1427040	1427168	3	129		hypothetical protein			-	-
ZMO1417	1427547	1428923	3	1377	ZP_0009677:	DNA and RNA helicases superfa	538	1.00E-152	COG0513	LKJ
ZMO1418	1429396	1429262	-2	135		hypothetical protein			-	-
ZMO1419	1430435	1429485	-3	951	NP_422215	4-hydroxybenzoate octaprenyltra	257	2.00E-67	COG0382	H
ZMO1420	1430675	1431214	2	540	NP_534248	phosphoribosylaminoimidazole c	228	5.00E-59	COG0041	F
ZMO1421	1431211	1432299	1	1089	NP_773755	phosphoribosylaminoimidazole c	307	3.00E-82	COG0026	F
ZMO1422	1435280	1432380	-3	2901	ZP_0009449:	predicted Zn-dependent peptida	904	0	COG0612	R
ZMO1423	1438188	1435417	-1	2772	ZP_0009449:	predicted Zn-dependent peptida	780	0	COG0612	R
ZMO1424	1438454	1441048	2	2595	NP_698844	heat shock protein, ATP-depend	1177	0	COG0542	O
ZMO1425	1441742	1441158	-3	585	ZP_0005578:	thiamine monophosphate syntha	76.6	3.00E-13	COG0352	H
ZMO1426	1441905	1442330	3	426	NP_622549	DNA repair proteins	79.3	1.00E-14	COG2003	L
ZMO1427	1442584	1442444	-2	141		hypothetical protein			-	-
ZMO1428	1442587	1442441	1	147	ZP_0001626:	sphingosine kinase	159	6.00E-38	COG1597	IR
ZMO1429	1445306	1443609	-3	1698	NP_902518	outer membrane component of n	360	5.00E-98	COG1538	MU
ZMO1430	1446400	1445309	-2	1092	NP_883923	secretion protein, multidrug resis	277	3.00E-73	COG1566	V
ZMO1431	1446642	1446415	-1	228	NP_541510	conserved hypothetical membrar	53.9	7.00E-07	-	-
ZMO1432	1448669	1446645	-3	2025	NP_889617	conserved hypothetical membrar	368	1.00E-100	COG1289	S
ZMO1433	1450131	1449124	-1	1008	ZP_0009579:	DNA polymerase III, delta subun	124	3.00E-27	COG1466	L
ZMO1434	1450692	1450147	-1	546	ZP_0009579:	conserved hypothetical protein	152	3.00E-36	COG5468	S
ZMO1435	1453292	1450758	-3	2535	ZP_0009580:	leucyl-tRNA synthetase	1145	0	COG0495	J
ZMO1436	1453750	1453316	-2	435	ZP_0009580:	conserved hypothetical protein	172	8.00E-43	-	-
ZMO1437	1454782	1454156	-2	627	NP_931341	conserved hypothetical protein	197	1.00E-49	COG1280	E
ZMO1438	1454986	1455447	1	462	AAL18479	transcriptional regulator, putative	187	7.00E-47	COG1522	K
ZMO1439	1456331	1455453	-3	879	NP_459623	hydrolase, putative	277	2.00E-73	COG0388	R
ZMO1440	1457121	1456297	-1	825	ZP_0009580:	conserved hypothetical protein	71.2	2.00E-11	-	-
ZMO1441	1457593	1458711	1	1119	ZP_0009410:	glycine/D-amino acid oxidases (c	348	1.00E-94	COG0665	E
ZMO1442	1459655	1458762	-3	894	NP_103522	conserved hypothetical protein	124	2.00E-27	-	-
ZMO1443	1459840	1461168	1	1329	NP_419982	conserved hypothetical protein	216	9.00E-55	COG2244	R
ZMO1444	1463589	1461547	-1	2043	ZP_0009393:	glycyl-tRNA synthetase, beta sut	622	1.00E-176	COG0751	J
ZMO1445	1464445	1464555	1	111		hypothetical protein			-	-
ZMO1446	1464465	1463599	-1	867	ZP_0001398:	glycyl-tRNA synthetase, alpha su	452	1.00E-126	COG0752	J
ZMO1447	1464799	1465860	1	1062	ZP_0009331:	conserved hypothetical protein	167	3.00E-40	COG3735	S
ZMO1448	1466454	1466068	-1	387		hypothetical protein			-	-
ZMO1449	1468200	1466695	-1	1506	BAB83933	L-sorbose reductase	420	1.00E-116	COG0246	G
ZMO1450	1468622	1470031	2	1410	NP_531913	DNA photolyase, blue-light phot	390	1.00E-107	COG0415	L
ZMO1451	1471223	1470132	-3	1092	NP_419006	purine nucleoside permease, put	267	2.00E-70	COG5042	F
ZMO1452	1472607	1471384	-1	1224	ZP_0003130:	arabinose efflux permease	315	1.00E-84	COG2814	G
ZMO1453	1472592	1472699	3	108		hypothetical protein			-	-
ZMO1454	1472763	1472614	-1	150		hypothetical protein			-	-
ZMO1455	1472781	1473377	3	597	NP_943127	Tn5501 resolvase, transposase	254	5.00E-67	COG1961	L
ZMO1456	1473684	1474340	3	657	NP_419275	efflux protein, LysE family	144	1.00E-33	COG1280	E
ZMO1457	1474414	1475832	1	1419	NP_819596	major facilitator family transport	173	8.00E-42	COG0477	GEPR
ZMO1458	1475864	1477645	2	1782		hypothetical protein			-	-
ZMO1459	1478281	1477664	-2	618	AAL07520	transporter, putative	143	2.00E-33	COG3201	H
ZMO1460	1479114	1478242	-1	873	NP_822511	thiosulfate sulfurtransferase (rho	222	8.00E-57	COG2897	P
ZMO1461	1480270	1479122	-2	1149	NP_636067	conserved hypothetical protein	301	2.00E-80	-	-

ZMO1462	1481195	1480269	-3	927	NP_822512	conserved hypothetical protein	287	2.00E-76	COG0715	P
ZMO1463	1483018	1481216	-2	1803	NP_902858	TonB-dependent receptor, probab	282	2.00E-74	COG1629	P
ZMO1464	1483981	1483760	-2	222		hypothetical protein				-
ZMO1465	1485542	1484220	-3	1323	NP_462153	transport protein, putative	584	1.00E-165	COG0814	E
ZMO1466	1486537	1485752	-2	786	NP_773784	oxidoreductase	214	2.00E-54	COG0596	R
ZMO1467	1486762	1487586	1	825	AAK26458	ABC-2 transporter, putative, poly	181	1.00E-44	COG1682	GM
ZMO1468	1490048	1487631	-3	2418		hypothetical protein				-
ZMO1469	1490405	1490518	2	114		hypothetical protein				-
ZMO1470	1491334	1490504	-2	831	NP_948727	conserved hypothetical protein	155	9.00E-37		-
ZMO1471	1493438	1491627	-3	1812	ZP_0009597	membrane GTPase involved in s	959	0	COG1217	T
ZMO1472	1493400	1493519	3	120		hypothetical protein				-
ZMO1473	1493885	1494622	2	738	NP_298118	conserved hypothetical protein	94.7	1.00E-18		-
ZMO1474	1494640	1494777	1	138		hypothetical protein				-
ZMO1475	1495116	1497578	3	2463	ZP_0002744	outer membrane receptor protei	683	0	COG1629	P
ZMO1476	1497814	1498137	1	324		hypothetical protein				-
ZMO1477	1499049	1498162	-1	888		hypothetical protein				-
ZMO1478	1499859	1499113	-1	747	ZP_0008984	6-phosphogluconolactonase/gluc	131	1.00E-29	COG0363	G
ZMO1479	1501079	1500153	-3	927	NP_104580	electron transfer flavoprotein alpl	347	2.00E-94	COG2025	C
ZMO1480	1501825	1501082	-2	744	NP_534091	electron transfer flavoprotein bet	343	2.00E-93	COG2086	C
ZMO1481	1503084	1501894	-1	1191	ZP_0009552	succinyl-CoA synthetase, beta su	487	1.00E-136	COG0045	C
ZMO1482	1506816	1503622	-1	3195	NP_947281	serine protease/outer membrane	73.2	3.00E-11	COG4625	S
ZMO1483	1507091	1506918	-3	174		hypothetical protein				-
ZMO1484	1510265	1507128	-3	3138	ZP_0005878	DNA and RNA helicases superfa	804	0	COG0210	L
ZMO1485	1510373	1511713	2	1341	ZP_0004495	dGTP triphosphohydrolase	297	4.00E-79	COG0232	F
ZMO1486	1511889	1512017	3	129		hypothetical protein				-
ZMO1487	1512806	1512036	-3	771	ZP_0008645	FOG: EAL domain	219	6.00E-56	COG2200	T
ZMO1488	1513817	1512945	-3	873	NP_890240	2-dehydro-3-deoxyphosphoctor	357	2.00E-97	COG2877	M
ZMO1489	1514634	1513840	-1	795	ZP_0000805	CMP-2-keto-3-deoxyoctulosonic	238	7.00E-62	COG1212	M
ZMO1490	1515030	1515644	3	615	NP_948710	outer membrane protein, putative	64.7	1.00E-09	COG3637	M
ZMO1491	1515939	1516742	3	804	NP_948710	outer membrane protein, putative	59.3	8.00E-08	COG3637	M
ZMO1492	1517206	1517030	-2	177		hypothetical protein				-
ZMO1493	1518121	1517549	-2	573	ZP_0004841	predicted membrane protein	194	1.00E-48	COG1238	S
ZMO1494	1519047	1518148	-1	900	ZP_0009672	acetylglutamate kinase	404	1.00E-111	COG0548	E
ZMO1495	1519762	1519199	-2	564	NP_386747	conserved hypothetical protein	162	2.00E-39	COG2096	S
ZMO1496	1520273	1522930	2	2658	NP_520479	phosphoenolpyruvate carboxylas	699	0	COG2352	E
ZMO1497	1524567	1523077	-1	1491	NP_840598	amino acid transporter	640	0	COG0531	C
ZMO1498	1525276	1524905	-2	372	ZP_0009594	diadenosine tetraphosphate (Ap	163	7.00E-40	COG0537	FGR
ZMO1499	1525745	1525428	-3	318	ZP_0009594	phosphoribosyl-ATP pyrophosph	111	3.00E-24	COG0140	E
ZMO1500	1526617	1525856	-2	762	ZP_0009594	imidazoleglycerol phosphate syn	401	1.00E-111	COG0107	E
ZMO1501	1527414	1526620	-1	795	ZP_0009593	phosphoribosylformimino-5-amin	315	8.00E-85	COG0106	E
ZMO1502	1528160	1527477	-3	684	ZP_0009593	glutamine amidotransferase	253	2.00E-66	COG0118	E
ZMO1503	1528734	1528120	-1	615	ZP_0009593	imidazoleglycerol-phosphate del	271	6.00E-72	COG0131	E
ZMO1504	1528795	1529286	1	492	ZP_0009593	conserved hypothetical protein	197	5.00E-50	COG3814	S
ZMO1505	1529317	1529502	1	186		hypothetical protein				-
ZMO1506	1529509	1529847	1	339		hypothetical protein				-
ZMO1507	1530448	1529921	-2	528	ZP_0009681	inorganic pyrophosphatase	262	3.00E-69	COG0221	C
ZMO1508	1530657	1530803	2	147	ZP_0009681	histidyl-tRNA synthetase	436	1.00E-121	COG0124	J
ZMO1509	1531912	1532988	1	1077	ZP_0009681	protein chain release factor A	424	1.00E-117	COG0216	J
ZMO1510	1532945	1533841	2	897	ZP_0009681	methylase of polypeptide chain r	228	9.00E-59	COG2890	J
ZMO1511	1534152	1535225	3	1074	NP_419693	conserved hypothetical protein	80.9	4.00E-14		-
ZMO1512	1537071	1535290	-1	1782	ZP_0009416	ABC-type transport system invol	644	0	COG5265	O
ZMO1513	1539517	1537154	-2	2364	NP_767345	phenylalanyl-tRNA synthetase be	717	0	COG0072	J
ZMO1514	1540614	1539520	-1	1095	ZP_0009475	phenylalanyl-tRNA synthetase al	534	1.00E-150	COG0016	J
ZMO1515	1541280	1540909	-1	372	ZP_0009475	ribosomal protein L20	197	3.00E-50	COG0292	J
ZMO1516	1541497	1541300	-2	198	ZP_0009475	ribosomal protein L35	116	1.00E-25	COG0291	J
ZMO1517	1541615	1541460	-3	156		hypothetical protein				-
ZMO1518	1542422	1541649	-3	774	ZP_0001482	archaeal fructose-1,6-bisphosph	260	2.00E-68	COG0483	G
ZMO1519	1543403	1542474	-3	930	ZP_0009590	phosphoribosylpyrophosphate sy	479	1.00E-134	COG0462	FE
ZMO1520	1543838	1543614	-3	225	NP_531398	conserved hypothetical protein	66	2.00E-10	COG3908	S
ZMO1521	1544565	1543993	-1	573	NP_421618	conserved hypothetical protein	91.3	9.00E-18		-
ZMO1522	1544960	1548106	2	3147	NP_299516	conserved hypothetical protein (r	530	1.00E-149	COG1629	P
ZMO1523	1548482	1548381	-3	102		hypothetical protein				-
ZMO1524	1548492	1549421	3	930	NP_699849	membrane protein, putative	246	4.00E-64	COG0697	GER
ZMO1525	1552581	1549492	-1	3090	ZP_0008826	outer membrane protein	322	2.00E-86	COG1538	MU
ZMO1526	1552794	1552678	-1	117		hypothetical protein				-
ZMO1527	1556023	1552730	-2	3294	ZP_0002819	cation/multidrug efflux pump	1122	0	COG0841	V
ZMO1528	1559118	1556026	-1	3093	ZP_0002815	cation/multidrug efflux pump	1113	0	COG0841	V
ZMO1529	1560453	1559164	-1	1290	NP_251218	probable RND efflux membrane t	305	1.00E-81	COG0845	M
ZMO1530	1560938	1561948	2	1011	ZP_0005496	FOG: CBS domain	303	4.00E-81	COG0794	M
ZMO1531	1562121	1562354	3	234	ZP_0009383	phosphoribosylformylglycinamidi	117	7.00E-26	COG1828	F
ZMO1532	1562354	1563019	2	666	ZP_0009383	phosphoribosylformylglycinamidi	311	5.00E-84	COG0047	F
ZMO1533	1563462	1564046	3	585	ZP_0011030	conserved hypothetical protein	100	2.00E-20	COG3247	S
ZMO1534	1564282	1564169	-2	114		hypothetical protein				-
ZMO1535	1564380	1564682	3	303	NP_109452	conserved hypothetical protein	61.2	4.00E-09	COG3293	L
ZMO1536	1566836	1565175	-3	1662	NP_763374	ATPase involved in DNA repair	343	4.00E-93		-
ZMO1537	1567694	1567593	-3	102		hypothetical protein				-
ZMO1538	1571143	1567775	-2	3369	ZP_0009486	DNA polymerase III, alpha subur	1190	0	COG0587	L

ZMO1539	1571503	1571634	1	132	hypothetical protein				-	P
ZMO1540	1571649	1571951	3	303	ZP_0002590; Fe2+ transport system protein A	58.9	2.00E-08	COG1918		P
ZMO1541	1571957	1573882	2	1926	ZP_0009641; Fe2+ transport system protein B	670	0	COG0370		P
ZMO1542	1573978	1574559	1	582	NP_532201 single-strand DNA binding protei	237	1.00E-61	COG0629		L
ZMO1543	1576492	1574636	-2	1857	ZP_0009525; cobalamin biosynthesis protein C	651	0	COG4547		H
ZMO1544	1577482	1576505	-2	978	ZP_0009637; MoxR-like ATPases	504	1.00E-141	COG0714		R
ZMO1545	1578134	1577517	-3	618	ZP_0009635; heat shock protein, DnaJ-class n	192	5.00E-48	COG2214		O
ZMO1546	1578331	1577690	-2	642	ZP_0009635; heat shock protein, DnaJ-class n	126	3.00E-28	COG2214		O
ZMO1547	1578272	1578838	2	567	ZP_0005126; transcriptional regulator	201	8.00E-51	COG1309		K
ZMO1548	1578854	1581031	2	2178	NP_951745 squalene-hopene cyclase	561	1.00E-158	COG1657		I
ZMO1549	1581396	1581701	3	306	NP_421805 BolA protein	84	6.00E-16	COG0271		T
ZMO1550	1581790	1582458	1	669	Q9RH04 HIS ATP phosphoribosyltransferase	431	1.00E-120	COG0040		E
ZMO1551	1582700	1583740	2	1041	Q9RH05 HIS; histidinol dehydrogenase (HDH)	633	1.00E-180	COG0141		E
ZMO1552	1583824	1584213	1	390	ZP_0009634; transcription termination factor	185	3.00E-46	COG0781		K
ZMO1553	1584226	1585197	1	972	NP_420174 thiamine-monophosphate kinase	177	3.00E-43	COG0611		H
ZMO1554	1585506	1586276	3	771	NP_422209 conserved hypothetical protein	204	1.00E-51	COG1385		S
ZMO1555	1586439	1586329	-1	111	hypothetical protein					-
ZMO1556	1586582	1587970	2	1389	AAF18278 gamma-glutamylcysteine synthel	948	0	COG3572		H
ZMO1557	1588393	1589919	1	1527	NP_108068 amidophosphoribosyltransferase	637	0	COG0034		F
ZMO1558	1590247	1590369	1	123	hypothetical protein					-
ZMO1559	1591018	1590911	-2	108	hypothetical protein					-
ZMO1560	1591219	1591106	-2	114	hypothetical protein					-
ZMO1561	1591364	1592068	2	705	ZP_0009344; dehydrogenases with different s;e	185	7.00E-46	COG1028		IQR
ZMO1562	1592135	1592602	2	468	ZP_0000760; NTP pyrophosphohydrolases inc	154	4.00E-37	COG0494		LR
ZMO1563	1592747	1593610	2	864	ZP_0009622; putative salt-induced outer mem	137	2.00E-31	COG3137		M
ZMO1564	1594398	1593838	-1	561	gb AAL07520; transporter, putative nicotinamid	142	3.00E-33	COG3201		H
ZMO1565	1594481	1594582	2	102	hypothetical protein					-
ZMO1566	1594871	1595194	2	324	NP_949175 conserved hypothetical protein	143	5.00E-34	COG1742		S
ZMO1567	1596374	1596024	-2	351	NP_636067 conserved hypothetical protein	230	2.00E-59			-
ZMO1568	1598123	1596390	-3	1734	NP_790852 TonB-dependent receptor, putati	288	3.00E-76	COG1629		P
ZMO1569	1599778	1598972	-2	807	NP_901083 pyruvate formate lyase activatin	261	1.00E-68	COG1180		O
ZMO1570	1602056	1599747	-3	2310	NP_681780 formate acetyltransferase, pfl	1077	0	COG1882		C
ZMO1571	1602823	1604253	1	1431	ZP_0009595; cytochrome bd-type quinol oxida	557	1.00E-157	COG1271		C
ZMO1572	1604260	1605282	1	1023	ZP_0008765; cytochrome bd-type quinol oxida	345	6.00E-94	COG1294		C
ZMO1573	1605592	1606521	1	930	ZP_0002448; predicted iron-dependent peroxic	359	4.00E-98	COG2837		P
ZMO1574	1606647	1607555	3	909	NP_771239 transcriptional regulatory protein	328	1.00E-88	COG0583		K
ZMO1575	1607654	1607770	2	117	hypothetical protein					-
ZMO1576	1607748	1608494	3	747	ZP_0008695; short-chain alcohol dehydrogena	244	1.00E-63	COG4221		R
ZMO1577	1608752	1609972	2	1221	ZP_000869; arabinose efflux permease	463	1.00E-129	COG2814		G
ZMO1578	1610019	1610783	3	765	ZP_000791; dehydrogenases with different s;e	293	2.00E-78	COG1028		IQR
ZMO1579	1610847	1611968	3	1122	CAE81060 alpha/beta hydrolase superfamily	456	1.00E-127	COG1073		R
ZMO1580	1616983	1617117	1	135	hypothetical protein					-
ZMO1581	1618669	1618965	1	297	ZP_0009031; conserved hypothetical protein	86.7	9.00E-17	COG1359		S
ZMO1582	1619501	1619016	-3	486	ZP_000948; G:T/U mismatch-specific DNA gl	161	4.00E-39	COG3663		L
ZMO1583	1622323	1619891	-2	2433	ZP_000967; Type IIA topoisomerase (DNA gy	1144	0	COG0187		L
ZMO1584	1623596	1622472	-3	1125	ZP_000948; Recombinational DNA repair ATF	290	3.00E-77	COG1195		L
ZMO1585	1623711	1623574	-1	138	hypothetical protein					-
ZMO1586	1623714	1623571	3	144	NP_935820 bacterioferritin (cytochrome b1)	169	2.00E-41	COG2193		P
ZMO1587	1624274	1624627	2	354	CAE69762 conserved hypothetical protein	50.4	7.00E-06			-
ZMO1588	1624785	1627625	3	2841	AAM12400 excinuclease ABC subunit A	1843	0	COG0178		L
ZMO1589	1627796	1628725	2	930	NP_798191 conserved hypothetical protein	168	1.00E-40			-
ZMO1590	1629594	1628839	-1	756	ZP_0001428; ABC-type transport system invol	259	3.00E-68	COG1127		Q
ZMO1591	1630364	1629609	-3	756	ZP_0005398; ABC-type transport system invol	288	9.00E-77	COG0767		Q
ZMO1592	1631474	1630431	-3	1044	NP_770710 alanine racemase	216	4.00E-55	COG0787		M
ZMO1593	1633492	1631564	-2	1929	ZP_000968; protease with the C-terminal PD;	619	1.00E-176	COG3975		R
ZMO1594	1633761	1633546	-1	216	hypothetical protein					-
ZMO1595	1633821	1633994	3	174	hypothetical protein					-
ZMO1596	1634679	1635830	3	1152	P06758 ADH; alcohol dehydrogenase II (ADH I	752	0	COG1454		C
ZMO1597	1635986	1636156	2	171	hypothetical protein					-
ZMO1598	1636224	1638206	3	1983	ZP_0009646; deoxyxylulose-5-phosphate synt	892	0	COG1154		HI
ZMO1599	1638299	1640908	2	2610	ZP_000309; exporters of the RND superfamil	659	0	COG2409		R
ZMO1600	1641142	1642104	1	963	ZP_000147; homoserine kinase type II	302	5.00E-81	COG2334		R
ZMO1601	1642109	1642579	2	471	O69014 RNH ribonuclease H (RNase H)	329	1.00E-89	COG0328		L
ZMO1602	1642720	1644177	1	1458	NP_404603 exported protein, putative	107	4.00E-22	COG4099		R
ZMO1603	1644461	1644907	2	447	ZP_0009352; conserved hypothetical protein	125	1.00E-28	COG3453		S
ZMO1604	1646229	1644946	-1	1284	NP_643133 phosphodiesterase-nucleotide py	338	1.00E-91	COG1524		R
ZMO1605	1647732	1646350	-1	1383	O66113 ODP pyruvate dehydrogenase E1 cor	898	0	COG0022		C
ZMO1606	1648798	1647740	-2	1059	O66112 ODP; pyruvate dehydrogenase E1 cor	720	0	COG1071		C
ZMO1607	1649533	1649171	-2	363	ZP_0009510; conserved hypothetical protein	56.6	9.00E-08	COG2919		D
ZMO1608	1650863	1649580	-3	1284	P33675 ENO enolase (2-phosphoglycerate del	823	0	COG0148		G
ZMO1609	1651068	1651697	3	630	ZP_0009403; conserved hypothetical protein	66.6	3.00E-10			-
ZMO1610	1651700	1652221	2	522	T33720 conserved hypothetical protein					-
ZMO1611	1652276	1652611	2	336	T33720 conserved hypothetical protein					-
ZMO1612	1652869	1653453	1	585	T33719 conserved hypothetical protein	379	1.00E-104	COG2854		Q
ZMO1613	1653595	1653708	1	114	hypothetical protein					-
ZMO1614	1654428	1653796	-1	633	ZP_0001335; conserved hypothetical transmer	85.5	6.00E-16	COG0705		R

ZMO1615	1654876	1654451	-2	426	O50237 GRE	transcription elongation factor gr	281	2.00E-75	COG0782	K
ZMO1616	1654985	1654869	-3	117		hypothetical protein			-	-
ZMO1617	1658345	1657491	-2	855	O50236 CAR	carbamoyl-phosphate synthase I	1502	0	COG0458	EF
ZMO1618	1659582	1658416	-1	1167	O50235 CAR	carbamoyl-phosphate synthase s	762	0	COG0505	EF
ZMO1619	1659771	1660295	3	525	ZP_000940	conserved hypothetical protein	162	3.00E-39	COG1610	S
ZMO1620	1660703	1660599	-3	105		hypothetical protein			-	-
ZMO1621	1660966	1661223	1	258		hypothetical protein			-	-
ZMO1622	1661223	1662284	3	1062	AAG42747	DNA primase	696	0	COG0358	L
ZMO1623	1663111	1665126	1	2016	AAG42748	RNA polymerase sigma 70 factor	1046	0	COG0568	K
ZMO1624	1666722	1665214	-1	1509	ZP_000968	ATPase with chaperone activity,	625	1.00E-178	COG0606	O
ZMO1625	1666996	1667460	1	465	NP_774737	ribonuclease P protein compone	83.6	1.00E-15	COG0230	J
ZMO1626	1667687	1669426	2	1740	ZP_000951	preprotein translocase subunit Yi	528	1.00E-148	COG0706	U
ZMO1627	1669435	1670073	1	639	NP_945984	GTPases, probable	229	2.00E-59	COG0218	R
ZMO1628	1671189	1670143	-1	1047	ZP_000163	uncharacterized iron-regulated r	310	5.00E-83	COG3182	S
ZMO1629	1672004	1671711	-3	294	ZP_000163	conserved hypothetical protein	57.4	6.00E-08	-	-
ZMO1630	1672288	1672007	-2	282		hypothetical protein			-	-
ZMO1631	1674561	1672276	-1	2286	NP_841158	TonB-dependent receptor proteir	467	1.00E-130	COG1629	P
ZMO1632	1674853	1675983	1	1131	ZP_000951	acetylornithine deacetylase/succ	395	1.00E-108	COG0624	E
ZMO1633	1676362	1676042	-2	321		hypothetical protein			-	-
ZMO1634	1677113	1676433	-3	681	ZP_000951	conserved hypothetical protein	147	2.00E-34	COG2840	S
ZMO1635	1678698	1678390	-1	309	ZP_000951	membrane-bound lytic murein tra	322	1.00E-86	COG2821	M
ZMO1636	1679390	1678743	-3	648	NP_945656	conserved hypothetical protein	106	3.00E-22	COG4395	S
ZMO1637	1679466	1679597	3	132		hypothetical protein			-	-
ZMO1638	1679860	1680354	1	495	ZP_000951	preprotein translocase subunit S	173	2.00E-42	COG1952	U
ZMO1639	1680439	1682052	1	1614	ZP_000545	uncharacterized membrane prote	395	1.00E-108	COG0728	R
ZMO1640	1682076	1683098	3	1023	AAG42413	tryptophanyl-tRNA synthase	671	0	COG0180	J
ZMO1641	1683217	1683879	1	663	ZP_000940	conserved hypothetical protein	177	1.00E-43	-	-
ZMO1642	1685092	1683953	-2	1140	ZP_000519	molecular chaperone distantly re	296	4.00E-79	COG2377	O
ZMO1643	1685213	1686442	2	1230	ZP_000939	tyrosyl-tRNA synthetase	582	1.00E-165	COG0162	J
ZMO1644	1688577	1686505	-1	2073	AAG42404	DNA helicase RecG, ATP-depen	1202	0	COG1200	LK
ZMO1645	1688665	1688880	1	216		hypothetical protein			-	-
ZMO1646	1688894	1692292	2	3399	NP_420651	transcription-repair coupling fact	1173	0	COG1197	LK
ZMO1647	1693096	1692551	-2	546	ZP_000945	7,8-dihydro-6-hydroxymethylpter	117	1.00E-25	COG0801	H
ZMO1648	1693272	1694009	3	738	NP_948032	uracil-DNA glycosylase	236	4.00E-61	COG1573	G
ZMO1649	1694256	1695326	3	1071	NP_420038	gluconolactonase	293	3.00E-78	COG3386	L
ZMO1650	1695701	1696684	2	984	ZP_000913	beta-lactamase class C, esterase	311	1.00E-83	COG1680	V
ZMO1651	1699064	1696782	-3	2283	NP_766857	phosphoenolpyruvate-protein ph	669	0	COG3605	R
ZMO1652	1700070	1699087	-1	984	ZP_000967	dioxygenases related to 2-nitropr	455	1.00E-127	COG2070	T
ZMO1653	1701428	1700163	-3	1266	ZP_000967	aspartokinases	541	1.00E-152	COG0527	E
ZMO1654	1701505	1702296	1	792	ZP_000967	2-polyprenyl-3-methyl-5-hydroxy-	241	1.00E-62	COG2227	H
ZMO1655	1702381	1702938	1	558	NP_420483	bacterioferritin comigratory prote	85.1	6.00E-16	COG1225	O
ZMO1656	1703125	1704030	1	906	ZP_000960	conserved hypothetical protein	92.8	8.00E-18	COG1426	S
ZMO1657	1704214	1705284	1	1071	ZP_000960	conserved hypothetical protein	171	3.00E-41	COG1729	S
ZMO1658	1705340	1706329	2	990	ZP_000081	ATPase implicated in cell cycle c	182	8.00E-45	COG0037	D
ZMO1659	1706551	1708464	1	1914	ZP_000143	ATP-dependent Zn proteases	816	0	COG0465	O
ZMO1660	1708591	1709004	1	414		hypothetical protein			-	-
ZMO1661	1709055	1710341	3	1287	ZP_000960	gamma-glutamyl phosphate redu	521	5.00E-163	COG0014	E
ZMO1662	1710399	1711034	3	636	ZP_000960	nicotinic acid mononucleotide ad	222	3.00E-57	COG1057	H
ZMO1663	1711043	1711444	2	402	ZP_000960	conserved hypothetical protein	157	3.00E-38	COG0799	S
ZMO1664	1711516	1711944	1	429	ZP_000960	conserved hypothetical protein	190	5.00E-48	COG1576	S
ZMO1665	1711944	1713131	3	1188	ZP_000960	membrane-bound metallopeptid	69.7	1.00E-10	COG4942	D
ZMO1666	1713317	1713171	-3	147		hypothetical protein			-	-
ZMO1667	1713304	1714650	1	1347	ZP_000966	periplasmic protease	479	1.00E-134	COG0793	M
ZMO1668	1714683	1715288	3	606	ZP_000966	disulfide bond formation protein I	138	6.00E-32	COG1495	O
ZMO1669	1715258	1715815	2	558	ZP_000966	ubiquinone biosynthesis protein I	213	2.00E-54	COG2941	H
ZMO1670	1715822	1716253	2	432		hypothetical protein			-	-
ZMO1671	1716363	1716782	3	420	ZP_000966	conserved hypothetical protein	57	7.00E-08	-	-
ZMO1672	1716917	1717396	2	480	ZP_000966	conserved hypothetical protein	83.2	2.00E-15	-	-
ZMO1673	1718322	1717507	-1	816	NP_519621	putative oxidoreductase	270	2.00E-71	COG0656	R
ZMO1674	1718481	1718359	-1	123		hypothetical protein			-	-
ZMO1675	1719276	1718512	-1	765	ZP_000958	protein-disulfide isomerase	175	9.00E-43	COG1651	O
ZMO1676	1720177	1719533	-2	645	ZP_000958	conserved hypothetical protein	117	1.00E-25	COG5389	S
ZMO1677	1720215	1721336	3	1122	ZP_000958	A/G-specific DNA glycosylase	363	3.00E-99	COG1194	L
ZMO1678	1722251	1721343	-3	909	ZP_000955	prephenate dehydratase	285	7.00E-76	COG0077	E
ZMO1679	1723225	1722353	-2	873	ZP_000955	Rossmann fold nucleotide-bindin	317	2.00E-85	COG1611	R
ZMO1680	1723930	1723274	-2	657	ZP_000960	conserved hypothetical protein	137	2.00E-31	COG3921	S
ZMO1681	1724393	1726087	2	1695	BAC65228	aspartate:alanine antiporter	684	0	COG2985	R
ZMO1682	1726117	1727709	1	1593	AAK58507	L-aspartate beta-decarboxylase	758	0	COG0436	E
ZMO1683	1727805	1728905	3	1101	NP_799884	L-asparaginase II, periplasmic	289	7.00E-77	COG0252	EJ
ZMO1684	1729367	1730527	2	1161	NP_949645	phosphoserine aminotransferase	531	1.00E-150	COG1932	HE
ZMO1685	1730599	1732182	1	1584	ZP_000553	phosphoglycerate dehydrogenas	666	0	COG0111	HE
ZMO1686	1732379	1733494	2	1116	ZP_000935	ATP phosphoribosyltransferase i	320	3.00E-86	COG3705	E
ZMO1687	1733559	1734848	3	1290	ZP_000935	adenylosuccinate synthase	643	0	COG0104	F
ZMO1688	1735759	1734941	-2	819	ZP_000938	aminomethyltransferase related I	235	8.00E-61	COG0354	R
ZMO1689	1735806	1737146	3	1341	ZP_000139	dihydroorotase and related cyclic	540	1.00E-152	COG0044	F

ZMO1690	1737595	1738536	1	942 ZP_0009662	heat shock protein, DnaJ-class n	372	1.00E-102	COG2214	O
ZMO1691	1738817	1739839	2	1023 ZP_0009662	conserved hypothetical membran	178	1.00E-43	COG1295	S
ZMO1692	1739850	1740668	3	819 ZP_0009662	enoyl-[acyl-carrier-protein] reduc	410	1.00E-113	COG0623	I
ZMO1693	1740665	1741741	2	1077 ZP_0009666	chorismate synthase	551	1.00E-156	COG0082	E
ZMO1694	1744297	1741823	-2	2475 ZP_0009577	outer membrane receptor protein	401	1.00E-110	COG1629	P
ZMO1695	1745100	1744567	-1	534 NP_422538	conserved hypothetical protein	137	1.00E-31	COG3786	S
ZMO1696	1746274	1745264	-2	1011 NP_108002	alginate lyase	440	1.00E-122	COG0604	CR
ZMO1697	1746392	1746736	2	345 NP_108001	conserved hypothetical protein	170	5.00E-42	COG1733	K
ZMO1698	1748036	1746918	-3	1119 ZP_0009582	GTP cyclohydrolase II	321	1.00E-86	COG0807	H
ZMO1699	1748808	1748005	-1	804 ZP_0009582	exonuclease III	337	1.00E-91	COG0708	L
ZMO1700	1749468	1749896	3	429	hypothetical protein	-	-	-	-
ZMO1701	1750588	1749905	-2	684 ZP_0009582	outer membrane lipoprotein-sorti	192	3.00E-48	COG2834	M
ZMO1702	1753101	1750672	-1	2430 ZP_0009653	DNA segregation ATPase FtsK/S	763	0	COG1674	D
ZMO1703	1753261	1754478	1	1218 ZP_0009385	2-polyprenyl-6-methoxyphenol h	397	1.00E-109	COG0654	HC
ZMO1704	1755208	1754522	-2	687 AG3011	ATP-dependent proteinase LA2 I	108	6.00E-23	COG2802	R
ZMO1705	1756074	1755166	-1	909 NP_418929	thioredoxin	153	5.00E-36	COG3118	O
ZMO1706	1756171	1756299	1	129	hypothetical protein	-	-	-	-
ZMO1707	1756289	1756900	2	612 ZP_0009374	orotate phosphoribosyltransferas	214	8.00E-55	COG0461	F
ZMO1708	1756922	1757692	2	771 ZP_0005421	pyridoxal phosphate biosynthesis	333	3.00E-90	COG0854	H
ZMO1709	1757689	1758093	1	405 ZP_0009437	phosphopantetheinyl transferase	122	1.00E-27	COG0736	I
ZMO1710	1758149	1759027	2	879 ZP_0009437	signal peptidase I	252	5.00E-66	COG0681	U
ZMO1711	1759037	1760155	2	1119 ZP_0009437	permease, predicted	288	2.00E-76	COG0628	U
ZMO1712	1760788	1760237	-2	552 NP_284471	peptidyl-prolyl isomerase	134	1.00E-30	COG0545	O
ZMO1713	1761274	1761074	-2	201 NP_104296	ribosomal protein S21	114	5.00E-25	COG0828	J
ZMO1714	1761429	1762049	3	621 ZP_0009666	biopolymer transport ExbD2 prot	143	2.00E-33	COG0848	U
ZMO1715	1762569	1762084	-1	486 ZP_0009666	biopolymer transport ExbD prote	127	6.00E-29	COG0848	U
ZMO1716	1763439	1762702	-1	738 ZP_0009666	biopolymer transport ExbB protei	259	4.00E-68	COG0811	U
ZMO1717	1764347	1763622	-3	726 NP_901653	conserved hypothetical protein	85.5	8.00E-16	COG0810	M
ZMO1718	1764707	1765564	2	858 ZP_0009666	conserved hypothetical protein	196	3.00E-49	-	-
ZMO1719	1766273	1767178	2	906 Q03417	SCR fructokinase	625	1.00E-178	COG1940	KG
ZMO1720	1767757	1767386	-2	372 ZP_0009644	DNA-directed RNA polymerase, :	152	1.00E-36	COG1758	K
ZMO1721	1768324	1767944	-2	381 ZP_0003306	lactoylglutathione lyase and relat	115	1.00E-25	COG0346	E
ZMO1722	1769475	1768372	-1	1104 NP_947300	glutathione dependent formaldeh	660	0	COG1062	C
ZMO1723	1770307	1769555	-2	753 ZP_0009674	conserved hypothetical protein	229	6.00E-59	COG1496	S
ZMO1724	1772124	1770850	-1	1275 ZP_0009652	UDP-N-acetylglucosamine enolp	606	1.00E-172	COG0766	M
ZMO1725	1772456	1772235	-3	222 ZP_0009365	conserved hypothetical protein	133	9.00E-31	COG2127	S
ZMO1726	1772497	1772748	1	252	hypothetical protein	-	-	-	-
ZMO1727	1772893	1774104	1	1212 ZP_0009365	aspartate/tyrosine/aromatic amin	643	0	COG0436	E
ZMO1728	1774590	1774111	-1	480	hypothetical protein	-	-	-	-
ZMO1729	1774956	1774717	-1	240 ZP_0009437	conserved hypothetical protein	110	7.00E-24	-	-
ZMO1730	1775825	1775058	-3	768 ZP_0009438	serine acetyltransferase	295	4.00E-79	COG1045	E
ZMO1731	1776030	1776176	3	147	hypothetical protein	-	-	-	-
ZMO1732	1776712	1776176	-2	537 AAD33340	alkyl hydroperoxide reductase	191	6.00E-48	COG0450	O
ZMO1733	1776907	1777848	1	942 ZP_0009467	transcriptional regulator, oxidativ	407	1.00E-112	COG0583	K
ZMO1734	1778201	1779388	2	1188 NP_419983	conserved hypothetical protein	239	7.00E-62	-	-
ZMO1735	1780310	1779402	-3	909 NP_279218	LPS glycosyltransferase; Lpg	107	3.00E-22	COG0438	M
ZMO1736	1780569	1780411	-1	159	hypothetical protein	-	-	-	-
ZMO1737	1780542	1780685	3	144	hypothetical protein	-	-	-	-
ZMO1738	1781537	1780743	-3	795 ZP_0009676	two-component response regula	412	1.00E-114	COG3279	KT
ZMO1739	1782777	1781545	-1	1233 ZP_0009676	two-component signal transducti	377	1.00E-103	COG3275	T
ZMO1740	1783194	1782928	-1	267 NP_420995	conserved hypothetical protein	120	8.00E-27	-	-
ZMO1741	1785055	1783253	-2	1803 ZP_0009601	membrane GTPase LepA	983	0	COG0481	M
ZMO1742	1785049	1785177	1	129	hypothetical protein	-	-	-	-
ZMO1743	1786069	1785167	-2	903 ZP_0009397	diadenosine tetraphosphate / s	185	9.00E-46	COG0639	T
ZMO1744	1786148	1786288	2	141	hypothetical protein	-	-	-	-
ZMO1745	1788914	1787931	-2	984 ZP_0009580	methionine synthase I (cobalami	761	0	COG1410	E
ZMO1746	1790016	1788967	-1	1050 ZP_0009580	methionine synthase I, cobalamii	481	1.00E-134	COG0646	E
ZMO1747	1790990	1790091	-3	900 AAD19402	5,10-methylenetetrahydrofolate r	377	1.00E-103	COG0685	E
ZMO1748	1791939	1791001	-1	939 ZP_0009580	transcriptional regulators, predict	270	2.00E-71	COG0500	QR
ZMO1749	1792197	1793306	3	1110 NP_521080	possible lipoprotein precursor (va	162	8.00E-39	COG2853	M
ZMO1750	1793789	1793457	-3	333 ZP_0013837	conserved hypothetical protein	50.4	7.00E-06	COG5513	S
ZMO1751	1794718	1795017	1	300	hypothetical protein	-	-	-	-
ZMO1752	1795195	1795476	1	282	hypothetical protein	-	-	-	-
ZMO1753	1795811	1796638	2	828 NP_422002	ferredoxin-NADP reductase	335	4.00E-91	COG1018	C
ZMO1754	1798150	1796780	-2	1371 NP_463378	NAD-dependent aldehyde dehyd	461	1.00E-128	COG1012	C
ZMO1755	1799356	1798838	-2	519 Q9Z671	[TYS] thymidylate synthase (TS) (TSas	342	2.00E-93	COG0207	F
ZMO1756	1799728	1801083	1	1356 ZP_000865	H <sup>+</sup> /gluconate symporter and rela	472	1.00E-132	COG2610	GE
ZMO1757	1801196	1801693	2	498 ZP_0003355	gluconate kinase	181	6.00E-45	COG3265	G
ZMO1758	1802803	1801769	-2	1035 ZP_000962	DNA uptake lipoprotein	338	1.00E-91	COG4105	R
ZMO1759	1803913	1802963	-2	951 AAN33038	conserved hypothetical protein	108	1.00E-22	COG3440	V
ZMO1760	1804694	1804008	-3	687 ZP_000949	ABC-type branched-chain amino	264	2.00E-69	-	-
ZMO1761	1805301	1806188	3	888 ZP_000949	methyltransferases, predicted	281	1.00E-74	COG0313	R
ZMO1762	1806181	1806567	1	387 ZP_0009493	endonuclease distantly related to	117	6.00E-26	COG0792	L
ZMO1763	1807231	1806617	-2	615	hypothetical protein	-	-	-	-
ZMO1764	1808711	1807290	-3	1422 NP_420322	peptidoglycan binding domain pr	434	1.00E-120	COG2989	S
ZMO1765	1809016	1808861	-2	156	hypothetical protein	-	-	-	-

ZMO1766	1809591	1809007	-1	585	NP_719514	magnesium transporter, putative	149	6.00E-35	COG0598	P
ZMO1767	1810925	1810065	-3	861	AAF61451	UDPG-pyrophosphorylase	338	1.00E-91	COG1210	M
ZMO1768	1812315	1811056	-1	1260	Q9Z661 DCD	diaminopimelate decarboxylase (	818	0	COG0019	E
ZMO1769	1812580	1812335	-2	246		hypothetical protein			-	-
ZMO1770	1813986	1812586	-1	1401	Q9Z660 ARL	argininosuccinate lyase (arginos	916	0	COG0165	E
ZMO1771	1815464	1814313	-3	1152	AAD19418	NADH-dependent butanol dehyd	769	0	COG1979	C
ZMO1772	1815702	1816697	3	996	ZP_000861	NADPH:quinone reductase/oxid	358	1.00E-97	COG0604	CR
ZMO1773	1817581	1816757	-2	825	ZP_000236	aldo/keto reductases	314	1.00E-84	COG0656	R
ZMO1774	1817740	1817627	-2	114		hypothetical protein			-	-
ZMO1775	1818385	1818056	-2	330		hypothetical protein			-	-
ZMO1776	1818907	1821462	1	2556	NP_636429	aminopeptidase N	627	1.00E-178	COG0308	E
ZMO1777	1821816	1822856	3	1041	NP_419983	conserved hypothetical protein	230	3.00E-59	-	-
ZMO1778	1823897	1822884	-3	1014	NP_437834	conserved hypothetical membrar	273	4.00E-72	COG2899	S
ZMO1779	1824507	1824100	-1	408		hypothetical protein			-	-
ZMO1780	1824851	1824549	-3	303	NP_826883	conserved hypothetical protein	66.6	1.00E-10	COG1359	S
ZMO1781	1826133	1825009	-1	1125	NP_522075	conserved hypothetical transmer	151	2.00E-35	COG0668	M
ZMO1782	1826318	1826587	2	270		hypothetical protein			-	-
ZMO1783	1826571	1826278	-1	294		hypothetical protein			-	-
ZMO1784	1826764	1827897	1	1134	NP_825693	conserved hypothetical transmer	68.6	2.00E-10	-	-
ZMO1785	1828788	1828087	-1	702	NP_522075	conserved hypothetical transmer	87	3.00E-16	COG0668	M
ZMO1786	1828973	1829938	2	966		hypothetical protein			-	-
ZMO1787	1830256	1830014	-2	243		hypothetical protein			-	-
ZMO1788	1832443	1830605	-2	1839		hypothetical protein			-	-
ZMO1789	1832418	1832552	3	135		hypothetical protein			-	-
ZMO1790	1832663	1834450	2	1788	ZP_0009583	ABC-type multidrug transport sys	720	0	COG1132	V
ZMO1791	1834587	1834462	-1	126		hypothetical protein			-	-
ZMO1792	1836418	1834568	-2	1851	NP_421838	dihydroxy-acid dehydratase	973	0	COG0129	EG
ZMO1793	1836523	1837437	1	915	NP_421839	isoleucine biosynthesis transcrip	315	9.00E-85	COG0583	K
ZMO1794	1838126	1837809	-3	318	ZP_0009308	conserved hypothetical protein	131	3.00E-30	COG4530	S
ZMO1795	1838158	1838394	1	237		hypothetical protein			-	-
ZMO1796	1838410	1839771	1	1362	ZP_0009308	5-enolpyruvylshikimate-3-phosph	585	1.00E-166	COG0128	E
ZMO1797	1839768	1840400	3	633	ZP_0009473	cytidylate kinase	207	1.00E-52	COG0283	F
ZMO1798	1840667	1842373	2	1707	ZP_0009472	ribosomal protein S1	923	0	COG0539	J
ZMO1799	1842402	1842503	3	102		hypothetical protein			-	-
ZMO1800	1843336	1842503	-2	834	NP_792432	phenazine biosynthesis protein, I	328	6.00E-89	COG0384	R
ZMO1801	1843616	1843900	2	285	Q9X4E2 IHF	integration host factor beta-subu	116	8.00E-26	COG0776	L
ZMO1802	1844247	1844080	-1	168		hypothetical protein			-	-
ZMO1803	1844394	1844284	-1	111		hypothetical protein			-	-
ZMO1804	1844396	1845829	2	1434	NP_644648	amino acid transporter	541	1.00E-153	COG0531	E
ZMO1805	1846539	1845892	-1	648	O33512 GPH	phosphoglycolate phosphatase (	95.9	5.00E-19	COG0546	R
ZMO1806	1847365	1846772	-2	594	NP_810376	acetyltransferase, putative	251	6.00E-66	COG0110	R
ZMO1807	1847550	1849934	3	2385	ZP_0009577	outer membrane receptor protein	99.8	2.00E-19	COG1629	P
ZMO1808	1850248	1849988	-2	261	ZP_0005360	conserved hypothetical protein	108	3.00E-23	COG2914	S
ZMO1809	1850935	1850267	-2	669	ZP_0005355	NADH:ubiquinone oxidoreductas	263	3.00E-69	COG4660	C
ZMO1810	1851557	1850931	-3	627	ZP_0005355	NADH:ubiquinone oxidoreductas	208	6.00E-53	COG4659	C
ZMO1811	1852708	1851638	-2	1071	ZP_0005355	NADH:ubiquinone oxidoreductas	469	1.00E-131	COG4658	C
ZMO1812	1854171	1852714	-1	1458	ZP_0005355	NADH:ubiquinone oxidoreductas	555	1.00E-156	COG4656	C
ZMO1813	1854844	1854188	-2	657	ZP_0005356	NADH:ubiquinone oxidoreductas	226	3.00E-58	COG2878	C
ZMO1814	1855442	1854867	-3	576	ZP_0005356	NADH:ubiquinone oxidoreductas	283	1.00E-75	COG4657	C
ZMO1815	1858118	1855917	-3	2202	ZP_0009275	outer membrane receptor protein	464	1.00E-129	COG1629	P
ZMO1816	1858831	1860537	1	1707	AAC99364	transcriptional regulator NifA	645	0	COG3604	KT
ZMO1817	1860746	1862215	2	1470	AAC99365	nitrogen fixation protein nifB	704	0	COG0535	R
ZMO1818	1862255	1862449	2	195	NP_768379	ferredoxin, FdxN	108	2.00E-23	COG1145	C
ZMO1819	1862483	1862737	2	255	AAG35393	NifZ; FixU	113	7.00E-25	-	-
ZMO1820	1862758	1862970	1	213	AAK27735	nitrogen fixation protein FixU	100	5.00E-21	COG5554	Q
ZMO1821	1862970	1863830	3	861	AAG35394	conserved hypothetical protein	282	6.00E-75	-	-
ZMO1822	1865969	1863846	-3	2124	NP_942765	ferrisiderophore receptor protein,	562	1.00E-159	COG1629	P
ZMO1823	1866350	1867237	2	888	Q9ZIE4 NIFH	nitrogenase iron protein, nitronge	534	1.00E-151	COG1348	P
ZMO1824	1867248	1868723	3	1476	AAD05047	nitrogenase FeMo alpha subunit,	828	0	COG2710	C
ZMO1825	1868783	1870318	2	1536	AAD05048	nitrogenase FeMo beta subunit	843	0	COG2710	C
ZMO1826	1870387	1871841	1	1455	AAG27065	nitrogenase reductase iron-molib	719	0	COG2710	C
ZMO1827	1871838	1873208	3	1371	AAG27066	nitrogenase molybdenum-iron pr	561	1.00E-159	COG2710	C
ZMO1828	1873201	1873695	1	495	AAG27067	nitrogenase molybdenum-iron pr	216	1.00E-55	-	-
ZMO1829	1873685	1874149	2	465	NP_659739	conserved hypothetical protein	171	3.00E-42	-	-
ZMO1830	1874500	1873991	-2	510	ZP_0005437	ferredoxin, FdxB	130	8.00E-30	COG1145	C
ZMO1831	1874486	1875073	2	588	AAG27071	nitrogen fixation protein nifQ	211	5.00E-54	-	-
ZMO1832	1875249	1875572	3	324	AAG27072	conserved hypothetical protein	126	7.00E-29	COG0316	S
ZMO1833	1875630	1875872	3	243	AAG27073	nitrogen fixation protein, NifU	90.1	9.00E-18	COG0694	O
ZMO1834	1875895	1877052	1	1158	P57794 NIFS	nitrogenase metallocusters bios	494	1.00E-138	COG1104	E
ZMO1835	1877109	1878269	3	1161	AAF13763	homocitrate synthase	742	0	COG0119	E
ZMO1836	1878314	1878646	2	333	P26481 NIFV	nitrogenase stabilizing/protective	95.1	2.00E-19	-	-
ZMO1837	1878718	1879587	1	870	NP_946353	molybdenum transport system pr	223	3.00E-57	COG0157	H
ZMO1838	1879920	1879714	-1	207	NP_103048	molybdo-pterin binding protein	85.1	3.00E-16	COG3585	H
ZMO1839	1880116	1880232	1	117		hypothetical protein			-	-
ZMO1840	1880847	1880308	-1	540	NP_767926	putative isochorismatase family	110	1.00E-23	COG1335	Q
ZMO1841	1881493	1880966	-2	528	ZP_0005355	sigma E factor positive regulator	86	4.00E-16	COG3086	T



ZMO1842	1882511	1881471	-3	1041	NP_699476	nosX protein	246	4.00E-64	COG1477	H
ZMO1843	1882665	1882769	3	105		hypothetical protein				
ZMO1844	1883923	1882853	-2	1071	NP_522622	probable oxidoreductase	362	5.00E-99	COG0673	R
ZMO1845	1884354	1884067	-1	288	NP_396628	alkylphosphonate uptake protein	108	2.00E-23	COG2824	P
ZMO1846	1885272	1884493	-1	780	NP_348608	ABC-type Fe3+ transport system	183	3.00E-45	COG1120	PH
ZMO1847	1886249	1885242	-3	1008	NP_907313	ABC-type Fe3+ transport system	271	1.00E-71	COG0609	P
ZMO1848	1887128	1886262	-3	867	NP_616161	ABC-type Fe3+ transport system	226	4.00E-58	COG0614	P
ZMO1849	1888120	1889850	1	1731	AAF13754	conserved hypothetical protein	933	0	-	-
ZMO1850	1890318	1889962	-1	357	ZP_0009247	conserved hypothetical protein	153	7.00E-37	-	-
ZMO1851	1890797	1890321	-3	477	ZP_0009247	flavodoxins	224	6.00E-58	COG0716	C
ZMO1852	1890873	1891019	3	147		hypothetical protein				
ZMO1853	1891958	1891068	-3	891	NP_531597	dihydrodipicolinate synthase	185	9.00E-46	COG0329	EM
ZMO1854	1893347	1892109	-3	1239	ZP_000050	transcriptional regulator	489	1.00E-137	COG1167	KE
ZMO1855	1893683	1894438	2	756	NP_461372	putative GMP synthase, glutamir	265	5.00E-70	COG0518	F
ZMO1856	1895861	1894605	-3	1257	NP_461314	transport protein, putative	328	2.00E-88	COG0477	GEPR
ZMO1857	1896023	1896916	2	894	NP_102796	transcriptional regulator, probabl	308	1.00E-82	COG0583	K
ZMO1858	1902155	1902289	2	135		hypothetical protein				
ZMO1859	1904490	1905614	3	1125	NP_642819	regulator of pathogenicity factors	380	1.00E-104	COG3659	M
ZMO1860	1906393	1905689	-2	705	NP_107091	similar to nodulin 21	255	6.00E-67	COG1814	S
ZMO1861	1907937	1906939	-1	999	ZP_001343	dioxygenases related to 2-nitropr	222	1.00E-56	COG2070	R
ZMO1862	1909117	1909013	-2	105		hypothetical protein				
ZMO1863	1909727	1909240	-1	483	CAE80593	putative phosphatase	63.5	1.00E-09	-	-
ZMO1864	1910097	1910576	3	480	BAA19758	transposase	67	1.00E-10	COG3293	L
ZMO1865	1916005	1916139	1	135		hypothetical protein				
ZMO1866	1919292	1917658	-1	1635	ZP_0009357	hydrolase of the metallo-beta-lac	667	0	COG0595	R
ZMO1867	1920167	1919346	-3	822	ZP_0009357	transcriptional regulator, putative	337	2.00E-91	COG1521	K
ZMO1868	1920999	1920202	-1	798	NP_420743	biotin protein ligase	152	5.00E-36	COG0340	H
ZMO1869	1921829	1921002	-3	828	ZP_0009675	ribonuclease I	116	4.00E-25	COG3719	J
ZMO1870	1922827	1921850	-2	978	ZP_0009676	nicotinate-nucleotide pyrophosph	326	5.00E-88	COG0157	H
ZMO1871	1923847	1922855	-2	993	ZP_0009605	quinolinate synthase	492	1.00E-138	COG0379	H
ZMO1872	1924488	1923868	-1	621	ZP_0009605	conserved hypothetical protein	80.1	3.00E-14	-	-
ZMO1873	1924856	1924530	-3	327	ZP_0009342	glutaredoxin-related protein	143	8.00E-34	COG0278	O
ZMO1874	1925138	1924911	-3	228	ZP_0009342	stress-induced morphogen (activ	99.4	1.00E-20	COG0271	T
ZMO1875	1925511	1925149	-1	363	ZP_0009341	conserved hypothetical protein	102	2.00E-21	COG5467	S
ZMO1876	1925874	1926371	3	498	NP_420132	conserved hypothetical protein	85.5	4.00E-16	COG3827	S
ZMO1877	1927376	1926531	-3	846	NP_637572	glutamine cyclotransferase	268	1.00E-70	COG3823	O
ZMO1878	1927522	1929387	1	1866	AAP46185	valyl-tRNA synthetase	991	0	COG0525	J
ZMO1879	1930308	1931309	3	1002	ZP_0009606	delta-aminolevulinic acid dehydr	478	1.00E-133	COG0113	H
ZMO1880	1931302	1931910	1	609		hypothetical protein				
ZMO1881	1932660	1932776	3	117		hypothetical protein				
ZMO1882	1932784	1933770	1	987	NP_415243	transport protein, putative	263	5.00E-69	COG3180	R
ZMO1883	1934831	1933896	-3	936	ZP_0000475	phosphoglycerate dehydrogenas	262	6.00E-69	COG0111	HE
ZMO1884	1935521	1934892	-3	630	NP_927865	conserved hypothetical protein	315	3.00E-85	COG1636	S
ZMO1885	1936778	1935708	-3	1071	ZP_000516	NADH:flavin oxidoreductases, xc	431	1.00E-119	COG1902	C
ZMO1886	1938074	1936971	-3	1104	NP_386204	transport protein, putative	293	5.00E-78	COG3180	R
ZMO1887	1938645	1938085	-1	561	BAA15678	Isochorismatase (EC 3.3.2.1)	169	2.00E-41	COG1335	Q
ZMO1888	1939122	1938979	-1	144		hypothetical protein				
ZMO1889	1940043	1939174	-1	870	ZP_0009375	SAM-dependent methyltransfera	334	1.00E-90	COG1092	R
ZMO1890	1941296	1940076	-3	1221	ZP_0005459	Zn-dependent peptidases, predic	312	9.00E-84	COG0612	R
ZMO1891	1942834	1941299	-2	1536	ZP_0009375	threonine synthase	598	1.00E-170	COG0498	E
ZMO1892	1943260	1942916	-2	345	ZP_0009645	conserved hypothetical protein	61.6	3.00E-09	-	-
ZMO1893	1943496	1943597	3	102		hypothetical protein				
ZMO1894	1943502	1943317	-1	186		hypothetical protein				
ZMO1895	1943628	1944635	3	1008	ZP_0009645	sugar kinases, ribokinase family	366	1.00E-100	COG0524	G
ZMO1896	1945670	1944759	-3	912	ZP_0009492	preprotein translocase subunit S	283	2.00E-75	COG0341	U
ZMO1897	1947270	1945693	-1	1578	ZP_0009492	preprotein translocase subunit S	588	1.00E-167	COG0342	U
ZMO1898	1947624	1947283	-1	342	NP_697903	preprotein translocase, YajC sub	106	1.00E-22	COG1862	U
ZMO1899	1949475	1948510	-1	966	ZP_0009427	3-oxoacyl-[acyl-carrier-protein] s	397	1.00E-109	COG0332	I
ZMO1900	1950527	1949478	-3	1050	ZP_0009427	fatty acid/phospholipid biosynthe	391	1.00E-107	COG0416	I
ZMO1901	1952003	1950936	-3	1068	ZP_0009385	conserved hypothetical protein	135	1.00E-30	-	-
ZMO1902	1952750	1952028	-3	723	ZP_0009385	uroporphyrinogen-III synthase	107	3.00E-22	COG1587	H
ZMO1903	1953711	1952791	-1	921	ZP_0009385	porphobilinogen deaminase	270	2.00E-71	COG0181	H
ZMO1904	1953713	1954804	2	1092	ZP_0009385	metal-dependent proteases with	459	1.00E-128	COG0533	O
ZMO1905	1954805	1955827	2	1023	ZP_0009385	glycerol-3-phosphate dehydroge	315	1.00E-84	COG0240	C
ZMO1906	1956441	1955908	-1	534	ZP_0009597	translation initiation factor 3 (IF-3	270	1.00E-71	COG0290	J
ZMO1907	1959228	1956559	-1	2670	ZP_0009672	DNA mismatch repair ATPase (N	997	0	COG0249	L
ZMO1908	1959784	1959296	-2	489	ZP_0009482	small protein A (tmRNA-binding)	149	2.00E-35	COG2913	J
ZMO1909	1960001	1960540	2	540	ZP_0009482	conserved hypothetical protein	123	1.00E-27	-	-
ZMO1910	1960707	1961369	3	663	ZP_0009331	ribosomal protein L25 (general s	225	6.00E-58	COG1825	J
ZMO1911	1961444	1962013	2	570	ZP_0009331	peptidyl-tRNA hydrolase	244	5.00E-64	COG0193	J
ZMO1912	1962063	1963163	3	1101	ZP_0009534	GTPase, probable translation fac	580	1.00E-164	COG0012	J
ZMO1913	1963494	1964444	3	951	ZP_0009493	glutathione synthase/ribosomal p	405	1.00E-112	COG0189	HJ
ZMO1914	1965369	1964452	-1	918	ZP_0000473	integrase/recombinase	251	1.00E-65	COG0582	L
ZMO1915	1966816	1965386	-2	1431	NP_889870	biotin synthesis protein, putative	330	4.00E-89	COG0132	H
ZMO1916	1967451	1966810	-1	642	NP_880813	conserved hypothetical protein	136	3.00E-31	-	-
ZMO1917	1968656	1967454	-3	1203	NP_889868	8-amino-7-oxononanoate syntha	401	1.00E-110	COG0156	H

ZMO1918	1968726	1969991	3	1266 NP_884047	adenosylmethionine-8-amino-7-c	543	1.00E-153	COG0161	H
ZMO1919	1970458	1969991	-2	468 ZP_0003873	thiol-disulfide isomerase and thi	79.3	3.00E-14	COG0526	OC
ZMO1920	1970774	1971193	2	420 NP_772219	conserved hypothetical protein	77.8	4.00E-14	-	-
ZMO1921	1971322	1973490	1	2169 ZP_0005462	Primosomal protein N' (replicatio	667	0	COG1198	L
ZMO1922	1974971	1973496	-3	1476 ZP_0009362	capsule polysaccharide export pi	296	5.00E-79	COG3562	M
ZMO1923	1975292	1976767	2	1476 NP_885142	capsular polysaccharide biosyntf	173	7.00E-42	COG1368	M
ZMO1924	1977729	1976782	-1	948 ZP_0005539	collagenase and related protease	267	2.00E-70	COG0826	O
ZMO1925	1979471	1977732	-3	1740 ZP_0005539	collagenase and related protease	371	1.00E-101	COG0826	O
ZMO1926	1979595	1979708	3	114	hypothetical protein	-	-	-	-
ZMO1927	1981615	1979708	-2	1908 ZP_0009431	periplasmic serine proteases (Cl	472	1.00E-131	COG0616	OU
ZMO1928	1981991	1982278	2	288 P48229 CH1	heat shock protein groEs, 10 kDa	188	2.00E-47	COG0234	O
ZMO1929	1982385	1984025	3	1641 JC2564	heat shock protein groEL, 60 kDa	1024	0	COG0459	O
ZMO1930	1984282	1985481	1	1200 NP_642539	phage-related integrase	795	0	COG0582	L
ZMO1931	1985478	1986644	3	1167 ZP_0013583	conserved hypothetical protein	651	0	COG4804	S
ZMO1932	1988336	1987551	-3	786	hypothetical protein	-	-	-	-
ZMO1933	1989715	1988342	-2	1374 NP_907780	type I restriction-modification enz	145	1.00E-33	COG0732	V
ZMO1934	1991742	1989730	-1	2013 NP_904837	type I restriction-modification enz	752	0	COG0286	V
ZMO1935	1993428	1992724	-1	705 NP_520729	conserved hypothetical protein	246	3.00E-64	COG5419	S
ZMO1936	1993041	1993811	3	771 ZP_0009138	conserved hypothetical protein	433	1.00E-120	COG5419	S
ZMO1937	1993866	1994207	3	342 ZP_0009138	conserved hypothetical protein	217	3.00E-56	-	-
ZMO1938	1994179	1995114	1	936 ZP_0002547	conserved hypothetical protein	465	1.00E-130	COG5534	L
ZMO1939	1995513	1995872	3	360 ZP_0002443	ATPases involved in chromosom	213	6.00E-55	COG1192	D
ZMO1940	1995958	1996572	1	615 ZP_0013585	conserved hypothetical protein	317	7.00E-86	-	-
ZMO1941	1996569	1997324	3	756 NP_520723	type IV secretory pathway, conju	280	2.00E-74	COG4959	OU
ZMO1942	1997998	1996949	-2	1050 ZP_0002548	type IV secretory pathway, VirD2	469	1.00E-131	COG3843	U
ZMO1943	1998005	1999264	2	1260 ZP_0002548	type IV secretory pathway, VirD2	747	0	COG3843	U
ZMO1944	2000656	1999289	-2	1368 NP_773256	transcriptional regulatory protein	238	2.00E-61	COG1167	KE
ZMO1945	2000759	2001646	2	888 ZP_000272	predicted epimerase, PhzC/PhzF	176	5.00E-43	COG0384	R
ZMO1946	2001676	2002419	1	744 NP_640740	oxidoreductase (short-chain alco	236	3.00E-61	COG1028	IQR
ZMO1947	2002476	2002922	3	447 NP_900598	translational inhibitor protein	99	1.00E-20	COG0251	J
ZMO1948	2002935	2003396	3	462 NP_250048	conserved hypothetical protein	200	8.00E-51	COG2606	S
ZMO1949	2003408	2004124	2	717 NP_745853	NAD(P)H quinone oxidoreductas	317	2.00E-85	COG2249	R
ZMO1950	2004121	2005305	1	1185 ZP_0003006	aspartate/tyrosine/aromatic amin	421	1.00E-116	COG0436	E
ZMO1951	2006220	2006927	3	708 NP_768922	demethylmenaquinone methyltra	93.2	4.00E-18	COG0684	H
ZMO1952	2007015	2007935	3	921 AAQ18192	3-methyl-2-oxobutanoate hydrox	293	3.00E-78	COG0413	H
ZMO1953	2008020	2007892	-1	129	hypothetical protein	-	-	-	-
ZMO1954	2008049	2009386	2	1338 T03562	type IV secretory pathway, VirB1	181	2.00E-54	COG2948	U
ZMO1955	2011159	2009462	-2	1698 CAE80616	malic enzyme, NAD-dependent	684	0	COG0281	C
ZMO1956	2012974	2011304	-2	1671 ZP_0009622	ATPase involved in DNA repair	558	1.00E-158	COG0497	L
ZMO1957	2014211	2013036	-3	1176 ZP_0009597	glycosyltransferase	502	1.00E-141	COG0438	M
ZMO1958	2014771	2014355	-2	417	hypothetical protein	-	-	-	-
ZMO1959	2017861	2014820	-2	3042 ZP_0009319	ATPase involved in DNA repair/c	200	2.00E-49	-	-
ZMO1960	2018050	2019399	1	1350	hypothetical protein	-	-	-	-
ZMO1961	2019543	2020706	3	1164 ZP_0001355	conserved hypothetical protein	99.4	1.00E-19	-	-
ZMO1962	2020697	2022124	2	1428 ZP_0007919	two-component signal transducti	135	2.00E-30	COG0642	T
ZMO1963	2023411	2022128	-2	1284 AAN77499	citrate synthase	573	1.00E-162	COG0372	C
ZMO1964	2025002	2023563	-3	1440 ZP_0001512	glutamyl- and glutamyl-tRNA sy	600	1.00E-170	COG0008	J
ZMO1965	2025180	2027741	3	2562 ZP_0009512	predicted membrane metal-bindi	365	2.00E-99	COG0658	R
ZMO1966	2027792	2028781	2	990 NP_716708	conserved hypothetical protein	115	1.00E-24	-	-
ZMO1967	2028807	2029727	3	921 NP_767581	beta-lactamase L2 precursor	275	6.00E-73	COG2367	V
ZMO1968	2029967	2030092	2	126	hypothetical protein	-	-	-	-
ZMO1969	2031561	2030557	-1	1005 ZP_0004325	FOG: TPR repeat, SEL1 subfam	253	4.00E-66	COG0790	R
ZMO1970	2032578	2031763	-1	816 NP_948437	3-methyl-2-oxobutanoate hydrox	313	2.00E-84	COG0413	H
ZMO1971	2033366	2032584	-3	783 NP_386268	pantoate--beta-alanine ligase	253	3.00E-66	COG0414	H
ZMO1972	2033394	2033558	3	165	hypothetical protein	-	-	-	-
ZMO1973	2034222	2033587	-1	636 ZP_0000775	lysine efflux permease	204	7.00E-52	COG1279	R
ZMO1974	2034300	2035208	3	909 ZP_0000775	transcriptional regulator	271	1.00E-71	COG0583	K
ZMO1975	2035205	2036137	2	933 ZP_0003417	ornithine cyclodeaminase, mu-cr	233	3.00E-60	COG2423	E
ZMO1976	2036408	2037265	2	858	hypothetical protein	-	-	-	-
ZMO1977	2037477	2038922	3	1446 ZP_0001471	permeases of the major facilitato	410	1.00E-113	COG0477	GEPR
ZMO1978	2039887	2038958	-2	930 NP_105340	chromosome partitioning protein,	246	3.00E-64	COG1475	K
ZMO1979	2040684	2039890	-1	795 NP_945645	chromosome partitioning protein,	304	1.00E-81	COG1192	D
ZMO1980	2041346	2040687	-3	660 NP_422548	glucose inhibited division protein	123	2.00E-27	COG0357	M
ZMO1981	2043115	2041349	-2	1767 NP_699036	glucose-inhibited division protein	571	1.00E-161	COG0445	D
ZMO1982	2043152	2043283	2	132	hypothetical protein	-	-	-	-
ZMO1983	2043576	2044565	3	990 NP_299031	conserved hypothetical protein	288	1.00E-76	COG3386	G
ZMO1984	2044595	2045581	2	987 NP_299013	sugar-phosphate dehydrogenase	526	1.00E-148	COG0667	C
ZMO1985	2045683	2045820	1	138	hypothetical protein	-	-	-	-
ZMO1986	2046165	2048576	3	2412 ZP_0002744	outer membrane receptor protei	652	0	COG1629	P
ZMO1987	2048686	2048552	-2	135	hypothetical protein	-	-	-	-
ZMO1988	2049881	2048583	-3	1299 NP_767274	tRNA modification GTPase	315	1.00E-84	COG0486	R
ZMO1989	2050073	2050573	2	501 ZP_0005454	methylated DNA-protein cysteine	110	1.00E-23	COG0350	L
ZMO1990	2050607	2050717	2	111	hypothetical protein	-	-	-	-
ZMO1991	2050668	2050552	-1	117	hypothetical protein	-	-	-	-
ZMO1992	2050677	2051378	3	702 ZP_0009643	dienelactone hydrolase	201	9.00E-51	COG0412	Q
ZMO1993	2051375	2052376	2	1002 ZP_0005454	NADPH:quinone reductase/Zn-d	261	1.00E-68	COG0604	CR

ZMO1994	2052414	2052518	3	105	hypothetical protein				
ZMO1995	2052537	2052653	3	117	hypothetical protein				
ZMO1996	2053922	2052672	-3	1251	ZP_0005454: transcription termination factor R	668	0	COG1158	K
ZMO1997	2054548	2054111	-2	438	ZP_0009692: membrane protein, predicted	168	2.00E-41	COG1981	S
ZMO1998	2055611	2054664	-3	948	ZP_0009692: uroporphyrinogen decarboxylase	421	1.00E-116	COG0407	H