

Table S1. Proteins (2,327) of *L. biflexa* identified by mass spectrometry

id_biflexa	locus_tag_L_biflexa	gene_L_biflexa	gene_product_L_biflexa	seq_type	localization	id_uniprot	orthologues_L_interrogat	c_value	functional_classification	Psport	SignalP	LipoP
WP_012387039.1	LEPBI_RS00020	dnaA	chromosomal replicat	chromosome	I	sBOSK31	WP_000478209.1	0.5904162	L	Cytoplasmic	NO_SP	CYT
WP_012387040.1	LEPBI_RS00025		DNA polymerase III su	chromosome	I	tBOSK32	WP_000695822.1	0.6434500000000001	L	Cytoplasmic	NO_SP	CYT
WP_012387043.1	LEPBI_RS00040	gyrB	DNA topoisomerase (	chromosome	I	tBOSK35	WP_000076460.1	0.8320059	L	Cytoplasmic	NO_SP	CYT
WP_012387044.1	LEPBI_RS00045	gyrA	DNA gyrase subunit A	chromosome	I	tBOSK36	WP_000076846.1	0.7848571500000001	L	Cytoplasmic	NO_SP	CYT
WP_012387047.1	LEPBI_RS00060		lipoprotein LipL21	chromosome	I	tBOSK39	WP_000610519.1	0.5274801		Unknown	LIPO	SpII
WP_012387048.1	LEPBI_RS00065		hypothetical protein	chromosome	I	tBOSK40	WP_000945708.1	0.30762765		Cytoplasmic	SP	CYT
WP_012387050.1	LEPBI_RS00075		DNA polymerase III su	chromosome	I	tBOSK42	WP_000212007.1	0.4343262		Cytoplasmic	NO_SP	CYT
WP_049755955.1	LEPBI_RS00090		hypothetical protein	chromosome	I	tBOSK45				Unknown	SP	SpII
WP_012387054.1	LEPBI_RS00095		SDR family oxidoredu	chromosome	I	tBOSK22	WP_000998676.1	0.697711	I	Cytoplasmic	NO_SP	CYT
WP_012387055.1	LEPBI_RS00100		threonylcarbamoyl-A	chromosome	I	tBOSK23	WP_000603802.1	0.722755	J	Cytoplasmic	NO_SP	CYT
WP_012387057.1	LEPBI_RS00110		alkaline phosphatase	chromosome	I	tBOSK25				Unknown	LIPO	SpII
WP_012387058.1	LEPBI_RS00115		VacB/RNase II family	chromosome	I	tBOSK26	WP_001022135.1	0.5927498999999999	K	Cytoplasmic	NO_SP	CYT
WP_012387060.1	LEPBI_RS00125	tsaE	tRNA (adenosine(37)-I	chromosome	I	tBOSK28	WP_000418142.1	0.3840825	J	Cytoplasmic	NO_SP	CYT
WP_012387061.1	LEPBI_RS00123		Hsp33 family molecu	chromosome	I	tBOSK29	WP_000551848.1	0.4314024	O	Cytoplasmic	NO_SP	CYT
WP_012387062.1	LEPBI_RS00135		beta-galactosidase	chromosome	I	tBOSK30	WP_000575933.1	0.70657785	G	Unknown	NO_SP	CYT
WP_012387063.1	LEPBI_RS00140		hypothetical protein	chromosome	I	tBOSK46	WP_000420355.1	0.45402885		Cytoplasmic	NO_SP	CYT
WP_012387064.1	LEPBI_RS00145		inositol phosphatase	chromosome	I	tBOSK55	WP_000400940.1	0.5784597	G	Cytoplasmic	NO_SP	CYT
WP_012387065.1	LEPBI_RS00150		superoxide dismutase	chromosome	I	tBOSK56			P	Periplasmic	NO_SP	CYT
WP_041769540.1	LEPBI_RS00155		anthranilate synthase	chromosome	I	tBOSK57	WP_000449766.1	0.4194768	E	Cytoplasmic	NO_SP	CYT
WP_012387067.1	LEPBI_RS00160		aminodeoxychorisma	chromosome	I	tBOSK58			E	Cytoplasmic	NO_SP	CYT
WP_012387068.1	LEPBI_RS00165		hypothetical protein	chromosome	I	tBOSK59	WP_000781311.1	0.36963150000000006		Unknown	SP	SpI
WP_012387071.1	LEPBI_RS00180	cysE	serine O-acetyltransfe	chromosome	I	tBOSK62	WP_000462634.1	0.737385	E	Cytoplasmic	NO_SP	CYT
WP_012387073.1	LEPBI_RS00190		hypothetical protein	chromosome	I	tBOSK64	WP_000347906.1	0.494448		Unknown	SP	SpI
WP_012476053.1	LEPBI_RS00205	add	adenosine deaminase	chromosome	I	tBOSK67	WP_001229174.1	0.7677549	F	Cytoplasmic	NO_SP	CYT
WP_012387078.1	LEPBI_RS00215		VOC family protein	chromosome	I	tBOSK69	WP_000079225.1	0.6181812	R	Unknown	NO_SP	SpI
WP_012387079.1	LEPBI_RS00220		ester cyclase	chromosome	I	tBOSK70				Unknown	NO_SP	CYT
WP_012387081.1	LEPBI_RS00230	ygiD	4,5-DOPA dioxygenas	chromosome	I	tBOSK47	WP_000184345.1	0.48885090000000003	Q	Unknown	NO_SP	CYT
WP_012387082.1	LEPBI_RS00235		esterase	chromosome	I	tBOSK48			R	Unknown	NO_SP	CYT
WP_012387085.1	LEPBI_RS00245		IS30-like element ISLb	chromosome	I	tBOSK51			X	Cytoplasmic	NO_SP	CYT
WP_012387087.1	LEPBI_RS00250		adenylosuccinate lyas	chromosome	I	tBOSK53	WP_000567237.1	0.8318871	F	Cytoplasmic	NO_SP	CYT
WP_002980273.1	LEPBI_RS00255		glucose 1-dehydrogen	chromosome	I	tBOSK54	WP_000043153.1	0.85293000000000001	I	Cytoplasmic	NO_SP	CYT
WP_012387089.1	LEPBI_RS00265		enoyl-CoA hydratase/	chromosome	I	tBOSJN6	WP_000761500.1	0.43316865	I	Cytoplasmic	NO_SP	CYT
WP_012387091.1	LEPBI_RS00275		EAL domain-containin	chromosome	I	tBOSJN8	WP_000214763.1	0.6045912999999999		Cytoplasmic	NO_SP	CYT
WP_012387093.1	LEPBI_RS00285		YebC/PmpR family DN	chromosome	I	sBOSJP0	WP_000014140.1	0.7409584	K	Cytoplasmic	NO_SP	CYT
WP_187148075.1	LEPBI_RS00290		acyl-CoA dehydrogen:	chromosome	I	tBOSJP1	WP_000393538.1	0.8361341999999999	I	Cytoplasmic	NO_SP	CYT
WP_012387096.1	LEPBI_RS00300		ABC transporter ATP-t	chromosome	I	tBOSJP3	WP_000667646.1	0.76936365000000001	V	CytoplasmicMembrane	NO_SP	CYT
WP_012387098.1	LEPBI_RS00310		HEAT repeat domain-	chromosome	I	tBOSJP5				Cytoplasmic	LIPO	SpII
WP_012387099.1	LEPBI_RS00315	hflX	GTPase HflX	chromosome	I	tBOSJP6	WP_000960086.1	0.67803	J	Cytoplasmic	NO_SP	CYT
WP_012387100.1	LEPBI_RS00320		STAS domain-containi	chromosome	I	tBOSJP7	WP_000124812.1	0.6802902499999999		Cytoplasmic	NO_SP	CYT
WP_012387101.1	LEPBI_RS00325		homoserine dehydrog	chromosome	I	tBOSJP8	WP_000439715.1	0.62644000000000001	E	Cytoplasmic	NO_SP	CYT
WP_012476056.1	LEPBI_RS00330		hypothetical protein	chromosome	I	tBOSJP9				Unknown	NO_SP	CYT

WP_012387103.1	LEPBI_RS00335	hypothetical protein	chromosome	I	tBOSJQ0	WP_000614023.1	0.4307615999999999		Cytoplasmic	NO_SP	CYT
WP_049755991.1	LEPBI_RS00340	SUMF1/EgtB/PvdO	far chromosome	I	tBOSJQ1	WP_000141824.1	0.50025	O	Unknown	SP	SpI
WP_012387106.1	LEPBI_RS00350	NAD(P)/FAD-depende	chromosome	I	tBOSJQ3			Q	Cytoplasmic	NO_SP	CYT
WP_012387107.1	LEPBI_RS00355	DUF4139 domain-con	chromosome	I	tBOSJQ4			S	OuterMembrane	LIPO	SpI
WP_012387108.1	LEPBI_RS00360	S-methyl-5'-thioadenc	chromosome	I	tBOSJQ5	WP_000121286.1	0.789195	F	Cytoplasmic	NO_SP	CYT
WP_012387109.1	LEPBI_RS00365	STAS domain-containi	chromosome	I	tBOSJQ6	WP_002068150.1	0.43927999999999995		Cytoplasmic	NO_SP	CYT
WP_012387111.1	LEPBI_RS00375	glucose-6-phosphate i	chromosome	I	sBOSJQ8	WP_000620160.1	0.6102656000000001	G	Cytoplasmic	NO_SP	CYT
WP_012387112.1	LEPBI_RS00380	nucleotidyltransferase	chromosome	I	tBOSJQ9	WP_000667727.1	0.49202369999999995	J	Cytoplasmic	NO_SP	CYT
WP_012387113.1	LEPBI_RS00385	phosphotransferase	chromosome	I	tBOSJS6	WP_001027030.1	0.47802439999999996		Cytoplasmic	NO_SP	CYT
WP_012387114.1	LEPBI_RS00390	response regulator	chromosome	I	tBOSJS7	WP_001983427.1	0.5464284	T	CytoplasmicMembrane	NO_SP	CYT
WP_041769547.1	LEPBI_RS00400	alpha/beta hydrolase	chromosome	I	tBOSJS9	WP_033108110.1	0.5145268	H	Cytoplasmic	NO_SP	CYT
WP_012387117.1	LEPBI_RS00405	ferredoxin	chromosome	I	tBOSJT0	WP_000764038.1	0.6688149999999999		Unknown	NO_SP	CYT
WP_012387118.1	LEPBI_RS00410	response regulator	chromosome	I	tBOSJT1			T	Cytoplasmic	NO_SP	CYT
WP_012387120.1	LEPBI_RS00420	polyprenyl synthetase	chromosome	I	tBOSJT3	WP_001970545.1	0.54326745	H	Cytoplasmic	NO_SP	CYT
WP_012387121.1	LEPBI_RS00425	nucleoside-diphospha	chromosome	I	sBOSJT4	WP_000091691.1	0.8589635999999999	F	Extracellular	NO_SP	CYT
WP_012387122.1	LEPBI_RS00430	cation:proton antipori	chromosome	I	tBOSJR0	WP_000165932.1	0.5192992000000001	P	CytoplasmicMembrane	NO_SP	TMH
WP_012387123.1	LEPBI_RS00435	pantetheine-phospha	chromosome	I	sBOSJR1	WP_000681221.1	0.7378371	H	Cytoplasmic	NO_SP	CYT
WP_012387124.1	LEPBI_RS00440	argininosuccinate syn	chromosome	I	sBOSJR2	WP_000068289.1	0.8311693500000001	E	Cytoplasmic	NO_SP	CYT
WP_012387125.1	LEPBI_RS00445	hypothetical protein	chromosome	I	tBOSJR3	WP_000465532.1	0.41692		CytoplasmicMembrane	LIPO	SpII
WP_012387129.1	LEPBI_RS00465	quinone-dependent d	chromosome	I	tBOSJR7	WP_002145910.1	0.6045324999999999	F	CytoplasmicMembrane	NO_SP	CYT
WP_012476061.1	LEPBI_RS00470	PAS domain S-box pro	chromosome	I	tBOSJR8			T	CytoplasmicMembrane	NO_SP	CYT
WP_012387131.1	LEPBI_RS00475	response regulator	chromosome	I	tBOSJR9			T	Cytoplasmic	NO_SP	CYT
WP_012387136.1	LEPBI_RS00500	EAL domain-containin	chromosome	I	tBOSJS4			T	CytoplasmicMembrane	NO_SP	CYT
WP_012387137.1	LEPBI_RS00505	TetR/AcrR family tran	chromosome	I	tBOSJS5				Unknown	NO_SP	CYT
WP_012387139.1	LEPBI_RS00515	GMC family oxidoredu	chromosome	I	tBOSJT6			I	Unknown	NO_SP	CYT
WP_012387141.1	LEPBI_RS00525	acyl-CoA/acyl-ACP del	chromosome	I	tBOSJT8			I	Cytoplasmic	NO_SP	CYT
WP_012387144.1	LEPBI_RS00540	AMP-binding protein	chromosome	I	tBOSJU1	WP_000845063.1	0.5453612999999999	I	Cytoplasmic	NO_SP	CYT
WP_012387146.1	LEPBI_RS00550	chemotaxis protein	chromosome	I	tBOSJU3	WP_001180837.1	0.49717835	T	CytoplasmicMembrane	NO_SP	TMH
WP_012387147.1	LEPBI_RS00555	DUF2804 domain-con	chromosome	I	tBOSJV1	WP_001047667.1	0.3376737		Unknown	LIPO	SpII
WP_012387149.1	LEPBI_RS00565	lyase	chromosome	I	tBOSJV3			V	Unknown	SP	SpI
WP_012387150.1	LEPBI_RS00570	NAD-dependent epim	chromosome	I	tBOSJV4			M	Cytoplasmic	NO_SP	CYT
WP_012387153.1	LEPBI_RS00585	chemotaxis protein	chromosome	I	tBOSJU6	WP_001180837.1	0.50176645	T	CytoplasmicMembrane	NO_SP	TMH
WP_041769551.1	LEPBI_RS00590	alpha/beta hydrolase	chromosome	I	tBOSJU7				Cytoplasmic	NO_SP	CYT
WP_041769553.1	LEPBI_RS00600	hypothetical protein	chromosome	I	tBOSJU9				Unknown	NO_SP	CYT
WP_012476066.1	LEPBI_RS00615	GyrI-like domain-cont	chromosome	I	tBOSJW1				Unknown	NO_SP	CYT
WP_012387161.1	LEPBI_RS00625	DUF1554 domain-con	chromosome	I	tBOSJW3				Unknown	LIPO	CYT
WP_012387163.1	LEPBI_RS00635	SDR family oxidoredu	chromosome	I	tBOSJW5			I	Cytoplasmic	NO_SP	CYT
WP_012387166.1	LEPBI_RS00650	hypothetical protein	chromosome	I	tBOSJW8				Unknown	SP	CYT
WP_012476068.1	LEPBI_RS00670	hypothetical protein	chromosome	I	tBOSJX2	WP_001067879.1	0.4938479		Unknown	LIPO	SpII
WP_012387173.1	LEPBI_RS00685	hypothetical protein	chromosome	I	tBOSJX5				Unknown	LIPO	SpII
WP_012387174.1	LEPBI_RS00690	hypothetical protein	chromosome	I	tBOSJV5	WP_000773476.1	0.35962649999999996		Unknown	LIPO	SpI
WP_012387178.1	LEPBI_RS00705	malate dehydrogenas	chromosome	I	tBOSJV9	WP_001974248.1	0.74252475	C	Cytoplasmic	NO_SP	CYT
WP_004785689.1	LEPBI_RS00710	hypothetical protein	chromosome	I	tBOSJX6	WP_000414808.1	0.76100865		Cytoplasmic	NO_SP	CYT
WP_012476069.1	LEPBI_RS00715	hypothetical protein	chromosome	I	tBOSJX7				Cytoplasmic	LIPO	SpII

WP_012387180.1	LEPBI_RS00720		energy transducer Tor chromosome	I	tBOSJX8	WP_000437522.1	0.6443465		Cytoplasmic	NO_SP	CYT
WP_012387181.1	LEPBI_RS00725		biopolymer transport chromosome	I	tBOSJX9	WP_000053705.1	0.8116762499999999		Unknown	NO_SP	SpI
WP_012387182.1	LEPBI_RS00730		biopolymer transport chromosome	I	tBOSJY0	WP_000619314.1	0.769775		Unknown	NO_SP	CYT
WP_012387183.1	LEPBI_RS00735		MotA/TolQ/ExbB prot chromosome	I	tBOSJY1	WP_000668014.1	0.5703326000000001	U	CytoplasmicMembrane	SP	SpI
WP_012387185.1	LEPBI_RS00745		TrkA family potassium chromosome	I	tBOSJZ0	WP_000985723.1	0.48970545	P	Cytoplasmic	NO_SP	CYT
WP_012476070.1	LEPBI_RS00755		hypothetical protein chromosome	I	tBOSJZ2				CytoplasmicMembrane	SP	SpI
WP_012476071.1	LEPBI_RS00760		adenosine deaminase chromosome	I	tBOSJZ3	WP_000805986.1	0.5569643		Cytoplasmic	NO_SP	CYT
WP_012387191.1	LEPBI_RS00775		SPFH domain-containing chromosome	I	tBOSJZ9	WP_001173870.1	0.6347499999999999	O	Cytoplasmic	NO_SP	CYT
WP_012387192.1	LEPBI_RS00780		hypothetical protein chromosome	I	tBOSK00	WP_001183762.1	0.432193		Cytoplasmic	NO_SP	CYT
WP_041769557.1	LEPBI_RS00785		hypothetical protein chromosome	I	tBOSK01				Cytoplasmic	NO_SP	CYT
WP_012387194.1	LEPBI_RS00790		DUF1553 domain-containing chromosome	I	tBOSJY3				Cytoplasmic	NO_SP	CYT
WP_012387196.1	LEPBI_RS00800		hypothetical protein chromosome	I	tBOSJY5				Unknown	SP	SpII
WP_012476074.1	LEPBI_RS00805		porin chromosome	I	tBOSJY6				Unknown	SP	SpI
WP_012387198.1	LEPBI_RS00810	gmd	GDP-mannose 4,6-dehydrogenase chromosome	I	tBOSJY7	WP_000709511.1	0.81717075	M	Cytoplasmic	NO_SP	CYT
WP_012387201.1	LEPBI_RS00820		STAS domain-containing chromosome	I	tBOSJZ5				Cytoplasmic	NO_SP	CYT
WP_012387202.1	LEPBI_RS00825		Crp/Fnr family transcription factor chromosome	I	tBOSJZ6	WP_000103068.1	0.784575	T	Cytoplasmic	NO_SP	CYT
WP_012387203.1	LEPBI_RS00830		hypothetical protein chromosome	I	tBOSJZ7				Cytoplasmic	NO_SP	SpI
WP_012476076.1	LEPBI_RS00835		VWA domain-containing chromosome	I	tBOSK72	WP_000479709.1	0.3724528		Unknown	NO_SP	CYT
WP_012387205.1	LEPBI_RS00840		CoA pyrophosphatase chromosome	I	tBOSK73	WP_001234817.1	0.4922613		Cytoplasmic	NO_SP	CYT
WP_012387206.1	LEPBI_RS00845		HRDC domain-containing chromosome	I	tBOSK74	WP_001166720.1	0.640827	J	Cytoplasmic	NO_SP	CYT
WP_012387207.1	LEPBI_RS00850		amidophosphoribosyl transferase chromosome	I	tBOSK75	WP_000086941.1	0.8227103999999999	F	Cytoplasmic	NO_SP	CYT
WP_012387208.1	LEPBI_RS00855	queD	6-carboxytetrahydropteridine synthase chromosome	I	tBOSK76	WP_000391049.1	0.7587728	H	Cytoplasmic	NO_SP	CYT
WP_012387209.1	LEPBI_RS00860	queC	7-cyano-7-deazaguaniine synthase chromosome	I	sBOSK77	WP_001088969.1	0.606453	J	Unknown	NO_SP	CYT
WP_012387210.1	LEPBI_RS00865		SGNH/GDSL hydrolase chromosome	I	tBOSK78				Unknown	SP	SpII
WP_012387212.1	LEPBI_RS00875		DUF1574 family protein chromosome	I	tBOSK80				Cytoplasmic	NO_SP	CYT
WP_012387215.1	LEPBI_RS00890		NAD(P)(+) transhydrogenase chromosome	I	tBOSK90	WP_000127254.1	0.7446334499999999	C	CytoplasmicMembrane	NO_SP	TMH
WP_012387216.1	LEPBI_RS00895		response regulator transcription factor chromosome	I	tBOSK91	WP_000805070.1	0.3875619999999999	T	Cytoplasmic	NO_SP	CYT
WP_012387217.1	LEPBI_RS00900		tetratricopeptide repeat domain-containing chromosome	I	tBOSK81	WP_000821095.1	0.3270881		Unknown	SP	SpI
WP_012476077.1	LEPBI_RS00905		hypothetical protein chromosome	I	tBOSK82	WP_001014594.1	0.4235638500000001	M	Cytoplasmic	NO_SP	CYT
WP_012387219.1	LEPBI_RS00910		spiro-SPASM protein chromosome	I	tBOSK83	WP_000671644.1	0.5353029		Cytoplasmic	NO_SP	CYT
WP_012387220.1	LEPBI_RS00915		putative peptidyl-prolyl isomerase chromosome	I	tBOSK84	WP_001083687.1	0.5502428		Unknown	SP	TMH
WP_012387221.1	LEPBI_RS00920		aspartate kinase chromosome	I	tBOSK85	WP_000181768.1	0.819225	E	Cytoplasmic	NO_SP	CYT
WP_012387222.1	LEPBI_RS00925		acyl-CoA desaturase chromosome	I	tBOSK86				CytoplasmicMembrane	NO_SP	TMH
WP_012387225.1	LEPBI_RS00940		LEA type 2 family protein chromosome	I	tBOSKA9	WP_000798179.1	0.35830110000000004		Cytoplasmic	SP	CYT
WP_012387226.1	LEPBI_RS00945		zinc-binding dehydrogenase chromosome	I	tBOSKB0	WP_001053085.1	0.5508959999999999	C	Cytoplasmic	NO_SP	CYT
WP_012387228.1	LEPBI_RS00955		glycosyltransferase chromosome	I	tBOSKB2	WP_000861276.1	0.7438542	M	Cytoplasmic	NO_SP	CYT
WP_012387230.1	LEPBI_RS00965		MotA/TolQ/ExbB protein chromosome	I	tBOSK94	WP_000345490.1	0.74231	N	CytoplasmicMembrane	NO_SP	TMH
WP_012387231.1	LEPBI_RS00970	motB	flagellar motor protein chromosome	I	tBOSK95	WP_001129912.1	0.7916238	N	CytoplasmicMembrane	NO_SP	CYT
WP_002972703.1	LEPBI_RS00975		flagellar basal body assembly protein chromosome	I	tBOSK96	WP_000501992.1	0.7142999999999999		Unknown	NO_SP	CYT
WP_012387232.1	LEPBI_RS00980	kdsB	3-deoxy-mannooctulose 6-phosphate synthase chromosome	I	sBOSK97	WP_000721859.1	0.6608125	M	Cytoplasmic	NO_SP	CYT
WP_012387233.1	LEPBI_RS00985		cation:proton antiporter chromosome	I	tBOSK98	WP_000399950.1	0.6105935	P	CytoplasmicMembrane	NO_SP	CYT
WP_012387234.1	LEPBI_RS00990		TolC family protein chromosome	I	tBOSK99				Unknown	SP	SpI
WP_187148077.1	LEPBI_RS00995		HlyD family efflux pump chromosome	I	tBOSKA0				Cytoplasmic	NO_SP	TMH
WP_012387238.1	LEPBI_RS01010		YceI family protein chromosome	I	tBOSKA3	WP_000821257.1	0.4275495		Unknown	SP	SpI

WP_012387239.1	LEPBI_RS01015		DUF1801 domain-con	chromosome	I	tBOSKA4			Unknown	NO_SP	CYT	
WP_012387244.1	LEPBI_RS01040		SRPBCC family proteir	chromosome	I	tBOSKB3			Unknown	NO_SP	CYT	
WP_012387246.1	LEPBI_RS01050		hypothetical protein	chromosome	I	tBOSKB7			Unknown	SP	CYT	
WP_012387248.1	LEPBI_RS01055		hypothetical protein	chromosome	I	tBOSKB9			Unknown	LIPO	SpI	
WP_012387250.1	LEPBI_RS01065	ligA	NAD-dependent DNA	chromosome	I	sBOSKC1	WP_001124828.1	0.6553015	L	Cytoplasmic	NO_SP	CYT
WP_012387256.1	LEPBI_RS01095		acyl-CoA dehydrogen:	chromosome	I	tBOSKC9	WP_001199925.1	0.64809855	I	Cytoplasmic	NO_SP	CYT
WP_012387260.1	LEPBI_RS01115		1-acyl-sn-glycerol-3-pl	chromosome	I	tBOSKB5	WP_000391163.1	0.5103448	C	Cytoplasmic	NO_SP	CYT
WP_012387262.1	LEPBI_RS01125		hypothetical protein	chromosome	I	tBOSKC2				Unknown	LIPO	SpII
WP_012476080.1	LEPBI_RS01130		CAP domain-containir	chromosome	I	tBOSKF8				Unknown	LIPO	CYT
WP_012387265.1	LEPBI_RS01135		EVE domain-containin	chromosome	I	tBOSKF9	WP_001110309.1	0.65250405	R	Cytoplasmic	NO_SP	CYT
WP_012387266.1	LEPBI_RS01140	ftsH	ATP-dependent zinc n	chromosome	I	tBOSKG0	WP_001038998.1	0.77795685	O	CytoplasmicMembrane	NO_SP	SpI
WP_012387267.1	LEPBI_RS01145		aminoacyl-tRNA hydr	chromosome	I	tBOSKG1	WP_000767698.1	0.8555900000000001	J	Cytoplasmic	NO_SP	CYT
WP_012387268.1	LEPBI_RS01150		50S ribosomal protein	chromosome	I	tBOSKG2	WP_000081487.1	0.60944805		Cytoplasmic	NO_SP	CYT
WP_012387269.1	LEPBI_RS01155		ribose-phosphate pyr	chromosome	I	tBOSKG4	WP_001012709.1	0.78751035	F	Cytoplasmic	NO_SP	CYT
WP_012387270.1	LEPBI_RS01160		NTP transferase doma	chromosome	I	tBOSKG6	WP_000805357.1	0.64073835	M	Cytoplasmic	NO_SP	CYT
WP_012387272.1	LEPBI_RS01175		WYL domain-containii	chromosome	I	tBOSKH0	WP_001049175.1	0.40027185	K	Cytoplasmic	NO_SP	CYT
WP_012387273.1	LEPBI_RS01180		ACP S-malonyltransfei	chromosome	I	tBOSKH1	WP_000951976.1	0.6133347	I	Unknown	NO_SP	CYT
WP_012387275.1	LEPBI_RS01190		sodium:solute sympoi	chromosome	I	tBOSKF3			E	CytoplasmicMembrane	NO_SP	TMH
WP_012476081.1	LEPBI_RS01195		hypothetical protein	chromosome	I	tBOSKF4				Cytoplasmic	NO_SP	CYT
WP_012476082.1	LEPBI_RS01200		M23 family metallope	chromosome	I	tBOSKF5				Cytoplasmic	LIPO	TMH
WP_012387278.1	LEPBI_RS01205		NAD(P)-binding doma	chromosome	I	tBOSKF6	WP_000055098.1	0.6609822499999999	P	Cytoplasmic	NO_SP	CYT
WP_012387280.1	LEPBI_RS01215		hypothetical protein	chromosome	I	tBOSKG3				Unknown	NO_SP	CYT
WP_012387283.1	LEPBI_RS01225		valine--tRNA ligase	chromosome	I	tBOSKG8	WP_000744009.1	0.71156745	J	Cytoplasmic	NO_SP	CYT
WP_012387284.1	LEPBI_RS01230		phosphoribosylamine	chromosome	I	tBOSTI2	WP_001197373.1	0.63965	F	Cytoplasmic	NO_SP	CYT
WP_012387285.1	LEPBI_RS01235		hypothetical protein	chromosome	I	tBOSTI3	WP_001116208.1	0.6600082499999999		Cytoplasmic	NO_SP	CYT
WP_012387286.1	LEPBI_RS01240	prfB	peptide chain release	chromosome	I	tBOSTI4	WP_000453256.1	0.7520436	J	Cytoplasmic	NO_SP	CYT
WP_012387287.1	LEPBI_RS01245		sigma-54-dependent f	chromosome	I	tBOSTI5			T	Cytoplasmic	NO_SP	CYT
WP_012387288.1	LEPBI_RS01250		OmpA family protein	chromosome	I	tBOSTI6	WP_001074459.1	0.364408099999999996	M	OuterMembrane	NO_SP	CYT
WP_012476083.1	LEPBI_RS01255		motility associated fax	chromosome	I	tBOSTI7	WP_000640630.1	0.4928762	S	Cytoplasmic	NO_SP	CYT
WP_012387290.1	LEPBI_RS01260		PASTA domain-contaii	chromosome	I	tBOSTI8	WP_001088499.1	0.62952259999999999	D	CytoplasmicMembrane	NO_SP	TMH
WP_012387292.1	LEPBI_RS01270	thrC	threonine synthase	chromosome	I	tBOSTJ0	WP_000626010.1	0.7504987	E	Unknown	NO_SP	CYT
WP_012476085.1	LEPBI_RS01275		hypothetical protein	chromosome	I	tBOSTJ1	WP_000389276.1	0.6015466		Cytoplasmic	NO_SP	CYT
WP_012387294.1	LEPBI_RS01280		hypothetical protein	chromosome	I	tBOSTJ2	WP_000433740.1	0.487208699999999994		Cytoplasmic	NO_SP	CYT
WP_012387295.1	LEPBI_RS01285		leucine--tRNA ligase	chromosome	I	sBOSTJ3	WP_001199946.1	0.748255	J	Cytoplasmic	NO_SP	CYT
WP_012387298.1	LEPBI_RS01300		ABC transporter ATP-t	chromosome	I	tBOSTJ6	WP_000942282.1	0.6429357	M	CytoplasmicMembrane	NO_SP	CYT
WP_012387300.1	LEPBI_RS01310		hypothetical protein	chromosome	I	tBOSTJ8	WP_000867010.1	0.8107308000000001		Cytoplasmic	SP	SpI
WP_012476089.1	LEPBI_RS01315		ATP-binding protein	chromosome	I	tBOSTJ9	WP_000601181.1	0.6521851	L	Cytoplasmic	NO_SP	CYT
WP_012387303.1	LEPBI_RS01325	panB	3-methyl-2-oxobutan	chromosome	I	sBOSTK1	WP_000789319.1	0.679265	H	Cytoplasmic	NO_SP	CYT
WP_012387304.1	LEPBI_RS01330		3-deoxy-7-phosphohe	chromosome	I	tBOSTK2			E	Cytoplasmic	NO_SP	CYT
WP_012387305.1	LEPBI_RS01335		rhodanese-like domai	chromosome	I	tBOSTK3	WP_000187969.1	0.60942975	P	Unknown	NO_SP	CYT
WP_012387306.1	LEPBI_RS01340		ABC-F family ATP-binc	chromosome	I	tBOSTK4	WP_000481720.1	0.66232485	R	Cytoplasmic	NO_SP	CYT
WP_012387310.1	LEPBI_RS01355		hypothetical protein	chromosome	I	tBOSJ05				Cytoplasmic	NO_SP	CYT
WP_012476090.1	LEPBI_RS01360		hypothetical protein	chromosome	I	tBOSJ06	WP_000672155.1	0.36961920000000004		Unknown	LIPO	SpII
WP_012387313.1	LEPBI_RS01370		EAL domain-containin	chromosome	I	tBOSJ08			T	CytoplasmicMembrane	NO_SP	CYT

WP_012387314.1	LEPBI_RS01375		hypothetical protein	chromosome	I	tBOSJ09			Unknown	TAT	CYT	
WP_012387315.1	LEPBI_RS01380		DsbA family oxidoreductase	chromosome	I	tBOSJ10	WP_000448278.1	0.463824	O	Unknown	NO_SP	CYT
WP_012387316.1	LEPBI_RS01385		efflux RND transporter	chromosome	I	tBOSJ11	WP_000838391.1	0.56548305	V	CytoplasmicMembrane	NO_SP	TMH
WP_012387317.1	LEPBI_RS01390		DUF2804 domain-containing	chromosome	I	tBOSJ19	WP_001047667.1	0.399227749999999994		Unknown	NO_SP	CYT
WP_012387318.1	LEPBI_RS01395		GMC family oxidoreductase	chromosome	I	tBOSJ20	WP_000759726.1	0.36046360000000005	I	Unknown	NO_SP	CYT
WP_012387319.1	LEPBI_RS01400		ankyrin repeat domain	chromosome	I	tBOSJ21				Cytoplasmic	NO_SP	CYT
WP_012387320.1	LEPBI_RS01405		hypothetical protein	chromosome	I	tBOSJ22				Cytoplasmic	SP	Spl
WP_012387321.1	LEPBI_RS01410		hypothetical protein	chromosome	I	tBOSJ23				Unknown	SP	Spl
WP_012387323.1	LEPBI_RS01420		Jag N-terminal domain	chromosome	I	tBOSJ12	WP_000432936.1	0.7799166	R	Cytoplasmic	NO_SP	CYT
WP_012387324.1	LEPBI_RS01425	gidC	membrane protein	in: chromosome	I	tBOSJ13	WP_000390190.1	0.61340895	M	CytoplasmicMembrane	NO_SP	Spl
WP_041769570.1	LEPBI_RS01440		helix-turn-helix transcription factor	chromosome	I	tBOSJ16	WP_000378131.1	0.302175		Unknown	NO_SP	CYT
WP_012387328.1	LEPBI_RS01445		hypothetical protein	chromosome	I	tBOSJ17				Cytoplasmic	NO_SP	CYT
WP_012387329.1	LEPBI_RS01450		glutathione S-transferase	chromosome	I	tBOSJ18	WP_000593328.1	0.30121875	O	Cytoplasmic	NO_SP	CYT
WP_012387332.1	LEPBI_RS01465		acyl-CoA thioesterase	chromosome	I	tBOSJE6			I	Cytoplasmic	NO_SP	CYT
WP_012387333.1	LEPBI_RS01470		DUF1330 domain-containing	chromosome	I	tBOSJE7				Cytoplasmic	NO_SP	CYT
WP_012387334.1	LEPBI_RS01475		class I SAM-dependent methyltransferase	chromosome	I	tBOSJE8				Cytoplasmic	NO_SP	CYT
WP_012387336.1	LEPBI_RS01485		gamma carbonic anhydrase	chromosome	I	tBOSJF0	WP_001020828.1	0.67332199999999999	R	Cytoplasmic	NO_SP	CYT
WP_012387337.1	LEPBI_RS01490		SpoIIIE family protein	in: chromosome	I	tBOSJF1			T	CytoplasmicMembrane	LIPO	SplI
WP_012387338.1	LEPBI_RS01495		phenylalanine--tRNA synthetase	chromosome	I	sBOSJF2	WP_000777483.1	0.59173499999999999	J	Cytoplasmic	NO_SP	CYT
WP_012387339.1	LEPBI_RS01500		bifunctional diguanylate cyclase	chromosome	I	tBOSJF3			T	CytoplasmicMembrane	NO_SP	CYT
WP_012387340.1	LEPBI_RS01505		amidohydrolase family	chromosome	I	tBOSJF4	WP_000591983.1	0.7342929	F	Cytoplasmic	NO_SP	CYT
WP_012387341.1	LEPBI_RS01510		ATP-dependent DNA topoisomerase	chromosome	I	tBOSJD4	WP_002095496.1	0.60622575	L	Cytoplasmic	NO_SP	CYT
WP_012387342.1	LEPBI_RS01515		MBOAT family protein	chromosome	I	tBOSJD5	WP_000577056.1	0.51341	M	CytoplasmicMembrane	NO_SP	TMH
WP_012387343.1	LEPBI_RS01520		hypothetical protein	chromosome	I	tBOSJD6	WP_000011185.1	0.432700799999999994		Cytoplasmic	NO_SP	CYT
WP_187148078.1	LEPBI_RS01525		caspase family protein	chromosome	I	tBOSJD7	WP_000837582.1	0.60727095		Unknown	SP	CYT
WP_012387345.1	LEPBI_RS01530		hypothetical protein	chromosome	I	tBOSJD8	WP_000700529.1	0.4844736		Unknown	SP	Spl
WP_012387347.1	LEPBI_RS01540	ftsA	cell division protein	Ft chromosome	I	tBOSJE0	WP_001294723.1	0.73906500000000001	D	Cytoplasmic	NO_SP	CYT
WP_012387348.1	LEPBI_RS01545	ftsZ	cell division protein	Ft chromosome	I	tBOSJE1	WP_000617710.1	0.7290459	D	Cytoplasmic	NO_SP	CYT
WP_012387349.1	LEPBI_RS01550		hypothetical protein	chromosome	I	tBOSJE2				Unknown	LIPO	SplI
WP_012387350.1	LEPBI_RS01555		hypothetical protein	chromosome	I	tBOSJE3				Unknown	LIPO	SplI
WP_012476092.1	LEPBI_RS01560		hypothetical protein	chromosome	I	tBOSJL4				Unknown	NO_SP	Spl
WP_012387352.1	LEPBI_RS01565		hypothetical protein	chromosome	I	tBOSJL5	WP_001971016.1	0.3356445		Unknown	SP	SplI
WP_012387353.1	LEPBI_RS01570	nadA	quinolinate synthase	chromosome	I	tBOSJL6	WP_000853488.1	0.76862115	H	Cytoplasmic	NO_SP	CYT
WP_012387354.1	LEPBI_RS01575		2-C-methyl-D-erythritol 2-C-methyltransferase	chromosome	I	sBOSJL7	WP_000285623.1	0.68539729999999999	I	Cytoplasmic	NO_SP	CYT
WP_012476094.1	LEPBI_RS01580		hypothetical protein	chromosome	I	tBOSJJ6				Unknown	NO_SP	CYT
WP_012387356.1	LEPBI_RS01585		SpoIIIE family protein	in: chromosome	I	tBOSJJ7			T	Cytoplasmic	NO_SP	CYT
WP_012476095.1	LEPBI_RS01590		carotenoid 1,2-hydroxylase	chromosome	I	tBOSJJ8	WP_000143898.1	0.4739245	R	Unknown	SP	Spl
WP_012387358.1	LEPBI_RS01595		ABC transporter permease	chromosome	I	tBOSJJ9	WP_000759810.1	0.81249	Q	CytoplasmicMembrane	NO_SP	TMH
WP_012387360.1	LEPBI_RS01605		ABC transporter ATP-binding cassette	chromosome	I	tBOSJK1	WP_000218838.1	0.61092	E	CytoplasmicMembrane	NO_SP	CYT
WP_012387361.1	LEPBI_RS01610		ATP-binding cassette	chromosome	I	tBOSJK2	WP_000619175.1	0.63711945000000001	E	Cytoplasmic	NO_SP	CYT
WP_012387362.1	LEPBI_RS01615		AsmA family protein	chromosome	I	tBOSJK3	WP_001116782.1	0.3549064		Unknown	NO_SP	TMH
WP_012387363.1	LEPBI_RS01620		hypothetical protein	chromosome	I	tBOSJK4				Unknown	LIPO	SplI
WP_012387364.1	LEPBI_RS01625		HEAT repeat domain-containing	chromosome	I	tBOSJK5				Unknown	SP	Spl
WP_012476096.1	LEPBI_RS01630		DNA mismatch repair	chromosome	I	tBOSJK6	WP_000200399.1	0.3592755	L	CytoplasmicMembrane	NO_SP	CYT

WP_012387368.1	LEPBI_RS01645		long-chain fatty acid-- chromosome	I	tBOSJK9	WP_000277632.1	0.7316595	I	Cytoplasmic	NO_SP	CYT
WP_012476098.1	LEPBI_RS01650		enoyl-CoA hydratase/ chromosome	I	tBOSJL0	WP_000947684.1	0.4928618499999999	I	Cytoplasmic	NO_SP	CYT
WP_012387371.1	LEPBI_RS01660		carboxymuconolactor chromosome	I	tBOSJL2				Unknown	NO_SP	CYT
WP_012387373.1	LEPBI_RS01670	map	type I methionyl amin chromosome	I	tBOSKD6			J	Cytoplasmic	NO_SP	CYT
WP_012387374.1	LEPBI_RS01675		alpha/beta hydrolase chromosome	I	tBOSKD7				Cytoplasmic	NO_SP	CYT
WP_012387375.1	LEPBI_RS01680		MAPEG family protein chromosome	I	tBOSKD8	WP_001067456.1	0.543678		CytoplasmicMembrane	NO_SP	CYT
WP_012387376.1	LEPBI_RS01685		NAD(P)-dependent gly chromosome	I	sBOSKD9	WP_000690432.1	0.83391165	C	Cytoplasmic	NO_SP	CYT
WP_012387378.1	LEPBI_RS01695		metallophosphoester; chromosome	I	tBOSKE1	WP_000692533.1	0.7054344000000001		Cytoplasmic	NO_SP	CYT
WP_012387379.1	LEPBI_RS01700		hypothetical protein chromosome	I	tBOSKE2	WP_000145547.1	0.5014896		Unknown	NO_SP	Spl
WP_081431644.1	LEPBI_RS01705	recG	ATP-dependent DNA I chromosome	I	tBOSKE3	WP_000798669.1	0.6609143499999999	L	Cytoplasmic	NO_SP	CYT
WP_012387381.1	LEPBI_RS01710		M15 family metallope chromosome	I	tBOSKE8	WP_000836548.1	0.5656074000000001		Unknown	LIPO	SplI
WP_012387382.1	LEPBI_RS01715	galE	UDP-glucose 4-epimei chromosome	I	tBOSKE9	WP_001984071.1	0.7331841	M	Cytoplasmic	NO_SP	CYT
WP_012387383.1	LEPBI_RS01720	lpxA	acyl-ACP--UDP-N-acet chromosome	I	tBOSKF0	WP_000690880.1	0.66218	M	Cytoplasmic	NO_SP	CYT
WP_012387385.1	LEPBI_RS01730		hypothetical protein chromosome	I	tBOSKF2				Cytoplasmic	NO_SP	CYT
WP_012387386.1	LEPBI_RS01735		acetyl-CoA C-acetyltra chromosome	I	tBOSKD3	WP_000390637.1	0.8056125	I	Cytoplasmic	NO_SP	CYT
WP_012387388.1	LEPBI_RS01745		peptidase domain-cor chromosome	I	tBOSKD5			V	CytoplasmicMembrane	NO_SP	CYT
WP_012387390.1	LEPBI_RS01755		ATP-binding cassette ( chromosome	I	tBOSKE5			V	CytoplasmicMembrane	NO_SP	CYT
WP_012387395.1	LEPBI_RS01780		NAD(P)/FAD-depende chromosome	I	tBOSIX9	WP_000613939.1	0.702603	R	Cytoplasmic	NO_SP	CYT
WP_012387397.1	LEPBI_RS01790		GNAT family N-acetyl chromosom	I	tBOSIY1	WP_001021825.1	0.5662107000000001		Cytoplasmic	NO_SP	CYT
WP_187148066.1	LEPBI_RS01830		copper chaperone PCi chromosome	I	tBOSIZ8			P	Unknown	SP	Spl
WP_012387413.1	LEPBI_RS01870	nosZ	Sec-dependent nitrou chromosome	I	tBOSIZ1			P	Unknown	LIPO	SplI
WP_012387414.1	LEPBI_RS01875		cytochrome c chromosome	I	tBOSIZ2				Cytoplasmic	LIPO	SplI
WP_012387415.1	LEPBI_RS01880		fasciclin domain-cont: chromosome	I	tBOSIZ3			R	CytoplasmicMembrane	LIPO	CYT
WP_012387419.1	LEPBI_RS01900		hypothetical protein chromosome	I	tBOSJH9				Cytoplasmic	NO_SP	TMH
WP_012387420.1	LEPBI_RS01905		outer membrane prot chromosome	I	tBOSJI0	WP_001172917.1	0.6146002		Unknown	SP	TMH
WP_012476110.1	LEPBI_RS01915		U32 family peptidase chromosome	I	tBOSJI2			J	Cytoplasmic	NO_SP	CYT
WP_012387424.1	LEPBI_RS01925		hypothetical protein chromosome	I	tBOSJI4				Unknown	SP	Spl
WP_012387426.1	LEPBI_RS01935	creC	two-component syste chromosome	I	tBOSJI6	WP_080011803.1	0.5560275	T	CytoplasmicMembrane	NO_SP	CYT
WP_012387431.1	LEPBI_RS01960		DUF4256 domain-con chromosome	I	tBOSJJ1	WP_000049027.1	0.6533932		Unknown	NO_SP	CYT
WP_012387434.1	LEPBI_RS01970		hypothetical protein chromosome	I	tBOSJJ4				Cytoplasmic	SP	Spl
WP_012387435.1	LEPBI_RS01975		hypothetical protein chromosome	I	tBOSJJ5				Cytoplasmic	LIPO	Spl
WP_012476113.1	LEPBI_RS02000		hypothetical protein chromosome	I	tBOSIX3				Unknown	SP	Spl
WP_012387443.1	LEPBI_RS02015		YdiU family protein chromosome	I	tBOSIX5			O	Unknown	NO_SP	CYT
WP_012387447.1	LEPBI_RS02030		hypothetical protein chromosome	I	tBOSIW6				Cytoplasmic	NO_SP	CYT
WP_012476115.1	LEPBI_RS02050		chemotaxis protein chromosome	I	tBOSK08			T	CytoplasmicMembrane	NO_SP	TMH
WP_012387454.1	LEPBI_RS02060		PAS domain-containin chromosome	I	tBOSK10			T	CytoplasmicMembrane	NO_SP	CYT
WP_012387456.1	LEPBI_RS02070		hypothetical protein chromosome	I	tBOSK12				Unknown	LIPO	Spl
WP_012387461.1	LEPBI_RS02085		SRPBCC family proteir chromosome	I	tBOSK17				Cytoplasmic	NO_SP	CYT
WP_012476119.1	LEPBI_RS02125		heavy metal transloca chromosome	I				P	CytoplasmicMembrane	NO_SP	CYT
WP_002972591.1	LEPBI_RS02170		rod shape-determini chromosome	I	tBOSJM9	WP_000575569.1	0.96326	D	Cytoplasmic	NO_SP	CYT
WP_012387473.1	LEPBI_RS02175		Ppx/GppA family pho: chromosome	I	tBOSJN0	WP_000249634.1	0.6069294	F	Cytoplasmic	NO_SP	CYT
WP_012387474.1	LEPBI_RS02180		SpoIIE family protein i chromosome	I	tBOSJN1	WP_000622415.1	0.52816985		CytoplasmicMembrane	SP	Spl
WP_012387476.1	LEPBI_RS02190		leucyl aminopeptidas: chromosome	I	tBOSJN3	WP_000762682.1	0.66633435	E	Cytoplasmic	NO_SP	CYT
WP_012387477.1	LEPBI_RS02195	bcp	thioredoxin-depender chromosome	I	tBOSJN4	WP_001292536.1	0.7224364	O	Cytoplasmic	NO_SP	CYT

WP_012387478.1	LEPBI_RS02200	hypothetical protein	chromosome	I	tBOSJL8	WP_000377460.1	0.62730875		Unknown	NO_SP	CYT
WP_012387481.1	LEPBI_RS02215	hypothetical protein	chromosome	I	tBOSJM1	WP_000453665.1	0.4577958		Unknown	NO_SP	CYT
WP_012387482.1	LEPBI_RS02220	signal peptide peptidase	chromosome	I	tBOSJM2	WP_000440816.1	0.69080715	O	CytoplasmicMembrane	NO_SP	TMH
WP_012387483.1	LEPBI_RS02225	hypothetical protein	chromosome	I	tBOSJM3	WP_000661083.1	0.4178818		CytoplasmicMembrane	NO_SP	CYT
WP_012387484.1	LEPBI_RS02230	5'/3'-nucleotidase Sur	chromosome	I	sBOSJM4	WP_001023250.1	0.6538176	L	Cytoplasmic	NO_SP	CYT
WP_012387485.1	LEPBI_RS02235	tetratricopeptide repeat	chromosome	I	tBOSJM5	WP_001280575.1	0.5073120000000001		Cytoplasmic	NO_SP	CYT
WP_012387488.1	LEPBI_RS02260	methyl-accepting chemotaxis	chromosome	I	tBOSJ33			T	CytoplasmicMembrane	NO_SP	TMH
WP_012387490.1	LEPBI_RS02270	ABC transporter substrate	chromosome	I	tBOSJ35				Cytoplasmic	SP	CYT
WP_012387495.1	LEPBI_RS02300	hypothetical protein	chromosome	I	tBOSJ40				Cytoplasmic	SP	Spl
WP_187148068.1	LEPBI_RS02305	tyrosine-type recombinase	chromosome	I	tBOSJ41			L	Cytoplasmic	NO_SP	CYT
WP_012387498.1	LEPBI_RS02315	L-aspartate oxidase	chromosome	I	tBOSJ43	WP_001137375.1	0.7447461	H	Cytoplasmic	NO_SP	CYT
WP_012387499.1	LEPBI_RS02320	S41 family peptidase	chromosome	I	tBOSJ44	WP_000053693.1	0.6670664	O	CytoplasmicMembrane	LIPO	Spl
WP_041769595.1	LEPBI_RS02325	hypothetical protein	chromosome	I	tBOSJ45	WP_001129541.1	0.3071404		Cytoplasmic	SP	SplI
WP_012387501.1	LEPBI_RS02330	pyridoxine 5'-phosphate	chromosome	I	sBOSJ25	WP_000865278.1	0.64308915	H	Cytoplasmic	NO_SP	CYT
WP_012387502.1	LEPBI_RS02335	FYDLN acid domain-containing	chromosome	I	tBOSJ26				Cytoplasmic	NO_SP	CYT
WP_012387504.1	LEPBI_RS02345	RNA chaperone Hfq	chromosome	I	sBOSJ28	WP_001274793.1	0.8213171999999999	T	Cytoplasmic	NO_SP	CYT
WP_012387505.1	LEPBI_RS02350	mannose-1-phosphate	chromosome	I	tBOSJ29	WP_001070780.1	0.7404061499999999	M	Cytoplasmic	NO_SP	CYT
WP_012387507.1	LEPBI_RS02360	purine-binding chemotaxis	chromosome	I	tBOSJ31	WP_000093551.1	0.7320129999999999	T	Cytoplasmic	NO_SP	CYT
WP_012387508.1	LEPBI_RS02365	PhoU family transcription	chromosome	I	tBOSJ32	WP_000465176.1	0.6966444999999999		Cytoplasmic	NO_SP	CYT
WP_012387509.1	LEPBI_RS02370	methyl-accepting chemotaxis	chromosome	I	tBOSJ72			T	CytoplasmicMembrane	NO_SP	TMH
WP_012476123.1	LEPBI_RS02380	two-component sensor	chromosome	I	tBOSJ75			T	CytoplasmicMembrane	NO_SP	TMH
WP_012387513.1	LEPBI_RS02385	hypothetical protein	chromosome	I	tBOSJ76	WP_000163651.1	0.6333312		Cytoplasmic	NO_SP	CYT
WP_012387514.1	LEPBI_RS02390	hypothetical protein	chromosome	I	tBOSJ77				Cytoplasmic	SP	CYT
WP_012387515.1	LEPBI_RS02395	hypothetical protein	chromosome	I	tBOSJ78				Cytoplasmic	NO_SP	CYT
WP_041769598.1	LEPBI_RS02405	poly-gamma-glutamate	chromosome	I	tBOSJ80	WP_001078607.1	0.4109911		Unknown	NO_SP	CYT
WP_012387520.1	LEPBI_RS02420	SpoII family protein	chromosome	I	tBOSJ83				CytoplasmicMembrane	NO_SP	CYT
WP_012387522.1	LEPBI_RS02430	serine hydrolase	chromosome	I	tBOSJ65			V	CytoplasmicMembrane	LIPO	SplI
WP_012387523.1	LEPBI_RS02435	2,3-bisphosphoglycerate	chromosome	I	tBOSJ66	WP_001069143.1	0.7161800999999999	G	Cytoplasmic	NO_SP	CYT
WP_012387525.1	LEPBI_RS02445	TonB-dependent receptor	chromosome	I	tBOSJ68	WP_000517759.1	0.572472	H	OuterMembrane	SP	Spl
WP_012476126.1	LEPBI_RS02450	adenosine kinase	chromosome	I	tBOSJ69	WP_000683574.1	0.7402081500000001	G	Cytoplasmic	NO_SP	CYT
WP_012387528.1	LEPBI_RS02460	PAS domain-containing	chromosome	I	tBOSJ71			T	CytoplasmicMembrane	NO_SP	CYT
WP_012387529.1	LEPBI_RS02465	ABC transporter ATP-binding	chromosome	I	tBOSJ46	WP_000598571.1	0.6467700000000001	V	Cytoplasmic	NO_SP	CYT
WP_012387531.1	LEPBI_RS02475	GldG family protein	chromosome	I	tBOSJ48	WP_000849194.1	0.5075532		CytoplasmicMembrane	NO_SP	CYT
WP_012387532.1	LEPBI_RS02480	hypothetical protein	chromosome	I	tBOSJ49	WP_000832927.1	0.33538315		Unknown	NO_SP	Spl
WP_012387534.1	LEPBI_RS02490	UDP-N-acetylmuramoyl	chromosome	I	tBOSJ51	WP_000708411.1	0.68143185	M	Cytoplasmic	NO_SP	CYT
WP_012387535.1	LEPBI_RS02495	phenylalanine--tRNA	chromosome	I	sBOSJ52	WP_001053743.1	0.81525	J	Cytoplasmic	NO_SP	CYT
WP_012387536.1	LEPBI_RS02500	acetyl-CoA acetyltransferase	chromosome	I	tBOSJ53	WP_001070403.1	0.55098		Unknown	NO_SP	CYT
WP_012387537.1	LEPBI_RS02505	hypothetical protein	chromosome	I	tBOSJ54	WP_000433586.1	0.59324265		Cytoplasmic	NO_SP	CYT
WP_012387538.1	LEPBI_RS02510	hypothetical protein	chromosome	I	tBOSJ55	WP_000932425.1	0.4253788		Cytoplasmic	NO_SP	CYT
WP_012387540.1	LEPBI_RS02520	30S ribosomal protein	chromosome	I	sBOSJ57	WP_001274025.1	0.6789805999999999		Cytoplasmic	NO_SP	CYT
WP_012387541.1	LEPBI_RS02530	phosphoglucosamine	chromosome	I	tBOSJ61	WP_001092943.1	0.6262689999999999	G	Cytoplasmic	NO_SP	CYT
WP_012387542.1	LEPBI_RS02535	glutamine--fructose-6-phosphate	chromosome	I	tBOSJ62	WP_000334327.1	0.5735300000000001	M	Cytoplasmic	NO_SP	CYT
WP_012387543.1	LEPBI_RS02540	GlmU family protein	chromosome	I	tBOSJ63	WP_001127234.1	0.5629394999999999		Cytoplasmic	NO_SP	CYT
WP_012387544.1	LEPBI_RS02545	alpha/beta hydrolase	chromosome	I	tBOSJ64				Cytoplasmic	NO_SP	CYT

WP_012387545.1	LEPBI_RS02550		methylcrotonoyl-CoA chromosome	I	tBOSJ58	WP_000402517.1	0.776105		I	Cytoplasmic	NO_SP	CYT
WP_012387547.1	LEPBI_RS02560		DJ-1/Pfpl family prote chromosome	I	tBOSJ60	WP_001127205.1	0.5576641		V	Cytoplasmic	NO_SP	CYT
WP_041769601.1	LEPBI_RS02565		trypsin-like peptidase chromosome	I	tBOSJG1	WP_000798837.1	0.6117507		O	Periplasmic	LIPO	Spl
WP_041769942.1	LEPBI_RS02570	ruvB	Holliday junction bran chromosome	I	tBOSJG2	WP_001129835.1	0.7057072500000001		L	Cytoplasmic	NO_SP	CYT
WP_012476128.1	LEPBI_RS02575		TonB family protein chromosome	I	tBOSJG3	WP_000361891.1	0.680466			Unknown	NO_SP	CYT
WP_012387551.1	LEPBI_RS02580		hypothetical protein chromosome	I	tBOSJG4					Unknown	NO_SP	Spl
WP_012387552.1	LEPBI_RS02585		serine hydrolase chromosome	I	tBOSJG5	WP_000742170.1	0.28715975		V	Unknown	LIPO	SplI
WP_012387553.1	LEPBI_RS02590		SufE family protein chromosome	I	tBOSJG6	WP_001084286.1	0.6709227		O	Cytoplasmic	NO_SP	CYT
WP_012387554.1	LEPBI_RS02595		hypothetical protein chromosome	I	tBOSJG7					Unknown	LIPO	CYT
WP_041769943.1	LEPBI_RS02600		hypothetical protein chromosome	I	tBOSJG8	WP_000966831.1	0.38211280000000003			CytoplasmicMembrane	NO_SP	CYT
WP_012387559.1	LEPBI_RS02620	pbpC	penicillin-binding prot chromosome	I	tBOSJH2	WP_002145395.1	0.50610285		M	CytoplasmicMembrane	SP	CYT
WP_012387561.1	LEPBI_RS02630		SpoII family protein chromosome	I	tBOSJH4				T	CytoplasmicMembrane	NO_SP	TMH
WP_012387563.1	LEPBI_RS02640		FAD-binding oxidored chromosome	I	tBOSJF6	WP_001018374.1	0.67202049999999999		C	Cytoplasmic	NO_SP	CYT
WP_012387564.1	LEPBI_RS02645		SDR family NAD(P)-de chromosome	I	tBOSJF7	WP_001074690.1	0.66599999999999999		R	CytoplasmicMembrane	NO_SP	CYT
WP_081431650.1	LEPBI_RS02650		NYN domain-containin chromosome	I	tBOSJF8	WP_000898859.1	0.427133			Cytoplasmic	NO_SP	CYT
WP_012387567.1	LEPBI_RS02660		DUF1574 domain-con chromosome	I	tBOSJG0	WP_000489551.1	0.55370700000000001			Cytoplasmic	NO_SP	CYT
WP_012387570.1	LEPBI_RS02675		FecR domain-containin chromosome	I	tBOSJC0					Unknown	NO_SP	CYT
WP_012387571.1	LEPBI_RS02680		HAMP domain-contain chromosome	I	tBOSJC1				T	Unknown	NO_SP	Spl
WP_012387572.1	LEPBI_RS02685		hypothetical protein chromosome	I	tBOSJC2	WP_000831279.1	0.565915			OuterMembrane	LIPO	SplI
WP_012476129.1	LEPBI_RS02690		hypothetical protein chromosome	I	tBOSJC3					CytoplasmicMembrane	SP	Spl
WP_012387575.1	LEPBI_RS02700		DUF2225 domain-con chromosome	I	tBOSJC5	WP_000127192.1	0.7450641		S	Cytoplasmic	NO_SP	CYT
WP_081431651.1	LEPBI_RS02705		hypothetical protein chromosome	I	tBOSJC6	WP_000825586.1	0.6344569			Cytoplasmic	SP	Spl
WP_012387580.1	LEPBI_RS02725		hypothetical protein chromosome	I	tBOSJD0					Unknown	SP	Spl
WP_012387581.1	LEPBI_RS02730		alkaline phosphatase chromosome	I	tBOSJD1				M	CytoplasmicMembrane	NO_SP	TMH
WP_012387582.1	LEPBI_RS02735		acetyl-CoA carboxylas chromosome	I	tBOSJD2	WP_000623974.1	0.62504860000000001		I	Cytoplasmic	NO_SP	CYT
WP_012387583.1	LEPBI_RS02740		acetyl-CoA carboxylas chromosome	I	tBOSJD3					Cytoplasmic	NO_SP	CYT
WP_012387584.1	LEPBI_RS02745		BamA/TamA family of chromosome	I	tBOSJA6					OuterMembrane	SP	Spl
WP_012387585.1	LEPBI_RS02750		DUF1566 domain-con chromosome	I	tBOSJA7	WP_000760764.1	0.428141250000000003			CytoplasmicMembrane	LIPO	CYT
WP_012387586.1	LEPBI_RS02755		hypothetical protein chromosome	I	tBOSJA8	WP_000689734.1	0.458160099999999996			Cytoplasmic	NO_SP	CYT
WP_041769947.1	LEPBI_RS02775		SpoII family protein chromosome	I	tBOSJB2				T	Cytoplasmic	NO_SP	CYT
WP_041769948.1	LEPBI_RS02780		sigma-54-dependent chromosome	I	tBOSJB3	WP_001974395.1	0.74385		K	Cytoplasmic	NO_SP	CYT
WP_012387592.1	LEPBI_RS02785	thiD	bifunctional hydroxyn chromosome	I	tBOSJB4	WP_000368308.1	0.61608960000000001		H	Unknown	NO_SP	Spl
WP_012387595.1	LEPBI_RS02800		hypothetical protein chromosome	I	tBOSJB7	WP_000721126.1	0.487965600000000005			Unknown	SP	Spl
WP_012387596.1	LEPBI_RS02805		porin chromosome	I	tBOSJ85					OuterMembrane	SP	Spl
WP_012387597.1	LEPBI_RS02810		efflux RND transporte chromosome	I	tBOSJ97	WP_000620782.1	0.85008859999999999		P	CytoplasmicMembrane	NO_SP	CYT
WP_012387599.1	LEPBI_RS02820		efflux RND transporte chromosome	I	tBOSJ99	WP_000690698.1	0.6967751			Cytoplasmic	NO_SP	Spl
WP_012387600.1	LEPBI_RS02825		TolC family protein chromosome	I	tBOSJA1	WP_000718034.1	0.71410559999999999		M	OuterMembrane	SP	CYT
WP_012387603.1	LEPBI_RS02840		FAD-binding oxidored chromosome	I	tBOSJA4	WP_002086035.1	0.7662204		C	Cytoplasmic	NO_SP	CYT
WP_012387604.1	LEPBI_RS02845	ppk1	polyphosphate kinase chromosome	I	tBOSJA5	WP_000045686.1	0.6933408		P	CytoplasmicMembrane	NO_SP	CYT
WP_012387605.1	LEPBI_RS02850	fliD	flagellar filament cap chromosome	I	tBOSJ86	WP_001110736.1	0.55628595		N	Periplasmic	NO_SP	CYT
WP_012387606.1	LEPBI_RS02855		hypothetical protein chromosome	I	tBOSJ87	WP_000409256.1	0.55346000000000001			Cytoplasmic	NO_SP	CYT
WP_012387608.1	LEPBI_RS02865		HAD family hydrolase chromosome	I	tBOSJ89	WP_001173175.1	0.3683208			Unknown	NO_SP	CYT
WP_012387609.1	LEPBI_RS02870		methyltransferase doi chromosome	I	tBOSJ90	WP_001082180.1	0.6810606			Cytoplasmic	NO_SP	CYT
WP_012476131.1	LEPBI_RS02875		diaminopimelate epin chromosome	I	tBOSJ91	WP_000157608.1	0.78345135		E	Cytoplasmic	NO_SP	CYT



WP_012387611.1	LEPBI_RS02880	1-acyl-sn-glycerol-3-pl chromosome	I	tBOSJ92	WP_000410308.1	0.65475425		Unknown	NO_SP	CYT
WP_012476132.1	LEPBI_RS02885	hypothetical protein chromosome	I	tBOSJ93	WP_001113793.1	0.5979300000000001		Unknown	NO_SP	CYT
WP_012476133.1	LEPBI_RS02895	DUF4468 domain-con chromosome	I	tBOSJ94				Cytoplasmic	SP	CYT
WP_041769615.1	LEPBI_RS02915	SpoIIE family protein chromosome	I	tBOSKH3				CytoplasmicMembrane	NO_SP	TMH
WP_012387619.1	LEPBI_RS02925	PAS domain S-box pro chromosome	I	tBOSKH5	WP_001230742.1	0.419387	T	CytoplasmicMembrane	NO_SP	CYT
WP_012387622.1	LEPBI_RS02940	acetyl-CoA acetyltran: chromosome	I	tBOSKH8	WP_001280808.1	0.88244	I	Cytoplasmic	NO_SP	CYT
WP_012387623.1	LEPBI_RS02945	3-hydroxyacyl-CoA de chromosome	I	tBOSKH9	WP_001206943.1	0.82108	I	Cytoplasmic	NO_SP	Spl
WP_012387625.1	LEPBI_RS02960	hypothetical protein chromosome	I	tBOSKI1				Cytoplasmic	LIPO	CYT
WP_012387631.1	LEPBI_RS02990	hypothetical protein chromosome	I	tBOSKI7				OuterMembrane	NO_SP	Spl
WP_012476135.1	LEPBI_RS03010	hypothetical protein chromosome	I	tBOSKJ0				Unknown	LIPO	SplI
WP_012387635.1	LEPBI_RS03015	hypothetical protein chromosome	I	tBOSKJ1				Cytoplasmic	SP	Spl
WP_012387639.1	LEPBI_RS03035	ABC transporter subst chromosome	I	tBOSKJ5			T	CytoplasmicMembrane	SP	Spl
WP_012387644.1	LEPBI_RS03060	SDR family oxidoredu chromosome	I	tBOSKK0	WP_000646914.1	0.4619442	R	Cytoplasmic	NO_SP	CYT
WP_012387645.1	LEPBI_RS03065	cyclic nucleotide-bind chromosome	I	tBOSKK1				Unknown	NO_SP	CYT
WP_012387646.1	LEPBI_RS03070	Crp/Fnr family transcr chromosome	I	tBOSKK2				Cytoplasmic	NO_SP	CYT
WP_012387647.1	LEPBI_RS03075	ankyrin repeat domaii chromosome	I	tBOSKK3				Unknown	SP	Spl
WP_012387648.1	LEPBI_RS03080	peptidoglycan DD-me chromosome	I	tBOSKK4			M	OuterMembrane	SP	SplI
WP_012387649.1	LEPBI_RS03085	transcriptional regulat chromosome	I	tBOSKK5	WP_000674089.1	0.5179305		CytoplasmicMembrane	NO_SP	TMH
WP_012387652.1	LEPBI_RS03100	GAF domain-containir chromosome	I	tBOSKK8				CytoplasmicMembrane	LIPO	CYT
WP_012387654.1	LEPBI_RS03110	phosphorylase chromosome	I	tBOSKL0				Cytoplasmic	NO_SP	CYT
WP_012387655.1	LEPBI_RS03115	glutathione peroxidas chromosome	I	tBOSKL1	WP_000657852.1	0.5240868999999999	V	Unknown	NO_SP	CYT
WP_012387657.1	LEPBI_RS03125	transglycosylase domi chromosome	I	tBOSKL3	WP_000783273.1	0.47114055000000005	M	CytoplasmicMembrane	NO_SP	CYT
WP_012387664.1	LEPBI_RS03170	transketolase chromosome	I	tBOSKM0	WP_001002663.1	0.7865253	G	Cytoplasmic	NO_SP	CYT
WP_012387666.1	LEPBI_RS03180	polyprenyl synthetase chromosome	I	tBOSKM2	WP_000868876.1	0.6250068	H	Cytoplasmic	NO_SP	CYT
WP_012387667.1	LEPBI_RS03185	GHKL domain-contain chromosome	I	tBOSKM3			T	CytoplasmicMembrane	SP	Spl
WP_012476140.1	LEPBI_RS03190	hypothetical protein chromosome	I	tBOSKM4	WP_000820064.1	0.5032901		Extracellular	LIPO	SplI
WP_012387670.1	LEPBI_RS03200	ATP-dependent zinc p chromosome	I	tBOSKM6			S	Cytoplasmic	LIPO	CYT
WP_012387672.1	LEPBI_RS03210	alpha-L-glutamate ligε chromosome	I	tBOSKM8				Cytoplasmic	NO_SP	CYT
WP_012387677.1	LEPBI_RS03235	lpxD UDP-3-O-(3-hydroxym chromosome	I	sBOSKN3	WP_000155196.1	0.5784853999999999	M	Cytoplasmic	NO_SP	CYT
WP_012387678.1	LEPBI_RS03240	DoxX family protein chromosome	I	tBOSKN4				CytoplasmicMembrane	NO_SP	TMH
WP_012387679.1	LEPBI_RS03245	RibD family protein chromosome	I	tBOSKN5	WP_001087012.1	0.5554695	H	Cytoplasmic	NO_SP	CYT
WP_012387682.1	LEPBI_RS03260	hypothetical protein chromosome	I	tBOSKN8	WP_001026144.1	0.518077		Cytoplasmic	SP	Spl
WP_012387683.1	LEPBI_RS03265	alpha/beta hydrolase chromosome	I	tBOSKN9			I	Cytoplasmic	NO_SP	CYT
WP_012387685.1	LEPBI_RS03275	WYL domain-containir chromosome	I	tBOSKP1	WP_001290040.1	0.417576		Cytoplasmic	NO_SP	CYT
WP_012387686.1	LEPBI_RS03280	hypothetical protein chromosome	I	tBOSKP2	WP_000175921.1	0.47279700000000001		Cytoplasmic	SP	CYT
WP_012387687.1	LEPBI_RS03285	hypothetical protein chromosome	I	tBOSKP3	WP_000941137.1	0.3987675		Unknown	LIPO	SplI
WP_012387689.1	LEPBI_RS03295	biliverdin-producing h chromosome	I	tBOSKP5	WP_000050531.1	0.548225	H	Cytoplasmic	NO_SP	CYT
WP_012387693.1	LEPBI_RS03315	polA DNA polymerase I chromosome	I	tBOSKP9	WP_000825971.1	0.65227635000000001	L	Cytoplasmic	NO_SP	CYT
WP_012387694.1	LEPBI_RS03320	glycosyltransferase chromosome	I	tBOSKQ0	WP_000600560.1	0.64875195	M	Cytoplasmic	NO_SP	CYT
WP_012387696.1	LEPBI_RS03330	glutamate--tRNA ligas chromosome	I	sBOSKQ2	WP_001076468.1	0.74540070000000001	J	Cytoplasmic	NO_SP	CYT
WP_012387697.1	LEPBI_RS03335	hypothetical protein chromosome	I	tBOSKQ3				Unknown	SP	TMH
WP_012476142.1	LEPBI_RS03340	DNA gyrase subunit A chromosome	I	tBOSKQ4	WP_001972951.1	0.8220533999999999	L	Cytoplasmic	NO_SP	CYT
WP_012387699.1	LEPBI_RS03345	DNA gyrase subunit B chromosome	I	tBOSKQ5	WP_000102225.1	0.8278281	L	Cytoplasmic	NO_SP	CYT
WP_012387700.1	LEPBI_RS03350	serine hydrolase chromosome	I	tBOSKQ6			V	CytoplasmicMembrane	NO_SP	CYT

WP_012387701.1	LEPBI_RS03355	hypothetical protein	chromosome	I	tBOSKQ7			Unknown	LIPO	SplI		
WP_012387702.1	LEPBI_RS03360	hypothetical protein	chromosome	I	tBOSKQ8			Unknown	LIPO	SplI		
WP_012476143.1	LEPBI_RS03365	hypothetical protein	chromosome	I	tBOSKQ9			Unknown	SP	Spl		
WP_012387705.1	LEPBI_RS03375	DUF445 family protei	chromosome	I	tBOSKR1			CytoplasmicMembrane	NO_SP	TMH		
WP_012387706.1	LEPBI_RS03380	SDR family oxidoredu	chromosome	I	tBOSKR2			R	Cytoplasmic	NO_SP	CYT	
WP_012387707.1	LEPBI_RS03385	GNAT family N-acetyl	chromosome	I	tBOSKR3	WP_001022053.1	0.460018399999999994		Cytoplasmic	NO_SP	CYT	
WP_012387708.1	LEPBI_RS03390	hypothetical protein	chromosome	I	tBOSKR4	WP_000816419.1	0.43635780000000001		Unknown	LIPO	CYT	
WP_012387709.1	LEPBI_RS03395	DNA-protecting prote	chromosome	I	tBOSKR5	WP_001081159.1	0.412263999999999996		L	CytoplasmicMembrane	NO_SP	CYT
WP_012387710.1	LEPBI_RS03400	calcium/sodium antip	chromosome	I	tBOSKR6				P	CytoplasmicMembrane	NO_SP	TMH
WP_041769623.1	LEPBI_RS03405	hypothetical protein	chromosome	I	tBOSKR7	WP_000854082.1	0.3759619			Cytoplasmic	SP	CYT
WP_012387712.1	LEPBI_RS03410	arginine/lysine/ornith	chromosome	I	tBOSKR8				E	Cytoplasmic	NO_SP	CYT
WP_012387713.1	LEPBI_RS03415	hypothetical protein	chromosome	I	tBOSKR9	WP_000446221.1	0.545188049999999999			Cytoplasmic	NO_SP	CYT
WP_012387715.1	LEPBI_RS03425	DegT/DnrJ/EryC1/StrS	chromosome	I	tBOSKS1	WP_001982414.1	0.6640722		M	Cytoplasmic	NO_SP	CYT
WP_012387719.1	LEPBI_RS03445	glutathione S-transfer	chromosome	I	tBOSKS5					Unknown	NO_SP	CYT
WP_012387722.1	LEPBI_RS03460	DUF2237 domain-con	chromosome	I	tBOSKS8				S	Unknown	NO_SP	CYT
WP_012387723.1	LEPBI_RS03465	hypothetical protein	chromosome	I	tBOSL29	WP_000594730.1	0.53125			Unknown	SP	Spl
WP_012387725.1	LEPBI_RS03475	hypothetical protein	chromosome	I	tBOSL31					Cytoplasmic	NO_SP	CYT
WP_012387726.1	LEPBI_RS03485	thiolase family protei	chromosome	I	tBOSL32	WP_000778965.1	0.79447995		I	Cytoplasmic	NO_SP	CYT
WP_012387727.1	LEPBI_RS03490	ketol-acid reductois	chromosome	I	sBOSL33	WP_001284348.1	0.89638		E	Cytoplasmic	NO_SP	CYT
WP_012387733.1	LEPBI_RS03520	ABC-F family ATP-binc	chromosome	I	tBOSL39	WP_001049205.1	0.5907924		R	Cytoplasmic	NO_SP	CYT
WP_012387734.1	LEPBI_RS03525	PAS domain-containin	chromosome	I	tBOSL40				T	CytoplasmicMembrane	NO_SP	CYT
WP_012387735.1	LEPBI_RS03530	hypothetical protein	chromosome	I	tBOSL41	WP_000803603.1	0.370252999999999994			Unknown	SP	Spl
WP_012387736.1	LEPBI_RS03535	HlyC/CorC family tran	chromosome	I	tBOSL42	WP_000420145.1	0.65517195		R	CytoplasmicMembrane	NO_SP	CYT
WP_012387737.1	LEPBI_RS03540	phosphopantothenoy	chromosome	I	tBOSL43	WP_000067295.1	0.752574499999999999		H	Cytoplasmic	NO_SP	CYT
WP_012387738.1	LEPBI_RS03545	DNA/pantothenate m	chromosome	I	tBOSL44	WP_001212530.1	0.601829749999999999		H	Cytoplasmic	NO_SP	CYT
WP_012387742.1	LEPBI_RS03565	cytochrome c-type bic	chromosome	I	tBOSL48	WP_000706226.1	0.4897755			Unknown	SP	Spl
WP_012387743.1	LEPBI_RS03570	heme lyase CcmF/NrfI	chromosome	I	tBOSL49	WP_000997635.1	0.76954		C	CytoplasmicMembrane	NO_SP	TMH
WP_012387748.1	LEPBI_RS03595	sodium:proton antipo	chromosome	I	tBOSL54	WP_000810537.1	0.707434		P	CytoplasmicMembrane	SP	Spl
WP_012387752.1	LEPBI_RS03615	4-hydroxy-tetrahydro	chromosome	I	sBOSL58	WP_001970781.1	0.75099420000000001		E	Cytoplasmic	NO_SP	CYT
WP_012387753.1	LEPBI_RS03620	4-hydroxy-tetrahydro	chromosome	I	tBOSL59	WP_000082216.1	0.6885153		E	Cytoplasmic	NO_SP	CYT
WP_012387754.1	LEPBI_RS03625	TIGR00159 family pro	chromosome	I	tBOSL60	WP_000464749.1	0.651		T	CytoplasmicMembrane	NO_SP	TMH
WP_012476150.1	LEPBI_RS03630	hypothetical protein	chromosome	I	tBOSL61	WP_000766592.1	0.514779			Cytoplasmic	NO_SP	CYT
WP_012387756.1	LEPBI_RS03635	alpha/beta hydrolase	chromosome	I	tBOSL62	WP_001047532.1	0.51069645		H	Unknown	NO_SP	CYT
WP_012387757.1	LEPBI_RS03640	adenylate/guanylate c	chromosome	I	tBOSL63				T	CytoplasmicMembrane	NO_SP	CYT
WP_012387758.1	LEPBI_RS03645	flagellar M-ring protei	chromosome	I	tBOSL64	WP_001115057.1	0.839930849999999999		N	CytoplasmicMembrane	NO_SP	CYT
WP_012387761.1	LEPBI_RS03660	aminotransferase clas	chromosome	I	tBOSL67				H	Cytoplasmic	NO_SP	CYT
WP_012387762.1	LEPBI_RS03665	TetR/AcrR family tran	chromosome	I	tBOSL68					Cytoplasmic	NO_SP	CYT
WP_012387764.1	LEPBI_RS03675	Hsp70 family protein	chromosome	I	tBOSL70				G	Cytoplasmic	NO_SP	CYT
WP_012387767.1	LEPBI_RS03690	MBL fold metallo-hyd	chromosome	I	tBOSL73	WP_000954148.1	0.545035199999999999			Cytoplasmic	NO_SP	CYT
WP_012387770.1	LEPBI_RS03705	flagellar basal body ro	chromosome	I	tBOSL76	WP_000522494.1	0.931395		N	Periplasmic	NO_SP	CYT
WP_187148069.1	LEPBI_RS03715	DUF3427 domain-con	chromosome	I	tBOSL78				K	Cytoplasmic	NO_SP	CYT
WP_012387777.1	LEPBI_RS03740	MCE family protein	chromosome	I	tBOSL83					Unknown	NO_SP	TMH
WP_012387778.1	LEPBI_RS03745	hypothetical protein	chromosome	I	tBOSL84					Unknown	SP	CYT
WP_012387779.1	LEPBI_RS03750	sterol desaturase fam	chromosome	I	tBOSL85				I	CytoplasmicMembrane	NO_SP	CYT

WP_012387780.1	LEPBI_RS03755	gloA	lactoylglutathione lyase	chromosome	I	tBOSL86				Cytoplasmic	NO_SP	CYT
WP_012387782.1	LEPBI_RS03765	pyk	pyruvate kinase	chromosome	I	tBOSL88	WP_000698533.1	0.7066867499999999	G	Cytoplasmic	NO_SP	CYT
WP_012387783.1	LEPBI_RS03770		histone deacetylase	chromosome	I	tBOSL89	WP_000410918.1	0.6356506999999999	Q	Cytoplasmic	NO_SP	CYT
WP_012387784.1	LEPBI_RS03775		hypothetical protein	chromosome	I	tBOSL90	WP_000510896.1	0.59328225		Cytoplasmic	NO_SP	CYT
WP_012387785.1	LEPBI_RS03780		response regulator	chromosome	I	tBOSL91	WP_000134482.1	0.60811245	T	Cytoplasmic	NO_SP	CYT
WP_012387789.1	LEPBI_RS03800		alpha-galactosidase	chromosome	I	tBOSL95	WP_001201672.1	0.57394755	G	Cytoplasmic	NO_SP	CYT
WP_012387790.1	LEPBI_RS03805		ribonuclease D	chromosome	I	tBOSL96	WP_001128627.1	0.757055	J	Cytoplasmic	NO_SP	CYT
WP_012387791.1	LEPBI_RS03810	radA	DNA repair protein RadA	chromosome	I	tBOSL97	WP_000728132.1	0.6665057499999999	L	Cytoplasmic	NO_SP	CYT
WP_012387793.1	LEPBI_RS03820		hypothetical protein	chromosome	I	tBOSL99				Unknown	NO_SP	CYT
WP_012387794.1	LEPBI_RS03825		hypothetical protein	chromosome	I	tBOSLA0				Unknown	SP	Spl
WP_012476154.1	LEPBI_RS03830		lipase	chromosome	I	tBOSLA1				Cytoplasmic	NO_SP	Spl
WP_012387796.1	LEPBI_RS03835		hypothetical protein	chromosome	I	tBOSLA2				Unknown	LIPO	SpII
WP_041769643.1	LEPBI_RS03840		hypothetical protein	chromosome	I	tBOSLA3				Cytoplasmic	NO_SP	CYT
WP_012387799.1	LEPBI_RS03850		hypothetical protein	chromosome	I	tBOSLA5	WP_000439958.1	0.44418170000000007		Cytoplasmic	NO_SP	CYT
WP_012387801.1	LEPBI_RS03860		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	chromosome	I	tBOSLA7			I	CytoplasmicMembrane	NO_SP	CYT
WP_012387803.1	LEPBI_RS03870		MaoC family dehydratase	chromosome	I	tBOSLA9	WP_000161597.1	0.79625	I	Unknown	NO_SP	CYT
WP_012387804.1	LEPBI_RS03875		MBL fold metallo-hydrolase	chromosome	I	tBOSLB0	WP_000862891.1	0.54968265		Cytoplasmic	NO_SP	CYT
WP_012387806.1	LEPBI_RS03885		hypothetical protein	chromosome	I	tBOSLB2	WP_001977544.1	0.6318864		Cytoplasmic	NO_SP	CYT
WP_012387807.1	LEPBI_RS03890	lepB	signal peptidase LepB	chromosome	I	tBOSLB3	WP_000764509.1	0.7117456500000001		CytoplasmicMembrane	NO_SP	CYT
WP_012387809.1	LEPBI_RS03900	ilvB	biosynthetic-type acetate kinase	chromosome	I	tBOSLB5	WP_001052471.1	0.5565532500000001	E	Cytoplasmic	NO_SP	CYT
WP_002975072.1	LEPBI_RS03905		P-II family nitrogen reductase	chromosome	I	tBOSLB6			T	CytoplasmicMembrane	NO_SP	CYT
WP_187148079.1	LEPBI_RS03910		ammonium transporter	chromosome	I	tBOSLB7	WP_000872256.1	0.7981111499999999	P	CytoplasmicMembrane	NO_SP	TMH
WP_012387811.1	LEPBI_RS03915		glutathione peroxidase	chromosome	I	tBOSLB8	WP_001983897.1	0.6210764999999999	V	Cytoplasmic	NO_SP	CYT
WP_012476156.1	LEPBI_RS03930	atpB	F0F1 ATP synthase subunit b	chromosome	I	tBOSLC2	WP_000281179.1	0.62095035	C	CytoplasmicMembrane	SP	Spl
WP_002975055.1	LEPBI_RS03935	atpE	ATP synthase F0 subunit e	chromosome	I	tBOSLC3	WP_000394249.1	0.5971139999999999		CytoplasmicMembrane	NO_SP	TMH
WP_012387816.1	LEPBI_RS03940		F0F1 ATP synthase subunit c	chromosome	I	sBOSLC4	WP_000243426.1	0.6889311	C	Cytoplasmic	NO_SP	CYT
WP_012387817.1	LEPBI_RS03945	atpH	ATP synthase F1 subunit h	chromosome	I	sBOSLC5	WP_000999999.1	0.44762969999999996	C	Cytoplasmic	NO_SP	CYT
WP_012387818.1	LEPBI_RS03950		F0F1 ATP synthase subunit c	chromosome	I	sBOSLC6	WP_000695329.1	0.85389	C	Cytoplasmic	NO_SP	CYT
WP_012387819.1	LEPBI_RS03955	atpG	ATP synthase F1 subunit g	chromosome	I	sBOSLC7	WP_000235141.1	0.71974	C	Cytoplasmic	NO_SP	CYT
WP_012387820.1	LEPBI_RS03960	atpD	F0F1 ATP synthase subunit d	chromosome	I	sBOSLC8	WP_001032431.1	0.86006	C	CytoplasmicMembrane	NO_SP	CYT
WP_012387821.1	LEPBI_RS03965	atpC	ATP synthase F1 subunit c	chromosome	I	tBOSLC9	WP_001275641.1	0.5370400000000001	C	Cytoplasmic	NO_SP	CYT
WP_012387823.1	LEPBI_RS03975		hypothetical protein	chromosome	I	tBOSLD1				Cytoplasmic	NO_SP	CYT
WP_012387824.1	LEPBI_RS03980		GAF domain-containing protein	chromosome	I	tBOSLD2	WP_000523717.1	0.50137		Cytoplasmic	NO_SP	CYT
WP_012476157.1	LEPBI_RS04000	carA	glutamine-hydrolyzing protein	chromosome	I	tBOSLP1	WP_000643183.1	0.7259967	E	Cytoplasmic	NO_SP	CYT
WP_012387830.1	LEPBI_RS04010		porin OmpL1	chromosome	I	tBOSLP3	WP_002072562.1	0.5101732999999999		CytoplasmicMembrane	SP	Spl
WP_012387837.1	LEPBI_RS04045		cyclic nucleotide-binding protein	chromosome	I	tBOSLQ0	WP_000645315.1	0.5897101	T	Unknown	NO_SP	CYT
WP_012387840.1	LEPBI_RS04060	bioB	biotin synthase BioB	chromosome	I	sBOSLQ3	WP_000921250.1	0.6667654999999999	H	Cytoplasmic	NO_SP	CYT
WP_041769960.1	LEPBI_RS04065		MFS transporter	chromosome	I	tBOSLQ4			G	CytoplasmicMembrane	NO_SP	TMH
WP_002975048.1	LEPBI_RS04070		hypothetical protein	chromosome	I	tBOSLQ5	WP_000875511.1	0.81036		Unknown	NO_SP	CYT
WP_012387842.1	LEPBI_RS04075		lipase	chromosome	I	tBOSLQ6	WP_001051394.1	0.5194991999999999		Cytoplasmic	NO_SP	CYT
WP_012387843.1	LEPBI_RS04080	serB	phosphoserine phosphatase	chromosome	I	tBOSLQ7	WP_000927928.1	0.4941728000000001	E	Cytoplasmic	NO_SP	CYT
WP_012476161.1	LEPBI_RS04085	mutS	DNA mismatch repair protein	chromosome	I	tBOSLQ8	WP_001047644.1	0.5993925000000001	L	Cytoplasmic	NO_SP	CYT
WP_012387845.1	LEPBI_RS04090		phosphoribosylanthranilate synthase	chromosome	I	tBOSLQ9	WP_001984951.1	0.5215584	E	Cytoplasmic	NO_SP	CYT
WP_012387846.1	LEPBI_RS04095		TetR/AcrR family transcription factor	chromosome	I	tBOSLR0				Cytoplasmic	NO_SP	CYT

WP_012387848.1	LEPBI_RS04105		shikimate dehydroger	chromosome	I	tBOSLR2	WP_002145264.1	0.5115354999999999	E	Cytoplasmic	NO_SP	CYT
WP_012387851.1	LEPBI_RS04120		hypothetical protein	chromosome	I	tBOSLR5	WP_000425174.1	0.7805258999999999		Cytoplasmic	NO_SP	CYT
WP_012387852.1	LEPBI_RS04125		hypothetical protein	chromosome	I	tBOSLR6	WP_001028161.1	0.47922939999999997		Unknown	SP	Spl
WP_012387853.1	LEPBI_RS04130		S1 RNA-binding doma	chromosome	I	tBOSLR7	WP_000664814.1	0.6248235	J	Cytoplasmic	NO_SP	CYT
WP_012387855.1	LEPBI_RS04140		ATP-binding protein	chromosome	I	tBOSLR9	WP_000144004.1	0.605855		Cytoplasmic	NO_SP	CYT
WP_012387856.1	LEPBI_RS04145	uvrB	excinuclease ABC sub	chromosome	I	sBOSLS0	WP_000179030.1	0.795465	L	Cytoplasmic	NO_SP	CYT
WP_012387857.1	LEPBI_RS04150	lon	endopeptidase La	chromosome	I	tBOSLS1	WP_000398444.1	0.701914	O	Unknown	NO_SP	CYT
WP_012387858.1	LEPBI_RS04155		transglycosylase dom	chromosome	I	tBOSLS2	WP_000010431.1	0.6222348	M	CytoplasmicMembrane	NO_SP	CYT
WP_012387859.1	LEPBI_RS04160		ABC transporter subst	chromosome	I	tBOSLS3	WP_000348634.1	0.4525659		Unknown	SP	CYT
WP_012387860.1	LEPBI_RS04165		ABC transporter ATP-t	chromosome	I	tBOSLS4	WP_000172202.1	0.71202285	V	CytoplasmicMembrane	NO_SP	Spl
WP_012387862.1	LEPBI_RS04175		succinate CoA transfe	chromosome	I	tBOSLS6			C	Cytoplasmic	NO_SP	CYT
WP_012387863.1	LEPBI_RS04180		NAD(P)-binding protei	chromosome	I	tBOSLS7	WP_000684307.1	0.48620765000000005	R	Cytoplasmic	NO_SP	CYT
WP_012476164.1	LEPBI_RS04190		metal-sensing transcri	chromosome	I	tBOSLS9				Unknown	NO_SP	CYT
WP_012387867.1	LEPBI_RS04200		ToIC family protein	chromosome	I	tBOSLT1				Unknown	SP	CYT
WP_012387868.1	LEPBI_RS04205		efflux RND transporte	chromosome	I	tBOSLT2			V	CytoplasmicMembrane	NO_SP	CYT
WP_012387869.1	LEPBI_RS04210		hypothetical protein	chromosome	I	tBOSLT3				Extracellular	SP	Spl
WP_012387870.1	LEPBI_RS04215		hypothetical protein	chromosome	I	tBOSLT4				Extracellular	SP	Spl
WP_012476166.1	LEPBI_RS04220		hypothetical protein	chromosome	I	tBOSLT5				Unknown	SP	Spl
WP_012387872.1	LEPBI_RS04225		HAMP domain-containi	chromosome	I	tBOSLT6			T	CytoplasmicMembrane	NO_SP	TMH
WP_012387874.1	LEPBI_RS04235		hypothetical protein	chromosome	I	tBOSLT8				Unknown	NO_SP	CYT
WP_012387875.1	LEPBI_RS04240		penicillin acylase fami	chromosome	I	tBOSLT9	WP_000821874.1	0.51739680000000001	Q	Periplasmic	NO_SP	Spl
WP_012387878.1	LEPBI_RS04255		hypothetical protein	chromosome	I	tBOSLU2	WP_000381195.1	0.60088545000000002		Cytoplasmic	NO_SP	CYT
WP_012387879.1	LEPBI_RS04260		enoyl-CoA hydratase/	chromosome	I	tBOSLU3	WP_000505733.1	0.6153569	I	Cytoplasmic	NO_SP	CYT
WP_012387880.1	LEPBI_RS04265		Crp/Fnr family transcr	chromosome	I	tBOSLU4	WP_000403598.1	0.5467344	T	Cytoplasmic	NO_SP	CYT
WP_012387882.1	LEPBI_RS04275		hypothetical protein	chromosome	I	tBOSLU6	WP_000068280.1	0.46452000000000004		Cytoplasmic	NO_SP	CYT
WP_049755973.1	LEPBI_RS04280	hisB	imidazoleglycerol-phc	chromosome	I	sBOSLU7	WP_000130165.1	0.80121369999999999	E	Cytoplasmic	NO_SP	CYT
WP_012387884.1	LEPBI_RS04285	hisH	imidazole glycerol phc	chromosome	I	tBOSLU8	WP_000560473.1	0.644193	E	Cytoplasmic	NO_SP	CYT
WP_012387885.1	LEPBI_RS04290	hisA	1-(5-phosphoribosyl)-	chromosome	I	sBOSLU9	WP_000635440.1	0.6047613	E	Cytoplasmic	NO_SP	CYT
WP_012387886.1	LEPBI_RS04295		thioredoxin domain-c	chromosome	I	tBOSLV0	WP_001071434.1	0.51023075		CytoplasmicMembrane	NO_SP	Spl
WP_012387887.1	LEPBI_RS04300		N-acetylneuraminat	chromosome	I	tBOSLV1	WP_001011675.1	0.5829138	M	Cytoplasmic	NO_SP	CYT
WP_012387891.1	LEPBI_RS04320		helicase	chromosome	I	tBOSLV5	WP_000063951.1	0.71964		Cytoplasmic	NO_SP	CYT
WP_012387892.1	LEPBI_RS04325		hypothetical protein	chromosome	I	tBOSLV6	WP_000454661.1	0.8335488		Unknown	NO_SP	CYT
WP_012387894.1	LEPBI_RS04335		lipase chaperone fami	chromosome	I	tBOSLV8	WP_000854852.1	0.53938305		Cytoplasmic	NO_SP	TMH
WP_012387897.1	LEPBI_RS04350		TPM domain-containi	chromosome	I	tBOSLW1			S	CytoplasmicMembrane	SP	Spl
WP_012476170.1	LEPBI_RS04360		glycine--tRNA ligase	chromosome	I	tBOSLW3	WP_000412102.1	0.7858224	J	Cytoplasmic	NO_SP	CYT
WP_012387902.1	LEPBI_RS04375		GyrI-like domain-cont	chromosome	I	tBOSLW6	WP_000656643.1	0.37741274999999996		Unknown	NO_SP	CYT
WP_012476172.1	LEPBI_RS04390		TetR/AcrR family tran	chromosome	I	tBOSLW8				Unknown	NO_SP	CYT
WP_012387908.1	LEPBI_RS04410		hypothetical protein	chromosome	I	tBOSLX2				OuterMembrane	SP	Spl
WP_012387910.1	LEPBI_RS04420		PAS domain-containin	chromosome	I	tBOSLX4			T	CytoplasmicMembrane	NO_SP	CYT
WP_002989181.1	LEPBI_RS04440		STAS domain-containi	chromosome	I	tBOSLX8	WP_000695903.1	0.89823000000000001		Cytoplasmic	NO_SP	CYT
WP_041769661.1	LEPBI_RS04445		hypothetical protein	chromosome	I	tBOSLX9	WP_000402226.1	0.4411029		Unknown	NO_SP	TMH
WP_012387916.1	LEPBI_RS04455		PD40 domain-containi	chromosome	I	tBOSLY1	WP_000251310.1	0.40368735		Unknown	LIPO	Spl
WP_012387918.1	LEPBI_RS04465		trypsin-like peptidase	chromosome	I	tBOSLY3	WP_001976240.1	0.67658579999999999	O	Periplasmic	NO_SP	TMH
WP_012387919.1	LEPBI_RS04470		pyridoxal phosphate-c	chromosome	I	tBOSLY4	WP_001253859.1	0.80709255	E	Cytoplasmic	NO_SP	CYT

WP_012387920.1	LEPBI_RS04475	murI	glutamate racemase	chromosome	I	tBOSLY5	WP_000662657.1	0.5502288000000001	M	Cytoplasmic	NO_SP	CYT
WP_012387921.1	LEPBI_RS04480		phosphoribosylformyl	chromosome	I	tBOSLY6	WP_001112646.1	0.6114724	F	Cytoplasmic	NO_SP	CYT
WP_012476176.1	LEPBI_RS04485		PAS domain-containin	chromosome	I	tBOSLY7				CytoplasmicMembrane	NO_SP	TMH
WP_012387924.1	LEPBI_RS04495		response regulator	chromosome	I	tBOSLY9			T	Cytoplasmic	NO_SP	CYT
WP_012387926.1	LEPBI_RS04505		chemotaxis response	chromosome	I	tBOSLZ1			T	Cytoplasmic	NO_SP	CYT
WP_012387927.1	LEPBI_RS04510		chemotaxis protein Ct	chromosome	I	tBOSLZ2			T	Cytoplasmic	NO_SP	CYT
WP_012387928.1	LEPBI_RS04515		purine-binding chemc	chromosome	I	tBOSLZ3			T	Cytoplasmic	NO_SP	CYT
WP_012387929.1	LEPBI_RS04520		MCP four helix bundle	chromosome	I	tBOSLZ4	WP_011172165.1	0.32878605	T	CytoplasmicMembrane	NO_SP	Spl
WP_012387934.1	LEPBI_RS04545		enoyl-CoA hydratase/	chromosome	I	tBOSMA7	WP_001291080.1	0.629454	I	Cytoplasmic	NO_SP	CYT
WP_012387936.1	LEPBI_RS04555		glycogen/starch/alph	chromosome	I	tBOSMA9			G	Cytoplasmic	NO_SP	CYT
WP_012387937.1	LEPBI_RS04560		response regulator	chromosome	I	tBOSMB0	WP_001032649.1	0.7544956999999999		Cytoplasmic	NO_SP	CYT
WP_135737503.1	LEPBI_RS04565		HEAT repeat domain-	chromosome	I	tBOSMB1				Cytoplasmic	NO_SP	CYT
WP_012387939.1	LEPBI_RS04570		hypothetical protein	chromosome	I	tBOSMB2	WP_000943435.1	0.36028000000000004		Cytoplasmic	SP	CYT
WP_012387941.1	LEPBI_RS04580		hypothetical protein	chromosome	I	tBOSMB4	WP_000586914.1	0.547315		Unknown	NO_SP	CYT
WP_012387944.1	LEPBI_RS04595		UDP-glucose/GDP-ma	chromosome	I	tBOSMB7	WP_000861675.1	0.7803081	M	Cytoplasmic	NO_SP	CYT
WP_012387945.1	LEPBI_RS04600		thioredoxin fold dom	chromosome	I	tBOSMB8				Cytoplasmic	SP	Spl
WP_012387946.1	LEPBI_RS04605	hisE	phosphoribosyl-ATP d	chromosome	I	sBOSMB9	WP_000394955.1	0.8260800000000001	E	Cytoplasmic	NO_SP	CYT
WP_012387948.1	LEPBI_RS04615	mnmC	FAD-dependent 5-carl	chromosome	I	tBOSMC1				Cytoplasmic	NO_SP	CYT
WP_012387951.1	LEPBI_RS04630		MinD/ParA family pro	chromosome	I	tBOSMC4	WP_000371641.1	0.834985	D	CytoplasmicMembrane	NO_SP	CYT
WP_012387953.1	LEPBI_RS04640	whiG	RNA polymerase sigma	chromosome	I	tBOSMC6	WP_000039671.1	0.9041399999999999	K	Cytoplasmic	NO_SP	CYT
WP_012387954.1	LEPBI_RS04645		FapA family protein	chromosome	I	tBOSMC7	WP_000535110.1	0.7154235	N	Cytoplasmic	NO_SP	CYT
WP_012387957.1	LEPBI_RS04660		DUF370 domain-cont	chromosome	I	sBOSMD0	WP_000077420.1	0.683844	M	Unknown	NO_SP	CYT
WP_012387958.1	LEPBI_RS04665		guanylate kinase	chromosome	I	tBOSMD1	WP_082274816.1	0.5834282499999999	F	Cytoplasmic	NO_SP	CYT
WP_012387959.1	LEPBI_RS04670		flagellar protein FliB	chromosome	I	tBOSMD2	WP_000157730.1	0.6569343		Cytoplasmic	NO_SP	TMH
WP_012387960.1	LEPBI_RS04675	fliJ	flagellar export protei	chromosome	I	tBOSMD3	WP_000819760.1	0.451295		Unknown	NO_SP	CYT
WP_041769964.1	LEPBI_RS04680		SpoIIE family protein	chromosome	I	tBOSMD4			T	CytoplasmicMembrane	SP	Spl
WP_012387962.1	LEPBI_RS04685		FliI/YscN family ATPas	chromosome	I	tBOSMD5	WP_000570583.1	0.72919	N	Cytoplasmic	NO_SP	CYT
WP_041769965.1	LEPBI_RS04690		hypothetical protein	chromosome	I	tBOSMD6				Unknown	NO_SP	CYT
WP_002973161.1	LEPBI_RS04695		hypothetical protein	chromosome	I	tBOSMD7	WP_000802848.1	0.6337905		Unknown	NO_SP	CYT
WP_012387965.1	LEPBI_RS04705	murA	UDP-N-acetylglucosan	chromosome	I	tBOSMD9	WP_001257925.1	0.831897	M	Cytoplasmic	NO_SP	CYT
WP_012387966.1	LEPBI_RS04710		hypothetical protein	chromosome	I	tBOSME0				Cytoplasmic	NO_SP	TMH
WP_012387967.1	LEPBI_RS04715		glycoside hydrolase fa	chromosome	I	tBOSME1	WP_000621166.1	0.5511312	G	CytoplasmicMembrane	SP	TMH
WP_012387968.1	LEPBI_RS04720		DUF3095 domain-con	chromosome	I	tBOSME2	WP_000616634.1	0.5167104		Cytoplasmic	NO_SP	CYT
WP_012476179.1	LEPBI_RS04725		hypothetical protein	chromosome	I	tBOSME3				Extracellular	LIPO	SplI
WP_012387972.1	LEPBI_RS04740		arylesterase	chromosome	I	tBOSME6	WP_000458621.1	0.56217525	D	Periplasmic	LIPO	SplI
WP_012387973.1	LEPBI_RS04745		TenA family protein	chromosome	I	tBOSME7			H	Unknown	NO_SP	CYT
WP_012387974.1	LEPBI_RS04755	tig	trigger factor	chromosome	I	tBOSME8	WP_000384982.1	0.5126417999999999	O	Cytoplasmic	NO_SP	CYT
WP_012387975.1	LEPBI_RS04760		ATP-dependent Clp pr	chromosome	I	tBOSME9	WP_000111455.1	0.7814960999999999	O	Cytoplasmic	NO_SP	CYT
WP_012387976.1	LEPBI_RS04765	clpX	ATP-dependent Clp pr	chromosome	I	sBOSMF0	WP_001085747.1	0.76279345	O	Cytoplasmic	NO_SP	CYT
WP_012387977.1	LEPBI_RS04770	bla	subclass B1 metallo-b	chromosome	I	tBOSMF1				Unknown	LIPO	TMH
WP_012387980.1	LEPBI_RS04785		twin-arginine transloc	chromosome	I	tBOSMF4	WP_000457916.1	0.6092609999999999		CytoplasmicMembrane	NO_SP	CYT
WP_012387981.1	LEPBI_RS04790		PAS domain S-box pro	chromosome	I	tBOSMF5				Unknown	NO_SP	CYT
WP_012387982.1	LEPBI_RS04795		alpha/beta hydrolase	chromosome	I	tBOSMF6	WP_000698133.1	0.5772048000000001		Cytoplasmic	LIPO	Spl
WP_167530794.1	LEPBI_RS04800		copper chaperone PCi	chromosome	I	tBOSMF7				Cytoplasmic	NO_SP	CYT

WP_012387985.1	LEPBI_RS04810		M3 family metallopep chromosome	I	tBOSMF9	WP_000483795.1	0.62467515	O	Cytoplasmic	NO_SP	CYT
WP_012387986.1	LEPBI_RS04815		DUF393 domain-cont chromosome	I	tBOSMG0	WP_001190402.1	0.48225799999999996	R	Unknown	NO_SP	CYT
WP_012387987.1	LEPBI_RS04820		glycosyltransferase fa chromosome	I	tBOSMG1			M	CytoplasmicMembrane	SP	TMH
WP_012387990.1	LEPBI_RS04835		hypothetical protein chromosome	I	tBOSMG4				CytoplasmicMembrane	LIPO	SpII
WP_012476181.1	LEPBI_RS04845		FecR domain-containi chromosome	I	tBOSMG6	WP_000581670.1	0.4362866		Unknown	SP	SpI
WP_143708627.1	LEPBI_RS04850		channel protein TolC chromosome	I	tBOSMG7				Unknown	NO_SP	CYT
WP_012387998.1	LEPBI_RS04875		efflux RND transporte chromosome	I	tBOSMH2	WP_000584329.1	0.29899200000000004		Cytoplasmic	NO_SP	TMH
WP_012387999.1	LEPBI_RS04880		efflux RND transporte chromosome	I	tBOSMH3			V	CytoplasmicMembrane	NO_SP	TMH
WP_012388001.1	LEPBI_RS04890		TIGR04388 family proi chromosome	I	tBOSMH5				Unknown	SP	CYT
WP_012388002.1	LEPBI_RS04895		hypothetical protein chromosome	I	tBOSMH6				Cytoplasmic	LIPO	CYT
WP_012388003.1	LEPBI_RS04900		adenylate/guanylate c chromosome	I	tBOSMH7			T	Cytoplasmic	NO_SP	CYT
WP_012388004.1	LEPBI_RS04905		cellulase family glycos chromosome	I	tBOSMH8	WP_000391771.1	0.4226112		Cytoplasmic	NO_SP	CYT
WP_012388005.1	LEPBI_RS04910		O-antigen ligase famil chromosome	I	tBOSMH9	WP_000004000.1	0.52140389999999999		CytoplasmicMembrane	NO_SP	TMH
WP_012388006.1	LEPBI_RS04915		glycosyltransferase chromosome	I	tBOSMI0	WP_001222086.1	0.71785819999999999	M	Cytoplasmic	NO_SP	CYT
WP_012476183.1	LEPBI_RS04935		DUF4254 domain-con chromosome	I	tBOSMI4	WP_001207830.1	0.66716114999999999		Cytoplasmic	NO_SP	CYT
WP_012388011.1	LEPBI_RS04940		NRDE family protein chromosome	I	tBOSMI5			R	Unknown	NO_SP	CYT
WP_012388012.1	LEPBI_RS04945		serine hydroxymethyl chromosome	I	sBOSMI6	WP_001160150.1	0.85182499999999999	E	Cytoplasmic	NO_SP	CYT
WP_012388013.1	LEPBI_RS04950		lipoate--protein ligase chromosome	I	tBOSMI7	WP_001258780.1	0.4515056	H	Cytoplasmic	NO_SP	CYT
WP_012388015.1	LEPBI_RS04960		MBL fold metallo-hydr chromosome	I	tBOSMI9	WP_000636970.1	0.61757685		Cytoplasmic	NO_SP	CYT
WP_041769968.1	LEPBI_RS04965		PBP1A family penicilli chromosome	I	tBOSMJ0	WP_000835640.1	0.7304136	M	CytoplasmicMembrane	NO_SP	SpI
WP_012388017.1	LEPBI_RS04970		tetratricopeptide repe chromosome	I	tBOSMJ1				Unknown	SP	SpI
WP_012388019.1	LEPBI_RS04980		MBOAT family proteir chromosome	I	tBOSMJ3	WP_000898568.1	0.63478499999999999	M	CytoplasmicMembrane	NO_SP	TMH
WP_012388020.1	LEPBI_RS04985	sppA	signal peptide peptidz chromosome	I	tBOSMJ4	WP_000682856.1	0.6306496	O	CytoplasmicMembrane	LIPO	CYT
WP_012388021.1	LEPBI_RS04990		aldose 1-epimerase chromosome	I	tBOSMJ5	WP_000461624.1	0.32723445	G	Cytoplasmic	NO_SP	CYT
WP_012388024.1	LEPBI_RS05005		TIGR00730 family Ros chromosome	I	tBOSMJ8			F	Cytoplasmic	NO_SP	CYT
WP_012388025.1	LEPBI_RS05010		50S ribosomal protein chromosome	I	sBOSMJ9	WP_000113840.1	0.735984	J	Cytoplasmic	NO_SP	CYT
WP_012388029.1	LEPBI_RS05025		UbiX family flavin prei chromosome	I	tBOSMK3	WP_000780086.1	0.72382370000000001	H	Unknown	NO_SP	CYT
WP_012476185.1	LEPBI_RS05030		acyl-CoA thioesterase chromosome	I	tBOSMK4	WP_000451642.1	0.58295510000000001	I	Cytoplasmic	NO_SP	CYT
WP_012388031.1	LEPBI_RS05035	pyrB	aspartate carbamoylri chromosome	I	sBOSMK5	WP_001982280.1	0.864055	F	Cytoplasmic	NO_SP	CYT
WP_012388033.1	LEPBI_RS05045		LL-diaminopimelate a chromosome	I	sBOSMK7	WP_001284168.1	0.811275	E	Cytoplasmic	NO_SP	CYT
WP_012388035.1	LEPBI_RS05055		hypothetical protein chromosome	I	tBOSMK9	WP_000478876.1	0.327276		Unknown	SP	CYT
WP_012388036.1	LEPBI_RS05060		transcriptional regulat chromosome	I	tBOSML0	WP_000687885.1	0.50795074999999999		Cytoplasmic	NO_SP	CYT
WP_012388037.1	LEPBI_RS05065	rho	transcription terminat chromosome	I	tBOSMW8	WP_000179609.1	0.81325245000000001	K	Cytoplasmic	NO_SP	CYT
WP_012388038.1	LEPBI_RS05070	rpmE	50S ribosomal protein chromosome	I	sBOSMW9	WP_000845534.1	0.72749400000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388039.1	LEPBI_RS05075		pentapeptide repeat- chromosome	I	tBOSMX0	WP_000115243.1	0.7889607		Cytoplasmic	NO_SP	CYT
WP_012388040.1	LEPBI_RS05080		hypothetical protein chromosome	I	tBOSMX1	WP_000802251.1	0.5863928		Unknown	NO_SP	CYT
WP_012388041.1	LEPBI_RS05085		STAS domain-containi chromosome	I	tBOSMX2	WP_000908508.1	0.55471710000000001		Unknown	NO_SP	CYT
WP_012388042.1	LEPBI_RS05090		hypothetical protein chromosome	I	tBOSMX3	WP_000683163.1	0.39643900000000004		Unknown	LIPO	SpII
WP_012388043.1	LEPBI_RS05095		DUF342 domain-cont chromosome	I	tBOSMX4	WP_001973629.1	0.70056794999999999	N	Cytoplasmic	NO_SP	CYT
WP_012388045.1	LEPBI_RS05105		RNA methyltransferas chromosome	I	tBOSMX6	WP_000280345.1	0.57271725000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388046.1	LEPBI_RS05110		class I SAM-dependen chromosome	I	tBOSMX7	WP_000844813.1	0.58449900000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388048.1	LEPBI_RS05120		citrate synthase chromosome	I	tBOSMX9	WP_000852462.1	0.87062	C	Cytoplasmic	NO_SP	CYT
WP_012388049.1	LEPBI_RS05125		lytic transglycosylase chromosome	I	tBOSMY0	WP_000712694.1	0.51059499999999999	M	Periplasmic	SP	SpI
WP_012388050.1	LEPBI_RS05130		hypothetical protein chromosome	I	tBOSMY1				Cytoplasmic	NO_SP	CYT

WP_012388051.1	LEPBI_RS05135		hypothetical protein	chromosome	I	tBOSMY2	WP_001008019.1	0.685565		Cytoplasmic	NO_SP	CYT
WP_012388052.1	LEPBI_RS05140		polymer-forming cyto	chromosome	I	tBOSMY3	WP_001229815.1	0.9417800000000001	Z	Cytoplasmic	NO_SP	CYT
WP_012388053.1	LEPBI_RS05145		4-hydroxythreonine-4	chromosome	I	tBOSMY4	WP_001079897.1	0.5125584	H	Cytoplasmic	NO_SP	CYT
WP_012388055.1	LEPBI_RS05155		DegT/DnrJ/EryC1/StrS	chromosome	I	tBOSMY6	WP_000538752.1	0.74580165	M	Cytoplasmic	NO_SP	CYT
WP_187148081.1	LEPBI_RS05160		hypothetical protein	chromosome	I	tBOSMY7	WP_000411557.1	0.442764		CytoplasmicMembrane	NO_SP	Spl
WP_135578823.1	LEPBI_RS05180		hypothetical protein	chromosome	I	tBOSMZ1				OuterMembrane	NO_SP	CYT
WP_012388061.1	LEPBI_RS05185		2-oxoglutarate dehydri	chromosome	I	tBOSMZ2	WP_000687652.1	0.73174365	C	Cytoplasmic	NO_SP	CYT
WP_012388062.1	LEPBI_RS05190	lpdA	dihydrolipoyl dehydro	chromosome	I	tBOSMZ3	WP_001271670.1	0.7169926500000001	C	Cytoplasmic	NO_SP	CYT
WP_012388063.1	LEPBI_RS05195	odhB	2-oxoglutarate dehydri	chromosome	I	tBOSMZ4	WP_000110035.1	0.739905	C	Cytoplasmic	NO_SP	CYT
WP_041769970.1	LEPBI_RS05200		gamma carbonic anhy	chromosome	I	tBOSMZ5	WP_000841462.1	0.69471465	R	Cytoplasmic	NO_SP	CYT
WP_012388067.1	LEPBI_RS05220		SpoII E family protein	chromosome	I	tBOSMZ8	WP_001136707.1	0.6599443500000001	T	Unknown	NO_SP	CYT
WP_012388072.1	LEPBI_RS05240		hypothetical protein	chromosome	I	tBOSN03				Extracellular	LIPO	CYT
WP_012476191.1	LEPBI_RS05250		response regulator	chromosome	I	tBOSN05	WP_000597511.1	0.3963080500000001	T	CytoplasmicMembrane	LIPO	CYT
WP_012388075.1	LEPBI_RS05255		sigma-70 family RNA	chromosome	I	tBOSN06			K	Cytoplasmic	NO_SP	CYT
WP_012388077.1	LEPBI_RS05265		OmpA family protein	chromosome	I	tBOSN08				Unknown	SP	TMH
WP_012388081.1	LEPBI_RS05290		PAS domain S-box pro	chromosome	I	tBOSN12			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388083.1	LEPBI_RS05300		adenylate/guanylate	chromosome	I	tBOSN14			T	CytoplasmicMembrane	NO_SP	TMH
WP_012388084.1	LEPBI_RS05305		GGDEF domain-contai	chromosome	I	tBOSN15			T	CytoplasmicMembrane	NO_SP	TMH
WP_012388086.1	LEPBI_RS05315		methyl-accepting chei	chromosome	I	tBOSN17			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388088.1	LEPBI_RS05330		histidine kinase	chromosome	I	tBOSN19				CytoplasmicMembrane	LIPO	CYT
WP_012388089.1	LEPBI_RS05335		hypothetical protein	chromosome	I	tBOSN20				Unknown	SP	Spl
WP_041769973.1	LEPBI_RS05345		hypothetical protein	chromosome	I	tBOSN22				Unknown	NO_SP	CYT
WP_012388092.1	LEPBI_RS05350		membrane protein	chromosome	I	tBOSN23				CytoplasmicMembrane	NO_SP	TMH
WP_012476194.1	LEPBI_RS05355		hypothetical protein	chromosome	I	tBOSN24				Unknown	SP	Spl
WP_012476195.1	LEPBI_RS05360		MBL fold metallo-hydri	chromosome	I	tBOSN25				Unknown	SP	SplI
WP_012476196.1	LEPBI_RS05370		MBL fold metallo-hydri	chromosome	I	tBOSN27	WP_000680449.1	0.34324185	G	Cytoplasmic	LIPO	CYT
WP_012388097.1	LEPBI_RS05375		SRPBCC domain-conta	chromosome	I	tBOSN28				Unknown	NO_SP	CYT
WP_012388100.1	LEPBI_RS05385		hypothetical protein	chromosome	I	tBOSN31				Cytoplasmic	SP	CYT
WP_012388107.1	LEPBI_RS05420		DUF4349 domain-con	chromosome	I	tBOSN38	WP_000927508.1	0.3580272		Unknown	LIPO	SplI
WP_012388108.1	LEPBI_RS05425		amidohydrolase famil	chromosome	I	tBOSN39				Cytoplasmic	NO_SP	CYT
WP_012388110.1	LEPBI_RS05435		sodium:solute sympoi	chromosome	I	tBOSN41	WP_002067908.1	0.52701725	E	CytoplasmicMembrane	NO_SP	TMH
WP_041769977.1	LEPBI_RS05445		long-chain fatty acid--	chromosome	I	tBOSN43			I	CytoplasmicMembrane	NO_SP	CYT
WP_012388113.1	LEPBI_RS05450		acyl-CoA dehydrogen:	chromosome	I	tBOSN44	WP_000898172.1	0.5925504	I	Cytoplasmic	NO_SP	CYT
WP_012388115.1	LEPBI_RS05460		MaoC family dehydrat	chromosome	I	tBOSN46	WP_000276952.1	0.8057021999999999	I	Unknown	NO_SP	CYT
WP_012388119.1	LEPBI_RS05480		FAD-dependent oxido	chromosome	I	tBOSN50	WP_000778114.1	0.43124895	E	Unknown	TAT	Spl
WP_012476199.1	LEPBI_RS05485		ATP-binding protein	chromosome	I	tBOSN51				CytoplasmicMembrane	SP	Spl
WP_012388121.1	LEPBI_RS05490		50S ribosomal protein	chromosome	I	tBOSN52	WP_001270455.1	0.5627358	J	Cytoplasmic	NO_SP	CYT
WP_012388122.1	LEPBI_RS05495		helix-turn-helix transc	chromosome	I	tBOSN53	WP_001067493.1	0.8335311000000001		Cytoplasmic	NO_SP	CYT
WP_012388124.1	LEPBI_RS05505		haloacid dehalogenas	chromosome	I	tBOSN55	WP_000176746.1	0.5173495		Cytoplasmic	NO_SP	CYT
WP_012388129.1	LEPBI_RS05535	trpS	tryptophan--tRNA liga	chromosome	I	tBOSN60	WP_001221811.1	0.6848000000000001	J	Cytoplasmic	NO_SP	CYT
WP_041769978.1	LEPBI_RS05540		hypothetical protein	chromosome	I	tBOSN61	WP_000016926.1	0.5849914		Cytoplasmic	NO_SP	CYT
WP_012388131.1	LEPBI_RS05545		outer membrane lipoi	chromosome	I	tBOSN62	WP_000874918.1	0.57978605		Unknown	SP	Spl
WP_012388132.1	LEPBI_RS05550		electron transfer flavc	chromosome	I	tBOSN63	WP_000072965.1	0.804075	C	Unknown	NO_SP	CYT
WP_012388133.1	LEPBI_RS05555		electron transfer flavc	chromosome	I	tBOSN64	WP_000692396.1	0.83598	C	Cytoplasmic	NO_SP	CYT

WP_012388137.1	LEPBI_RS05580		acyl-CoA dehydrogenase	chromosome	I	tBOSN68	WP_001202091.1	0.8349207999999999	I	Cytoplasmic	NO_SP	CYT
WP_012388138.1	LEPBI_RS05585		FAD-dependent oxidoreductase	chromosome	I	tBOSN69			Q	Unknown	NO_SP	CYT
WP_012388139.1	LEPBI_RS05590	thrB	homoserine kinase	chromosome	I	tBOSN70	WP_000095033.1	0.52838325	E	Unknown	NO_SP	CYT
WP_012388141.1	LEPBI_RS05600		hypothetical protein	chromosome	I	tBOSN72				Unknown	NO_SP	CYT
WP_012388142.1	LEPBI_RS05605		thioredoxin domain-containing	chromosome	I	tBOSN73	WP_000651714.1	0.5085822999999999	O	Unknown	NO_SP	Spl
WP_012388143.1	LEPBI_RS05610		malate dehydrogenase	chromosome	I	sBOSN74	WP_000048017.1	0.843575	C	Unknown	NO_SP	CYT
WP_012388146.1	LEPBI_RS05625	prmC	peptide chain release factor	chromosome	I	tBOSNI3	WP_001164600.1	0.55264275	J	Cytoplasmic	NO_SP	CYT
WP_039936944.1	LEPBI_RS05635		Crp/Fnr family transcription factor	chromosome	I	tBOSNI4	WP_000367409.1	0.7248569999999999	T	Cytoplasmic	NO_SP	CYT
WP_012388147.1	LEPBI_RS05640		tetratricopeptide repeat	chromosome	I	tBOSNI5	WP_000918546.1	0.65482065		Cytoplasmic	NO_SP	CYT
WP_012388150.1	LEPBI_RS05655		elongation factor G	chromosome	I	tBOSNI8	WP_000102023.1	0.85553	J	Cytoplasmic	NO_SP	CYT
WP_012388152.1	LEPBI_RS05665		hypothetical protein	chromosome	I	tBOSNJ0				Cytoplasmic	NO_SP	CYT
WP_041769980.1	LEPBI_RS05675		TlpA family protein domain	chromosome	I	tBOSNJ2	WP_000675947.1	0.3938664		CytoplasmicMembrane	NO_SP	TMH
WP_012388157.1	LEPBI_RS05690		polyhydroxyalkanoate synthase	chromosome	I	tBOSNJ5	WP_000771343.1	0.7589708		Cytoplasmic	NO_SP	CYT
WP_012476205.1	LEPBI_RS05695		HEAT repeat domain-containing	chromosome	I	tBOSNJ6	WP_000475809.1	0.40229760000000003		Unknown	SP	Spl
WP_012388159.1	LEPBI_RS05700	cysK	cysteine synthase A	chromosome	I	tBOSNJ7	WP_000644947.1	0.8150562	E	Cytoplasmic	NO_SP	CYT
WP_081431657.1	LEPBI_RS05705	topA	type I DNA topoisomerase	chromosome	I	tBOSNJ8	WP_000054706.1	0.45215239999999995	L	Cytoplasmic	NO_SP	CYT
WP_012388161.1	LEPBI_RS05710	hemH	ferrochelatase	chromosome	I	sBOSNJ9	WP_080011809.1	0.57956639999999999	H	Cytoplasmic	NO_SP	CYT
WP_012388162.1	LEPBI_RS05715		NAD(P)-binding protein	chromosome	I	tBOSNK0	WP_001260288.1	0.4198608	H	Cytoplasmic	NO_SP	CYT
WP_012388163.1	LEPBI_RS05720	hemN	oxygen-independent class I	chromosome	I	tBOSNK1	WP_001982947.1	0.66146355	H	Cytoplasmic	NO_SP	CYT
WP_012388164.1	LEPBI_RS05725		uroporphyrinogen decarboxylase	chromosome	I	tBOSNK2	WP_001132417.1	0.5797044	H	Cytoplasmic	NO_SP	CYT
WP_012388165.1	LEPBI_RS05730		glutamate-1-semialdehyde lyase	chromosome	I	sBOSNK3	WP_001075132.1	0.706344	H	Cytoplasmic	NO_SP	CYT
WP_012388166.1	LEPBI_RS05735	hemB	prophobilinogen synthase	chromosome	I	tBOSNK4	WP_000448656.1	0.70347	H	Cytoplasmic	NO_SP	CYT
WP_012388167.1	LEPBI_RS05740		uroporphyrinogen synthase	chromosome	I	tBOSNK5	WP_000086813.1	0.48360000000000003	H	Cytoplasmic	NO_SP	CYT
WP_012388169.1	LEPBI_RS05750	msrB	peptide-methionine S-methyltransferase	chromosome	I	tBOSNK7	WP_002070109.1	0.6708276	O	Cytoplasmic	NO_SP	CYT
WP_012476206.1	LEPBI_RS05770		hypothetical protein	chromosome	I	tBOSNL2				Cytoplasmic	LIPO	CYT
WP_012476207.1	LEPBI_RS05780	cobA	uroporphyrinogen-III cosynthase	chromosome	I	tBOSNL4	WP_000930524.1	0.49984000000000006	H	Cytoplasmic	NO_SP	CYT
WP_012388177.1	LEPBI_RS05785		sulfite reductase subunit alpha	chromosome	I	tBOSNL5			F	CytoplasmicMembrane	NO_SP	CYT
WP_012388178.1	LEPBI_RS05790		NADPH-dependent aspartate aminotransferase	chromosome	I	sBOSNL6	WP_001287342.1	0.4608205	P	Cytoplasmic	NO_SP	CYT
WP_012388179.1	LEPBI_RS05795		50S ribosome-binding protein	chromosome	I	tBOSNL7	WP_000365065.1	0.76478985000000001	P	Cytoplasmic	NO_SP	CYT
WP_012388180.1	LEPBI_RS05800	cysD	sulfate adenylyltransferase	chromosome	I	tBOSNL8	WP_001972962.1	0.88273350000000001	E	Cytoplasmic	NO_SP	CYT
WP_012388181.1	LEPBI_RS05805		phosphoadenylyl-sulfite lyase	chromosome	I	tBOSNL9	WP_000993603.1	0.5856582	E	Cytoplasmic	NO_SP	CYT
WP_012388182.1	LEPBI_RS05810		sulfate/molybdate ABC transporter	chromosome	I	tBOSNM0	WP_000510777.1	0.76406000000000001	P	CytoplasmicMembrane	NO_SP	CYT
WP_187148082.1	LEPBI_RS05825		sulfate ABC transporter	chromosome	I	tBOSNM3	WP_000842617.1	0.649848	P	Periplasmic	SP	CYT
WP_012388186.1	LEPBI_RS05835		flagellar hook-length control	chromosome	I	tBOSNM4				Unknown	NO_SP	CYT
WP_012388188.1	LEPBI_RS05845	flgE	flagellar hook protein	chromosome	I	tBOSNM6	WP_000986372.1	0.85451500000000001	N	Extracellular	NO_SP	CYT
WP_012388189.1	LEPBI_RS05850		tetratricopeptide repeat	chromosome	I	tBOSNM7				Unknown	NO_SP	CYT
WP_041769700.1	LEPBI_RS05860		GAF domain-containing protein	chromosome	I	tBOSNM9	WP_000802798.1	0.6825063	T	Unknown	NO_SP	CYT
WP_012388193.1	LEPBI_RS05870	murD	UDP-N-acetylmuramic acid deacetylase	chromosome	I	tBOSNN1	WP_000671558.1	0.496872	M	Cytoplasmic	NO_SP	CYT
WP_012388194.1	LEPBI_RS05875		STAS domain-containing protein	chromosome	I	tBOSNN2	WP_000884017.1	0.86365	T	Unknown	NO_SP	CYT
WP_012388195.1	LEPBI_RS05880		indole-3-glycerol phosphate synthase	chromosome	I	tBOSNN3	WP_000099241.1	0.62046535	E	Cytoplasmic	NO_SP	CYT
WP_012388196.1	LEPBI_RS05885		MASE1 domain-containing protein	chromosome	I	tBOSNN4			T	CytoplasmicMembrane	NO_SP	TMH
WP_012388198.1	LEPBI_RS05900		clan AA aspartic protease	chromosome	I	tBOSNN6				Cytoplasmic	NO_SP	CYT
WP_012388201.1	LEPBI_RS05915		ankyrin repeat domain-containing	chromosome	I	tBOSNN9				CytoplasmicMembrane	NO_SP	TMH
WP_012388202.1	LEPBI_RS05920		right-handed parallel beta-sheet	chromosome	I	tBOSNPO				Unknown	SP	Spl



WP_012388203.1	LEPBI_RS05925		cytochrome-c peroxid	chromosome	I	tBOSNP1			O	Unknown	SP	CYT
WP_012476210.1	LEPBI_RS05955		hypothetical protein	chromosome	I	tBOSNP8				Extracellular	SP	CYT
WP_143708628.1	LEPBI_RS05965		IS3 family transposase	chromosome	I	tBOSNQ0				Cytoplasmic	NO_SP	CYT
WP_012388222.1	LEPBI_RS06010		hypothetical protein	chromosome	I	tBOSNR0	WP_000611763.1	0.6404715999999999		OuterMembrane	SP	Spl
WP_012388224.1	LEPBI_RS06020	leuC	3-isopropylmalate del	chromosome	I	tBOSNR2	WP_000855526.1	0.6632059499999999	E	Cytoplasmic	NO_SP	CYT
WP_012388227.1	LEPBI_RS06035		chemotaxis protein	chromosome	I	tBOSNR5			T	CytoplasmicMembrane	NO_SP	CYT
WP_012476212.1	LEPBI_RS06040		ankyrin repeat domain	chromosome	I	tBOSNR6				Cytoplasmic	NO_SP	CYT
WP_012388229.1	LEPBI_RS06045		hypothetical protein	chromosome	I	tBOSNR7				Unknown	LIPO	TMH
WP_012388231.1	LEPBI_RS06055		transcription initiator	chromosome	I	tBOSNR9				Unknown	NO_SP	CYT
WP_012388234.1	LEPBI_RS06070		dihydrofolate reductase	chromosome	I	tBOSNS2				Cytoplasmic	NO_SP	CYT
WP_012388239.1	LEPBI_RS06100		hypothetical protein	chromosome	I	tBOSNS7				Unknown	LIPO	Spl
WP_041769983.1	LEPBI_RS06130		hypothetical protein	chromosome	I	tBOSNT3	WP_000488656.1	0.7456379000000001		Unknown	SP	Spl
WP_012388246.1	LEPBI_RS06135		hypothetical protein	chromosome	I	tBOSNT4	WP_000669416.1	0.4857125		Unknown	NO_SP	Spl
WP_012388247.1	LEPBI_RS06140		HEAT repeat domain	chromosome	I	tBOSNT5	WP_001984000.1	0.49098060000000004		Unknown	LIPO	SplI
WP_012476217.1	LEPBI_RS06150		GTP-binding protein	chromosome	I	tBOSP44			R	Cytoplasmic	NO_SP	CYT
WP_041769726.1	LEPBI_RS06160		chemotaxis protein	chromosome	I	tBOSP46			T	CytoplasmicMembrane	NO_SP	TMH
WP_012388252.1	LEPBI_RS06165		acyl-CoA dehydrogenase	chromosome	I	tBOSP47	WP_000572090.1	0.6878618999999999	I	Cytoplasmic	NO_SP	CYT
WP_187148083.1	LEPBI_RS06180		hypothetical protein	chromosome	I	tBOSP50				Unknown	SP	Spl
WP_012388256.1	LEPBI_RS06185		zinc ABC transporter	chromosome	I	tBOSP51			P	Periplasmic	SP	Spl
WP_012388259.1	LEPBI_RS06200		class I SAM-dependent	chromosome	I	tBOSP54	WP_000402845.1	0.6241650000000001		Cytoplasmic	NO_SP	CYT
WP_012388260.1	LEPBI_RS06205	tmk	dTMP kinase	chromosome	I	tBOSP55	WP_000791380.1	0.50225	F	Cytoplasmic	NO_SP	CYT
WP_041769729.1	LEPBI_RS06215		B12-binding domain	chromosome	I	tBOSP57			R	Unknown	NO_SP	CYT
WP_012388263.1	LEPBI_RS06220		DUF1577 domain	chromosome	I	tBOSP58	WP_000447930.1	0.5462063999999999		Cytoplasmic	NO_SP	CYT
WP_012388264.1	LEPBI_RS06225	guaB	IMP dehydrogenase	chromosome	I	tBOSP59	WP_000070955.1	0.823835	F	Cytoplasmic	NO_SP	CYT
WP_012388265.1	LEPBI_RS06230		outer membrane lipoprotein	chromosome	I	tBOSP60	WP_000374062.1	0.6134931		Unknown	SP	CYT
WP_012388266.1	LEPBI_RS06235		16S rRNA (uracil1498)	chromosome	I	tBOSP61	WP_000656570.1	0.44188835000000004	J	Cytoplasmic	NO_SP	CYT
WP_012476223.1	LEPBI_RS06240		hypothetical protein	chromosome	I		WP_001228481.1	0.485		Unknown	LIPO	Spl
WP_012388267.1	LEPBI_RS06245		hypothetical protein	chromosome	I	tBOSP62	WP_000016317.1	0.3899665		Cytoplasmic	NO_SP	CYT
WP_012388269.1	LEPBI_RS06255		hypothetical protein	chromosome	I	tBOSP64				CytoplasmicMembrane	NO_SP	TMH
WP_012388270.1	LEPBI_RS06260		peptidase	chromosome	I	tBOSP65	WP_001015936.1	0.47501424999999997	R	Unknown	SP	Spl
WP_041769734.1	LEPBI_RS06265		sulfatase-like hydrolase	chromosome	I	tBOSP66	WP_000847257.1	0.5200374		CytoplasmicMembrane	NO_SP	TMH
WP_012388272.1	LEPBI_RS06270	carB	carbamoyl-phosphate	chromosome	I	tBOSP67	WP_001137995.1	0.820025	E	Unknown	NO_SP	CYT
WP_187148084.1	LEPBI_RS06275		DUF1499 domain	chromosome	I	tBOSP68			S	Cytoplasmic	NO_SP	CYT
WP_012388274.1	LEPBI_RS06280		hypothetical protein	chromosome	I	tBOSP69				Unknown	SP	CYT
WP_012388276.1	LEPBI_RS06290	ispG	(E)-4-hydroxy-3-methyl	chromosome	I	tBOSP71	WP_001011583.1	0.6384114	I	Cytoplasmic	NO_SP	CYT
WP_012476225.1	LEPBI_RS06305		GHL domain	chromosome	I	tBOSP74	WP_000558136.1	0.44161200000000006	T	CytoplasmicMembrane	NO_SP	TMH
WP_012388280.1	LEPBI_RS06310		response regulator	chromosome	I	tBOSP75	WP_000655500.1	0.6925392		Cytoplasmic	NO_SP	CYT
WP_012388282.1	LEPBI_RS06320		2-isopropylmalate synthase	chromosome	I	tBOSP77	WP_000169688.1	0.7177797	E	Cytoplasmic	NO_SP	CYT
WP_012388283.1	LEPBI_RS06325		aminoacyl-tRNA hydrolase	chromosome	I	tBOSP78	WP_001284985.1	0.5505234999999999	J	Cytoplasmic	NO_SP	CYT
WP_012388286.1	LEPBI_RS06340		replication-associated	chromosome	I	tBOSP81	WP_001281336.1	0.5891613	L	Cytoplasmic	NO_SP	CYT
WP_012388288.1	LEPBI_RS06350		NADH-quinone oxidoreductase	chromosome	I	sBOSP83	WP_000524416.1	0.8856243	C	CytoplasmicMembrane	NO_SP	CYT
WP_012388289.1	LEPBI_RS06355		NADH-quinone oxidoreductase	chromosome	I	tBOSP84	WP_000660863.1	0.62881705	C	Cytoplasmic	NO_SP	CYT
WP_012388290.1	LEPBI_RS06360		NADH-quinone oxidoreductase	chromosome	I	sBOSP85	WP_000990075.1	0.89257	C	Cytoplasmic	NO_SP	CYT
WP_012476227.1	LEPBI_RS06365		NAD(P)H-dependent	chromosome	I	tBOSP86	WP_000540770.1	0.7299468	C	Unknown	NO_SP	CYT

WP_012388292.1	LEPBI_RS06370	nuoF	NADH-quinone oxidor	chromosome	I	tBOSP87	WP_000829480.1	0.7077964999999999	C	Cytoplasmic	NO_SP	CYT
WP_012388293.1	LEPBI_RS06375	nuoH	NADH-quinone oxidor	chromosome	I	sBOSP88	WP_001104353.1	0.76341375	C	CytoplasmicMembrane	NO_SP	TMH
WP_041769742.1	LEPBI_RS06380		NADH-quinone oxidor	chromosome	I	tBOSP89	WP_000010969.1	0.48214559999999995		CytoplasmicMembrane	NO_SP	TMH
WP_012388296.1	LEPBI_RS06390	nuoL	NADH-quinone oxidor	chromosome	I	tBOSP91	WP_000406351.1	0.6149286	C	CytoplasmicMembrane	NO_SP	CYT
WP_012388297.1	LEPBI_RS06395		NADH-quinone oxidor	chromosome	I	tBOSP92	WP_000347200.1	0.5970107499999999	C	CytoplasmicMembrane	NO_SP	TMH
WP_041769985.1	LEPBI_RS06405		cupin domain-contain	chromosome	I	sBOSP94	WP_000201440.1	0.6300211499999999	E	Cytoplasmic	NO_SP	CYT
WP_049755978.1	LEPBI_RS06410	recJ	single-stranded-DNA-:	chromosome	I	tBOSP95	WP_000615876.1	0.5053628	L	Cytoplasmic	NO_SP	CYT
WP_012388301.1	LEPBI_RS06415		polymer-forming cyto	chromosome	I	tBOSP96	WP_001278842.1	0.693405	Z	Cytoplasmic	NO_SP	CYT
WP_012388303.1	LEPBI_RS06425		efflux RND transporte	chromosome	I	tBOSP98	WP_000565850.1	0.7215070499999998	P	CytoplasmicMembrane	NO_SP	TMH
WP_012388304.1	LEPBI_RS06430		inorganic pyrophosph	chromosome	I	tBOSP99	WP_000233562.1	0.4083072	C	Cytoplasmic	NO_SP	CYT
WP_012388305.1	LEPBI_RS06435		TolC family protein	chromosome	I	tBOSPA0	WP_000254988.1	0.4872645		OuterMembrane	LIPO	CYT
WP_012388307.1	LEPBI_RS06445	lexA	transcriptional repres:	chromosome	I	sBOSPA2	WP_000654116.1	0.79063	K	Cytoplasmic	NO_SP	CYT
WP_012388308.1	LEPBI_RS06450		hypothetical protein	chromosome	I	tBOSPA3	WP_000283525.1	0.42464694999999997		Unknown	LIPO	SpII
WP_012388309.1	LEPBI_RS06455		S41 family peptidase	chromosome	I	tBOSPA4	WP_000790723.1	0.6025138	O	CytoplasmicMembrane	SP	CYT
WP_012388313.1	LEPBI_RS06475		MBL fold metallo-hydi	chromosome	I	tBOSPA8	WP_001220497.1	0.779895	P	Cytoplasmic	NO_SP	CYT
WP_012388314.1	LEPBI_RS06480	glpK	glycerol kinase GlpK	chromosome	I	sBOSPA9	WP_001286755.1	0.7746947999999999	C	Cytoplasmic	NO_SP	CYT
WP_012388317.1	LEPBI_RS06495		iron-containing alcoh	chromosome	I	tBOSPB2	WP_001122022.1	0.7590250000000001	C	Cytoplasmic	NO_SP	CYT
WP_012388318.1	LEPBI_RS06500		flagellar biosynthesis :	chromosome	I	tBOSPB3	WP_000150993.1	0.6682250000000001		Unknown	NO_SP	CYT
WP_012388319.1	LEPBI_RS06505	rsmI	16S rRNA (cytidine(14	chromosome	I	sBOSPB4	WP_001083572.1	0.5698608999999999	J	Cytoplasmic	NO_SP	CYT
WP_012388321.1	LEPBI_RS06515		hypothetical protein	chromosome	I	tBOSPB6	WP_000623631.1	0.46783935		Unknown	NO_SP	CYT
WP_012388322.1	LEPBI_RS06520	nadE	NAD(+) synthase	chromosome	I	tBOSPB7	WP_001192276.1	0.5699182500000001	H	Cytoplasmic	NO_SP	CYT
WP_012388325.1	LEPBI_RS06535		hypothetical protein	chromosome	I	tBOSPC0				Unknown	NO_SP	SpI
WP_012388326.1	LEPBI_RS06540		YggS family pyridoxal	chromosome	I	tBOSPC1	WP_000538451.1	0.5876890499999999	H	Cytoplasmic	NO_SP	CYT
WP_012476228.1	LEPBI_RS06545	proC	pyrroline-5-carboxylat	chromosome	I	tBOSPC2	WP_002080974.1	0.53802	E	Cytoplasmic	NO_SP	CYT
WP_012388328.1	LEPBI_RS06555		sensor domain-contai	chromosome	I	tBOSPC3	WP_000623745.1	0.7418020499999999	T	Cytoplasmic	NO_SP	CYT
WP_012388331.1	LEPBI_RS06570	mnmA	tRNA 2-thiouridine(34	chromosome	I	sBOSPC6	WP_000033461.1	0.7741375999999999	J	Cytoplasmic	NO_SP	CYT
WP_012388332.1	LEPBI_RS06575		alpha-hydroxy-acid ox	chromosome	I	tBOSPC7	WP_000058904.1	0.7201970999999999	C	Cytoplasmic	NO_SP	CYT
WP_012476230.1	LEPBI_RS06580		PilZ domain-containin	chromosome	I	tBOSPC8	WP_000357129.1	0.49998		Cytoplasmic	NO_SP	CYT
WP_012388336.1	LEPBI_RS06595		hypothetical protein	chromosome	I	tBOSPD1	WP_000735123.1	0.4332018999999999		Unknown	LIPO	SpII
WP_012388337.1	LEPBI_RS06600		lipoprotein	chromosome	I	tBOSPD2	WP_000836305.1	0.33231174999999996		Unknown	LIPO	SpII
WP_012476231.1	LEPBI_RS06605		hypothetical protein	chromosome	I	tBOSPD3	WP_000087417.1	0.33719085000000004		Cytoplasmic	SP	CYT
WP_012388339.1	LEPBI_RS06610		insulinase family prot	chromosome	I	tBOSPD4	WP_000333575.1	0.5349345	R	Cytoplasmic	SP	SpI
WP_012388340.1	LEPBI_RS06615		insulinase family prot	chromosome	I	tBOSPD5	WP_000649940.1	0.6442862999999999	R	Cytoplasmic	SP	SpI
WP_012388341.1	LEPBI_RS06620		MBL fold metallo-hydi	chromosome	I	tBOSPD6	WP_000271588.1	0.6393123		Cytoplasmic	NO_SP	CYT
WP_012476232.1	LEPBI_RS06630		hypothetical protein	chromosome	I	tBOSPD8	WP_000096242.1	0.42858270000000004		Unknown	SP	SpI
WP_012476233.1	LEPBI_RS06635		N-acetylMuramoyl-L-a	chromosome	I	tBOSPD9	WP_001252402.1	0.5494148		Cytoplasmic	SP	SpI
WP_012388345.1	LEPBI_RS06640		hypothetical protein	chromosome	I	tBOSPE0	WP_000427173.1	0.49712685000000006		Cytoplasmic	NO_SP	CYT
WP_002973585.1	LEPBI_RS06650		Paal family thioestera	chromosome	I	tBOSPE1	WP_000648186.1	0.891775		Cytoplasmic	NO_SP	CYT
WP_012388346.1	LEPBI_RS06655		hypothetical protein	chromosome	I	tBOSPE2	WP_000209452.1	0.44078125		Cytoplasmic	NO_SP	CYT
WP_012388348.1	LEPBI_RS06665		peroxiredoxin	chromosome	I	tBOSPE4	WP_001136732.1	0.84773	V	Cytoplasmic	NO_SP	CYT
WP_012388349.1	LEPBI_RS06670	sufB	Fe-S cluster assembly	chromosome	I	tBOSPE5	WP_000438391.1	0.8674032	O	Cytoplasmic	NO_SP	CYT
WP_012476235.1	LEPBI_RS06680		PQQ-dependent suga	chromosome	I	tBOSPE7	WP_000485070.1	0.4864203	G	Unknown	LIPO	SpI
WP_012388354.1	LEPBI_RS06695	rlmN	23S rRNA (adenine(25	chromosome	I	sBOSPE8	WP_000622607.1	0.6874293	J	Cytoplasmic	NO_SP	CYT
WP_012476236.1	LEPBI_RS06700		Cys-rich protein	chromosome	I		WP_001068430.1	0.39629625000000007		Unknown	SP	CYT

WP_012388356.1	LEPBI_RS06705		glycosyltransferase fa	chromosome	I	tBOSPR0	WP_001071951.1	0.5138787499999999	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388357.1	LEPBI_RS06710		cytochrome c3 family	chromosome	I	tBOSPR1	WP_001064927.1	0.7823450000000001		Unknown	NO_SP	Spl
WP_041769987.1	LEPBI_RS06715		TAT-variant-translocase	chromosome	I	tBOSPR2	WP_000372296.1	0.661945	C	CytoplasmicMembrane	NO_SP	CYT
WP_012388359.1	LEPBI_RS06720	nrfD	polysulfide reductase	chromosome	I	tBOSPR3	WP_000063680.1	0.85825		CytoplasmicMembrane	NO_SP	CYT
WP_012388360.1	LEPBI_RS06725		DUF3341 domain-con	chromosome	I	tBOSPR4	WP_000277765.1	0.713135		Unknown	NO_SP	CYT
WP_012388361.1	LEPBI_RS06730		cytochrome c	chromosome	I	tBOSPR5	WP_000878646.1	0.6266604		Unknown	LIPO	SplI
WP_012388362.1	LEPBI_RS06735		hypothetical protein	chromosome	I	tBOSPR6	WP_000453372.1	0.6450741		CytoplasmicMembrane	NO_SP	TMH
WP_012388363.1	LEPBI_RS06740		SH3 domain-containin	chromosome	I	tBOSPR7	WP_000827840.1	0.54266		Unknown	LIPO	SplI
WP_041769988.1	LEPBI_RS06760		adenylate/guanylate c	chromosome	I	tBOSPS1				Unknown	NO_SP	CYT
WP_012476237.1	LEPBI_RS06765		AAA family ATPase	chromosome	I	tBOSPS2	WP_000654973.1	0.34595549999999997	L	Cytoplasmic	NO_SP	CYT
WP_012388371.1	LEPBI_RS06775		crotonase/enoyl-CoA	chromosome	I	tBOSPS5	WP_000848056.1	0.66115095	I	Cytoplasmic	NO_SP	CYT
WP_012388372.1	LEPBI_RS06780		prolipoprotein diacylg	chromosome	I	tBOSPS6	WP_000567061.1	0.7362085499999999		CytoplasmicMembrane	NO_SP	TMH
WP_012388374.1	LEPBI_RS06790		M23 family metallope	chromosome	I	tBOSPS8	WP_000625244.1	0.56359425	M	Unknown	NO_SP	CYT
WP_012476238.1	LEPBI_RS06795	pcnB	polynucleotide adeny	chromosome	I	tBOSPS9	WP_000670773.1	0.68112	J	Cytoplasmic	NO_SP	CYT
WP_012388376.1	LEPBI_RS06800	thiL	thiamine-phosphate k	chromosome	I	tBOSPT0	WP_000662272.1	0.5241873	H	Unknown	NO_SP	CYT
WP_012388377.1	LEPBI_RS06805	rplM	50S ribosomal protein	chromosome	I	tBOSPT1	WP_000115097.1	0.7651	J	Periplasmic	NO_SP	CYT
WP_012388378.1	LEPBI_RS06810	rpsI	30S ribosomal protein	chromosome	I	tBOSPT2	WP_001966744.1	0.731283	J	Cytoplasmic	NO_SP	CYT
WP_012388380.1	LEPBI_RS06820	alaS	alanine--tRNA ligase	chromosome	I	sBOSPT4	WP_000802930.1	0.6126466500000001	J	Cytoplasmic	NO_SP	CYT
WP_012388381.1	LEPBI_RS06825		YajQ family cyclic di-G	chromosome	I	sBOSPT5	WP_001283275.1	0.7348077	T	Cytoplasmic	NO_SP	CYT
WP_012388382.1	LEPBI_RS06830		DNA translocase FtsK	chromosome	I	tBOSPT6	WP_000444199.1	0.52708095	D	CytoplasmicMembrane	NO_SP	TMH
WP_012388383.1	LEPBI_RS06835		outer membrane lipoi	chromosome	I	tBOSPT7	WP_000196651.1	0.6428745	M	Unknown	SP	Spl
WP_012388384.1	LEPBI_RS06840		helix-turn-helix domai	chromosome	I	tBOSPT8	WP_001072290.1	0.696585	D	Unknown	NO_SP	CYT
WP_012388385.1	LEPBI_RS06845		30S ribosomal protein	chromosome	I	sBOSPT9	WP_000358325.1	0.7043750999999999	J	Cytoplasmic	NO_SP	CYT
WP_012476239.1	LEPBI_RS06855	trpD	anthranilate phospho	chromosome	I	tBOSPU1	WP_000433680.1	0.6045227999999999	E	Cytoplasmic	NO_SP	CYT
WP_012388388.1	LEPBI_RS06860	yajC	preprotein translocas	chromosome	I	tBOSPU2	WP_000141830.1	0.6499948000000001		Unknown	NO_SP	CYT
WP_012388389.1	LEPBI_RS06865		SRP-less Sec system pi	chromosome	I	tBOSPU3				CytoplasmicMembrane	SP	Spl
WP_012388390.1	LEPBI_RS06870	secD	protein translocase su	chromosome	I	tBOSPU4	WP_000833715.1	0.72113085	U	CytoplasmicMembrane	NO_SP	TMH
WP_012388391.1	LEPBI_RS06875	secF	protein translocase su	chromosome	I	tBOSPU5	WP_000459252.1	0.6669184499999999	U	CytoplasmicMembrane	NO_SP	TMH
WP_012388393.1	LEPBI_RS06885		riboflavin synthase	chromosome	I	tBOSPU7	WP_000494006.1	0.58296645	H	Cytoplasmic	NO_SP	CYT
WP_012388394.1	LEPBI_RS06890		STAS domain-containi	chromosome	I	tBOSPU8				Unknown	NO_SP	CYT
WP_012388395.1	LEPBI_RS06895		bifunctional 3,4-dihyd	chromosome	I	tBOSPU9	WP_000615785.1	0.8278874999999999	H	Cytoplasmic	NO_SP	CYT
WP_012388396.1	LEPBI_RS06900	pdxH	pyridoxamine 5'-phos	chromosome	I	sBOSPV0	WP_000371278.1	0.5996668999999999	H	Cytoplasmic	NO_SP	CYT
WP_187148086.1	LEPBI_RS06910		aminotransferase clas	chromosome	I	tBOSPV2	WP_000895444.1	0.76237425	E	Cytoplasmic	NO_SP	CYT
WP_012388399.1	LEPBI_RS06915		AAA family ATPase	chromosome	I	tBOSPV3	WP_000450798.1	0.69408	J	Cytoplasmic	NO_SP	CYT
WP_012388400.1	LEPBI_RS06925	der	ribosome biogenesis C	chromosome	I	tBOSPV5	WP_001029804.1	0.5302869	J	Cytoplasmic	NO_SP	CYT
WP_012388402.1	LEPBI_RS06935		hypothetical protein	chromosome	I	tBOSPV7				Cytoplasmic	NO_SP	CYT
WP_012388403.1	LEPBI_RS06940		motility associated fax	chromosome	I	tBOSPV8	WP_000019139.1	0.57167	S	Unknown	NO_SP	CYT
WP_012388404.1	LEPBI_RS06945		AAA family ATPase	chromosome	I	tBOSPV9	WP_000281020.1	0.680229	D	Cytoplasmic	NO_SP	CYT
WP_012388405.1	LEPBI_RS06950		Cys-rich protein	chromosome	I	tBOSPW0				Unknown	SP	Spl
WP_012388406.1	LEPBI_RS06960	glnA	type I glutamate--amr	chromosome	I	tBOSPW1	WP_000091770.1	0.82292265	E	Cytoplasmic	NO_SP	CYT
WP_012388407.1	LEPBI_RS06965		SpolIE family protein	chromosome	I	tBOSPW2				Cytoplasmic	NO_SP	CYT
WP_012388408.1	LEPBI_RS06970		hypothetical protein	chromosome	I	tBOSPW3	WP_001258973.1	0.752085		Cytoplasmic	SP	Spl
WP_012388409.1	LEPBI_RS06975		response regulator tra	chromosome	I	tA5JUR5	WP_001201862.1	0.60738975	T	Cytoplasmic	NO_SP	CYT
WP_012388411.1	LEPBI_RS06985		class I fructose-bispho	chromosome	I	tBOSPW6	WP_000565746.1	0.7446037500000001	G	Cytoplasmic	NO_SP	CYT

WP_012388412.1	LEPBI_RS06990		4-alpha-glucanotransf chromosome	I	tBOSPW7			G	Cytoplasmic	NO_SP	CYT
WP_012388416.1	LEPBI_RS07010		alpha/beta hydrolase chromosome	I	tBOSPX1	WP_000698726.1	0.5495292	R	Cytoplasmic	SP	CYT
WP_012388418.1	LEPBI_RS07020		polymer-forming cyto chromosome	I	tBOSPX3	WP_000974282.1	0.8487306000000001	Z	Cytoplasmic	NO_SP	CYT
WP_012388419.1	LEPBI_RS07025		PBP1A family penicilli chromosome	I	tBOSPX4	WP_000808190.1	0.67806585	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388420.1	LEPBI_RS07030		zinc dependent phosph chromosome	I	tBOSPX5	WP_000907506.1	0.6609339000000001		Cytoplasmic	NO_SP	CYT
WP_012388421.1	LEPBI_RS07035		diaminopimelate dec chromosome	I	tBOSPX6	WP_001190627.1	0.7200963	E	Cytoplasmic	NO_SP	CYT
WP_012388422.1	LEPBI_RS07040		2-C-methyl-D-erythrit chromosome	I	tBOSPX7	WP_000838282.1	0.4631354	I	Cytoplasmic	NO_SP	CYT
WP_012388423.1	LEPBI_RS07045		PilZ domain-containin chromosome	I	tBOSPX8				CytoplasmicMembrane	NO_SP	TMH
WP_012388425.1	LEPBI_RS07055		cyclic nucleotide-bind chromosome	I	tBOSPY0				Cytoplasmic	NO_SP	CYT
WP_012388426.1	LEPBI_RS07065		hypothetical protein chromosome	I	tBOSPY1				Cytoplasmic	NO_SP	CYT
WP_012388428.1	LEPBI_RS07075		SH3 domain-containin chromosome	I	tBOSPY3				Cytoplasmic	NO_SP	CYT
WP_041769772.1	LEPBI_RS07090		AraC family transcript chromosome	I	tBOSPY5				Cytoplasmic	NO_SP	CYT
WP_143708644.1	LEPBI_RS07095		VOC family protein chromosome	I	tBOSPY6			R	Unknown	SP	CYT
WP_012388432.1	LEPBI_RS07100		hypothetical protein chromosome	I	tBOSPY7				Cytoplasmic	SP	SpI
WP_143708629.1	LEPBI_RS07105		FG-GAP repeat protei chromosome	I	tBOSPY8				Extracellular	NO_SP	CYT
WP_012388434.1	LEPBI_RS07110		DUF937 domain-cont chromosome	I	tBOSPY9				Unknown	NO_SP	CYT
WP_012388436.1	LEPBI_RS07120		SPOR domain-contain chromosome	I	tBOSPZ1	WP_000659917.1	0.3838032		CytoplasmicMembrane	NO_SP	SpI
WP_012388437.1	LEPBI_RS07125		dephospho-CoA kinas chromosome	I	tBOSPZ2	WP_001181520.1	0.48404265	H	Cytoplasmic	NO_SP	CYT
WP_012388438.1	LEPBI_RS07130		alpha/beta hydrolase chromosome	I	tBOSPZ3			H	Cytoplasmic	LIPO	SpII
WP_012388439.1	LEPBI_RS07140		hypothetical protein chromosome	I	tBOSPZ4	WP_000876121.1	0.7957818		Unknown	NO_SP	CYT
WP_012388443.1	LEPBI_RS07155		hypothetical protein chromosome	I	tBOSPZ8				Unknown	NO_SP	CYT
WP_012388445.1	LEPBI_RS07165		radical SAM protein chromosome	I	tBOSQ00	WP_000454163.1	0.8242343999999999		Cytoplasmic	NO_SP	CYT
WP_012388446.1	LEPBI_RS07170		lipoprotein LipL45 chromosome	I	tBOSQ01	WP_000714033.1	0.63122895		Cytoplasmic	LIPO	SpII
WP_012388448.1	LEPBI_RS07180	lipA	lipoyl synthase chromosome	I	sBOSQ03	WP_001068719.1	0.6743870000000001	H	Cytoplasmic	NO_SP	CYT
WP_012388450.1	LEPBI_RS07190		DUF1574 domain-con chromosome	I	tBOSQ05				Unknown	NO_SP	CYT
WP_012388452.1	LEPBI_RS07200	fsa	fructose-6-phosphate chromosome	I	sBOSQ07	WP_000424879.1	0.7780150000000001	G	Cytoplasmic	NO_SP	CYT
WP_012476244.1	LEPBI_RS07205		hypothetical protein chromosome	I	tBOSQ08	WP_001217817.1	0.69165145		Unknown	SP	SpI
WP_012388455.1	LEPBI_RS07215	purH	bifunctional phosphor chromosome	I	sBOSQ10	WP_000614725.1	0.7661	F	Cytoplasmic	NO_SP	CYT
WP_012388456.1	LEPBI_RS07220		phosphoribosylglycin chromosome	I	tBOSQB9	WP_000212325.1	0.635721	F	Cytoplasmic	NO_SP	SpI
WP_012388457.1	LEPBI_RS07225	fliS	flagellar export chape chromosome	I	tBOSQC0	WP_000050477.1	0.7138100000000001	N	Cytoplasmic	NO_SP	CYT
WP_012388461.1	LEPBI_RS07245		TRAP transporter sma chromosome	I	tBOSQC4				CytoplasmicMembrane	NO_SP	TMH
WP_012388462.1	LEPBI_RS07250	dctP	TRAP transporter sub chromosome	I	tBOSQC5			G	Periplasmic	SP	SpI
WP_012388463.1	LEPBI_RS07255		hypothetical protein chromosome	I	tBOSQC6				Cytoplasmic	LIPO	SpII
WP_012388464.1	LEPBI_RS07260		hypothetical protein chromosome	I	tBOSQC7	WP_000827044.1	0.42670060000000004		CytoplasmicMembrane	LIPO	TMH
WP_012388465.1	LEPBI_RS07265		DedA family protein chromosome	I	tBOSQC8	WP_000395055.1	0.65672	M	CytoplasmicMembrane	NO_SP	TMH
WP_012388468.1	LEPBI_RS07280		phosphorylase chromosome	I	tBOSQD1	WP_000694669.1	0.36582240000000005		Unknown	NO_SP	CYT
WP_012476246.1	LEPBI_RS07285		N-acetyl-gamma-gluta chromosome	I	tBOSQD2	WP_000808030.1	0.68303565	E	Cytoplasmic	NO_SP	CYT
WP_012388471.1	LEPBI_RS07295		DUF3365 domain-con chromosome	I	tBOSQD4	WP_000019011.1	0.36576899999999996		Unknown	LIPO	SpII
WP_012388472.1	LEPBI_RS07300		PAS domain S-box pro chromosome	I	tBOSQD5			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388473.1	LEPBI_RS07305		hypothetical protein chromosome	I	tBOSQD6				OuterMembrane	SP	CYT
WP_012388476.1	LEPBI_RS07320		S41 family peptidase chromosome	I	tBOSQD9			O	Cytoplasmic	LIPO	SpII
WP_012476247.1	LEPBI_RS07325		YbjN domain-containi chromosome	I	tBOSQE0				Unknown	SP	SpI
WP_012388478.1	LEPBI_RS07330		VOC family protein chromosome	I	tBOSQE1	WP_001247263.1	0.7985835		Cytoplasmic	NO_SP	CYT
WP_012388481.1	LEPBI_RS07345		histidine triad nucleot chromosome	I	tBOSQE4	WP_000131883.1	0.6149315	F	Cytoplasmic	NO_SP	CYT

WP_012388482.1	LEPBI_RS07350		ROK family protein	chromosome	I	tB0SQE5	WP_000834630.1	0.5606815500000001	G	Cytoplasmic	NO_SP	CYT
WP_012388483.1	LEPBI_RS07355		ABC transporter ATP-t	chromosome	I	tB0SQE6	WP_000603361.1	0.70138	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388485.1	LEPBI_RS07365		restriction endonucle:	chromosome	I	tB0SQE8	WP_000576229.1	0.5698192499999999		Cytoplasmic	NO_SP	CYT
WP_012388487.1	LEPBI_RS07375		Holliday junction ATP-	chromosome	I	sB0SQF0	WP_000623186.1	0.56603745	L	Cytoplasmic	NO_SP	CYT
WP_012388488.1	LEPBI_RS07380		patatin-like phospholi	chromosome	I	tB0SQF1	WP_000826015.1	0.37331999999999993	R	Cytoplasmic	NO_SP	CYT
WP_012388489.1	LEPBI_RS07385		C40 family peptidase	chromosome	I	tB0SQF2	WP_000488432.1	0.3875441		Unknown	SP	CYT
WP_012388490.1	LEPBI_RS07390		patatin-like phospholi	chromosome	I	tB0SQF3	WP_000816747.1	0.6458859	R	Unknown	NO_SP	Spl
WP_187148087.1	LEPBI_RS07395		outer membrane prot	chromosome	I	tB0SQF4				OuterMembrane	NO_SP	TMH
WP_041769991.1	LEPBI_RS07405		M48 family metallopr	chromosome	I	tB0SQF6			M	Unknown	SP	Spl
WP_012388494.1	LEPBI_RS07410		adenylate/guanylate c	chromosome	I	tB0SQF7			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388495.1	LEPBI_RS07415		methyl-accepting chei	chromosome	I	tB0SQF8	WP_001071261.1	0.53379315	T	CytoplasmicMembrane	NO_SP	TMH
WP_012388496.1	LEPBI_RS07420		BamA/TamA family o	chromosome	I	tB0SQF9	WP_000786858.1	0.6658953000000001		Unknown	SP	Spl
WP_041769992.1	LEPBI_RS07450		hypothetical protein	chromosome	I	tB0SQG3				Unknown	SP	Spl
WP_012476251.1	LEPBI_RS07455		hydrolase	chromosome	I	tB0SQG4	WP_001278382.1	0.41171009999999997		Cytoplasmic	NO_SP	CYT
WP_012388502.1	LEPBI_RS07460		polyphosphate kinase	chromosome	I	tB0SQG5			C	Cytoplasmic	NO_SP	CYT
WP_012388503.1	LEPBI_RS07465		UDP-galactose-lipid c	chromosome	I	tB0SQG6	WP_001237262.1	0.39621464999999995	C	Cytoplasmic	NO_SP	CYT
WP_012388507.1	LEPBI_RS07485		NAD(P)H-hydrate epi	chromosome	I	tB0SQH0	WP_000403128.1	0.35167054999999997	F	Cytoplasmic	NO_SP	CYT
WP_012388508.1	LEPBI_RS07490		hypothetical protein	chromosome	I	tB0SQH1	WP_001243475.1	0.4573382		OuterMembrane	SP	CYT
WP_135575622.1	LEPBI_RS07495	rimP	ribosome maturation	chromosome	I	sB0SQH2	WP_011172333.1	0.52759		Cytoplasmic	NO_SP	CYT
WP_012388510.1	LEPBI_RS07500	nusA	transcription terminat	chromosome	I	tB0SQH3	WP_000279228.1	0.7324564499999999	K	Cytoplasmic	NO_SP	CYT
WP_012388511.1	LEPBI_RS07505	infB	translation initiation f	chromosome	I	sB0SQH4				Cytoplasmic	NO_SP	CYT
WP_012388512.1	LEPBI_RS07510	rbfA	30S ribosome-binding	chromosome	I	sB0SQH5			J	Cytoplasmic	NO_SP	CYT
WP_012388514.1	LEPBI_RS07520	rpsO	30S ribosomal protein	chromosome	I	sB0SQH7	WP_000562102.1	0.7386250000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388515.1	LEPBI_RS07525	pnp	polyribonucleotide nu	chromosome	I	sB0SQH8	WP_000149893.1	0.7728534	J	Cytoplasmic	NO_SP	CYT
WP_012388516.1	LEPBI_RS07530		insulinase family prot	chromosome	I	tB0SQH9	WP_001157779.1	0.54036	R	Cytoplasmic	NO_SP	CYT
WP_012388517.1	LEPBI_RS07535	dut	dUTP diphosphatase	chromosome	I	tB0SQI0	WP_000689546.1	0.60538185	F	Unknown	NO_SP	CYT
WP_012388518.1	LEPBI_RS07540	flgG	flagellar basal-body	rc chromosome	I	tB0SQI1	WP_001257272.1	0.907205	N	Extracellular	NO_SP	Spl
WP_012388519.1	LEPBI_RS07545	flgA	flagellar basal body P-	chromosome	I	tB0SQI2	WP_001020205.1	0.3674		Unknown	SP	Spl
WP_049756002.1	LEPBI_RS07550		flagellar basal body L-	chromosome	I	tB0SQI3				Cytoplasmic	NO_SP	TMH
WP_143708645.1	LEPBI_RS07555	flgl	flagellar basal body P-	chromosome	I	tB0SQI4	WP_000838056.1	0.5432975999999999	N	Periplasmic	NO_SP	CYT
WP_012388522.1	LEPBI_RS07560		rod-binding protein	chromosome	I	tB0SQI5	WP_000972415.1	0.60091015		Cytoplasmic	NO_SP	CYT
WP_012388525.1	LEPBI_RS07575		class I SAM-dependen	chromosome	I	tB0SQI8	WP_001069834.1	0.5343888		Cytoplasmic	NO_SP	CYT
WP_012388527.1	LEPBI_RS07585		RNA-binding protein	chromosome	I	tB0SQJ0	WP_001165331.1	0.4843035		Unknown	NO_SP	CYT
WP_012388530.1	LEPBI_RS07600		NADP-dependent oxi	chromosome	I	tB0SQJ3			C	Cytoplasmic	NO_SP	CYT
WP_012476255.1	LEPBI_RS07615		SDR family oxidoreduc	chromosome	I	tB0SQJ6			I	Cytoplasmic	NO_SP	CYT
WP_012388534.1	LEPBI_RS07625		PAS domain S-box pro	chromosome	I	tB0SQJ7			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388535.1	LEPBI_RS07630		response regulator	chromosome	I	tB0SQJ8			T	Cytoplasmic	NO_SP	CYT
WP_012388541.1	LEPBI_RS07665	fliG	flagellar motor switch	chromosome	I	tB0SQK4	WP_000412660.1	0.6375263999999999	N	Cytoplasmic	NO_SP	CYT
WP_012476256.1	LEPBI_RS07675		pyruvate dehydrogen:	chromosome	I	tB0SQK6	WP_001062325.1	0.57451185	C	Cytoplasmic	NO_SP	CYT
WP_012388544.1	LEPBI_RS07680		pyruvate dehydrogen:	chromosome	I	tB0SQK7	WP_000279894.1	0.81071595	C	Cytoplasmic	NO_SP	CYT
WP_012388545.1	LEPBI_RS07685	pdhA	pyruvate dehydrogen:	chromosome	I	tB0SQK8	WP_000980946.1	0.7867293000000001	C	Cytoplasmic	NO_SP	CYT
WP_012388546.1	LEPBI_RS07690		hypothetical protein	chromosome	I	tB0SQK9	WP_000869088.1	0.45009455		Cytoplasmic	NO_SP	CYT
WP_012388547.1	LEPBI_RS07695		hypothetical protein	chromosome	I	tB0SQL0				Unknown	LIPO	SplI
WP_012476257.1	LEPBI_RS07700	fbp	class 1 fructose-bisph	chromosome	I	sB0SQL1	WP_000110726.1	0.7966332	G	Unknown	NO_SP	CYT

WP_187148088.1	LEPBI_RS07705		hypothetical protein	chromosome	I	tBOSQL2				Cytoplasmic	NO_SP	CYT
WP_012388550.1	LEPBI_RS07710		30S ribosomal protein	chromosome	I	tBOSQL3	WP_000232823.1	0.8614085		Cytoplasmic	NO_SP	CYT
WP_012388551.1	LEPBI_RS07715		GatB/YqeY domain-co	chromosome	I	tBOSQL4	WP_000058095.1	0.593985	R	Cytoplasmic	NO_SP	CYT
WP_012388552.1	LEPBI_RS07720	dnaG	DNA primase	chromosome	I	tBOSQL5	WP_000066266.1	0.5144526	L	Cytoplasmic	NO_SP	CYT
WP_012388553.1	LEPBI_RS07725	rpoD	RNA polymerase sigma	chromosome	I	tBOSQL6	WP_000429410.1	0.8668836	K	Cytoplasmic	NO_SP	CYT
WP_143708646.1	LEPBI_RS07730		hypothetical protein	chromosome	I	tBOSQL7				Cytoplasmic	NO_SP	CYT
WP_012388555.1	LEPBI_RS07735		glycerol-3-phosphate	chromosome	I	tBOSQL8	WP_001165152.1	0.6418368	C	Cytoplasmic	NO_SP	CYT
WP_187148089.1	LEPBI_RS07740		tyrosine--tRNA ligase	chromosome	I	tBOSQL9	WP_000354445.1	0.804955	J	Cytoplasmic	NO_SP	CYT
WP_012388557.1	LEPBI_RS07745		polysaccharide deace	chromosome	I	tBOSQM0	WP_000947641.1	0.5596767	G	Cytoplasmic	NO_SP	CYT
WP_012388558.1	LEPBI_RS07750		efflux RND transporte	chromosome	I	tBOSQM1	WP_000839345.1	0.73813905	V	CytoplasmicMembrane	NO_SP	TMH
WP_012388559.1	LEPBI_RS07755		peptide deformylase	chromosome	I	sBOSQM2	WP_000116243.1	0.79888	J	Cytoplasmic	NO_SP	CYT
WP_012388560.1	LEPBI_RS07765		hypothetical protein	chromosome	I	tBOSQM3	WP_000004280.1	0.7296569999999999		Cytoplasmic	NO_SP	CYT
WP_012388561.1	LEPBI_RS07770		SpoII E family protein	chromosome	I	tBOSQY1	WP_000612752.1	0.52577415	T	Cytoplasmic	NO_SP	CYT
WP_012388562.1	LEPBI_RS07775		STAS domain-containi	chromosome	I	tBOSQY2	WP_000406879.1	0.5632501000000001		Unknown	NO_SP	CYT
WP_012388563.1	LEPBI_RS07780		acetyl-CoA carboxylas	chromosome	I	tBOSQY3	WP_001973770.1	0.868175	I	Cytoplasmic	NO_SP	CYT
WP_012388564.1	LEPBI_RS07785		biotin/lipoyl-binding p	chromosome	I	tBOSQY4	WP_000564919.1	0.7054442999999999	I	Cytoplasmic	NO_SP	CYT
WP_012388565.1	LEPBI_RS07790		chemotaxis response i	chromosome	I	tBOSQY5	WP_000616854.1	0.6975837	T	Cytoplasmic	NO_SP	CYT
WP_012388567.1	LEPBI_RS07800		purine-binding chemc	chromosome	I	tBOSQY7	WP_000114482.1	0.5918635999999999	T	Cytoplasmic	NO_SP	CYT
WP_012388568.1	LEPBI_RS07805		methyl-accepting chei	chromosome	I	tBOSQY8			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388569.1	LEPBI_RS07810		chemotaxis protein Ct	chromosome	I	tBOSQY9	WP_000365940.1	0.47564435	T	Cytoplasmic	NO_SP	CYT
WP_012388570.1	LEPBI_RS07815		STAS domain-containi	chromosome	I	tBOSQZ0				Cytoplasmic	NO_SP	CYT
WP_012388571.1	LEPBI_RS07820		response regulator	chromosome	I	tBOSQZ1	WP_000821665.1	0.7778826	T	Cytoplasmic	NO_SP	CYT
WP_012388572.1	LEPBI_RS07825		hybrid sensor histidin	chromosome	I	tBOSQZ2	WP_000402080.1	0.53339815		Cytoplasmic	NO_SP	CYT
WP_012388573.1	LEPBI_RS07830		HAMP domain-containi	chromosome	I	tBOSQZ3			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388574.1	LEPBI_RS07835	ispH	4-hydroxy-3-methylbu	chromosome	I	tBOSQZ4	WP_000890370.1	0.7694478	I	Cytoplasmic	NO_SP	CYT
WP_002974229.1	LEPBI_RS07840		flagellin	chromosome	I	tBOSQZ5	WP_000586157.1	0.9379449999999999	N	Periplasmic	NO_SP	CYT
WP_012388576.1	LEPBI_RS07850	metW	methionine biosynthe	chromosome	I	tBOSQZ7	WP_000188047.1	0.6630974000000001		Cytoplasmic	NO_SP	CYT
WP_012388578.1	LEPBI_RS07860		O-acetylhomoserine a	chromosome	I	tBOSQZ9	WP_001137844.1	0.8836550000000001	E	Cytoplasmic	NO_SP	CYT
WP_187148090.1	LEPBI_RS07865		hypothetical protein	chromosome	I	tBOSR00	WP_000166979.1	0.5128879		OuterMembrane	SP	CYT
WP_041769800.1	LEPBI_RS07875		hypothetical protein	chromosome	I	tBOSR02				Unknown	NO_SP	CYT
WP_012388582.1	LEPBI_RS07880		hypothetical protein	chromosome	I	tBOSR03	WP_000775825.1	0.6131197		Unknown	SP	Spl
WP_012388583.1	LEPBI_RS07885		ATP-binding protein	chromosome	I	tBOSR04	WP_000098174.1	0.575784	M	CytoplasmicMembrane	LIPO	CYT
WP_012388584.1	LEPBI_RS07890	fliN	flagellar motor switch	chromosome	I	tBOSR05	WP_000503773.1	0.643235	N	Unknown	NO_SP	CYT
WP_012388585.1	LEPBI_RS07895		GNAT family N-acetyl	chromosome	I	tBOSR06				Unknown	NO_SP	CYT
WP_012388587.1	LEPBI_RS07905		paraslipin	chromosome	I	tBOSR08	WP_000447378.1	0.6767154	O	Cytoplasmic	NO_SP	CYT
WP_012388588.1	LEPBI_RS07910		paraslipin	chromosome	I	tBOSR09	WP_001272390.1	0.7192128	O	Cytoplasmic	NO_SP	CYT
WP_012388590.1	LEPBI_RS07920		heme-binding domain	chromosome	I	tBOSR11	WP_000726283.1	0.548064		Unknown	NO_SP	Spl
WP_012388591.1	LEPBI_RS07925	argH	argininosuccinate lyas	chromosome	I	sBOSR12	WP_000136475.1	0.6706875	E	Cytoplasmic	NO_SP	CYT
WP_012388592.1	LEPBI_RS07930		peptidylprolyl isomer	chromosome	I	tBOSR13	WP_001220028.1	0.67731675	O	Unknown	SP	Spl
WP_012388593.1	LEPBI_RS07935		hypothetical protein	chromosome	I	tBOSR14	WP_000141650.1	0.49160119999999999		Cytoplasmic	NO_SP	CYT
WP_012388594.1	LEPBI_RS07940		hypothetical protein	chromosome	I	tBOSR15	WP_000621805.1	0.5141178		Unknown	SP	CYT
WP_012388595.1	LEPBI_RS07945	fliM	flagellar motor switch	chromosome	I	tBOSR16	WP_000136083.1	0.9193499999999999	N	CytoplasmicMembrane	NO_SP	CYT
WP_012388596.1	LEPBI_RS07950		alkaline phosphatase	chromosome	I	tBOSR17			T	Periplasmic	NO_SP	CYT
WP_012388597.1	LEPBI_RS07955		ferredoxin	chromosome	I	tBOSR18	WP_000201605.1	0.7748784000000001		Unknown	NO_SP	CYT

WP_012388599.1	LEPBI_RS07965	queF	NADPH-dependent 7-i chromosome	I	tBOSR20	WP_000856053.1	0.7124962499999999	J	Cytoplasmic	NO_SP	CYT
WP_012388600.1	LEPBI_RS07970	guaA	glutamine-hydrolyzing chromosome	I	tBOSR21	WP_000234667.1	0.647575	F	Cytoplasmic	NO_SP	CYT
WP_012388601.1	LEPBI_RS07975		hypothetical protein chromosome	I	tBOSR22				Unknown	SP	Spl
WP_012476262.1	LEPBI_RS07990		O-antigen ligase family chromosome	I	tBOSR24	WP_000875499.1	0.33087374999999997		CytoplasmicMembrane	NO_SP	TMH
WP_012476263.1	LEPBI_RS08000		hypothetical protein chromosome	I	tBOSR26	WP_000500892.1	0.56001		Cytoplasmic	NO_SP	CYT
WP_012388606.1	LEPBI_RS08005		D-sedoheptulose 7-ph chromosome	I	sBOSR27	WP_000351733.1	0.67931175	G	Cytoplasmic	NO_SP	CYT
WP_012476264.1	LEPBI_RS08010		ABC transporter ATP-t chromosome	I	tBOSR28	WP_001089500.1	0.45486210000000005	E	CytoplasmicMembrane	NO_SP	CYT
WP_012388610.1	LEPBI_RS08025	leuC	3-isopropylmalate deH chromosome	I	tBOSR31	WP_000855526.1	0.81612	E	Cytoplasmic	NO_SP	CYT
WP_012388611.1	LEPBI_RS08030	leuD	3-isopropylmalate deH chromosome	I	tBOSR32	WP_000802156.1	0.74248515	E	Cytoplasmic	NO_SP	CYT
WP_012388612.1	LEPBI_RS08035		FKBP-type peptidyl-pr chromosome	I	tBOSR33			O	Periplasmic	SP	Spl
WP_012388613.1	LEPBI_RS08040		PLP-dependent cystein chromosome	I	tBOSR34	WP_000459126.1	0.5625576000000001	E	Cytoplasmic	NO_SP	CYT
WP_012388614.1	LEPBI_RS08045		patatin-like phospholi chromosome	I	tBOSR35			R	Extracellular	NO_SP	CYT
WP_012388615.1	LEPBI_RS08050	recN	DNA repair protein Re chromosome	I	tBOSR36	WP_000920921.1	0.5551425	L	Cytoplasmic	NO_SP	CYT
WP_012388616.1	LEPBI_RS08055		MotA/TolQ/ExbB prot chromosome	I	tBOSR37	WP_000477701.1	0.6442474499999999	U	CytoplasmicMembrane	NO_SP	CYT
WP_012388617.1	LEPBI_RS08060		biopolymer transport chromosome	I	tBOSR38	WP_000672100.1	0.7679102	U	CytoplasmicMembrane	NO_SP	CYT
WP_012388618.1	LEPBI_RS08065		outer membrane prot chromosome	I	tBOSR39	WP_000580974.1	0.6921312000000001	M	OuterMembrane	SP	Spl
WP_012388619.1	LEPBI_RS08070		UvrD-helicase domain chromosome	I	tBOSR40	WP_000378420.1	0.62333865	L	Cytoplasmic	NO_SP	CYT
WP_012388620.1	LEPBI_RS08075		hypothetical protein chromosome	I	tBOSR41	WP_000721620.1	0.4333522000000001		Unknown	SP	CYT
WP_012388621.1	LEPBI_RS08080		3'(2'),5'-bisphosphate chromosome	I	tBOSR42	WP_001084700.1	0.4362722	G	Cytoplasmic	NO_SP	CYT
WP_041769805.1	LEPBI_RS08095		TlpA family protein di chromosome	I	tBOSR45	WP_000267308.1	0.4344144		CytoplasmicMembrane	LIPO	Spl
WP_012388625.1	LEPBI_RS08100		AMP-binding protein chromosome	I	tBOSR46	WP_000829707.1	0.7191557999999999	I	Cytoplasmic	NO_SP	CYT
WP_041769807.1	LEPBI_RS08115	rfaE1	D-glycero-beta-D-mar chromosome	I	tBOSR49	WP_000291591.1	0.6615081	M	Cytoplasmic	NO_SP	CYT
WP_012388629.1	LEPBI_RS08120	rfaE2	D-glycero-beta-D-mar chromosome	I	tBOSR50	WP_000364507.1	0.6466602	M	Cytoplasmic	NO_SP	CYT
WP_012388630.1	LEPBI_RS08125		CTP synthase chromosome	I	tBOSR51	WP_000091728.1	0.8176162499999999	F	Cytoplasmic	NO_SP	Spl
WP_012388631.1	LEPBI_RS08130	kdsA	3-deoxy-8-phosphooc chromosome	I	tBOSR52	WP_001056080.1	0.73678675	M	Cytoplasmic	NO_SP	CYT
WP_012476266.1	LEPBI_RS08135	lptC	LPS export ABC transp chromosome	I	tBOSR53	WP_000791967.1	0.54826965		Unknown	LIPO	SplI
WP_012388633.1	LEPBI_RS08140		hypothetical protein chromosome	I	tBOSR54	WP_000621222.1	0.4306326		Unknown	SP	Spl
WP_041769999.1	LEPBI_RS08145	lptB	LPS export ABC transp chromosome	I	tBOSR55	WP_000047473.1	0.8924419	M	Cytoplasmic	NO_SP	CYT
WP_012388636.1	LEPBI_RS08155		HPr kinase/phosphory chromosome	I	sBOSR57	WP_000062490.1	0.7701507	T	Cytoplasmic	NO_SP	CYT
WP_012388642.1	LEPBI_RS08185	fmt	methionyl-tRNA form chromosome	I	tBOSR63	WP_000690652.1	0.5227794	J	Cytoplasmic	NO_SP	CYT
WP_012388643.1	LEPBI_RS08190		PASTA domain-containi chromosome	I	tBOSR64	WP_001071110.1	0.5073847499999999		Cytoplasmic	NO_SP	TMH
WP_012388644.1	LEPBI_RS08195	rpe	ribulose-phosphate 3- chromosome	I	tBOSR65	WP_000702812.1	0.72040815	G	Cytoplasmic	NO_SP	CYT
WP_015675939.1	LEPBI_RS08200	rpsP	30S ribosomal protein chromosome	I		WP_000240010.1	0.6882021999999999	J	Cytoplasmic	NO_SP	CYT
WP_012388646.1	LEPBI_RS08205		KH domain-containing chromosome	I	tBOSR67	WP_000391865.1	0.72368	R	Unknown	NO_SP	CYT
WP_012388648.1	LEPBI_RS08215	trmD	tRNA (guanosine(37)-I chromosome	I	tBOSR69	WP_000671159.1	0.6466082	J	Cytoplasmic	NO_SP	CYT
WP_012388649.1	LEPBI_RS08220	rplS	50S ribosomal protein chromosome	I	tBOSR70	WP_001072660.1	0.74638	J	Cytoplasmic	NO_SP	CYT
WP_012388653.1	LEPBI_RS08240		HD domain-containing chromosome	I	tBOSR74	WP_000712870.1	0.5503014	T	Cytoplasmic	NO_SP	CYT
WP_167530805.1	LEPBI_RS08260		type II secretion syste chromosome	I	tBOSR78	WP_000488361.1	0.44905075000000005		Unknown	LIPO	CYT
WP_012388659.1	LEPBI_RS08270		general secretion pati chromosome	I	tBOSR80	WP_000991320.1	0.60518		Unknown	NO_SP	TMH
WP_012388660.1	LEPBI_RS08275	gspD	type II secretion syste chromosome	I	tBOSR81	WP_000017090.1	0.6803615999999999	U	Unknown	SP	Spl
WP_012388661.1	LEPBI_RS08280	gspE	type II secretion syste chromosome	I	tBOSR82	WP_000853744.1	0.7932473999999999	N	Cytoplasmic	NO_SP	CYT
WP_012388662.1	LEPBI_RS08285		type II secretion syste chromosome	I	tBOSR83	WP_001029466.1	0.74143	N	CytoplasmicMembrane	NO_SP	CYT
WP_012388663.1	LEPBI_RS08290		type II secretion syste chromosome	I	tBOSR84	WP_001054085.1	0.5958908999999999		CytoplasmicMembrane	PILIN	CYT
WP_012388668.1	LEPBI_RS08315		pilus assembly proteir chromosome	I	tBOSRJ5	WP_000471275.1	0.5299056		Cytoplasmic	NO_SP	CYT

WP_012388669.1	LEPBI_RS08320		hypothetical protein	chromosome	I	tBOSRJ6	WP_000459773.1	0.61733925		Cytoplasmic	NO_SP	TMH
WP_012388670.1	LEPBI_RS08325	gspN	type II secretion syste	chromosome	I	tBOSRJ7	WP_000711612.1	0.42203179999999996		Cytoplasmic	NO_SP	CYT
WP_012388671.1	LEPBI_RS08330		vitamin B12-dependei	chromosome	I	tBOSRJ8	WP_000783496.1	0.809065	F	Cytoplasmic	NO_SP	CYT
WP_012388673.1	LEPBI_RS08345		NAD(P)/FAD-depende	chromosome	I	tBOSRK0			P	Unknown	NO_SP	CYT
WP_012388676.1	LEPBI_RS08360		hypothetical protein	chromosome	I	tBOSRK3				Unknown	LIPO	SpII
WP_012388681.1	LEPBI_RS08385		succinate dehydrogen	chromosome	I	tBOSRK8	WP_000345920.1	0.62092799999999999		CytoplasmicMembrane	NO_SP	TMH
WP_012388682.1	LEPBI_RS08390		fumarate reductase/s	chromosome	I	tBOSRK9	WP_000050920.1	0.83332499999999999	C	CytoplasmicMembrane	NO_SP	CYT
WP_041770003.1	LEPBI_RS08395		succinate dehydrogen	chromosome	I	tBOSRL0	WP_000364422.1	0.821	C	CytoplasmicMembrane	NO_SP	CYT
WP_012388684.1	LEPBI_RS08400		hypothetical protein	chromosome	I	tBOSRL1				Unknown	SP	SpI
WP_012388687.1	LEPBI_RS08415	lepA	elongation factor 4	chromosome	I	sBOSRL4	WP_001280999.1	0.81730934999999999	J	CytoplasmicMembrane	NO_SP	CYT
WP_012388688.1	LEPBI_RS08420	eno	phosphopyruvate hyd	chromosome	I	sBOSRL5	WP_000018115.1	0.834475	G	Cytoplasmic	NO_SP	CYT
WP_012388690.1	LEPBI_RS08430		ATP-dependent Clp pr	chromosome	I	tBOSRL7	WP_001115288.1	0.754875	O	Cytoplasmic	NO_SP	CYT
WP_012388692.1	LEPBI_RS08440		TldD/PmbA family prc	chromosome	I	tBOSRL9	WP_001024549.1	0.3701607	R	Cytoplasmic	NO_SP	CYT
WP_041770004.1	LEPBI_RS08445		TldD/PmbA family prc	chromosome	I	tBOSRM0	WP_001047263.1	0.35169749999999994	R	Cytoplasmic	NO_SP	CYT
WP_012388697.1	LEPBI_RS08465		STAS domain-containi	chromosome	I	tBOSRM4	WP_000602531.1	0.567256		Unknown	NO_SP	CYT
WP_012388699.1	LEPBI_RS08475		hypothetical protein	chromosome	I	tBOSRM6	WP_000810942.1	0.41092379999999995		Cytoplasmic	LIPO	SpII
WP_041769816.1	LEPBI_RS08480		transcriptional regulat	chromosome	I	tBOSRM7	WP_001969787.1	0.8418528		Unknown	NO_SP	CYT
WP_143708647.1	LEPBI_RS08485		sodium-dependent tri	chromosome	I	tBOSRM8	WP_001969726.1	0.67193775	R	CytoplasmicMembrane	NO_SP	TMH
WP_012388703.1	LEPBI_RS08490		helicase	chromosome	I	tBOSRN0	WP_001082079.1	0.5980150000000001	L	Cytoplasmic	NO_SP	CYT
WP_041769819.1	LEPBI_RS08495		hypothetical protein	chromosome	I	tBOSRN1	WP_001009261.1	0.40373059999999994		Unknown	SP	SpI
WP_012388705.1	LEPBI_RS08500		hypothetical protein	chromosome	I	tBOSRN2	WP_000531352.1	0.46350569999999996		Cytoplasmic	NO_SP	CYT
WP_012388706.1	LEPBI_RS08505	asnS	asparagine--tRNA liga	chromosome	I	tBOSRN3	WP_000005292.1	0.71249524999999999	J	Cytoplasmic	NO_SP	CYT
WP_012388707.1	LEPBI_RS08510	fold	bifunctional methylen	chromosome	I	sBOSRN4	WP_001070308.1	0.76803705	H	Cytoplasmic	NO_SP	CYT
WP_012388708.1	LEPBI_RS08515		acetylxlylan esterase	chromosome	I	tBOSRN5	WP_001007972.1	0.6548507	Q	Cytoplasmic	NO_SP	CYT
WP_012388709.1	LEPBI_RS08520		cysteine--tRNA ligase	chromosome	I	tBOSRN6	WP_000570129.1	0.66175065000000001	J	Cytoplasmic	NO_SP	CYT
WP_012476276.1	LEPBI_RS08525	rlmB	23S rRNA (guanosine)	chromosome	I	tBOSRN7	WP_060589244.1	0.5343655	J	Cytoplasmic	NO_SP	CYT
WP_012388712.1	LEPBI_RS08535		Na+:solute symporter	chromosome	I	tBOSRN9	WP_000490756.1	0.49287620000000001		CytoplasmicMembrane	NO_SP	TMH
WP_012388713.1	LEPBI_RS08540	hisF	imidazole glycerol phc	chromosome	I	sBOSRP0	WP_000067921.1	0.82696679999999999	E	Cytoplasmic	NO_SP	CYT
WP_012388714.1	LEPBI_RS08545	gatA	Asp-tRNA(Asn)/Glu-tR	chromosome	I	sBOSRP1	WP_001002770.1	0.717195	J	Cytoplasmic	NO_SP	CYT
WP_012388715.1	LEPBI_RS08550	gatC	Asp-tRNA(Asn)/Glu-tR	chromosome	I	tBOSRP2	WP_001024432.1	0.5473545		Cytoplasmic	NO_SP	CYT
WP_012388716.1	LEPBI_RS08555		undecaprenyl-phosph	chromosome	I	tBOSRP3	WP_000910880.1	0.67903	M	CytoplasmicMembrane	NO_SP	TMH
WP_081431662.1	LEPBI_RS08560		LPS-assembly protein	chromosome	I	tBOSRP4	WP_001131037.1	0.5662848		OuterMembrane	NO_SP	CYT
WP_012388721.1	LEPBI_RS08580		hypothetical protein	chromosome	I	tBOSRP8				Unknown	LIPO	SpII
WP_012388722.1	LEPBI_RS08585		M48 family metallope	chromosome	I	tBOSRP9			M	Unknown	SP	SpII
WP_012388723.1	LEPBI_RS08590		phosphodiesterase	chromosome	I	tBOSRQ0			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388725.1	LEPBI_RS08600		STAS domain-containi	chromosome	I	tBOSRQ2				Unknown	NO_SP	CYT
WP_012388726.1	LEPBI_RS08605		hypothetical protein	chromosome	I	tBOSRQ3	WP_000747976.1	0.32635200000000003		Unknown	SP	SpI
WP_012388728.1	LEPBI_RS08615		hypothetical protein	chromosome	I	tBOSRQ5				Cytoplasmic	SP	SpI
WP_012388730.1	LEPBI_RS08625		VWA domain-containi	chromosome	I	tBOSRQ7	WP_000470536.1	0.5491728	S	Cytoplasmic	NO_SP	CYT
WP_012388731.1	LEPBI_RS08630		MoxR family ATPase	chromosome	I	tBOSRQ8	WP_000778163.1	0.71068989999999999	R	Cytoplasmic	NO_SP	CYT
WP_012388732.1	LEPBI_RS08635		hypothetical protein	chromosome	I	tBOSRQ9	WP_000807170.1	0.556035		Unknown	NO_SP	CYT
WP_012388733.1	LEPBI_RS08640		amidohydrolase	chromosome	I	tBOSRR0	WP_000135393.1	0.48910309999999996		Unknown	NO_SP	CYT
WP_012388735.1	LEPBI_RS08650		AarF/ABC1/UbiB kina	chromosome	I	tBOSRR2	WP_000961616.1	0.406474	H	CytoplasmicMembrane	NO_SP	CYT
WP_012388737.1	LEPBI_RS08660		UDP-N-acetylmuramo	chromosome	I	tBOSRR4	WP_000841157.1	0.56555729999999999	M	Cytoplasmic	NO_SP	CYT



WP_012388738.1	LEPBI_RS08665	purE	5-(carboxyamino)imid chromosome	I	tBOSRR5	WP_001093510.1	0.7704515	F	Unknown	NO_SP	CYT
WP_012388741.1	LEPBI_RS08680		UDP-N-acetylglucosam chromosome	I	tBOSRR8	WP_000836517.1	0.5976135	M	CytoplasmicMembrane	NO_SP	Spl
WP_012388744.1	LEPBI_RS08695		UDP-N-acetylmuramo chromosome	I	tBOSRS1	WP_000782604.1	0.56194875	M	Cytoplasmic	NO_SP	CYT
WP_012388746.1	LEPBI_RS08705	rsmH	16S rRNA (cytosine(14 chromosome	I	sBOSRS3	WP_000445616.1	0.5315765	J	Cytoplasmic	NO_SP	CYT
WP_0124276277.1	LEPBI_RS08710		HIT domain-contains chromosome	I	tBOSRS4	WP_000390240.1	0.7100457	F	Cytoplasmic	NO_SP	CYT
WP_041770007.1	LEPBI_RS08715		protein-glutamate O- chromosome	I	tBOSRS5	WP_002145390.1	0.6810515500000001	T	Cytoplasmic	NO_SP	CYT
WP_012388750.1	LEPBI_RS08725		hypothetical protein chromosome	I	tBOSRS7	WP_000017889.1	0.4808193		Cytoplasmic	LIPO	CYT
WP_012388751.1	LEPBI_RS08730	amt	ammonium transport chromosome	I	tBOSRS8			P	CytoplasmicMembrane	SP	Spl
WP_012388754.1	LEPBI_RS08745		hypothetical protein chromosome	I	tBOSRT1	WP_001216953.1	0.6391742499999999		Cytoplasmic	NO_SP	CYT
WP_012388755.1	LEPBI_RS08750		AsmA family protein chromosome	I	tBOSRT2				Unknown	NO_SP	TMH
WP_012388756.1	LEPBI_RS08755	typA	translational GTPase 1 chromosome	I	tBOSRT3	WP_000405900.1	0.8255708999999999	T	CytoplasmicMembrane	NO_SP	CYT
WP_012388757.1	LEPBI_RS08760	rplU	50S ribosomal protein chromosome	I	sBOSRT4	WP_000270913.1	0.6968313	J	Cytoplasmic	NO_SP	CYT
WP_012388759.1	LEPBI_RS08770	rpmA	50S ribosomal protein chromosome	I	sBOSRT6	WP_000940600.1	0.767835	J	Cytoplasmic	NO_SP	CYT
WP_012388760.1	LEPBI_RS08775	obgE	GTPase ObgE chromosome	I	sBOSRT7	WP_000443450.1	0.6680486	D	Cytoplasmic	NO_SP	CYT
WP_012388761.1	LEPBI_RS08780	proB	glutamate 5-kinase chromosome	I	tBOSRT8	WP_000801906.1	0.6016770000000001	E	Cytoplasmic	NO_SP	CYT
WP_012388762.1	LEPBI_RS08785		glutamate-5-semialde chromosome	I	sBOSRT9	WP_000658458.1	0.6730614	E	Cytoplasmic	NO_SP	CYT
WP_012388765.1	LEPBI_RS08800		LytR C-terminal doma chromosome	I	tBOSRU2	WP_000133081.1	0.42877515000000005		Cytoplasmic	NO_SP	TMH
WP_012388766.1	LEPBI_RS08805	rsfS	ribosome silencing fac chromosome	I	tBOSRU3	WP_001070122.1	0.50870535	J	Unknown	NO_SP	CYT
WP_012388767.1	LEPBI_RS08810		thioredoxin domain-c chromosome	I	tBOSRU4	WP_001984949.1	0.5471487	R	Cytoplasmic	NO_SP	CYT
WP_041770009.1	LEPBI_RS08815		ToiC family protein chromosome	I	tBOSRU5	WP_000291493.1	0.5444499		Cytoplasmic	NO_SP	CYT
WP_187148092.1	LEPBI_RS08820		amidohydrolase chromosome	I	tBOSRU6	WP_000683294.1	0.7273579499999999	R	Cytoplasmic	NO_SP	CYT
WP_012388770.1	LEPBI_RS08825		enoyl-CoA hydratase/ chromosome	I	tBOSRU7			I	Cytoplasmic	NO_SP	CYT
WP_012388771.1	LEPBI_RS08830		MarR family transcrip chromosome	I	tBOSRU8	WP_000074962.1	0.6000120000000001		Cytoplasmic	NO_SP	CYT
WP_012388772.1	LEPBI_RS08835		aminopeptidase P N-t chromosome	I	tBOSS04	WP_000205143.1	0.69646995	E	Cytoplasmic	NO_SP	CYT
WP_012388775.1	LEPBI_RS08850	bfr	bacterioferritin chromosome	I	tBOSS07	WP_000677991.1	0.78427305	P	Cytoplasmic	NO_SP	CYT
WP_012388776.1	LEPBI_RS08855		N-6 DNA methylase chromosome	I	tBOSS08	WP_000181059.1	0.39746424999999996	J	Cytoplasmic	NO_SP	CYT
WP_012388777.1	LEPBI_RS08860		acetylglutamate kinas chromosome	I	tBOSS09	WP_001016365.1	0.4820755500000001		Cytoplasmic	NO_SP	CYT
WP_012388780.1	LEPBI_RS08875		D-alanine--D-alanine l chromosome	I	tBOSS12	WP_001038596.1	0.41725035	M	Cytoplasmic	NO_SP	CYT
WP_012388782.1	LEPBI_RS08885		HAD family hydrolase chromosome	I	tBOSS14	WP_000215708.1	0.6266735999999999	C	Cytoplasmic	NO_SP	CYT
WP_012388784.1	LEPBI_RS08895		GGDEF domain-contai chromosome	I	tBOSS16	WP_001239790.1	0.4324987	T	CytoplasmicMembrane	NO_SP	CYT
WP_012388785.1	LEPBI_RS08900	mqnC	dehypoxanthine futal chromosome	I	tBOSS17	WP_000146501.1	0.8205168	H	Cytoplasmic	NO_SP	CYT
WP_012388786.1	LEPBI_RS08905		(Fe-S)-binding protein chromosome	I	tBOSS18	WP_001018338.1	0.80199405	C	CytoplasmicMembrane	NO_SP	CYT
WP_012388787.1	LEPBI_RS08910		FecR domain-contains chromosome	I	tBOSS19				Unknown	NO_SP	CYT
WP_012388788.1	LEPBI_RS08915		hypothetical protein chromosome	I	tBOSS20				Unknown	SP	CYT
WP_012388790.1	LEPBI_RS08925		peptide chain release chromosome	I	tBOSS22	WP_001207220.1	0.7140994	J	Cytoplasmic	NO_SP	CYT
WP_012388791.1	LEPBI_RS08930		6-bladed beta-propell chromosome	I	tBOSS23	WP_000545443.1	0.47960055		Cytoplasmic	SP	CYT
WP_143708630.1	LEPBI_RS08935		tetratricopeptide repe chromosome	I	tBOSS24	WP_000603580.1	0.3367902		Unknown	SP	CYT
WP_012476281.1	LEPBI_RS08945		hypothetical protein chromosome	I	tBOSS26				Unknown	NO_SP	CYT
WP_012388795.1	LEPBI_RS08950		methylglyoxal synthas chromosome	I	tBOSS27	WP_000665953.1	0.7188274	G	Cytoplasmic	NO_SP	CYT
WP_012388796.1	LEPBI_RS08955		hypothetical protein chromosome	I	tBOSS28	WP_000682938.1	0.44008415000000006		Cytoplasmic	SP	Spl
WP_012388797.1	LEPBI_RS08960		hypothetical protein chromosome	I	tBOSS29	WP_000078824.1	0.62867475		Cytoplasmic	NO_SP	CYT
WP_012388798.1	LEPBI_RS08965		YjgP/YjgQ family perm chromosome	I	tBOSS30	WP_000651423.1	0.5819420499999999	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388801.1	LEPBI_RS08980		DUF1574 domain-con chromosome	I	tBOSS33				Cytoplasmic	NO_SP	CYT
WP_012388802.1	LEPBI_RS08985		MBOAT family proteir chromosome	I	tBOSS34	WP_000578203.1	0.537355	M	CytoplasmicMembrane	NO_SP	TMH

WP_012476282.1	LEPBI_RS08995		SpoIIIE family protein $\gamma$ chromosome	I	tBOSS36				CytoplasmicMembrane	SP	CYT
WP_012388805.1	LEPBI_RS09000		undecaprenyl-diphosph chromosome	I	sBOSS37	WP_001070489.1	0.6272	I	CytoplasmicMembrane	NO_SP	TMH
WP_012388806.1	LEPBI_RS09005		lipoprotein LipL31 chromosome	I	tBOSS38	WP_000742261.1	0.5474216		Cytoplasmic	LIPO	SpII
WP_012388807.1	LEPBI_RS09010	mfd	transcription-repair cc chromosome	I	tBOSS39	WP_000654025.1	0.6571606	L	Cytoplasmic	NO_SP	CYT
WP_012388808.1	LEPBI_RS09015		pantoate--beta-alanine chromosome	I	sBOSS40	WP_000634421.1	0.5562685	H	Cytoplasmic	NO_SP	CYT
WP_012388809.1	LEPBI_RS09020	hisD	histidinol dehydrogen chromosome	I	sBOSS41	WP_001007462.1	0.65652345	E	Cytoplasmic	NO_SP	CYT
WP_012388812.1	LEPBI_RS09035		HAMP domain-contain chromosome	I	tBOSS44			T	CytoplasmicMembrane	NO_SP	CYT
WP_012388814.1	LEPBI_RS09045		LEA type 2 family prot chromosome	I	tBOSS46				Unknown	LIPO	SpII
WP_012388815.1	LEPBI_RS09050		hypothetical protein chromosome	I	tBOSS47	WP_001274122.1	0.46443999999999996		Cytoplasmic	LIPO	SpII
WP_012388817.1	LEPBI_RS09060		hypothetical protein chromosome	I	tBOSS49				Cytoplasmic	LIPO	CYT
WP_187148093.1	LEPBI_RS09065		OmpA family protein chromosome	I	tBOSS50	WP_000802062.1	0.6083154	N	Unknown	SP	CYT
WP_041769828.1	LEPBI_RS09080	uvrA	excinuclease ABC sub chromosome	I	tBOSS53	WP_001156251.1	0.80236530000000001	L	Cytoplasmic	NO_SP	CYT
WP_012388822.1	LEPBI_RS09085		S49 family peptidase chromosome	I	tBOSS54	WP_000489489.1	0.382427500000000003	O	CytoplasmicMembrane	NO_SP	CYT
WP_012388824.1	LEPBI_RS09095		hydrolase chromosome	I	tBOSS56	WP_000940638.1	0.60294779999999999	D	Unknown	NO_SP	TMH
WP_012388826.1	LEPBI_RS09105		glycerophosphoryl die chromosome	I	tBOSS58	WP_000572014.1	0.400240750000000003	I	Cytoplasmic	NO_SP	CYT
WP_012476286.1	LEPBI_RS09120		2-isopropylmalate syn chromosome	I	tBOSS61	WP_000116258.1	0.74045375	E	Cytoplasmic	NO_SP	CYT
WP_012388830.1	LEPBI_RS09125	hisC	histidinol-phosphate t chromosome	I	tBOSS62	WP_000538654.1	0.433963450000000003	E	Cytoplasmic	NO_SP	CYT
WP_041769831.1	LEPBI_RS09130		Hsp20/alpha crystallin chromosome	I	tBOSS63	WP_000180222.1	0.48235775000000001	O	Cytoplasmic	NO_SP	CYT
WP_012388832.1	LEPBI_RS09135		Hsp20/alpha crystallin chromosome	I	tBOSS64	WP_001001876.1	0.425010999999999997	O	Cytoplasmic	NO_SP	CYT
WP_012476287.1	LEPBI_RS09140		RidA family protein chromosome	I	tBOSS65	WP_001023796.1	0.59637899999999999		Unknown	NO_SP	CYT
WP_012388835.1	LEPBI_RS09150	clpA	ATP-dependent Clp pr chromosome	I	tBOSS67	WP_001982061.1	0.65579999999999999	O	Cytoplasmic	NO_SP	CYT
WP_012388837.1	LEPBI_RS09160		GNAT family N-acetyl t chromosome	I	tBOSS69	WP_001083543.1	0.5086772	R	Cytoplasmic	NO_SP	CYT
WP_012388838.1	LEPBI_RS09165		SpoIIIE family protein $\gamma$ chromosome	I	tBOSS70				CytoplasmicMembrane	NO_SP	TMH
WP_041769833.1	LEPBI_RS09175		hypothetical protein chromosome	I	tBOSS72				Unknown	LIPO	CYT
WP_012388842.1	LEPBI_RS09185		exodeoxyribonuclease chromosome	I	tBOSS74	WP_000390225.1	0.56742575	L	Cytoplasmic	NO_SP	CYT
WP_012388843.1	LEPBI_RS09190		exodeoxyribonuclease chromosome	I	tBOSS75	WP_000230450.1	0.49201450000000001		Cytoplasmic	NO_SP	CYT
WP_012388845.1	LEPBI_RS09200		D-alanine--D-alanine l chromosome	I	sBOSS77	WP_001062346.1	0.5289795	M	Cytoplasmic	NO_SP	CYT
WP_012388847.1	LEPBI_RS09210		ABC transporter perm chromosome	I	tBOSS79	WP_000147518.1	0.7844018	M	CytoplasmicMembrane	NO_SP	TMH
WP_012388848.1	LEPBI_RS09215		ABC transporter ATP-t chromosome	I	tBOSS80	WP_000433117.1	0.7837731	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388849.1	LEPBI_RS09220		MCE family protein chromosome	I	tBOSS81	WP_001087254.1	0.6727896		Unknown	NO_SP	TMH
WP_012388850.1	LEPBI_RS09225		UDP-3-O-acyl-N-acetyl chromosome	I	sBOSS82	WP_000447207.1	0.65851719999999999	M	Cytoplasmic	NO_SP	CYT
WP_012388851.1	LEPBI_RS09230	ptsP	phosphoenolpyruvate chromosome	I	tBOSS83	WP_000621271.1	0.485514699999999997	G	Cytoplasmic	NO_SP	CYT
WP_012388853.1	LEPBI_RS09240		cob(I)yrinic acid a,c-di chromosome	I	tBOSS85	WP_000708723.1	0.6111105	H	Cytoplasmic	NO_SP	CYT
WP_012476288.1	LEPBI_RS09245		flagellin chromosome	I	tBOSS86	WP_000586161.1	0.7179084	N	Periplasmic	NO_SP	CYT
WP_041770012.1	LEPBI_RS09250		OmpA family protein chromosome	I	tBOSS87			M	OuterMembrane	LIPO	SpII
WP_012388856.1	LEPBI_RS09255		YbaB/EbfC family nucl chromosome	I	tBOSS88	WP_000492446.1	0.5345088		Unknown	NO_SP	CYT
WP_012388858.1	LEPBI_RS09265		ParA family protein chromosome	I	tBOSS90			D	CytoplasmicMembrane	NO_SP	CYT
WP_041769838.1	LEPBI_RS09270		hypothetical protein chromosome	I	tBOSS91				Unknown	NO_SP	CYT
WP_012388861.1	LEPBI_RS09280		AMP-binding protein chromosome	I	tBOSS93			I	CytoplasmicMembrane	NO_SP	CYT
WP_012388862.1	LEPBI_RS09285	pepN	aminopeptidase N chromosome	I	tBOSS94			E	Cytoplasmic	NO_SP	CYT
WP_012388863.1	LEPBI_RS09290		RNA-binding protein chromosome	I	tBOSS95				Unknown	NO_SP	CYT
WP_012388864.1	LEPBI_RS09295		EAL domain-containin chromosome	I	tBOSS96	WP_000348938.1	0.53313119999999999	T	CytoplasmicMembrane	NO_SP	CYT
WP_012388865.1	LEPBI_RS09300		TonB-dependent rece chromosome	I	tBOSS97	WP_001983065.1	0.57693659999999999	P	OuterMembrane	SP	SpI
WP_012388867.1	LEPBI_RS09310		hypothetical protein chromosome	I	tBOSS99				Unknown	LIPO	SpII

WP_012388869.1	LEPBI_RS09320		hypothetical protein	chromosome	I	tBOSSA1			Unknown	NO_SP	CYT		
WP_012388873.1	LEPBI_RS09340		alpha/beta hydrolase	chromosome	I	tBOSSA5			Unknown	NO_SP	SpI		
WP_012388875.1	LEPBI_RS09350		hypothetical protein	chromosome	I	tBOSSA7			Cytoplasmic	NO_SP	CYT		
WP_012388877.1	LEPBI_RS09360		hypothetical protein	chromosome	I	tBOSSA9	WP_000115765.1	0.392612349999999994			CytoplasmicMembrane	NO_SP	TMH
WP_187148094.1	LEPBI_RS09365	lysS	lysine--tRNA ligase	chromosome	I	tBOSSB0	WP_000004519.1	0.84142	J		Cytoplasmic	NO_SP	CYT
WP_012388879.1	LEPBI_RS09370		hypothetical protein	chromosome	I	tBOSSB1	WP_000701525.1	0.4535979			Unknown	LIPO	SpII
WP_012388880.1	LEPBI_RS09375	serA	phosphoglycerate de	chromosome	I	tBOSSB2	WP_001982325.1	0.76538	H		Cytoplasmic	NO_SP	CYT
WP_012388884.1	LEPBI_RS09395		dihydrolipoyl dehydro	chromosome	I	tBOSSB6	WP_000666066.1	0.61199325	C		Cytoplasmic	NO_SP	CYT
WP_012388886.1	LEPBI_RS09405		ABC transporter ATP-t	chromosome	I	tBOSSB8	WP_000666552.1	0.72620955	V		CytoplasmicMembrane	NO_SP	CYT
WP_012388889.1	LEPBI_RS09420		glutathione S-transfer	chromosome	I	tBOSSC1			O		Cytoplasmic	NO_SP	CYT
WP_012388890.1	LEPBI_RS09425		BolA/IbaG family iron-	chromosome	I	tBOSSC2	WP_000150944.1	0.7599888			Cytoplasmic	NO_SP	CYT
WP_012388891.1	LEPBI_RS09430	grxD	Grx4 family monothio	chromosome	I	tBOSSC3	WP_001058137.1	0.73111525	O		Unknown	NO_SP	CYT
WP_012388892.1	LEPBI_RS09435		glutathione S-transfer	chromosome	I	tBOSSC4	WP_000780847.1	0.7			Unknown	NO_SP	CYT
WP_012388893.1	LEPBI_RS09440	gshAB	bifunctional glutamat	chromosome	I	tBOSSC5	WP_001191099.1	0.63120325	M		Cytoplasmic	NO_SP	CYT
WP_012388895.1	LEPBI_RS09450	ggt	gamma-glutamyltrans	chromosome	I	tBOSSC7	WP_000809986.1	0.48305075000000003	E		Periplasmic	LIPO	TMH
WP_012388896.1	LEPBI_RS09455		metal-sulfur cluster a	chromosome	I	tBOSSC8	WP_000888483.1	0.69624	O		Periplasmic	NO_SP	CYT
WP_012476291.1	LEPBI_RS09470		Rieske 2Fe-2S domain	chromosome	I	tBOSSD1	WP_000010051.1	0.59206949999999999	P		Unknown	NO_SP	CYT
WP_012388900.1	LEPBI_RS09475		SufD family Fe-S clust	chromosome	I	tBOSSD2			O		Cytoplasmic	NO_SP	CYT
WP_012388901.1	LEPBI_RS09480	sufC	Fe-S cluster assembly	chromosome	I	tBOSSD3	WP_000136057.1	0.79576	O		Cytoplasmic	NO_SP	CYT
WP_012388903.1	LEPBI_RS09490		hypothetical protein	chromosome	I	tBOSSD5			G		Cytoplasmic	NO_SP	CYT
WP_012388904.1	LEPBI_RS09495	purQ	phosphoribosylformyl	chromosome	I	tBOSSD6	WP_000686200.1	0.62548695	F		Cytoplasmic	NO_SP	CYT
WP_012388905.1	LEPBI_RS09500	purS	phosphoribosylformyl	chromosome	I	tBOSSD7	WP_000275007.1	0.60426960000000001	F		Unknown	NO_SP	CYT
WP_012388906.1	LEPBI_RS09505		phosphoribosylamino	chromosome	I	tBOSSD8	WP_001070066.1	0.67406130000000001	F		Cytoplasmic	NO_SP	CYT
WP_012388907.1	LEPBI_RS09510		fused response regula	chromosome	I	tBOSSD9	WP_000075442.1	0.61309215000000001	T		Cytoplasmic	NO_SP	CYT
WP_012388912.1	LEPBI_RS09535		ATP-binding cassette	chromosome	I	tBOSSD4	WP_001141158.1	0.440405749999999993	E		Cytoplasmic	NO_SP	CYT
WP_012388913.1	LEPBI_RS09540		hydroxymethylglutary	chromosome	I	tBOSSD5	WP_000403254.1	0.71499329999999999	E		Cytoplasmic	NO_SP	CYT
WP_012388915.1	LEPBI_RS09555		adenylosuccinate synt	chromosome	I	tBOSSD7	WP_001111751.1	0.7430742	F		Cytoplasmic	NO_SP	CYT
WP_012476293.1	LEPBI_RS09560		ATP phosphoribosyltr	chromosome	I	tBOSSD8	WP_001075198.1	0.4921392	E		Cytoplasmic	NO_SP	CYT
WP_012388917.1	LEPBI_RS09565		1-acyl-sn-glycerol-3-pl	chromosome	I	tBOSSD9	WP_000229482.1	0.73808000000000001	C		Cytoplasmic	NO_SP	CYT
WP_012476294.1	LEPBI_RS09570		PAS domain-containin	chromosome	I	tBOSSD0			T		CytoplasmicMembrane	NO_SP	CYT
WP_012388919.1	LEPBI_RS09575	rplQ	50S ribosomal protein	chromosome	I	sBOSSF1	WP_001042619.1	0.4958827	J		Cytoplasmic	NO_SP	CYT
WP_012388920.1	LEPBI_RS09580		DNA-directed RNA po	chromosome	I	sBOSSF2	WP_000054108.1	0.926175	K		Cytoplasmic	NO_SP	CYT
WP_012388921.1	LEPBI_RS09585	rpsD	30S ribosomal protein	chromosome	I	sBOSSF3	WP_000135260.1	0.790495	J		Cytoplasmic	NO_SP	CYT
WP_012388922.1	LEPBI_RS09590	rpsK	30S ribosomal protein	chromosome	I	tBOSSF4	WP_000752686.1	0.75759649999999999	J		Cytoplasmic	NO_SP	CYT
WP_012388923.1	LEPBI_RS09595	rpsM	30S ribosomal protein	chromosome	I	sBOSSF5	WP_000090769.1	0.848	J		Cytoplasmic	NO_SP	CYT
WP_012476295.1	LEPBI_RS09600	infA	translation initiation f	chromosome	I	tBOSSF6	WP_001040194.1	0.98611	J		Cytoplasmic	NO_SP	CYT
WP_012388924.1	LEPBI_RS09605		adenylate kinase	chromosome	I	sBOSSF7	WP_000789400.1	0.75047939999999999	F		Cytoplasmic	NO_SP	CYT
WP_012388926.1	LEPBI_RS09615	rplO	50S ribosomal protein	chromosome	I	tBOSSF9	WP_000712192.1	0.56404965000000001	J		Cytoplasmic	NO_SP	CYT
WP_012388927.1	LEPBI_RS09620	rpmD	50S ribosomal protein	chromosome	I	sBOSSG0	WP_000427711.1	0.68646			Unknown	NO_SP	CYT
WP_002983215.1	LEPBI_RS09625	rpsE	30S ribosomal protein	chromosome	I	tBOSSG1	WP_000331210.1	0.8065134	J		Cytoplasmic	NO_SP	CYT
WP_012388928.1	LEPBI_RS09630	rplR	50S ribosomal protein	chromosome	I	sBOSSG2	WP_000567189.1	0.66803499999999999	J		Cytoplasmic	NO_SP	CYT
WP_012388929.1	LEPBI_RS09635	rplF	50S ribosomal protein	chromosome	I	sBOSSG3	WP_000086547.1	0.796065	J		Cytoplasmic	NO_SP	CYT
WP_002973604.1	LEPBI_RS09640	rpsH	30S ribosomal protein	chromosome	I	sBOSSG4	WP_000062824.1	0.78752024999999999	J		Cytoplasmic	NO_SP	CYT
WP_012388930.1	LEPBI_RS09645	rplE	50S ribosomal protein	chromosome	I	sBOSSG5	WP_000741297.1	0.78099615	J		Cytoplasmic	NO_SP	CYT

WP_012388931.1	LEPBI_RS09650		50S ribosomal protein chromosome	I	sBOSSG6	WP_001096782.1	0.6836333		Cytoplasmic	NO_SP	CYT
WP_002974152.1	LEPBI_RS09655	rplN	50S ribosomal protein chromosome	I	sBOSSG7	WP_000615917.1	0.92306	J	Cytoplasmic	NO_SP	CYT
WP_012388932.1	LEPBI_RS09660	rpsQ	30S ribosomal protein chromosome	I	tBOSSG8	WP_000123883.1	0.675	J	Cytoplasmic	NO_SP	CYT
WP_012388933.1	LEPBI_RS09665	rpmC	50S ribosomal protein chromosome	I	tBOSSG9				Unknown	NO_SP	CYT
WP_012388934.1	LEPBI_RS09670	rplP	50S ribosomal protein chromosome	I	sBOSSH0	WP_000950835.1	0.9014550000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388935.1	LEPBI_RS09675	rpsC	30S ribosomal protein chromosome	I	sBOSSH1	WP_000529953.1	0.84665	J	Cytoplasmic	NO_SP	CYT
WP_012476297.1	LEPBI_RS09680	rplV	50S ribosomal protein chromosome	I	sBOSSH2	WP_000387530.1	0.73637	J	Cytoplasmic	NO_SP	CYT
WP_002974021.1	LEPBI_RS09685	rpsS	30S ribosomal protein chromosome	I	sBOSSH3	WP_000124499.1	0.8656	J	Cytoplasmic	NO_SP	CYT
WP_012388937.1	LEPBI_RS09690	rplB	50S ribosomal protein chromosome	I	sBOSSH4	WP_000511542.1	0.797485	J	Cytoplasmic	NO_SP	CYT
WP_012388938.1	LEPBI_RS09695		50S ribosomal protein chromosome	I	sBOSSH5	WP_001053134.1	0.7589952999999998	J	Unknown	NO_SP	CYT
WP_012388939.1	LEPBI_RS09700	rplD	50S ribosomal protein chromosome	I	sBOSSH6	WP_000647275.1	0.735	J	Cytoplasmic	NO_SP	CYT
WP_012388940.1	LEPBI_RS09705	rplC	50S ribosomal protein chromosome	I	sBOSSH7	WP_001051846.1	0.69323	J	Cytoplasmic	NO_SP	CYT
WP_002974412.1	LEPBI_RS09710	rpsJ	30S ribosomal protein chromosome	I	sBOSSH8	WP_000918607.1	0.97059	J	Cytoplasmic	NO_SP	CYT
WP_012388941.1	LEPBI_RS09715	tuf	elongation factor Tu chromosome	I	sBOSSH9	WP_001040571.1	0.9102250000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388942.1	LEPBI_RS09720		elongation factor G-lik chromosome	I	tBOSSI0	WP_001166546.1	0.45721665	J	Cytoplasmic	NO_SP	CYT
WP_012388943.1	LEPBI_RS09725	rpsG	30S ribosomal protein chromosome	I	sBOSSI1	WP_000091209.1	0.863065	J	Cytoplasmic	NO_SP	CYT
WP_004783543.1	LEPBI_RS09730		30S ribosomal protein chromosome	I	sBOSSI2	WP_001142358.1	0.955625	J	Cytoplasmic	NO_SP	CYT
WP_012388944.1	LEPBI_RS09735	rpoC	DNA-directed RNA po chromosome	I	sBOSSI3	WP_001256473.1	0.8473374	K	Cytoplasmic	NO_SP	CYT
WP_012388945.1	LEPBI_RS09740	rpoB	DNA-directed RNA po chromosome	I	sBOSSI4	WP_000274334.1	0.865458	K	Cytoplasmic	NO_SP	CYT
WP_012388946.1	LEPBI_RS09745	rplL	50S ribosomal protein chromosome	I	tBOSSI5	WP_000102400.1	0.8070900000000001	J	Unknown	NO_SP	CYT
WP_012388947.1	LEPBI_RS09750		50S ribosomal protein chromosome	I	sBOSSI6	WP_000013204.1	0.7637305499999999	J	Cytoplasmic	NO_SP	CYT
WP_012388948.1	LEPBI_RS09755		50S ribosomal protein chromosome	I	sBOSSI7	WP_001188789.1	0.852175	J	Cytoplasmic	NO_SP	CYT
WP_012388949.1	LEPBI_RS09760	rplK	50S ribosomal protein chromosome	I	sBOSSI8	WP_000729204.1	0.9057609000000001	J	Cytoplasmic	NO_SP	CYT
WP_012388950.1	LEPBI_RS09765	nusG	transcription terminat chromosome	I	tBOSSI9	WP_000536871.1	0.8360429	K	Cytoplasmic	NO_SP	CYT
WP_012388951.1	LEPBI_RS09785		hypothetical protein chromosome	I	tBOSSJ1	WP_001129800.1	0.7317954		Cytoplasmic	NO_SP	CYT
WP_012388952.1	LEPBI_RS09790		SDR family NAD(P)-de chromosome	I	tBOSSJ2	WP_000351752.1	0.751945	I	Cytoplasmic	NO_SP	CYT
WP_187148095.1	LEPBI_RS09795		metalloregulator ArsR chromosome	I	tBOSSJ3	WP_000031888.1	0.7626861		Unknown	NO_SP	CYT
WP_012388954.1	LEPBI_RS09800	rfaD	ADP-glyceromanno-hε chromosome	I	tBOSSJ4	WP_001074785.1	0.6908467500000001	M	Cytoplasmic	NO_SP	CYT
WP_012388955.1	LEPBI_RS09805		UbiD family decarboxi chromosome	I	tBOSSJ5	WP_000695319.1	0.6759918	H	Cytoplasmic	NO_SP	CYT
WP_012388956.1	LEPBI_RS09810		hypothetical protein chromosome	I	tBOSSJ6	WP_001005189.1	0.626717		Cytoplasmic	NO_SP	CYT
WP_012388959.1	LEPBI_RS09825		hypothetical protein chromosome	I	tBOSSJ9	WP_000615042.1	0.3283588		CytoplasmicMembrane	NO_SP	CYT
WP_012476299.1	LEPBI_RS09830		hypothetical protein chromosome	I	tBOSSK1				CytoplasmicMembrane	NO_SP	TMH
WP_012388963.1	LEPBI_RS09835		glycosyltransferase fa chromosome	I	tBOSSK3	WP_000840858.1	0.5354302999999999	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388964.1	LEPBI_RS09840		dolichyl-phosphate-m chromosome	I	tBOSSK4	WP_000231203.1	0.32700075		CytoplasmicMembrane	NO_SP	TMH
WP_012388965.1	LEPBI_RS09845		hypothetical protein chromosome	I	tBOSSK5	WP_000934683.1	0.37917300000000004		CytoplasmicMembrane	NO_SP	TMH
WP_012388966.1	LEPBI_RS09850		glycosyltransferase fa chromosome	I	tBOSSK6	WP_000728671.1	0.6439108499999999	M	CytoplasmicMembrane	NO_SP	CYT
WP_012476300.1	LEPBI_RS09860		glycosyltransferase fa chromosome	I	tBOSSK8	WP_000868621.1	0.5778382499999999		CytoplasmicMembrane	NO_SP	CYT
WP_012388969.1	LEPBI_RS09865		glycosyltransferase fa chromosome	I	tBOSSK9	WP_000282880.1	0.32500035000000005	M	CytoplasmicMembrane	NO_SP	CYT
WP_012388970.1	LEPBI_RS09870	glf	UDP-galactopyranose chromosome	I	tBOSSL0			M	Unknown	NO_SP	Spl
WP_012388971.1	LEPBI_RS09875		glycosyltransferase chromosome	I	tBOSSL1				CytoplasmicMembrane	NO_SP	CYT
WP_012388977.1	LEPBI_RS09905		phosphoglycerate def chromosome	I	tBOSSL7	WP_000675255.1	0.6259407	C	Cytoplasmic	NO_SP	CYT
WP_012388981.1	LEPBI_RS09920		glycosyltransferase chromosome	I	tBOSSM1				Unknown	NO_SP	CYT
WP_012388984.1	LEPBI_RS09935		DegT/DnrJ/EryC1/StrS chromosome	I	tBOSSM4	WP_000575178.1	0.661695	M	Cytoplasmic	NO_SP	CYT
WP_012388987.1	LEPBI_RS09950		methyltransferase, TK chromosome	I	tBOSSM7				Cytoplasmic	NO_SP	CYT

WP_012388988.1	LEPBI_RS09955		FkbM family methyltr; chromosome	I	tBOSSM8				Cytoplasmic	NO_SP	CYT	
WP_012388989.1	LEPBI_RS09960		ABC transporter ATP-t chromosome	I	tBOSSM9				G	CytoplasmicMembrane	NO_SP	CYT
WP_041769855.1	LEPBI_RS09970		CatB-related O-acetylI chromosome	I	tBOSSN1				R	Cytoplasmic	NO_SP	CYT
WP_012388992.1	LEPBI_RS09975		phytanoyl-CoA dioxyg chromosome	I	tBOSSN2					Cytoplasmic	NO_SP	CYT
WP_012388993.1	LEPBI_RS09980		capsular polysaccharic chromosome	I	tBOSSN3					Cytoplasmic	NO_SP	CYT
WP_012388994.1	LEPBI_RS09985		GNAT family N-acetylI chromosome	I	tBOSSN4				J	Cytoplasmic	NO_SP	CYT
WP_012388996.1	LEPBI_RS09995		DegT/DnrJ/EryC1/StrS chromosome	I	tBOSSN6	WP_000582222.1	0.599985		M	Cytoplasmic	NO_SP	CYT
WP_012388997.1	LEPBI_RS10000		Gfo/Idh/MocA family chromosome	I	tBOSSN7				R	Cytoplasmic	NO_SP	CYT
WP_012388998.1	LEPBI_RS10005		glycosyltransferase fa; chromosome	I	tBOSSN8				M	Cytoplasmic	NO_SP	CYT
WP_012388999.1	LEPBI_RS10010	pseI	pseudaminic acid synt chromosome	I	tBOSSN9	WP_001230564.1	0.40615989999999996		M	Cytoplasmic	NO_SP	CYT
WP_012389000.1	LEPBI_RS10015		methionyl-tRNA form; chromosome	I	tBOSSP0				J	Cytoplasmic	NO_SP	CYT
WP_012476302.1	LEPBI_RS10020		PIG-L family deacetyla chromosome	I	tBOSSP1				G	Cytoplasmic	NO_SP	CYT
WP_012389003.1	LEPBI_RS10030		hypothetical protein chromosome	I	tBOSSP3					Unknown	NO_SP	CYT
WP_012389005.1	LEPBI_RS10040		aminotransferase clas chromosome	I	tBOSSP5				M	Cytoplasmic	NO_SP	CYT
WP_012389006.1	LEPBI_RS10045		GNAT family N-acetylI chromosome	I	tBOSSP6				J	Cytoplasmic	NO_SP	CYT
WP_012389007.1	LEPBI_RS10050		aldo/keto reductase chromosome	I	tBOSSP7				H	Cytoplasmic	NO_SP	CYT
WP_012389008.1	LEPBI_RS10055	pseC	UDP-4-amino-4,6-dide chromosome	I	tBOSSP8				M	Cytoplasmic	NO_SP	CYT
WP_012389009.1	LEPBI_RS10060	pseB	UDP-N-acetylglucosan chromosome	I	tBOSSP9	WP_000475904.1	0.47928669999999995		M	Cytoplasmic	NO_SP	CYT
WP_012389010.1	LEPBI_RS10065		GDP-L-fucose synthas chromosome	I	tBOSSQ0	WP_000410273.1	0.85107824999999999		M	Cytoplasmic	NO_SP	CYT
WP_012389012.1	LEPBI_RS10075	rfbA	glucose-1-phosphate I chromosome	I	tBOSSQ2	WP_000842260.1	0.6544881		M	Cytoplasmic	NO_SP	CYT
WP_012389016.1	LEPBI_RS10095		hypothetical protein chromosome	I	tBOSSQ6					Unknown	LIPO	SpII
WP_012389017.1	LEPBI_RS10100		RNA methyltransferas chromosome	I	tBOSSQ7				J	Cytoplasmic	NO_SP	CYT
WP_012389018.1	LEPBI_RS10105		FAD-dependent oxido chromosome	I	tBOSSQ8				C	Cytoplasmic	NO_SP	CYT
WP_012476304.1	LEPBI_RS10115		PAS domain S-box pro chromosome	I	tBOSSR0				T	CytoplasmicMembrane	NO_SP	CYT
WP_012389021.1	LEPBI_RS10120		SDR family NAD(P)-de chromosome	I	tBOSSR1				R	Unknown	NO_SP	CYT
WP_012476305.1	LEPBI_RS10125		SpoIIE family protein ; chromosome	I	tBOSSR2					CytoplasmicMembrane	NO_SP	TMH
WP_012389023.1	LEPBI_RS10130		DUF1566 domain-con chromosome	I	tBOSSR3					Extracellular	LIPO	CYT
WP_012389026.1	LEPBI_RS10145		hypothetical protein chromosome	I	tBOSSR6					Unknown	SP	SpII
WP_012476307.1	LEPBI_RS10155	sucC	ADP-forming succinat; chromosome	I	tBOSSR8	WP_000690686.1	0.8258382000000002		C	Cytoplasmic	NO_SP	CYT
WP_012389029.1	LEPBI_RS10160	sucD	succinate--CoA ligase chromosome	I	tBOSSR9	WP_000279904.1	0.84522735		C	Cytoplasmic	NO_SP	CYT
WP_012389031.1	LEPBI_RS10170		hypothetical protein chromosome	I	tBOSSS1	WP_001231967.1	0.416685			Cytoplasmic	NO_SP	TMH
WP_012389033.1	LEPBI_RS10180	lpxI	UDP-2,3-diacylglucose chromosome	I	tBOSSS3	WP_000517126.1	0.6447276000000001		S	Cytoplasmic	NO_SP	CYT
WP_012476308.1	LEPBI_RS10185	lpxB	lipid-A-disaccharide sy chromosome	I	tBOSSS4	WP_000212586.1	0.55739365		M	Cytoplasmic	NO_SP	CYT
WP_012389036.1	LEPBI_RS10195		hypothetical protein chromosome	I	tBOSSS6	WP_000124996.1	0.3261696			Cytoplasmic	NO_SP	CYT
WP_012389037.1	LEPBI_RS10200		hypothetical protein chromosome	I	tBOSSS7	WP_001974900.1	0.4018158			Cytoplasmic	LIPO	SpII
WP_012476309.1	LEPBI_RS10205		UvrD-helicase domain chromosome	I	tBOSSS8	WP_000777808.1	0.6538950000000001		L	Cytoplasmic	NO_SP	CYT
WP_012389039.1	LEPBI_RS10210		glutathione S-transfer chromosome	I	tBOSSS9				O	Unknown	NO_SP	CYT
WP_012389041.1	LEPBI_RS10220		FecR domain-containi chromosome	I	tBOSSST1					Cytoplasmic	SP	CYT
WP_012389042.1	LEPBI_RS10225		hypothetical protein chromosome	I	tBOSSST2					Unknown	LIPO	CYT
WP_012389045.1	LEPBI_RS10240		hypothetical protein chromosome	I	tBOSSST5					Unknown	LIPO	CYT
WP_012389048.1	LEPBI_RS10255	uvrC	excinuclease ABC sub; chromosome	I	sBOSSST8	WP_001114131.1	0.68122394999999999		L	Cytoplasmic	NO_SP	CYT
WP_041769858.1	LEPBI_RS10260		HAMP domain-contain; chromosome	I	tBOSSST9				T	CytoplasmicMembrane	NO_SP	TMH
WP_012389050.1	LEPBI_RS10265	lepB	signal peptidase I chromosome	I	tBOSSU0	WP_000091635.1	0.3554838			CytoplasmicMembrane	NO_SP	TMH
WP_012389052.1	LEPBI_RS10275	gap	type I glyceraldehyde- chromosome	I	tBOSSU2	WP_000196721.1	0.882065		G	Cytoplasmic	NO_SP	CYT

WP_012389053.1	LEPBI_RS10280		phosphoglycerate kinase	chromosome	I	sBOSSU3	WP_000422649.1	0.77588775	G	Cytoplasmic	NO_SP	CYT
WP_012389054.1	LEPBI_RS10285		triose-phosphate isomerase	chromosome	I	sBOSSU4	WP_001232578.1	0.682	G	Cytoplasmic	NO_SP	CYT
WP_012389055.1	LEPBI_RS10290	secG	preprotein translocase	chromosome	I	tBOSSU5	WP_000931842.1	0.48328245		CytoplasmicMembrane	NO_SP	TMH
WP_012389057.1	LEPBI_RS10300		HAMP domain-containing	chromosome	I	tBOSSU7	WP_000096813.1	0.6364946	T	CytoplasmicMembrane	NO_SP	CYT
WP_012389058.1	LEPBI_RS10305		response regulator	chromosome	I	tBOSSU8	WP_000282348.1	0.7138097999999999		Cytoplasmic	NO_SP	CYT
WP_012389061.1	LEPBI_RS10320		arginine--tRNA ligase	chromosome	I	sBOSSV1	WP_000662000.1	0.6352800000000001	J	Cytoplasmic	NO_SP	CYT
WP_012389063.1	LEPBI_RS10330	recO	DNA repair protein RecA	chromosome	I	sBOSSV3	WP_000016451.1	0.4354135	L	Cytoplasmic	NO_SP	CYT
WP_012389065.1	LEPBI_RS10340		HDIG domain-containing	chromosome	I	tBOSSV5	WP_000097929.1	0.6609774	T	CytoplasmicMembrane	NO_SP	CYT
WP_187148096.1	LEPBI_RS10345		PhoH family protein	chromosome	I	tBOSSV6	WP_000351423.1	0.6762046500000001	T	Cytoplasmic	NO_SP	CYT
WP_012389067.1	LEPBI_RS10350	aspS	aspartate--tRNA ligase	chromosome	I	sBOSSV7	WP_000683520.1	0.7346999999999999	J	Cytoplasmic	NO_SP	CYT
WP_012389069.1	LEPBI_RS10360		50S ribosomal protein	chromosome	I	sBOSSV9	WP_001263864.1	0.7106413999999999	J	Cytoplasmic	NO_SP	CYT
WP_012389070.1	LEPBI_RS10365		30S ribosomal protein	chromosome	I	sBOSSW0	WP_001293444.1	0.6074067999999999	J	Cytoplasmic	NO_SP	CYT
WP_012389071.1	LEPBI_RS10370	ssb	single-stranded DNA-binding	chromosome	I	tBOSSW1	WP_001262509.1	0.645545	L	Cytoplasmic	NO_SP	CYT
WP_012389072.1	LEPBI_RS10375		30S ribosomal protein	chromosome	I	sBOSSW2	WP_001246923.1	0.5714199999999999		Unknown	NO_SP	CYT
WP_012389075.1	LEPBI_RS10390		hypothetical protein	chromosome	I	tBOSSW5	WP_000669875.1	0.44004535		Cytoplasmic	LIPO	SpII
WP_012476311.1	LEPBI_RS10395		tetratricopeptide repeat	chromosome	I	tBOSSW6	WP_001070615.1	0.42176749999999996		Unknown	SP	SpI
WP_012389077.1	LEPBI_RS10400		hypothetical protein	chromosome	I	tBOSSW7	WP_000959052.1	0.40255		Cytoplasmic	NO_SP	CYT
WP_012389078.1	LEPBI_RS10405		aminotransferase class II	chromosome	I	tBOSSW8			E	Cytoplasmic	NO_SP	CYT
WP_012389079.1	LEPBI_RS10410		CHAT domain-containing	chromosome	I	tBOSSW9				Cytoplasmic	NO_SP	CYT
WP_012389081.1	LEPBI_RS10420		sigma-70 family RNA polymerase	chromosome	I	tBOSSX1				Cytoplasmic	NO_SP	CYT
WP_012389082.1	LEPBI_RS10425		hypothetical protein	chromosome	I	tBOSSX2				Unknown	NO_SP	CYT
WP_012389083.1	LEPBI_RS10430	ychF	redox-regulated ATPase	chromosome	I	tBOSSX3	WP_000055665.1	0.789065	J	Cytoplasmic	NO_SP	CYT
WP_012476312.1	LEPBI_RS10440		RNA pseudouridine synthase	chromosome	I	tBOSSX5			J	Cytoplasmic	NO_SP	CYT
WP_012389086.1	LEPBI_RS10445		DUF2797 domain-containing	chromosome	I	tBOSSX6	WP_000809310.1	0.6167777		Unknown	NO_SP	CYT
WP_012476313.1	LEPBI_RS10455		DUF1343 domain-containing	chromosome	I	tBOSSX8	WP_000935311.1	0.6035631	S	Periplasmic	LIPO	SpII
WP_012389089.1	LEPBI_RS10460		lipoprotein LipL46	chromosome	I	tBOSSX9	WP_001079033.1	0.5727375		Unknown	LIPO	SpII
WP_041769859.1	LEPBI_RS10465		response regulator	chromosome	I	tBOSSY0				Cytoplasmic	NO_SP	CYT
WP_012389091.1	LEPBI_RS10470		histidine kinase	chromosome	I	tBOSSY1			T	CytoplasmicMembrane	NO_SP	CYT
WP_041770016.1	LEPBI_RS10475		rhodanese-like domain	chromosome	I	tBOSSY2	WP_001982097.1	0.6843780000000002		Unknown	SP	CYT
WP_041769860.1	LEPBI_RS10480		peptidylprolyl isomerase	chromosome	I	tBOSSY3	WP_001141641.1	0.5669068	O	Cytoplasmic	NO_SP	CYT
WP_012389096.1	LEPBI_RS10490		NAD(P)H-dependent class II	chromosome	I	tBOSSY6			R	Cytoplasmic	NO_SP	CYT
WP_012389097.1	LEPBI_RS10495		VTT domain-containing	chromosome	I	tBOSSY7			M	CytoplasmicMembrane	NO_SP	CYT
WP_012389102.1	LEPBI_RS10520		hypothetical protein	chromosome	I	tBOSSZ2				Extracellular	LIPO	SpI
WP_012389104.1	LEPBI_RS10530		flagellin	chromosome	I	tBOSSZ4	WP_000586170.1	0.8237987999999999	N	Periplasmic	NO_SP	CYT
WP_012389105.1	LEPBI_RS10535		flagellin	chromosome	I	tBOSSZ5	WP_000586163.1	0.898595	N	Periplasmic	NO_SP	CYT
WP_041769861.1	LEPBI_RS10540		hypothetical protein	chromosome	I	tBOSSZ6	WP_001104455.1	0.32078670000000004		Cytoplasmic	NO_SP	CYT
WP_012389108.1	LEPBI_RS10550		DEAD/DEAH box helicase	chromosome	I	tBOSSZ8	WP_000667199.1	0.61673535	L	Cytoplasmic	NO_SP	CYT
WP_012389110.1	LEPBI_RS10560		tetratricopeptide repeat	chromosome	I	tBOST00	WP_000356651.1	0.5759709		Cytoplasmic	NO_SP	CYT
WP_012389111.1	LEPBI_RS10565	nusB	transcription antiterminal	chromosome	I	sBOST01	WP_001276210.1	0.6333905999999999	K	Cytoplasmic	NO_SP	CYT
WP_012389112.1	LEPBI_RS10570		6,7-dimethyl-8-ribitylthio	chromosome	I	sBOST02	WP_000613920.1	0.7156401	H	Cytoplasmic	NO_SP	CYT
WP_012389114.1	LEPBI_RS10575		SET domain-containing	chromosome	I	tBOST04	WP_001177028.1	0.671481		Unknown	NO_SP	CYT
WP_012389116.1	LEPBI_RS10585		DUF1957 domain-containing	chromosome	I	tBOST06			G	Cytoplasmic	NO_SP	CYT
WP_012389117.1	LEPBI_RS10590		hypothetical protein	chromosome	I	tBOST07				Cytoplasmic	NO_SP	CYT
WP_012389118.1	LEPBI_RS10595	raiA	ribosome-associated protein	chromosome	I	tBOST08	WP_000701011.1	0.7210650000000001		Unknown	NO_SP	CYT

WP_012389122.1	LEPBI_RS10610		sigma-70 family RNA 7 chromosome	I	tBOST12	WP_000378482.1	0.7222078499999999	K	Cytoplasmic	NO_SP	CYT
WP_012389123.1	LEPBI_RS10615	mutL	DNA mismatch repair chromosome	I	sBOST13	WP_000516444.1	0.6103152000000001	L	Cytoplasmic	NO_SP	CYT
WP_012389125.1	LEPBI_RS10625		flavin reductase chromosome	I	tBOST15	WP_000704507.1	0.5314249999999999	C	Unknown	NO_SP	CYT
WP_012389126.1	LEPBI_RS10630	purL	phosphoribosylformyl chromosome	I	sBOST16	WP_000409822.1	0.7352135999999999	F	Cytoplasmic	NO_SP	CYT
WP_012389128.1	LEPBI_RS10640		penicillin-binding prot chromosome	I	tBOST18				Unknown	LIPO	SpII
WP_041769863.1	LEPBI_RS10650		hypothetical protein chromosome	I	tBOST19				CytoplasmicMembrane	NO_SP	TMH
WP_012389132.1	LEPBI_RS10665		DNA-directed DNA po chromosome	I	tBOST22			L	Cytoplasmic	NO_SP	CYT
WP_012389135.1	LEPBI_RS10680		VOC family protein chromosome	I	tBOST25				Cytoplasmic	NO_SP	CYT
WP_012389142.1	LEPBI_RS10715		hypothetical protein chromosome	I	tBOST32				Cytoplasmic	NO_SP	CYT
WP_012389144.1	LEPBI_RS10725		AAA family ATPase chromosome	I	tBOST34				Cytoplasmic	NO_SP	CYT
WP_012389147.1	LEPBI_RS10740		hypothetical protein chromosome	I	tBOST37				Unknown	LIPO	CYT
WP_012389149.1	LEPBI_RS10750		hypothetical protein chromosome	I	tBOST39				CytoplasmicMembrane	SP	SpI
WP_012389152.1	LEPBI_RS10765		hypothetical protein chromosome	I	tBOST42				Cytoplasmic	NO_SP	CYT
WP_012389162.1	LEPBI_RS10815		DUF4209 domain-con chromosome	I	tBOST52				Cytoplasmic	NO_SP	CYT
WP_012389170.1	LEPBI_RS10855		hypothetical protein chromosome	I	tBOST61				Unknown	LIPO	SpII
WP_012389172.1	LEPBI_RS10865		DUF3368 domain-con chromosome	I	tBOST63			R	Cytoplasmic	NO_SP	CYT
WP_012389173.1	LEPBI_RS10870		DUF559 domain-cont chromosome	I	tBOST64				Cytoplasmic	NO_SP	CYT
WP_012389174.1	LEPBI_RS10880		DUF3800 domain-con chromosome	I	tBOST65				Cytoplasmic	NO_SP	CYT
WP_012389175.1	LEPBI_RS10885		ATP-binding protein chromosome	I	tBOST66				Cytoplasmic	NO_SP	CYT
WP_012389184.1	LEPBI_RS10940		helix-turn-helix transc chromosome	I	tBOST76				Unknown	NO_SP	CYT
WP_012389189.1	LEPBI_RS10965		putative DNA binding chromosome	I	tBOST81			K	Cytoplasmic	NO_SP	CYT
WP_012389201.1	LEPBI_RS11040		hypothetical protein chromosome	I	tBOST95				Unknown	NO_SP	CYT
WP_012389202.1	LEPBI_RS11045		PIN domain-containin chromosome	I	tBOST96				Unknown	NO_SP	CYT
WP_012476326.1	LEPBI_RS11105		helix-turn-helix transc chromosome	I					Unknown	NO_SP	CYT
WP_004787073.1	LEPBI_RS11150		transcriptional regulat chromosome	I	tBOSTB5			V	Cytoplasmic	NO_SP	CYT
WP_012389229.1	LEPBI_RS11200		multidrug efflux SMR chromosome	I	tBOSTC4			V	CytoplasmicMembrane	NO_SP	TMH
WP_012389232.1	LEPBI_RS11215		rRNA pseudouridine s chromosome	I	tBOSTC7			J	Cytoplasmic	NO_SP	CYT
WP_012389234.1	LEPBI_RS11225		chemotaxis protein chromosome	I	tBOSTC9			T	CytoplasmicMembrane	NO_SP	CYT
WP_012389237.1	LEPBI_RS11240		SDR family oxidoreduc chromosome	I	tBOSTD2	WP_001983276.1	0.7466817499999999		Cytoplasmic	NO_SP	CYT
WP_012389241.1	LEPBI_RS11260		polyprenol monophos chromosome	I	tBOSTD6			M	CytoplasmicMembrane	NO_SP	CYT
WP_012389245.1	LEPBI_RS11275	speD	adenosylmethionine c chromosome	I	tBOSTE0			E	Cytoplasmic	NO_SP	CYT
WP_187148055.1	LEPBI_RS11285		chemotaxis protein chromosome	I	tBOSTE2			T	CytoplasmicMembrane	NO_SP	TMH
WP_012389248.1	LEPBI_RS11290		hypothetical protein chromosome	I	tBOSTE3				Cytoplasmic	NO_SP	CYT
WP_012389249.1	LEPBI_RS11295		hypothetical protein chromosome	I	tBOSTE4	WP_001010184.1	0.4636949999999999		Extracellular	LIPO	CYT
WP_012389250.1	LEPBI_RS11300	ileS	isoleucine--tRNA ligas chromosome	I	sBOSTE5	WP_000005312.1	0.721908	J	Cytoplasmic	NO_SP	CYT
WP_012389252.1	LEPBI_RS11310		STAS domain-containi chromosome	I	tBOSTE7	WP_000405946.1	0.3557039999999999		Cytoplasmic	NO_SP	CYT
WP_012476332.1	LEPBI_RS11325		DUF4065 domain-con chromosome	I	tBOSTF0	WP_000413244.1	0.6534		Cytoplasmic	NO_SP	CYT
WP_012389256.1	LEPBI_RS11330		aspartate 1-decarboxy chromosome	I	sBOSTF1	WP_001167578.1	0.82758	H	Cytoplasmic	NO_SP	CYT
WP_012389257.1	LEPBI_RS11335		hypothetical protein chromosome	I	tBOSTF2	WP_000834696.1	0.5425397999999999		Unknown	SP	SpI
WP_041769871.1	LEPBI_RS11345		hypothetical protein chromosome	I	tBOSTF4	WP_001197044.1	0.6960429		Cytoplasmic	NO_SP	CYT
WP_012389260.1	LEPBI_RS11350	trxA	thioredoxin chromosome	I	tBOSTF5	WP_001970524.1	0.79806	O	Cytoplasmic	NO_SP	CYT
WP_012389261.1	LEPBI_RS11355		cAMP/cGMP-depende chromosome	I	tBOSTF6	WP_000910893.1	0.7524891		Cytoplasmic	NO_SP	CYT
WP_012389262.1	LEPBI_RS11360		acyl-CoA dehydrogen: chromosome	I	tBOSTF7	WP_000374065.1	0.8829849999999999	I	Cytoplasmic	NO_SP	CYT
WP_041770023.1	LEPBI_RS11365	thiC	phosphomethylpyrimi chromosome	I	tBOSTF8	WP_002072371.1	0.7776336	H	Cytoplasmic	NO_SP	CYT

WP_012476334.1	LEPBI_RS11380		hypothetical protein	chromosome	I	tBOSTG1	WP_000982211.1	0.4619724		CytoplasmicMembrane	SP	Spl
WP_012389267.1	LEPBI_RS11385		hypothetical protein	chromosome	I	tBOSTG2	WP_000616810.1	0.5169119999999999		Cytoplasmic	NO_SP	CYT
WP_012389269.1	LEPBI_RS11395		hypothetical protein	chromosome	I	tBOSTG4	WP_000099422.1	0.5264776		Unknown	NO_SP	CYT
WP_012389270.1	LEPBI_RS11400		bifunctional nuclease	chromosome	I	tBOSTG5	WP_000366622.1	0.8010250000000001	R	Cytoplasmic	NO_SP	CYT
WP_012476337.1	LEPBI_RS11415	hemW	radical SAM family he	chromosome	I	tBOSTG6	WP_000582255.1	0.538327	H	Cytoplasmic	NO_SP	CYT
WP_012389272.1	LEPBI_RS11430		CBS domain-containin	chromosome	I	tBOSTG7	WP_000275600.1	0.5516665		Cytoplasmic	NO_SP	CYT
WP_012389274.1	LEPBI_RS11440		pyridoxal phosphate-c	chromosome	I	tBOSTG9	WP_000433715.1	0.5589143999999999	E	Cytoplasmic	NO_SP	CYT
WP_012389275.1	LEPBI_RS11445		phospho-sugar mutas	chromosome	I	tBOSTH0	WP_001015901.1	0.70518195	G	Cytoplasmic	NO_SP	CYT
WP_012389276.1	LEPBI_RS11450		aspartate aminotransl	chromosome	I	tBOSTH1	WP_000995952.1	0.6488286	E	Cytoplasmic	NO_SP	CYT
WP_012389277.1	LEPBI_RS11455	leuB	3-isopropylmalate del	chromosome	I	tBOSTH2	WP_000799846.1	0.84358	C	Cytoplasmic	NO_SP	CYT
WP_012389278.1	LEPBI_RS11460		response regulator	chromosome	I	tBOSTH3	WP_000643584.1	0.7353000000000001		Cytoplasmic	NO_SP	CYT
WP_012389280.1	LEPBI_RS11470		hypothetical protein	chromosome	I	tBOSTH5	WP_000875640.1	0.3706037999999999		CytoplasmicMembrane	NO_SP	TMH
WP_012389281.1	LEPBI_RS11475		hypothetical protein	chromosome	I	tBOSTH6	WP_001042626.1	0.7480707999999999		Cytoplasmic	NO_SP	CYT
WP_012389282.1	LEPBI_RS11480		ABC transporter subst	chromosome	I	tBOSTH7	WP_001970104.1	0.6778758	E	Unknown	NO_SP	CYT
WP_012389284.1	LEPBI_RS11495	nadC	carboxylating nicotina	chromosome	I	tBOSTH9	WP_000266735.1	0.58677225	H	Cytoplasmic	NO_SP	CYT
WP_012389285.1	LEPBI_RS11500		lipoprotein LipL71	chromosome	I	tBOSTI0	WP_000843310.1	0.43571285000000004		OuterMembrane	LIPO	SpII
WP_002975418.1	LEPBI_RS11505		STAS domain-containi	chromosome	I	tBOSTI1	WP_000406878.1	0.9234	T	Unknown	NO_SP	CYT
WP_012389287.1	LEPBI_RS11515		transcriptional repres	chromosome	I	tBOSKT0	WP_001078417.1	0.6999239	P	Cytoplasmic	NO_SP	CYT
WP_012389288.1	LEPBI_RS11520		hypothetical protein	chromosome	I	tBOSKT1	WP_000469242.1	0.6266592		Cytoplasmic	LIPO	SpII
WP_012389289.1	LEPBI_RS11525		M23 family metallope	chromosome	I	tBOSKT2	WP_001163208.1	0.4047316		Unknown	SP	Spl
WP_012389290.1	LEPBI_RS11530	greA	transcription elongati	chromosome	I	tBOSKT3	WP_000064092.1	0.6870682	S	Cytoplasmic	NO_SP	CYT
WP_012389291.1	LEPBI_RS11535		flagellar filament oute	chromosome	I	tBOSKT4	WP_001972005.1	0.6013805999999999		Unknown	SP	Spl
WP_041770026.1	LEPBI_RS11540		endoflagellar filament	chromosome	I	tBOSKT5	WP_001227585.1	0.75123105		Unknown	SP	Spl
WP_015678642.1	LEPBI_RS11545		PurA ssDNA and RNA-	chromosome	I					Unknown	NO_SP	CYT
WP_012389294.1	LEPBI_RS11550		cyclic nucleotide-bind	chromosome	I	tBOSKT7	WP_001164879.1	0.5785086999999999	T	Cytoplasmic	NO_SP	CYT
WP_012389295.1	LEPBI_RS11555		response regulator trc	chromosome	I	tBOSKT8			T	Cytoplasmic	NO_SP	CYT
WP_187148056.1	LEPBI_RS11560		response regulator	chromosome	I	tBOSKT9			T	CytoplasmicMembrane	LIPO	SpII
WP_012389297.1	LEPBI_RS11565		DUF853 family proteir	chromosome	I	tBOSKU0			L	Cytoplasmic	NO_SP	CYT
WP_012389298.1	LEPBI_RS11570		co-chaperone GroES	chromosome	I	sBOSKU1	WP_000146552.1	0.8497041000000001	O	Cytoplasmic	NO_SP	CYT
WP_012389299.1	LEPBI_RS11575	groL	chaperonin GroEL	chromosome	I	sBOSKU2	WP_001029963.1	0.8726314	O	Cytoplasmic	NO_SP	CYT
WP_012389303.1	LEPBI_RS11595		hypothetical protein	chromosome	I	tBOSKU6	WP_000667225.1	0.705245		Cytoplasmic	NO_SP	CYT
WP_012389304.1	LEPBI_RS11600		Mrp/NBP35 family AT	chromosome	I	tBOSKU7	WP_000190880.1	0.75545415	D	CytoplasmicMembrane	NO_SP	CYT
WP_012389305.1	LEPBI_RS11605		metallophosphoester:	chromosome	I	tBOSKU8	WP_000697460.1	0.59044	T	Cytoplasmic	NO_SP	CYT
WP_012389307.1	LEPBI_RS11615		hypothetical protein	chromosome	I	tBOSKV0	WP_000013261.1	0.7014549999999999		Cytoplasmic	NO_SP	CYT
WP_012389308.1	LEPBI_RS11620		chorismate-binding pr	chromosome	I	tBOSKV1	WP_001217386.1	0.4403035	E	Cytoplasmic	NO_SP	CYT
WP_012389309.1	LEPBI_RS11625	hslU	ATP-dependent prote	chromosome	I	tBOSKV2	WP_001273642.1	0.7427250000000001	O	Cytoplasmic	NO_SP	CYT
WP_012389310.1	LEPBI_RS11630	hslV	ATP-dependent prote	chromosome	I	sBOSKV3	WP_001114726.1	0.8139124499999999	O	Cytoplasmic	NO_SP	CYT
WP_012389311.1	LEPBI_RS11635		ATP-binding protein	chromosome	I	tBOSKV4	WP_000377010.1	0.5739399999999999		Cytoplasmic	NO_SP	CYT
WP_012389312.1	LEPBI_RS11640	xerD	site-specific tyrosine r	chromosome	I	tBOSKV5	WP_000204200.1	0.8826147000000001	L	Cytoplasmic	NO_SP	CYT
WP_012389313.1	LEPBI_RS11645		hypothetical protein	chromosome	I	tBOSKV6				Cytoplasmic	LIPO	CYT
WP_012389314.1	LEPBI_RS11650	trxB	thioredoxin-disulfide r	chromosome	I	tBOSKV7	WP_000940585.1	0.8350432999999999	O	Cytoplasmic	NO_SP	Spl
WP_012389315.1	LEPBI_RS11655		hypothetical protein	chromosome	I	tBOSKV8				Unknown	SP	Spl
WP_012389316.1	LEPBI_RS11660	ilvN	acetolactate synthase	chromosome	I	tBOSKV9	WP_000680555.1	0.6884696	E	Cytoplasmic	NO_SP	CYT
WP_012476347.1	LEPBI_RS11665	ilvB	biosynthetic-type aceI	chromosome	I	tBOSKW0	WP_001272051.1	0.83400075	E	Cytoplasmic	NO_SP	CYT



WP_041770029.1	LEPBI_RS11670		tetratricopeptide repeat	chromosome	I	tBOSKW1	WP_000431183.1	0.7593547500000001		Cytoplasmic	NO_SP	CYT
WP_012389320.1	LEPBI_RS11680		hypothetical protein	chromosome	I	tBOSKW3	WP_000488503.1	0.48654539999999996		Cytoplasmic	LIPO	Spl
WP_012389321.1	LEPBI_RS11685	serC	3-phosphoserine/phosphoserine	chromosome	I	sBOSKW4	WP_001973456.1	0.64308915	H	Cytoplasmic	NO_SP	CYT
WP_012389322.1	LEPBI_RS11690		hypothetical protein	chromosome	I	tBOSKW5				Unknown	SP	CYT
WP_012389323.1	LEPBI_RS11695	rpiB	ribose 5-phosphate isomerase	chromosome	I	tBOSKW6	WP_000719443.1	0.7725371	G	Cytoplasmic	NO_SP	CYT
WP_041770031.1	LEPBI_RS11700		hypothetical protein	chromosome	I	tBOSKW7	WP_002070138.1	0.34081320000000004		Unknown	NO_SP	CYT
WP_012476350.1	LEPBI_RS11720		hypothetical protein	chromosome	I	tBOSKX1				CytoplasmicMembrane	NO_SP	TMH
WP_012389329.1	LEPBI_RS11725		metalloenzyme	chromosome	I	tBOSKX2	WP_000578515.1	0.5713344		Cytoplasmic	NO_SP	CYT
WP_012389330.1	LEPBI_RS11730		tetratricopeptide repeat	chromosome	I	tBOSKX3	WP_001082055.1	0.566115		OuterMembrane	NO_SP	Spl
WP_012389331.1	LEPBI_RS11735		tetratricopeptide repeat	chromosome	I	tBOSKX4	WP_000604760.1	0.48069945		Unknown	SP	Spl
WP_012476351.1	LEPBI_RS11740		SAM-dependent methyltransferase	chromosome	I	tBOSKX5	WP_001973506.1	0.63170399999999999		Cytoplasmic	NO_SP	CYT
WP_012389333.1	LEPBI_RS11745		UvrD-helicase domain	chromosome	I	tBOSKX6	WP_000792448.1	0.48751885000000006	L	Cytoplasmic	NO_SP	CYT
WP_012389336.1	LEPBI_RS11765		hypothetical protein	chromosome	I	tBOSKX9	WP_000675685.1	0.5246185		Cytoplasmic	NO_SP	TMH
WP_041770032.1	LEPBI_RS11775		LemA family protein	chromosome	I	tBOSKY1	WP_000850110.1	0.66688469999999999	M	Unknown	LIPO	Spl
WP_012389341.1	LEPBI_RS11790	pheA	prephenate dehydratase	chromosome	I	tBOSKY4	WP_001281293.1	0.66185955	E	Cytoplasmic	NO_SP	CYT
WP_012389342.1	LEPBI_RS11795	scpB	SMC-Scp complex subunit	chromosome	I	tBOSKY5	WP_000439024.1	0.762166	K	Cytoplasmic	NO_SP	CYT
WP_012389343.1	LEPBI_RS11800		segregation/condensation	chromosome	I	tBOSKY6	WP_000426654.1	0.6348644	L	Cytoplasmic	NO_SP	CYT
WP_002975323.1	LEPBI_RS11805		response regulator	chromosome	I	tBOSKY7	WP_000101124.1	0.8818672500000001	T	Cytoplasmic	NO_SP	CYT
WP_012389345.1	LEPBI_RS11815		chemotaxis protein C	chromosome	I	tBOSKY9	WP_000907362.1	0.63112499999999999	T	Cytoplasmic	NO_SP	CYT
WP_012389346.1	LEPBI_RS11820		purine-binding chemotaxis protein	chromosome	I	tBOSKZ0	WP_000200285.1	0.629432	T	Cytoplasmic	NO_SP	CYT
WP_012389347.1	LEPBI_RS11825		5-formyltetrahydrofolate dehydrogenase	chromosome	I	tBOSKZ1	WP_000776292.1	0.479766849999999997		Cytoplasmic	NO_SP	CYT
WP_012389348.1	LEPBI_RS11830		cell division protein Z	chromosome	I	tBOSKZ2	WP_000365849.1	0.53084850000000001		Cytoplasmic	NO_SP	CYT
WP_002975326.1	LEPBI_RS11840	rpIT	50S ribosomal protein I	chromosome	I	sBOSKZ5	WP_001136837.1	0.81506699999999999	J	Cytoplasmic	NO_SP	CYT
WP_002975302.1	LEPBI_RS11845	rpmI	50S ribosomal protein M1	chromosome	I	sBOSKZ6	WP_001125262.1	0.63424904999999999		Cytoplasmic	NO_SP	CYT
WP_012389351.1	LEPBI_RS11850		translation initiation factor	chromosome	I	sBOSKZ7	WP_001189133.1	0.74799945	J	Cytoplasmic	NO_SP	CYT
WP_012389353.1	LEPBI_RS11860	thrS	threonine--tRNA ligase	chromosome	I	tBOSKZ9	WP_000284477.1	0.7558254	J	Cytoplasmic	NO_SP	CYT
WP_012389354.1	LEPBI_RS11865		WHG domain-containing protein	chromosome	I	tBOSL00				Cytoplasmic	NO_SP	CYT
WP_143708650.1	LEPBI_RS11870		alpha/beta hydrolase	chromosome	I	tBOSL01				CytoplasmicMembrane	SP	Spl
WP_012389358.1	LEPBI_RS11885		P-II family nitrogen reductase	chromosome	I	tBOSL04	WP_000767694.1	0.951775	T	CytoplasmicMembrane	NO_SP	CYT
WP_012389363.1	LEPBI_RS11910		adenylate/guanylate cyclase	chromosome	I	tBOSL09				CytoplasmicMembrane	SP	CYT
WP_012389366.1	LEPBI_RS11925		HDOD domain-containing protein	chromosome	I	tBOSL12				Cytoplasmic	NO_SP	CYT
WP_012389368.1	LEPBI_RS11935		4Fe-4S dicluster domain protein	chromosome	I	tBOSL14	WP_000835444.1	0.56986999999999999	C	CytoplasmicMembrane	NO_SP	CYT
WP_012389372.1	LEPBI_RS11955		NADH-quinone oxidoreductase	chromosome	I	tBOSL18	WP_000402670.1	0.5139168		CytoplasmicMembrane	NO_SP	CYT
WP_012389373.1	LEPBI_RS11960		formate hydrogenase	chromosome	I	tBOSL19	WP_000636540.1	0.435883199999999997		CytoplasmicMembrane	NO_SP	TMH
WP_012389374.1	LEPBI_RS11970		ABC transporter ATP-binding domain	chromosome	I	tBOSL20	WP_000184524.1	0.53356275000000001	M	CytoplasmicMembrane	NO_SP	CYT
WP_012389376.1	LEPBI_RS11980		hypothetical protein	chromosome	I	tBOSL22	WP_001275305.1	0.4982222		Cytoplasmic	NO_SP	CYT
WP_012389378.1	LEPBI_RS11990	pyrE	orotate phosphoribosyltransferase	chromosome	I	sBOSL24	WP_000913341.1	0.5965569	F	Cytoplasmic	NO_SP	CYT
WP_012389380.1	LEPBI_RS12000		c-type cytochrome	chromosome	I	tBOSL26	WP_000804899.1	0.6818497	O	Periplasmic	LIPO	Spl
WP_012389382.1	LEPBI_RS12010		ornithine carbamoyltransferase	chromosome	I	tBOSL28	WP_000004530.1	0.77233860000000001	E	Cytoplasmic	NO_SP	CYT
WP_012389385.1	LEPBI_RS12020		aldolase	chromosome	I	tBOSLD8	WP_000041092.1	0.87194250000000001	G	Cytoplasmic	NO_SP	CYT
WP_012389386.1	LEPBI_RS12025		methyl-accepting chemotaxis protein	chromosome	I	tBOSLD9	WP_000027600.1	0.59885595	T	CytoplasmicMembrane	NO_SP	TMH
WP_012476357.1	LEPBI_RS12030		FecR domain-containing protein	chromosome	I	tBOSLE0	WP_001168703.1	0.457424799999999996		Cytoplasmic	LIPO	Spl
WP_012389388.1	LEPBI_RS12035		hypothetical protein	chromosome	I	tBOSLE1				CytoplasmicMembrane	NO_SP	TMH
WP_012389391.1	LEPBI_RS12045		1-acyl-sn-glycerol-3-phosphate	chromosome	I	tBOSLE4				Cytoplasmic	NO_SP	TMH

WP_012389392.1	LEPBI_RS12050		PAS domain S-box pro chromosome	I	tBOSLE5			T	CytoplasmicMembrane	NO_SP	CYT
WP_012389395.1	LEPBI_RS12065		tyrosine recombinase chromosome	I	tBOSLE8	WP_002079116.1	0.6956187	L	Cytoplasmic	NO_SP	CYT
WP_012389396.1	LEPBI_RS12070	recA	recombinase RecA chromosome	I	sBOSLE9	WP_000504720.1	0.7805847	L	Cytoplasmic	NO_SP	CYT
WP_012389397.1	LEPBI_RS12075		hypothetical protein chromosome	I	tBOSLF0				Cytoplasmic	SP	CYT
WP_012389398.1	LEPBI_RS12080		aldo/keto reductase chromosome	I	tBOSLF1	WP_001060166.1	0.65566665	Q	Cytoplasmic	NO_SP	CYT
WP_012389399.1	LEPBI_RS12085		AAA family ATPase chromosome	I	tBOSLF2			O	Cytoplasmic	NO_SP	CYT
WP_012476358.1	LEPBI_RS12100		PAS domain S-box pro chromosome	I	tBOSLF5			T	CytoplasmicMembrane	NO_SP	CYT
WP_012389403.1	LEPBI_RS12105		patatin-like phospholi chromosome	I	tBOSLF6	WP_001159609.1	0.5948844999999999	R	Cytoplasmic	NO_SP	TMH
WP_012389404.1	LEPBI_RS12110		cation-translocating P chromosome	I	tBOSLF7	WP_000402038.1	0.35876274999999996	P	CytoplasmicMembrane	NO_SP	CYT
WP_012389405.1	LEPBI_RS12115		C69 family dipeptidasi chromosome	I	tBOSLF8	WP_000332925.1	0.49196080000000003	E	Unknown	NO_SP	CYT
WP_041769876.1	LEPBI_RS12150		hypothetical protein chromosome	I	tBOSLG5	WP_000854884.1	0.66664125000000001		CytoplasmicMembrane	LIPO	TMH
WP_012389414.1	LEPBI_RS12160		ArsR family transcripti chromosome	I	tBOSLG7				Unknown	NO_SP	CYT
WP_012389416.1	LEPBI_RS12170		cyclic nucleotide-bind chromosome	I	tBOSLG9			T	Cytoplasmic	NO_SP	CYT
WP_012389421.1	LEPBI_RS12195		TatD family hydrolase chromosome	I	tBOSLH4			R	Cytoplasmic	NO_SP	CYT
WP_012389423.1	LEPBI_RS12205		alginate export family chromosome	I	tBOSLH6	WP_000739012.1	0.391059		OuterMembrane	SP	Spl
WP_012476360.1	LEPBI_RS12220		hypothetical protein chromosome	I					Unknown	SP	Spl
WP_012476361.1	LEPBI_RS12230		hypothetical protein chromosome	I	tBOSLI1				Unknown	SP	Spl
WP_012389429.1	LEPBI_RS12235		acyl-CoA dehydrogeni chromosome	I	tBOSLI2			I	Cytoplasmic	NO_SP	CYT
WP_187148098.1	LEPBI_RS12240		FAD-dependent oxido chromosome	I	tBOSLI3	WP_000877551.1	0.663696	C	Cytoplasmic	NO_SP	CYT
WP_012389432.1	LEPBI_RS12250		TetR family transcripti chromosome	I	tBOSLI5				Cytoplasmic	NO_SP	CYT
WP_012389433.1	LEPBI_RS12255		neutral/alkaline ceran chromosome	I	tBOSLI6				Unknown	LIPO	SplI
WP_143708636.1	LEPBI_RS12280		poly(3-hydroxybutyrai chromosome	I	tBOSLJ1			G	Unknown	NO_SP	CYT
WP_012389439.1	LEPBI_RS12285		hypothetical protein chromosome	I	tBOSLJ2				Unknown	LIPO	SplI
WP_012389440.1	LEPBI_RS12295	eutC	ethanolamine ammon chromosome	I	tBOSLJ3			E	Cytoplasmic	NO_SP	CYT
WP_012389441.1	LEPBI_RS12300		ethanolamine ammon chromosome	I	tBOSLJ4			E	Cytoplasmic	NO_SP	CYT
WP_012389443.1	LEPBI_RS12310	katG	catalase/peroxidase H chromosome	I	sBOSLJ6			P	Cytoplasmic	SP	Spl
WP_041769879.1	LEPBI_RS12355		adenylate/guanylate r chromosome	I	tBOSLK7			T	CytoplasmicMembrane	NO_SP	TMH
WP_012389466.1	LEPBI_RS12420		patatin-like phospholi chromosome	I	tBOSLL9			R	Unknown	NO_SP	CYT
WP_012389470.1	LEPBI_RS12440		GAF domain-containir chromosome	I	tBOSLM3			T	CytoplasmicMembrane	SP	CYT
WP_012389471.1	LEPBI_RS12445		response regulator tra chromosome	I	tBOSLM4	WP_000244073.1	0.3681033	T	Cytoplasmic	NO_SP	CYT
WP_012389472.1	LEPBI_RS12450		7TM-DISM domain-co chromosome	I	tBOSLM5				CytoplasmicMembrane	LIPO	SplI
WP_012476370.1	LEPBI_RS12455		hypothetical protein chromosome	I	tBOSLM7				Cytoplasmic	NO_SP	CYT
WP_012389475.1	LEPBI_RS12460		DUF3696 domain-con chromosome	I	tBOSLM8			R	Cytoplasmic	NO_SP	CYT
WP_012389476.1	LEPBI_RS12465		DUF262 domain-conti chromosome	I	tBOSLM9				Cytoplasmic	NO_SP	CYT
WP_012389479.1	LEPBI_RS12485		hypothetical protein chromosome	I	tBOSLN2				OuterMembrane	SP	CYT
WP_012389480.1	LEPBI_RS12490		alpha/beta hydrolase chromosome	I	tBOSLN3				Unknown	NO_SP	Spl
WP_041770038.1	LEPBI_RS12495		curli assembly protein chromosome	I	tBOSLN4				Cytoplasmic	NO_SP	CYT
WP_012389482.1	LEPBI_RS12500		DNA starvation/statio chromosome	I	tBOSLN5	WP_000658301.1	0.68393280000000001	P	Cytoplasmic	NO_SP	CYT
WP_012389483.1	LEPBI_RS12505		alpha/beta fold hydro chromosome	I	tBOSLN6	WP_001277162.1	0.52445060000000001	H	Cytoplasmic	NO_SP	CYT
WP_012389484.1	LEPBI_RS12510		SH3 domain-containin chromosome	I	tBOSLN7	WP_001971371.1	0.436743		Cytoplasmic	SP	CYT
WP_012389485.1	LEPBI_RS12515		pyridoxal phosphate-c chromosome	I	tBOSLN8	WP_000365890.1	0.74506000000000001	E	Cytoplasmic	NO_SP	CYT
WP_012389486.1	LEPBI_RS12520		DEAD/DEAH box helic chromosome	I	tBOSLN9	WP_000042798.1	0.88114739999999999	K	Cytoplasmic	NO_SP	CYT
WP_012389487.1	LEPBI_RS12525	dusA	tRNA dihydrouridine( chromosome	I	tBOSLP0	WP_000891135.1	0.5742908	J	Cytoplasmic	NO_SP	CYT
WP_012389488.1	LEPBI_RS12530		FH1PEP family type III chromosome	I	tBOSLZ7	WP_000412863.1	0.69370785	N	CytoplasmicMembrane	NO_SP	TMH

WP_012389492.1	LEPBI_RS12550	fliP	flagellar type III secret chromosome	I	tBOSM01	WP_000783972.1	0.7875152999999999	N	CytoplasmicMembrane	NO_SP	TMH
WP_041770040.1	LEPBI_RS12555		flagellar biosynthetic   chromosome	I	tBOSM02	WP_001211503.1	0.3935295000000001		Unknown	SP	Spl
WP_012389494.1	LEPBI_RS12560	fliN	flagellar motor switch chromosome	I	tBOSM03	WP_000503780.1	0.6252443999999999	N	Unknown	NO_SP	CYT
WP_012389495.1	LEPBI_RS12565		DUF971 domain-cont: chromosome	I	tBOSM04	WP_000057945.1	0.6067380000000001		Unknown	NO_SP	CYT
WP_012389496.1	LEPBI_RS12570	psd	phosphatidylserine de chromosome	I	tBOSM05	WP_000938817.1	0.6886885500000001	E	CytoplasmicMembrane	NO_SP	TMH
WP_012389497.1	LEPBI_RS12575		hypothetical protein chromosome	I	tBOSM06	WP_001202901.1	0.39512949999999997		Unknown	SP	Spl
WP_012389500.1	LEPBI_RS12590		hypothetical protein chromosome	I	tBOSM09				Unknown	NO_SP	CYT
WP_012389501.1	LEPBI_RS12595	lpxD	UDP-3-O-(3-hydroxym chromosome	I	tBOSM10	WP_000644954.1	0.6944652000000001	M	Cytoplasmic	NO_SP	CYT
WP_012476374.1	LEPBI_RS12600		OmpA family protein chromosome	I	tBOSM11				Cytoplasmic	NO_SP	CYT
WP_012389505.1	LEPBI_RS12615		glycosyltransferase fa  chromosome	I	tBOSM14				Unknown	NO_SP	CYT
WP_049755984.1	LEPBI_RS12620		cytochrome C554 and chromosome	I	tBOSM15				Cytoplasmic	NO_SP	TMH
WP_012389507.1	LEPBI_RS12625		thiosulfate sulfurtrans chromosome	I	tBOSM16			P	Cytoplasmic	SP	Spl
WP_012476377.1	LEPBI_RS12635		aminotransferase clas chromosome	I	tBOSM18			E	Cytoplasmic	NO_SP	CYT
WP_012389510.1	LEPBI_RS12640		ABC transporter ATP-t chromosome	I	tBOSM19	WP_001161019.1	0.5692408000000001	M	CytoplasmicMembrane	NO_SP	CYT
WP_041770041.1	LEPBI_RS12650		efflux RND transporte chromosome	I	tBOSM21	WP_001100379.1	0.69125		Cytoplasmic	NO_SP	TMH
WP_012389513.1	LEPBI_RS12655	mtaB	tRNA (N(6)-L-threonyl chromosome	I	tBOSM22	WP_000555988.1	0.6551711999999998	J	Cytoplasmic	NO_SP	CYT
WP_012389514.1	LEPBI_RS12660		tetratricopeptide repe chromosome	I	tBOSM23	WP_00059958.1	0.5431250000000001		Cytoplasmic	SP	Spl
WP_012389516.1	LEPBI_RS12670		ATP-dependent Clp pr chromosome	I	tBOSM25	WP_000889241.1	0.84875	O	Cytoplasmic	NO_SP	CYT
WP_012389518.1	LEPBI_RS12680		ABC transporter ATP-t chromosome	I	tBOSM27	WP_000052667.1	0.7139202000000001	M	CytoplasmicMembrane	NO_SP	CYT
WP_012389519.1	LEPBI_RS12685		ABC transporter perm chromosome	I	tBOSM28	WP_000867622.1	0.7295512	M	CytoplasmicMembrane	NO_SP	TMH
WP_012389520.1	LEPBI_RS12690		hypothetical protein chromosome	I	tBOSM29	WP_000097761.1	0.4061561000000001		Unknown	NO_SP	CYT
WP_012476378.1	LEPBI_RS12700		hypothetical protein chromosome	I	tBOSM31	WP_001049438.1	0.4140135		Unknown	NO_SP	Spl
WP_012389523.1	LEPBI_RS12705		mechanosensitive ion chromosome	I	tBOSM32	WP_000397489.1	0.5910143999999999		CytoplasmicMembrane	NO_SP	CYT
WP_012389524.1	LEPBI_RS12710		3-dehydroquinate syn chromosome	I	tBOSM33	WP_000052388.1	0.6100368	E	Cytoplasmic	NO_SP	CYT
WP_012389525.1	LEPBI_RS12715		NUDIX hydrolase chromosome	I	tBOSM34	WP_002069656.1	0.6708537		Cytoplasmic	NO_SP	CYT
WP_012389526.1	LEPBI_RS12720	rnc	ribonuclease III chromosome	I	tBOSM35	WP_000008630.1	0.47318180000000004	K	Cytoplasmic	NO_SP	CYT
WP_002974954.1	LEPBI_RS12725	acpP	acyl carrier protein chromosome	I	sBOSM36	WP_000753030.1	0.94154	I	Cytoplasmic	NO_SP	CYT
WP_012389529.1	LEPBI_RS12740		hypothetical protein chromosome	I	tBOSM39				Cytoplasmic	NO_SP	CYT
WP_012389530.1	LEPBI_RS12745	fabG	3-oxoacyl-ACP reduct: chromosome	I	tBOSM40	WP_000566240.1	0.7652639999999999	I	Cytoplasmic	NO_SP	CYT
WP_012389531.1	LEPBI_RS12750	plsX	phosphate acyltransfe chromosome	I	sBOSM41	WP_000990052.1	0.82598175	I	Cytoplasmic	NO_SP	CYT
WP_012389532.1	LEPBI_RS12755		ATP phosphoribosyltri: chromosome	I	sBOSM42	WP_000956489.1	0.7204576500000001	E	Cytoplasmic	NO_SP	CYT
WP_012389533.1	LEPBI_RS12760		hypothetical protein chromosome	I	tBOSM43	WP_000833112.1	0.425		Cytoplasmic	NO_SP	CYT
WP_012389534.1	LEPBI_RS12765		30S ribosomal protein chromosome	I	tBOSM44	WP_000182263.1	0.7149186	J	Cytoplasmic	NO_SP	CYT
WP_012389535.1	LEPBI_RS12770		(d)CMP kinase chromosome	I	tBOSM45	WP_001005055.1	0.57789205	F	Cytoplasmic	NO_SP	CYT
WP_012389536.1	LEPBI_RS12775		PAS domain S-box pro chromosome	I	tBOSM46			T	Cytoplasmic	NO_SP	CYT
WP_012389537.1	LEPBI_RS12780	aroA	3-phosphoshikimate 1 chromosome	I	sBOSM47	WP_000612432.1	0.6588549	E	Cytoplasmic	NO_SP	CYT
WP_012389538.1	LEPBI_RS12785		cyclic nucleotide-bind chromosome	I	tBOSM48	WP_000863354.1	0.590915		Cytoplasmic	NO_SP	CYT
WP_012389540.1	LEPBI_RS12795		hypothetical protein chromosome	I	tBOSM50	WP_000390247.1	0.820165		Cytoplasmic	NO_SP	CYT
WP_012389542.1	LEPBI_RS12805		hypothetical protein chromosome	I	tBOSM52	WP_000651384.1	0.4285544		Cytoplasmic	NO_SP	CYT
WP_012389544.1	LEPBI_RS12815		1-deoxy-D-xylulose-5- chromosome	I	tBOSM54	WP_001183723.1	0.7054971	H	Cytoplasmic	NO_SP	CYT
WP_012389545.1	LEPBI_RS12820		adenylate/guanylate r chromosome	I	tBOSM55	WP_001291001.1	0.7049493	T	CytoplasmicMembrane	NO_SP	TMH
WP_012389546.1	LEPBI_RS12825		tryptophan synthase ε chromosome	I	sQ5MI53	WP_001084828.1	0.6257691000000001	E	Cytoplasmic	NO_SP	CYT
WP_012389547.1	LEPBI_RS12830	trpB	tryptophan synthase ε chromosome	I	sBOSM57	WP_000514163.1	0.7857786999999999	E	Cytoplasmic	NO_SP	CYT
WP_012389548.1	LEPBI_RS12835		proline--tRNA ligase chromosome	I	sBOSM58	WP_000647839.1	0.6667723999999999	J	Cytoplasmic	NO_SP	CYT

WP_012389549.1	LEPBI_RS12840		site-2 protease family chromosome	I	tBOSM59	WP_000906630.1	0.668675	O	CytoplasmicMembrane	NO_SP	TMH
WP_012389550.1	LEPBI_RS12845		1-deoxy-D-xylulose-5- chromosome	I	sBOSM60	WP_000213814.1	0.6378528	I	Unknown	NO_SP	CYT
WP_012389552.1	LEPBI_RS12855		isoprenyl transferase chromosome	I	tBOSM62	WP_000522360.1	0.7168895999999998	I	Cytoplasmic	NO_SP	CYT
WP_012389553.1	LEPBI_RS12860	frr	ribosome recycling fa chromosome	I	sBOSM63	WP_000135448.1	0.7553153999999999	J	Cytoplasmic	NO_SP	CYT
WP_012389554.1	LEPBI_RS12865		UMP kinase chromosome	I	tBOSM64	WP_000179852.1	0.832665	F	Cytoplasmic	NO_SP	CYT
WP_012389555.1	LEPBI_RS12870	tsf	translation elongation chromosome	I	sBOSM65	WP_000741905.1	0.7599753	J	Cytoplasmic	NO_SP	CYT
WP_012389556.1	LEPBI_RS12875	rpsB	30S ribosomal protein chromosome	I	tBOSM66	WP_000111480.1	0.7823745	J	Cytoplasmic	NO_SP	CYT
WP_012389558.1	LEPBI_RS12885		bifunctional alpha,alp chromosome	I	tBOSM68			G	Cytoplasmic	NO_SP	CYT
WP_012389559.1	LEPBI_RS12890		glycoside hydrolase fa chromosome	I	tBOSM69			G	Cytoplasmic	NO_SP	CYT
WP_012389560.1	LEPBI_RS12895		PAS domain S-box pro chromosome	I	tBOSM70			T	CytoplasmicMembrane	NO_SP	CYT
WP_012389565.1	LEPBI_RS12915		SGNH/GDSL hydrolase chromosome	I	tBOSM75				Cytoplasmic	LIPO	SpII
WP_012389566.1	LEPBI_RS12920		chemotaxis protein chromosome	I	tBOSM76			T	CytoplasmicMembrane	NO_SP	TMH
WP_012389569.1	LEPBI_RS12935		MBL fold metallo-hydri chromosome	I	tBOSM79			R	Cytoplasmic	NO_SP	CYT
WP_012389570.1	LEPBI_RS12940		sulfite exporter TauE/ chromosome	I	tBOSM80				CytoplasmicMembrane	NO_SP	TMH
WP_012389572.1	LEPBI_RS12950	msrA	peptide-methionine (t chromosome	I	tBOSM82			O	Unknown	LIPO	TMH
WP_012389573.1	LEPBI_RS12955		HDOD domain-contair chromosome	I	tBOSM83	WP_001076957.1	0.6675272999999999	T	Cytoplasmic	NO_SP	CYT
WP_012389576.1	LEPBI_RS12970		SMP-30/gluconolactoi chromosome	I	tBOSM86	WP_000476420.1	0.3531297	G	Cytoplasmic	LIPO	SpI
WP_012389577.1	LEPBI_RS12975		acyltransferase chromosome	I	tBOSM87			I	CytoplasmicMembrane	NO_SP	TMH
WP_012389578.1	LEPBI_RS12980		SpoIIE family protein i chromosome	I	tBOSM88			T	Cytoplasmic	NO_SP	CYT
WP_012389580.1	LEPBI_RS12990		SDR family NAD(P)-de chromosome	I	tBOSM90			I	Cytoplasmic	NO_SP	CYT
WP_012389582.1	LEPBI_RS13000		polymer-forming cyto chromosome	I	tBOSM92	WP_000039429.1	0.75046455	Z	Unknown	NO_SP	CYT
WP_041770044.1	LEPBI_RS13005		tetratricopeptide repe chromosome	I		WP_000622506.1	0.67807		Unknown	NO_SP	CYT
WP_012389584.1	LEPBI_RS13010	acpS	holo-ACP synthase chromosome	I	sBOSM94	WP_000704154.1	0.7155617	I	Cytoplasmic	NO_SP	CYT
WP_012389585.1	LEPBI_RS13015		AAA family ATPase chromosome	I	tBOSM95	WP_000686848.1	0.402696	R	Unknown	NO_SP	CYT
WP_012389586.1	LEPBI_RS13020		glucose 1-dehydrogen chromosome	I	tBOSM96	WP_000653653.1	0.584645	I	Cytoplasmic	NO_SP	CYT
WP_012476383.1	LEPBI_RS13025		PilZ domain-containin chromosome	I	tBOSM97				Cytoplasmic	NO_SP	CYT
WP_012389588.1	LEPBI_RS13030		universal stress protei chromosome	I	tBOSM98	WP_001188723.1	0.7430399999999999	T	Cytoplasmic	NO_SP	CYT
WP_012389589.1	LEPBI_RS13035		ABC transporter perm chromosome	I	tBOSM99			E	CytoplasmicMembrane	NO_SP	TMH
WP_012389590.1	LEPBI_RS13040		ABC transporter perm chromosome	I	tBOSMA0			E	CytoplasmicMembrane	NO_SP	TMH
WP_012389591.1	LEPBI_RS13045		ABC transporter ATP-t chromosome	I	tBOSMA1			E	CytoplasmicMembrane	NO_SP	CYT
WP_012389592.1	LEPBI_RS13050		ABC transporter subst chromosome	I	tBOSMA2			E	Periplasmic	LIPO	SpII
WP_012389593.1	LEPBI_RS13055		NAD-dependent succi chromosome	I	tBOSMA3			I	Cytoplasmic	NO_SP	CYT
WP_012389594.1	LEPBI_RS13060	gabT	4-aminobutyrate--2-o. chromosome	I	tBOSMA4			E	Cytoplasmic	NO_SP	CYT
WP_012389595.1	LEPBI_RS13065		gamma-aminobutyral chromosome	I	tBOSML1			I	Cytoplasmic	NO_SP	CYT
WP_041769885.1	LEPBI_RS13070		DUF389 domain-contz chromosome	I	tBOSML2	WP_001170205.1	0.4968960000000000	S	CytoplasmicMembrane	NO_SP	CYT
WP_012389597.1	LEPBI_RS13075		hypothetical protein chromosome	I	tBOSML3	WP_000979308.1	0.3665592000000000		Unknown	NO_SP	CYT
WP_012476384.1	LEPBI_RS13080		SurA N-terminal domz chromosome	I	tBOSML4	WP_000281386.1	0.755625		Unknown	NO_SP	TMH
WP_012389599.1	LEPBI_RS13085		chemotaxis protein Ct chromosome	I	tBOSML5	WP_001167022.1	0.7699873500000001	N	Unknown	NO_SP	CYT
WP_012389600.1	LEPBI_RS13090		tetratricopeptide repe chromosome	I	tBOSML6				Cytoplasmic	SP	SpI
WP_012389601.1	LEPBI_RS13095		hypothetical protein chromosome	I	tBOSML7				Cytoplasmic	NO_SP	CYT
WP_012389602.1	LEPBI_RS13100		OmpA family protein chromosome	I	tBOSML8	WP_000557278.1	0.5460524999999999	M	Unknown	SP	CYT
WP_012389603.1	LEPBI_RS13105		ATP-binding cassette i chromosome	I	tBOSML9	WP_000626143.1	0.7992467999999999	R	Cytoplasmic	NO_SP	CYT
WP_012476385.1	LEPBI_RS13115	rdgB	RdgB/HAM1 family nc chromosome	I	tBOSMM1	WP_000828653.1	0.6162926000000001	F	Cytoplasmic	NO_SP	CYT
WP_012476386.1	LEPBI_RS13120		STAS domain-containi chromosome	I		WP_000406975.1	0.6510933		Cytoplasmic	NO_SP	CYT

WP_012389608.1	LEPBI_RS13130	hypothetical protein	chromosome	I	tBOSMM4	WP_000678902.1	0.552		Unknown	SP	Spl
WP_012389610.1	LEPBI_RS13140	hypothetical protein	chromosome	I	tBOSMM6	WP_001007329.1	0.4709835		Cytoplasmic	NO_SP	CYT
WP_012476387.1	LEPBI_RS13145	hypothetical protein	chromosome	I	tBOSMM7				Cytoplasmic	NO_SP	TMH
WP_012389612.1	LEPBI_RS13150	apolipoprotein N-acyl	chromosome	I	tBOSMM8	WP_000958086.1	0.5100585	M	CytoplasmicMembrane	NO_SP	TMH
WP_012389613.1	LEPBI_RS13155	PIN/TRAM domain-co	chromosome	I	tBOSMM9	WP_000581182.1	0.7378224	R	CytoplasmicMembrane	NO_SP	TMH
WP_012389614.1	LEPBI_RS13160	transcriptional regulat	chromosome	I	tBOSMN0	WP_000729197.1	0.788754	K	Cytoplasmic	NO_SP	CYT
WP_143708638.1	LEPBI_RS13170	hypothetical protein	chromosome	I	tBOSMN2				Unknown	LIPO	SpII
WP_012389618.1	LEPBI_RS13180	SpoII E family protein	chromosome	I	tBOSMN4				CytoplasmicMembrane	NO_SP	CYT
WP_012389619.1	LEPBI_RS13185	cytochrome C oxidase	chromosome	I	tBOSMN5	WP_000418707.1	0.4432092		CytoplasmicMembrane	NO_SP	TMH
WP_012389620.1	LEPBI_RS13190	cytochrome c oxidase	chromosome	I	tBOSMN6	WP_000100797.1	0.59449	C	CytoplasmicMembrane	NO_SP	TMH
WP_012389621.1	LEPBI_RS13195	cbb3-type cytochrome	chromosome	I	tBOSMN7	WP_000102005.1	0.8212545	C	CytoplasmicMembrane	NO_SP	CYT
WP_012389622.1	LEPBI_RS13200	cytochrome c oxidase	chromosome	I	tBOSMN8	WP_000220059.1	0.63325	C	CytoplasmicMembrane	NO_SP	CYT
WP_143708652.1	LEPBI_RS13205	SCO family protein	chromosome	I	tBOSMN9	WP_000885550.1	0.5618585		Unknown	SP	CYT
WP_012389626.1	LEPBI_RS13220	hypothetical protein	chromosome	I	tBOSMP2			S	CytoplasmicMembrane	NO_SP	CYT
WP_012389627.1	LEPBI_RS13225	YgcG family protein	chromosome	I	tBOSMP3			S	CytoplasmicMembrane	NO_SP	TMH
WP_012389628.1	LEPBI_RS13230	SpoII E family protein	chromosome	I	tBOSMP4	WP_001160641.1	0.30753450000000004		CytoplasmicMembrane	LIPO	SpII
WP_012389629.1	LEPBI_RS13235	citrate synthase	chromosome	I	tBOSMP5	WP_001288561.1	0.725345	C	Cytoplasmic	NO_SP	CYT
WP_012389630.1	LEPBI_RS13240	STAS domain-containi	chromosome	I	tBOSMP6	WP_001287684.1	0.7490934		Unknown	NO_SP	CYT
WP_012389632.1	LEPBI_RS13250	cytochrome c	chromosome	I	tBOSMP8	WP_001086272.1	0.68706		Unknown	LIPO	SpII
WP_012389634.1	LEPBI_RS13260	hypothetical protein	chromosome	I	tBOSMQ0	WP_002083627.1	0.43566239999999995		Cytoplasmic	NO_SP	CYT
WP_012389635.1	LEPBI_RS13265	AAA family ATPase	chromosome	I	tBOSMQ1				Cytoplasmic	NO_SP	CYT
WP_012389640.1	LEPBI_RS13290	AAA family ATPase	chromosome	I	tBOSMQ6			H	Cytoplasmic	NO_SP	CYT
WP_012389641.1	LEPBI_RS13295	hypothetical protein	chromosome	I	tBOSMQ7				Cytoplasmic	NO_SP	CYT
WP_012389643.1	LEPBI_RS13305	lipid A Kdo2 1-phosph	chromosome	I	tBOSMQ9	WP_001173879.1	0.67392		CytoplasmicMembrane	NO_SP	TMH
WP_012389644.1	LEPBI_RS13310	1-acyl-sn-glycerol-3-pl	chromosome	I	tBOSMR0				Cytoplasmic	NO_SP	CYT
WP_012389645.1	LEPBI_RS13315	hypothetical protein	chromosome	I	tBOSMR1				Cytoplasmic	NO_SP	CYT
WP_041770045.1	LEPBI_RS13320	rubrerythrin	chromosome	I	tBOSMR2	WP_000219378.1	0.48999405		Unknown	NO_SP	CYT
WP_012389647.1	LEPBI_RS13325	hypothetical protein	chromosome	I	tBOSMR3	WP_000510657.1	0.48329819999999996		Unknown	NO_SP	CYT
WP_012389648.1	LEPBI_RS13330	hypothetical protein	chromosome	I	tBOSMR4	WP_000907541.1	0.75729655		Unknown	NO_SP	CYT
WP_012389649.1	LEPBI_RS13335	type I methionyl amin	chromosome	I	tBOSMR5	WP_002077265.1	0.80511255	J	Cytoplasmic	NO_SP	CYT
WP_012389652.1	LEPBI_RS13345	hydroxyethylthiazole	chromosome	I	sBOSMR8	WP_000047876.1	0.49196224999999993	H	Unknown	NO_SP	CYT
WP_012389653.1	LEPBI_RS13350	thiamine phosphate s	chromosome	I	sBOSMR9	WP_001202539.1	0.31112639999999997	H	Unknown	NO_SP	CYT
WP_012389656.1	LEPBI_RS13365	acyl-CoA thioesterase	chromosome	I	tBOSMS2	WP_000626110.1	0.511518	I	Cytoplasmic	NO_SP	CYT
WP_012389658.1	LEPBI_RS13375	hypothetical protein	chromosome	I	tBOSMS4				OuterMembrane	SP	CYT
WP_012389661.1	LEPBI_RS13390	DUF1577 domain-con	chromosome	I	tBOSMS7	WP_000455718.1	0.5150292		Cytoplasmic	NO_SP	CYT
WP_012476392.1	LEPBI_RS13400	FKBP-type peptidyl-pr	chromosome	I	tBOSMS9	WP_000673420.1	0.62832245	O	Periplasmic	NO_SP	CYT
WP_187148099.1	LEPBI_RS13405	YHYH protein	chromosome	I	tBOSMT0	WP_000615243.1	0.6106663		Extracellular	NO_SP	Spl
WP_012389668.1	LEPBI_RS13425	ABC transporter ATP-t	chromosome	I	tBOSMT4	WP_001982953.1	0.7339311000000001	V	CytoplasmicMembrane	NO_SP	CYT
WP_012389669.1	LEPBI_RS13430	ABC-F family ATP-binc	chromosome	I	tBOSMT5	WP_000590867.1	0.8719999999999999	R	Cytoplasmic	NO_SP	CYT
WP_012389673.1	LEPBI_RS13445	formate-dependent p	chromosome	I	tBOSMT9	WP_000727141.1	0.5610528	F	CytoplasmicMembrane	NO_SP	CYT
WP_012389676.1	LEPBI_RS13460	copper-translocating	chromosome	I	tBOSMU2	WP_001982140.1	0.5694034499999999	P	CytoplasmicMembrane	NO_SP	CYT
WP_012389682.1	LEPBI_RS13490	hypothetical protein	chromosome	I	tBOSMU8				Unknown	NO_SP	CYT
WP_012389684.1	LEPBI_RS13500	STAS domain-containi	chromosome	I	tBOSMV0				Unknown	NO_SP	CYT
WP_012389685.1	LEPBI_RS13505	hypothetical protein	chromosome	I	tBOSMV1				Unknown	LIPO	CYT

WP_012389688.1	LEPBI_RS13520	hypothetical protein	chromosome	I	tBOSMV4				Unknown	SP	CYT
WP_012389689.1	LEPBI_RS13525	SDR family NAD(P)-de	chromosome	I	tBOSMV5	WP_000581855.1	0.43427340000000003	R	Cytoplasmic	NO_SP	CYT
WP_041770047.1	LEPBI_RS13530	neutral/alkaline non-l	chromosome	I	tBOSMV6				Unknown	SP	Spl
WP_012389692.1	LEPBI_RS13540	lipid A deacylase LpxR	chromosome	I	tBOSMV8				OuterMembrane	SP	Spl
WP_012389695.1	LEPBI_RS13555	alpha/beta hydrolase	chromosome	I	tBOSMW1			R	CytoplasmicMembrane	NO_SP	TMH
WP_012389696.1	LEPBI_RS13560	DUF4334 domain-con	chromosome	I	tBOSMW2				Unknown	NO_SP	CYT
WP_012389697.1	LEPBI_RS13565	CoA-binding protein	chromosome	I	tBOSMW3			R	Unknown	NO_SP	CYT
WP_012389699.1	LEPBI_RS13575	lipoprotein	chromosome	I	tBOSMW5	WP_000738272.1	0.48446999999999996		Cytoplasmic	LIPO	SplI
WP_012389702.1	LEPBI_RS13590	molybdopterin-depen	chromosome	I	tBOSN75			C	Cytoplasmic	NO_SP	CYT
WP_012389703.1	LEPBI_RS13600	nirB nitrite reductase large	chromosome	I	tBOSN76			C	Cytoplasmic	NO_SP	CYT
WP_012389706.1	LEPBI_RS13615	bifunctional molybde	chromosome	I	tBOSN79			H	Cytoplasmic	NO_SP	CYT
WP_012389709.1	LEPBI_RS13630	molybdopterin-depen	chromosome	I	tBOSN82			C	Cytoplasmic	NO_SP	CYT
WP_012389710.1	LEPBI_RS13635	ThiF family adenyltr	chromosome	I	tBOSN83			H	Cytoplasmic	NO_SP	CYT
WP_012476393.1	LEPBI_RS13655	NTP transferase doma	chromosome	I	tBOSN87				Cytoplasmic	NO_SP	CYT
WP_012389716.1	LEPBI_RS13665	sensor histidine kinas	chromosome	I	tBOSN89			T	CytoplasmicMembrane	NO_SP	TMH
WP_012389722.1	LEPBI_RS13695	hypothetical protein	chromosome	I	tBOSN95				Unknown	SP	Spl
WP_012389725.1	LEPBI_RS13710	OmpA family protein	chromosome	I	tBOSN98				CytoplasmicMembrane	LIPO	CYT
WP_012389726.1	LEPBI_RS13715	hypothetical protein	chromosome	I	tBOSN99				Extracellular	LIPO	SplI
WP_012389727.1	LEPBI_RS13720	NAD(P)/FAD-depende	chromosome	I	tBOSNA0			I	Unknown	NO_SP	CYT
WP_012389728.1	LEPBI_RS13725	sensor histidine kinas	chromosome	I	tBOSNA1			T	CytoplasmicMembrane	SP	Spl
WP_012389733.1	LEPBI_RS13745	hypothetical protein	chromosome	I	tBOSNA6				Extracellular	SP	TMH
WP_012389745.1	LEPBI_RS13795	hypothetical protein	chromosome	I	tBOSNB8				Unknown	NO_SP	Spl
WP_012389746.1	LEPBI_RS13800	hypothetical protein	chromosome	I	tBOSNB9	WP_000734051.1	0.47253		Unknown	LIPO	SplI
WP_012389747.1	LEPBI_RS13805	hypothetical protein	chromosome	I	tBOSNC0	WP_000018492.1	0.5357552499999999		Unknown	LIPO	SplI
WP_012389752.1	LEPBI_RS13830	tetratricopeptide repe	chromosome	I	tBOSNC5				Cytoplasmic	LIPO	SplI
WP_012389760.1	LEPBI_RS13865	right-handed parallel	chromosome	I	tBOSND3				Unknown	SP	SplI
WP_012389761.1	LEPBI_RS13870	DEAD/DEAH box helic	chromosome	I	tBOSND4			L	Cytoplasmic	NO_SP	CYT
WP_012389764.1	LEPBI_RS13885	GNAT family N-acetyl	chromosome	I	tBOSND8				Unknown	NO_SP	CYT
WP_012389765.1	LEPBI_RS13890	PEGA domain-contain	chromosome	I	tBOSND9	WP_000620380.1	0.44439120000000004		CytoplasmicMembrane	SP	Spl
WP_012389768.1	LEPBI_RS13905	PTS sugar transporter	chromosome	I	tBOSNE2	WP_041160702.1	0.6868278999999999	G	Cytoplasmic	NO_SP	CYT
WP_041769889.1	LEPBI_RS13915	4Fe-4S binding protei	chromosome	I	tBOSNE4	WP_000804576.1	0.3649861		Cytoplasmic	NO_SP	CYT
WP_002973362.1	LEPBI_RS13920	hypothetical protein	chromosome	I	tBOSNE5	WP_001291938.1	0.9146808000000001		Unknown	NO_SP	CYT
WP_012389772.1	LEPBI_RS13930	hypothetical protein	chromosome	I	tBOSNE7				CytoplasmicMembrane	NO_SP	TMH
WP_012389773.1	LEPBI_RS13935	MotA/ToIQ/ExbB prot	chromosome	I	tBOSNE8	WP_001070118.1	0.6803349999999999	N	CytoplasmicMembrane	NO_SP	TMH
WP_012389782.1	LEPBI_RS13980	HAMP domain-contain	chromosome	I	tBOSNF7			T	CytoplasmicMembrane	NO_SP	TMH
WP_012389784.1	LEPBI_RS13990	hypothetical protein	chromosome	I	tBOSNF9				Unknown	LIPO	SplI
WP_012389785.1	LEPBI_RS13995	LIC_13355 family lipo	chromosome	I	tBOSNG0	WP_000742409.1	0.42309945		Unknown	LIPO	CYT
WP_012389786.1	LEPBI_RS14000	preprotein translocas	chromosome	I	sBOSNG1	WP_000615621.1	0.7527069000000001	U	Cytoplasmic	NO_SP	CYT
WP_012389787.1	LEPBI_RS14005	type 1 glutamine amic	chromosome	I	tBOSNG2	WP_001257136.1	0.4924335	F	Cytoplasmic	NO_SP	CYT
WP_041770050.1	LEPBI_RS14010	hypothetical protein	chromosome	I	tBOSNG3	WP_000863243.1	0.41718704999999995		Unknown	LIPO	Spl
WP_012389789.1	LEPBI_RS14015	hypothetical protein	chromosome	I	tBOSNG4				Unknown	NO_SP	CYT
WP_012389793.1	LEPBI_RS14035	ATP-binding cassette	chromosome	I	tBOSNG8	WP_000675807.1	0.48233399999999993	P	CytoplasmicMembrane	NO_SP	CYT
WP_041770052.1	LEPBI_RS14045	hypothetical protein	chromosome	I	tBOSNH0				CytoplasmicMembrane	NO_SP	CYT
WP_012389796.1	LEPBI_RS14050	NAD(P)-dependent ox	chromosome	I	tBOSNH1	WP_001003555.1	0.43608959999999997	M	Unknown	NO_SP	CYT

WP_012476399.1	LEPBI_RS14055	hypothetical protein	chromosome	I	tBOSNH2			Unknown	SP	Spl	
WP_012389799.1	LEPBI_RS14065	arsenate reductase Ar	chromosome	I	tBOSNH4			Cytoplasmic	NO_SP	CYT	
WP_012389802.1	LEPBI_RS14080	NADH:flavin oxidore	chromosome	I	tBOSNH7			Cytoplasmic	NO_SP	CYT	
WP_012389803.1	LEPBI_RS14085	GGDEF domain-contai	chromosome	I	tBOSNH8			CytoplasmicMembrane	NO_SP	CYT	
WP_012389805.1	LEPBI_RS14095	PAS domain S-box pro	chromosome	I	tBOSNI0			CytoplasmicMembrane	NO_SP	CYT	
WP_012389807.1	LEPBI_RS14110	acyl-CoA dehydrogen:	chromosome	I	tBOSNT7	WP_000232010.1	0.782223	I	Cytoplasmic	NO_SP	CYT
WP_041769891.1	LEPBI_RS14115	alpha/beta hydrolase	chromosome	I	tBOSNT8			Unknown	LIPO	CYT	
WP_012389809.1	LEPBI_RS14120	SDR family NAD(P)-de	chromosome	I	tBOSNT9			I	Cytoplasmic	NO_SP	CYT
WP_012389811.1	LEPBI_RS14130	SRPBCC family proteir	chromosome	I	tBOSNU1			I	Cytoplasmic	NO_SP	CYT
WP_012389814.1	LEPBI_RS14145	hypothetical protein	chromosome	I	tBOSNU4				Unknown	SP	CYT
WP_012389815.1	LEPBI_RS14150	hypothetical protein	chromosome	I	tBOSNU5				Unknown	NO_SP	CYT
WP_012389817.1	LEPBI_RS14160	adenylate/guanylate c	chromosome	I	tBOSNU7	WP_000651726.1	0.34664520000000004	T	Unknown	NO_SP	CYT
WP_012389818.1	LEPBI_RS14165	NADP-dependent isoc	chromosome	I	tBOSNU8	WP_001062719.1	0.8555349999999999	C	Cytoplasmic	NO_SP	CYT
WP_041769892.1	LEPBI_RS14170	hypothetical protein	chromosome	I	tBOSNU9	WP_001983916.1	0.6000165		Unknown	NO_SP	CYT
WP_012389822.1	LEPBI_RS14185	MBL fold metallo-hydr	chromosome	I	tBOSNV2	WP_000694733.1	0.6206149999999999	P	Cytoplasmic	NO_SP	CYT
WP_012389824.1	LEPBI_RS14195	tetratricopeptide repe	chromosome	I	tBOSNV4	WP_000677438.1	0.3934494		OuterMembrane	LIPO	SpII
WP_012389825.1	LEPBI_RS14200	PEGA domain-containi	chromosome	I	tBOSNV5	WP_001257938.1	0.36788400000000004		Unknown	LIPO	CYT
WP_012389826.1	LEPBI_RS14205	FecR domain-containi	chromosome	I	tBOSNV6	WP_000833301.1	0.51096		Unknown	LIPO	SpII
WP_041769894.1	LEPBI_RS14220	fatty acid desaturase	chromosome	I	tBOSNV9			I	CytoplasmicMembrane	NO_SP	TMH
WP_012389831.1	LEPBI_RS14230	thiol peroxidase	chromosome	I	tBOSNW1	WP_000170133.1	0.7804719999999999	O	Unknown	NO_SP	CYT
WP_012389832.1	LEPBI_RS14235	AAA family ATPase	chromosome	I	tBOSNW2	WP_000622214.1	0.3194598		Cytoplasmic	NO_SP	CYT
WP_187148100.1	LEPBI_RS14260	sulfatase-like hydrola	chromosome	I	tBOSNW6			P	Unknown	LIPO	CYT
WP_049755987.1	LEPBI_RS14270	alpha/beta hydrolase	chromosome	I	tBOSNW8	WP_000944882.1	0.54857	H	Cytoplasmic	NO_SP	CYT
WP_012389843.1	LEPBI_RS14295	DUF2071 domain-con	chromosome	I	tBOSNX3			S	Cytoplasmic	NO_SP	CYT
WP_012389846.1	LEPBI_RS14310	dihydrolipoyl dehydro	chromosome	I	tBOSNX6	WP_001115276.1	0.62663535	C	Cytoplasmic	NO_SP	CYT
WP_012389850.1	LEPBI_RS14330	hypothetical protein	chromosome	I	tBOSNY0	WP_001132139.1	0.43889105		Unknown	SP	CYT
WP_012389851.1	LEPBI_RS14335	DUF342 domain-cont	chromosome	I	tBOSNY1	WP_000993253.1	0.5464512	N	Cytoplasmic	NO_SP	CYT
WP_012389852.1	LEPBI_RS14340	peptide-methionine (	chromosome	I	tBOSNY2	WP_000434146.1	0.632286	O	Unknown	NO_SP	CYT
WP_012389853.1	LEPBI_RS14345	S-methyl-5-thioribose	chromosome	I	sBOSNY3	WP_001158185.1	0.5907648	E	Cytoplasmic	NO_SP	CYT
WP_012476404.1	LEPBI_RS14350	hypothetical protein	chromosome	I	tBOSNY4				Unknown	NO_SP	CYT
WP_012389855.1	LEPBI_RS14355	hypothetical protein	chromosome	I	tBOSNY5	WP_000050593.1	0.47300000000000003		Cytoplasmic	NO_SP	CYT
WP_012389856.1	LEPBI_RS14360	CHAT domain-contain	chromosome	I	tBOSNY6	WP_000933331.1	0.6118679		Cytoplasmic	NO_SP	CYT
WP_012389857.1	LEPBI_RS14365	hypothetical protein	chromosome	I	tBOSNY7				Cytoplasmic	NO_SP	CYT
WP_012389860.1	LEPBI_RS14380	M23 family metallope	chromosome	I	tBOSNZ0	WP_000714135.1	0.6149849999999999	M	Unknown	SP	Spl
WP_012389861.1	LEPBI_RS14385	long-chain fatty acid--	chromosome	I	tBOSNZ1			I	Cytoplasmic	NO_SP	CYT
WP_041769897.1	LEPBI_RS14395	DNA polymerase III su	chromosome	I	tBOSNZ3	WP_001150496.1	0.7280262000000001	L	Cytoplasmic	NO_SP	CYT
WP_012476405.1	LEPBI_RS14400	nicotinate-nucleotide-	chromosome	I	tBOSNZ4	WP_001067584.1	0.54868535	H	Cytoplasmic	NO_SP	CYT
WP_012389867.1	LEPBI_RS14415	Asp-tRNA(Asn)/Glu-tR	chromosome	I	sBOSNZ7	WP_000807227.1	0.7399358999999999	J	Cytoplasmic	NO_SP	CYT
WP_012389868.1	LEPBI_RS14420	hemerythrin family pr	chromosome	I	tBOSNZ8				Cytoplasmic	NO_SP	CYT
WP_012389869.1	LEPBI_RS14425	aldehyde dehydrogen	chromosome	I	tBOSNZ9	WP_001142685.1	0.6779960500000001	I	Cytoplasmic	NO_SP	CYT
WP_012476407.1	LEPBI_RS14430	adenylate/guanylate c	chromosome	I	tBOSPO0			T	CytoplasmicMembrane	LIPO	SpII
WP_012476408.1	LEPBI_RS14435	adenylate/guanylate c	chromosome	I	tBOSPO1	WP_000251358.1	0.3676272	T	CytoplasmicMembrane	SP	CYT
WP_012389873.1	LEPBI_RS14445	flagellar assembly pro	chromosome	I	tBOSPO3	WP_001096786.1	0.9153249999999999	N	Cytoplasmic	NO_SP	CYT
WP_012389874.1	LEPBI_RS14450	sensor histidine kinas	chromosome	I	tBOSPO4			T	CytoplasmicMembrane	SP	Spl

WP_012389876.1	LEPBI_RS14460		Crp/Fnr family transcr	chromosome	I	tBOSP06			T	Unknown	NO_SP	CYT
WP_012389878.1	LEPBI_RS14470		nitric oxide reductase	chromosome	I	tBOSP08			P	Cytoplasmic	NO_SP	CYT
WP_012389879.1	LEPBI_RS14475		CbbQ/NirQ/NorQ/Gpx	chromosome	I	tBOSP09			R	Cytoplasmic	NO_SP	CYT
WP_012389880.1	LEPBI_RS14480		cbb3-type cytochrome	chromosome	I	tBOSP10			P	CytoplasmicMembrane	NO_SP	TMH
WP_012389881.1	LEPBI_RS14485		c-type cytochrome	chromosome	I	tBOSP11				CytoplasmicMembrane	NO_SP	TMH
WP_012389884.1	LEPBI_RS14490		cytochrome c oxidase	chromosome	I	tBOSP14			C	CytoplasmicMembrane	NO_SP	TMH
WP_012389886.1	LEPBI_RS14500	mtnC	acireductone synthase	chromosome	I	sBOSP16	WP_001022662.1	0.47832330000000006	E	Cytoplasmic	NO_SP	CYT
WP_012389887.1	LEPBI_RS14505		MFS transporter	chromosome	I	tBOSP17	WP_001972114.1	0.6885351		CytoplasmicMembrane	NO_SP	TMH
WP_012389888.1	LEPBI_RS14510		hypothetical protein	chromosome	I	tBOSP18	WP_000846596.1	0.5166413		CytoplasmicMembrane	SP	Spl
WP_012389889.1	LEPBI_RS14515		WecB/TagA/CpsF fam	chromosome	I	tBOSP19	WP_000742876.1	0.67629375	M	Cytoplasmic	NO_SP	CYT
WP_012389890.1	LEPBI_RS14520		hypothetical protein	chromosome	I	tBOSP20	WP_000796624.1	0.49029749999999994		Unknown	NO_SP	CYT
WP_167530807.1	LEPBI_RS14525		carbohydrate-binding	chromosome	I	tBOSP21	WP_000898918.1	0.5557468		Cytoplasmic	SP	Spl
WP_012389893.1	LEPBI_RS14535		transketolase family p	chromosome	I	tBOSP23	WP_000501205.1	0.845325	G	Cytoplasmic	NO_SP	CYT
WP_012389894.1	LEPBI_RS14540		methionine adenosylt	chromosome	I	tBOSP24	WP_000053346.1	0.86240385000000001	H	Cytoplasmic	NO_SP	CYT
WP_012389895.1	LEPBI_RS14545		lysophospholipid acylt	chromosome	I	tBOSP25			S	Unknown	NO_SP	CYT
WP_012389896.1	LEPBI_RS14550		nucleoside-diphospha	chromosome	I	tBOSP26	WP_000680173.1	0.3496311		Cytoplasmic	NO_SP	CYT
WP_012389899.1	LEPBI_RS14565		DUF3332 family prote	chromosome	I	tBOSP29	WP_001186895.1	0.48890400000000006		Unknown	NO_SP	SpII
WP_012389900.1	LEPBI_RS14570		hypothetical protein	chromosome	I	tBOSP30				Cytoplasmic	LIPO	SpII
WP_012389902.1	LEPBI_RS14580		PAS domain S-box pro	chromosome	I	tBOSP32	WP_001288616.1	0.47045	T	CytoplasmicMembrane	NO_SP	CYT
WP_012389903.1	LEPBI_RS14585		response regulator	chromosome	I	tBOSP33	WP_001012319.1	0.4511234		Unknown	NO_SP	CYT
WP_041770054.1	LEPBI_RS14605		hypothetical protein	chromosome	I	tBOSP37				Unknown	SP	Spl
WP_012389909.1	LEPBI_RS14615		hypothetical protein	chromosome	I	tBOSP39				CytoplasmicMembrane	LIPO	SpII
WP_012389910.1	LEPBI_RS14620		carboxypeptidase regi	chromosome	I	tBOSP40				Extracellular	LIPO	SpII
WP_041770055.1	LEPBI_RS14625		TPM domain-containii	chromosome	I	tBOSP41			S	CytoplasmicMembrane	NO_SP	CYT
WP_012389914.1	LEPBI_RS14640	pckA	phosphoenolpyruvate	chromosome	I	sBOSPF0	WP_001148872.1	0.8278281	C	Cytoplasmic	NO_SP	CYT
WP_012389915.1	LEPBI_RS14645		glycogen synthase	chromosome	I	sBOSPF1			G	Cytoplasmic	NO_SP	CYT
WP_012476413.1	LEPBI_RS14655		hypothetical protein	chromosome	I	tBOSPF4				Unknown	LIPO	CYT
WP_012389921.1	LEPBI_RS14670		AraC family transcript	chromosome	I	tBOSPF7			K	Cytoplasmic	NO_SP	CYT
WP_012389923.1	LEPBI_RS14680		hypothetical protein	chromosome	I	tBOSPF9				Unknown	SP	Spl
WP_012389927.1	LEPBI_RS14700		TetR family transcripti	chromosome	I	tBOSPG3				Cytoplasmic	NO_SP	CYT
WP_012389929.1	LEPBI_RS14710		transglycosylase domi	chromosome	I	tBOSPG5			M	CytoplasmicMembrane	NO_SP	CYT
WP_012389930.1	LEPBI_RS14715		peptidase	chromosome	I	tBOSPG6			R	OuterMembrane	LIPO	SpII
WP_012389931.1	LEPBI_RS14720		hypothetical protein	chromosome	I	tBOSPG7				Unknown	NO_SP	CYT
WP_012389934.1	LEPBI_RS14735	ahpC	peroxiredoxin	chromosome	I	tBOSPH0			V	Cytoplasmic	NO_SP	CYT
WP_012389935.1	LEPBI_RS14740		hydrogen peroxide-ini	chromosome	I	tBOSPH1			K	Cytoplasmic	NO_SP	CYT
WP_012389938.1	LEPBI_RS14755		hypothetical protein	chromosome	I	tBOSPH4	WP_000689175.1	0.51708274999999999		CytoplasmicMembrane	LIPO	TMH
WP_143708641.1	LEPBI_RS14760		hypothetical protein	chromosome	I	tBOSPH5				Unknown	LIPO	SpII
WP_012389940.1	LEPBI_RS14765		hypothetical protein	chromosome	I	tBOSPH6	WP_000922522.1	0.41334000000000004		Unknown	LIPO	SpII
WP_012476416.1	LEPBI_RS14770		TonB-dependent rece	chromosome	I	tBOSPH7	WP_000790264.1	0.57869249999999999		OuterMembrane	SP	Spl
WP_012389943.1	LEPBI_RS14780		MotA/TolQ/ExbB prot	chromosome	I	tBOSPH9			U	CytoplasmicMembrane	NO_SP	CYT
WP_012389944.1	LEPBI_RS14785		biopolymer transporti	chromosome	I	tBOSPI0	WP_000919048.1	0.83209	U	CytoplasmicMembrane	NO_SP	CYT
WP_012389945.1	LEPBI_RS14790		energy transducer Tor	chromosome	I	tBOSPI1	WP_000776116.1	0.66765105		Cytoplasmic	NO_SP	CYT
WP_012389946.1	LEPBI_RS14795		histidine kinase	chromosome	I	tBOSPI2			T	CytoplasmicMembrane	NO_SP	CYT
WP_012389950.1	LEPBI_RS14815		right-handed parallel	chromosome	I	tBOSPI6	WP_000698486.1	0.6041112		CytoplasmicMembrane	LIPO	SpII



WP_012389952.1	LEPBI_RS14825		MacB family efflux pu	chromosome	I	tBOSPI8			M	CytoplasmicMembrane	NO_SP	CYT
WP_012389953.1	LEPBI_RS14830		efflux RND transporte	chromosome	I	tBOSPI9				Unknown	NO_SP	CYT
WP_041769900.1	LEPBI_RS14840		TPM domain-containii	chromosome	I	tBOSPJ1			S	CytoplasmicMembrane	SP	CYT
WP_012389959.1	LEPBI_RS14860		alginate export family	chromosome	I	tBOSPJ5				OuterMembrane	SP	CYT
WP_012389960.1	LEPBI_RS14865		TetR/AcrR family tran:	chromosome	I	tBOSPJ6	WP_000219100.1	0.6510735		Cytoplasmic	NO_SP	CYT
WP_012389964.1	LEPBI_RS14885		class I SAM-dependen	chromosome	I	tBOSPK0				Cytoplasmic	NO_SP	CYT
WP_012389965.1	LEPBI_RS14890		histidine kinase	chromosome	I	tBOSPK1	WP_001109024.1	0.705	S	Cytoplasmic	NO_SP	CYT
WP_012389966.1	LEPBI_RS14895		hypothetical protein	chromosome	I	tBOSPK2	WP_000406163.1	0.4145616	R	Unknown	NO_SP	CYT
WP_012389967.1	LEPBI_RS14900		GNAT family N-acetyl	chromosome	I	tBOSPK3				Cytoplasmic	NO_SP	CYT
WP_012389970.1	LEPBI_RS14910		adenylate/guanylate c	chromosome	I	tBOSPK6			T	Cytoplasmic	NO_SP	CYT
WP_012389971.1	LEPBI_RS14915		histidine kinase	chromosome	I	tBOSPK7				Cytoplasmic	NO_SP	CYT
WP_012476418.1	LEPBI_RS14920		TetR/AcrR family tran:	chromosome	I	tBOSPK8				Cytoplasmic	NO_SP	CYT
WP_012389974.1	LEPBI_RS14930		DUF4281 domain-con	chromosome	I	tBOSPL0				CytoplasmicMembrane	NO_SP	TMH
WP_012389975.1	LEPBI_RS14935		ankyrin repeat domai	chromosome	I	tBOSPL1				Cytoplasmic	NO_SP	CYT
WP_012389988.1	LEPBI_RS15000		hypothetical protein	chromosome	I	tBOSPM4				Cytoplasmic	LIPO	CYT
WP_012389989.1	LEPBI_RS15005		hypothetical protein	chromosome	I	tBOSPM5				Cytoplasmic	LIPO	CYT
WP_012389990.1	LEPBI_RS15010		type II toxin-antitoxin	chromosome	I	tBOSPM6	WP_000617907.1	0.74057	V	Unknown	NO_SP	CYT
WP_012389992.1	LEPBI_RS15020		ankyrin repeat domai	chromosome	I	tBOSPM8				Cytoplasmic	LIPO	SpII
WP_012389996.1	LEPBI_RS15040		hypothetical protein	chromosome	I	tBOSPN2				Unknown	NO_SP	CYT
WP_012389997.1	LEPBI_RS15045	mreC	rod shape-determinin	chromosome	I	tBOSPN3	WP_000964329.1	0.6455202499999999	D	CytoplasmicMembrane	NO_SP	TMH
WP_012389999.1	LEPBI_RS15055	mrda	penicillin-binding prot	chromosome	I	tBOSPN5	WP_000900432.1	0.73332	D	CytoplasmicMembrane	NO_SP	CYT
WP_012390000.1	LEPBI_RS15060	rodA	rod shape-determinin	chromosome	I	tBOSPN6	WP_000801434.1	0.74646	D	CytoplasmicMembrane	NO_SP	TMH
WP_012390001.1	LEPBI_RS15065		hypothetical protein	chromosome	I	tBOSPN7	WP_000371581.1	0.35383095		Cytoplasmic	NO_SP	CYT
WP_012390002.1	LEPBI_RS15070		bifunctional riboflavin	chromosome	I	tBOSPN8	WP_000627565.1	0.53224385	H	Cytoplasmic	NO_SP	CYT
WP_012390004.1	LEPBI_RS15080		STAS domain-containi	chromosome	I	tBOSPP0	WP_000406135.1	0.71155755		Unknown	NO_SP	CYT
WP_012390005.1	LEPBI_RS15085		hypothetical protein	chromosome	I	tBOSPP1	WP_000660163.1	0.38550225		Unknown	SP	SpI
WP_012390007.1	LEPBI_RS15095		class I mannose-6-phc	chromosome	I	tBOSPP3	WP_001174417.1	0.5389362000000001	G	Unknown	NO_SP	CYT
WP_012390008.1	LEPBI_RS15100		pirin family protein	chromosome	I	tBOSPP4	WP_000691890.1	0.6408256499999999	R	Cytoplasmic	NO_SP	CYT
WP_012390011.1	LEPBI_RS15110		SRPBCC family proteir	chromosome	I	tBOSPP7	WP_002145501.1	0.47941659999999997		CytoplasmicMembrane	NO_SP	CYT
WP_012390012.1	LEPBI_RS15115		MFS transporter	chromosome	I	tBOSPP8	WP_000625277.1	0.6622407	G	CytoplasmicMembrane	NO_SP	CYT
WP_012390013.1	LEPBI_RS15120		cysteine synthase A	chromosome	I	tBOSPP9			E	Cytoplasmic	NO_SP	CYT
WP_187148061.1	LEPBI_RS15125		glucanase	chromosome	I	tBOSPPQ0				Unknown	LIPO	TMH
WP_012390015.1	LEPBI_RS15130		IS30-like element ISLb	chromosome	I	tBOSPPQ1			X	Cytoplasmic	NO_SP	CYT
WP_012390019.1	LEPBI_RS15150		acetoacetate--CoA lig:	chromosome	I	tBOSPPQ5	WP_000372281.1	0.5806052999999999	I	Cytoplasmic	NO_SP	CYT
WP_012390021.1	LEPBI_RS15160		DUF1574 family prote	chromosome	I	tBOSQ11				Cytoplasmic	SP	CYT
WP_012390023.1	LEPBI_RS15170		TolC family protein	chromosome	I	tBOSQ13				Cytoplasmic	SP	CYT
WP_012390024.1	LEPBI_RS15175		efflux RND transporte	chromosome	I	tBOSQ14			M	Cytoplasmic	NO_SP	CYT
WP_012390025.1	LEPBI_RS15180		efflux RND transporte	chromosome	I	tBOSQ15	WP_000565850.1	0.49062360000000005	P	CytoplasmicMembrane	NO_SP	CYT
WP_012390026.1	LEPBI_RS15185		dienelactone hydrolas	chromosome	I	tBOSQ16			Q	Unknown	LIPO	SpI
WP_012390027.1	LEPBI_RS15190		acyl-CoA dehydrogen:	chromosome	I	tBOSQ17	WP_000572090.1	0.5771661	I	Cytoplasmic	NO_SP	CYT
WP_012390029.1	LEPBI_RS15200		iron-sulfur cluster-bin	chromosome	I	tBOSQ19			C	Cytoplasmic	NO_SP	CYT
WP_012476422.1	LEPBI_RS15210		PAS domain S-box pro	chromosome	I	tBOSQ21			T	Cytoplasmic	NO_SP	CYT
WP_012390032.1	LEPBI_RS15215		hypothetical protein	chromosome	I	tBOSQ22	WP_000769736.1	0.4327092		Unknown	LIPO	SpI
WP_012390033.1	LEPBI_RS15220		hypothetical protein	chromosome	I	tBOSQ23	WP_000720240.1	0.5642975		Unknown	LIPO	SpII

WP_012390035.1	LEPBI_RS15230		hypothetical protein	chromosome	I	tBOSQ25			Unknown	SP	CYT	
WP_012390036.1	LEPBI_RS15235		6-carboxytetrahydrop	chromosome	I	tBOSQ26	WP_000465997.1	0.7572955499999999	H	Cytoplasmic	NO_SP	CYT
WP_012476423.1	LEPBI_RS15250		NAD(P)-dependent alk	chromosome	I	tBOSQ29			C	Cytoplasmic	NO_SP	CYT
WP_012390040.1	LEPBI_RS15255		VOC family protein	chromosome	I	tBOSQ30	WP_001183065.1	0.8166487		Unknown	NO_SP	CYT
WP_012390041.1	LEPBI_RS15260	ccrA	crotonyl-CoA carboxyl	chromosome	I	tBOSQ31	WP_000078168.1	0.865045	C	Cytoplasmic	NO_SP	CYT
WP_041770067.1	LEPBI_RS15265		hypothetical protein	chromosome	I	tBOSQ32	WP_000812385.1	0.56683445		Unknown	SP	SpI
WP_012390043.1	LEPBI_RS15270		hypothetical protein	chromosome	I	tBOSQ33	WP_000620882.1	0.41569835		Unknown	SP	SpI
WP_012390044.1	LEPBI_RS15275		di-heme enzyme	chromosome	I	tBOSQ34	WP_001211842.1	0.52348	O	Periplasmic	LIPO	SpII
WP_012390045.1	LEPBI_RS15280		metallo-mystery pair	chromosome	I	tBOSQ35	WP_000163348.1	0.39240864999999997		Unknown	LIPO	SpII
WP_012390048.1	LEPBI_RS15295		SpoII E family protein	chromosome	I	tBOSQ38			T	CytoplasmicMembrane	SP	SpI
WP_012390049.1	LEPBI_RS15300		Na/Pi cotransporter	chromosome	I	tBOSQ39			P	CytoplasmicMembrane	NO_SP	TMH
WP_012390050.1	LEPBI_RS15305		peptidylprolyl isomer	chromosome	I	tBOSQ40	WP_000842388.1	0.521064	O	Cytoplasmic	NO_SP	CYT
WP_012390051.1	LEPBI_RS15310		RNA-binding protein	chromosome	I	tBOSQ41	WP_000115710.1	0.750025		Unknown	NO_SP	CYT
WP_012390054.1	LEPBI_RS15325	fumC	class II fumarate hydr	chromosome	I	tBOSQ44	WP_000857390.1	0.78465915	C	Cytoplasmic	NO_SP	CYT
WP_012476426.1	LEPBI_RS15350		fumarate reductase/s	chromosome	I	tBOSQ49	WP_000050920.1	0.66232485	C	Unknown	NO_SP	CYT
WP_012390060.1	LEPBI_RS15355		fumarate hydratase	chromosome	I	tBOSQ50			C	Cytoplasmic	NO_SP	CYT
WP_012390062.1	LEPBI_RS15365		DUF3703 domain-con	chromosome	I	tBOSQ52				Unknown	NO_SP	CYT
WP_012390064.1	LEPBI_RS15375	cadA	cadmium-translocatin	chromosome	I	tBOSQ54			P	CytoplasmicMembrane	NO_SP	CYT
WP_012390065.1	LEPBI_RS15385		efflux RND transporte	chromosome	I	tBOSQ55	WP_000952676.1	0.61468605	P	CytoplasmicMembrane	NO_SP	TMH
WP_187148102.1	LEPBI_RS15420		OmpA family protein	chromosome	I	tBOSQ62	WP_000239305.1	0.6239525000000001		Unknown	LIPO	SpII
WP_012390073.1	LEPBI_RS15425		RluA family pseudouri	chromosome	I	tBOSQ63	WP_001047544.1	0.61797284999999999	J	Cytoplasmic	NO_SP	CYT
WP_012390075.1	LEPBI_RS15435		TerC family protein	chromosome	I	tBOSQ65	WP_000422110.1	0.67385834999999999	P	CytoplasmicMembrane	NO_SP	TMH
WP_012390077.1	LEPBI_RS15445		response regulator	chromosome	I	tBOSQ67			T	CytoplasmicMembrane	LIPO	SpI
WP_012390078.1	LEPBI_RS15450		response regulator tr	chromosome	I	tBOSQ68			T	Cytoplasmic	NO_SP	CYT
WP_012390079.1	LEPBI_RS15455		histidine phosphatase	chromosome	I	tBOSQ69	WP_000145482.1	0.45944325	T	Unknown	NO_SP	CYT
WP_012390080.1	LEPBI_RS15460	hpt	hypoxanthine phosph	chromosome	I	tBOSQ70	WP_000723581.1	0.46591545	F	Cytoplasmic	NO_SP	CYT
WP_012390083.1	LEPBI_RS15470		phosphate ABC trans	chromosome	I	tBOSQ73	WP_000768212.1	0.58393665	P	CytoplasmicMembrane	LIPO	SpII
WP_049755989.1	LEPBI_RS15475		OmpA family protein	chromosome	I	tBOSQ74	WP_002970704.1	0.45780025	M	CytoplasmicMembrane	SP	SpI
WP_012390085.1	LEPBI_RS15480		acyltransferase	chromosome	I	tBOSQ75				Cytoplasmic	NO_SP	CYT
WP_012476428.1	LEPBI_RS15490		alpha/beta hydrolase	chromosome	I	tBOSQ77	WP_001011734.1	0.5717846	I	Cytoplasmic	NO_SP	CYT
WP_020776763.1	LEPBI_RS15495		MaoC family dehydrat	chromosome	I	tBOSQ78	WP_001274661.1	0.677616		Cytoplasmic	NO_SP	CYT
WP_012390088.1	LEPBI_RS15500		MaoC family dehydrat	chromosome	I	tBOSQ79	WP_000034360.1	0.77537	I	Unknown	NO_SP	CYT
WP_012390090.1	LEPBI_RS15510		hypothetical protein	chromosome	I	tBOSQ81				Unknown	LIPO	SpII
WP_012390091.1	LEPBI_RS15515		WG repeat-containing	chromosome	I	tBOSQ82				Unknown	SP	SpI
WP_012390092.1	LEPBI_RS15520		M15 family metallope	chromosome	I	tBOSQ83			M	Cytoplasmic	SP	CYT
WP_012390095.1	LEPBI_RS15535		discoïdin domain-con	chromosome	I	tBOSQ86				Unknown	SP	SpI
WP_012390096.1	LEPBI_RS15540	trxA	thioredoxin	chromosome	I	tBOSQ87			O	Cytoplasmic	NO_SP	CYT
WP_012476429.1	LEPBI_RS15550		type 1 glutamine amic	chromosome	I	tBOSQ89				Unknown	SP	CYT
WP_012390099.1	LEPBI_RS15555		MBL fold metallo-hyd	chromosome	I	tBOSQ90				Unknown	NO_SP	CYT
WP_041770078.1	LEPBI_RS15565		aldehyde reductase	chromosome	I	tBOSQ92			M	Unknown	NO_SP	CYT
WP_012390106.1	LEPBI_RS15590		suppressor of fused di	chromosome	I	tBOSQ97	WP_000200272.1	0.6108487		Unknown	NO_SP	CYT
WP_012390108.1	LEPBI_RS15600		zinc-binding dehydrog	chromosome	I	tBOSQA0	WP_001189850.1	0.58581765	C	CytoplasmicMembrane	NO_SP	CYT
WP_012390109.1	LEPBI_RS15605	gcvT	glycine cleavage syste	chromosome	I	sBOSQA1	WP_001973508.1	0.68519385	E	Cytoplasmic	NO_SP	CYT
WP_012390110.1	LEPBI_RS15610	gcvH	glycine cleavage syste	chromosome	I	sBOSQA2	WP_000852369.1	0.7346250000000001	E	Unknown	NO_SP	CYT

WP_049756017.1	LEPBI_RS15615	gcvP	aminomethyl-transfer	chromosome	I	tB0SQA3	WP_001089345.1	0.7362691	E	Cytoplasmic	NO_SP	CYT
WP_012390114.1	LEPBI_RS15635		cysteine protease	chromosome	I	tB0SQA6				OuterMembrane	SP	Spl
WP_012476434.1	LEPBI_RS15650		methylmalonyl-CoA rr	chromosome	I	tB0SQA9	WP_000449876.1	0.80301	I	Unknown	NO_SP	CYT
WP_012476435.1	LEPBI_RS15655		1-acyl-sn-glycerol-3-pl	chromosome	I	tB0SQB0	WP_000431423.1	0.64332675		Cytoplasmic	NO_SP	CYT
WP_012390123.1	LEPBI_RS15680		serine protease	chromosome	I	tB0SQB5	WP_000675215.1	0.72		Unknown	SP	Spl
WP_012390124.1	LEPBI_RS15685		trypsin-like peptidase	chromosome	I	tB0SQB6	WP_000039575.1	0.5350300000000001	O	Periplasmic	SP	Spl
WP_012390126.1	LEPBI_RS15695		sulfurtransferase	chromosome	I	tB0SQB8	WP_001983600.1	0.7204725	P	Cytoplasmic	NO_SP	CYT
WP_012390127.1	LEPBI_RS15700		alpha-glucosidase	chromosome	I	tB0SQM4	WP_000466026.1	0.5857117	G	Unknown	LIPO	SplI
WP_012390129.1	LEPBI_RS15710		OsmC family protein	chromosome	I	tB0SQM6			R	Cytoplasmic	NO_SP	CYT
WP_012390130.1	LEPBI_RS15715		lysophospholipid acylI	chromosome	I	tB0SQM7	WP_000392265.1	0.71341695	S	Cytoplasmic	NO_SP	CYT
WP_012390131.1	LEPBI_RS15720	csrA	carbon storage regula	chromosome	I	sB0SQM8	WP_000960595.1	0.8346052500000001	T	Unknown	NO_SP	CYT
WP_012476436.1	LEPBI_RS15725	fliW	flagellar assembly pro	chromosome	I	tB0SQM9	WP_000510649.1	0.6199968	N	Unknown	NO_SP	CYT
WP_012390133.1	LEPBI_RS15730		flagellar hook-associa	chromosome	I	tB0SQN0	WP_001223330.1	0.8634000000000001	N	Unknown	NO_SP	CYT
WP_012390134.1	LEPBI_RS15735	flgK	flagellar hook-associa	chromosome	I	tB0SQN1	WP_000535887.1	0.780245	N	Extracellular	NO_SP	CYT
WP_012390137.1	LEPBI_RS15750		hypothetical protein	chromosome	I	tB0SQN4	WP_000802848.1	0.6817517		Unknown	NO_SP	CYT
WP_012390139.1	LEPBI_RS15760		hypothetical protein	chromosome	I	tB0SQN6				Cytoplasmic	LIPO	CYT
WP_012390141.1	LEPBI_RS15770		hypothetical protein	chromosome	I	tB0SQN8				Cytoplasmic	SP	Spl
WP_012476437.1	LEPBI_RS15775		DUF4228 domain-con	chromosome	I	tB0SQN9				Unknown	NO_SP	CYT
WP_012390146.1	LEPBI_RS15795		hypothetical protein	chromosome	I	tB0SQP3				Unknown	SP	Spl
WP_012390147.1	LEPBI_RS15800		response regulator tra	chromosome	I	tB0SQP4	WP_000795919.1	0.882	T	Cytoplasmic	NO_SP	CYT
WP_012390148.1	LEPBI_RS15805		HAMP domain-contain	chromosome	I	tB0SQP5	WP_001254665.1	0.5834745000000001	T	CytoplasmicMembrane	NO_SP	TMH
WP_012390149.1	LEPBI_RS15810	argJ	bifunctional glutamat	chromosome	I	tB0SQP6	WP_001123874.1	0.7088251499999999	E	Cytoplasmic	NO_SP	CYT
WP_012390153.1	LEPBI_RS15830		SDR family oxidoredu	chromosome	I	tB0SQQ0	WP_000744700.1	0.8216045500000001	M	Cytoplasmic	NO_SP	CYT
WP_012390154.1	LEPBI_RS15835		Re/Si-specific NAD(P)	chromosome	I	tB0SQQ1	WP_001020567.1	0.665616	C	CytoplasmicMembrane	NO_SP	CYT
WP_012390157.1	LEPBI_RS15850		histidine--tRNA ligase	chromosome	I	sB0SQQ4	WP_000431287.1	0.663552	J	Cytoplasmic	NO_SP	CYT
WP_012390158.1	LEPBI_RS15855		DUF1577 domain-con	chromosome	I	tB0SQQ5	WP_000116023.1	0.43505079999999996		Cytoplasmic	NO_SP	CYT
WP_012390159.1	LEPBI_RS15860		OmpA family protein	chromosome	I	tB0SQQ6	WP_001247305.1	0.51402285	M	Unknown	SP	Spl
WP_012390160.1	LEPBI_RS15865	folP	dihydropteroate synt	chromosome	I	tB0SQQ7	WP_000444207.1	0.5353582	H	Cytoplasmic	NO_SP	CYT
WP_012390161.1	LEPBI_RS15870		hypothetical protein	chromosome	I	tB0SQQ8	WP_000263748.1	0.37313640000000003		Cytoplasmic	LIPO	SplI
WP_012390163.1	LEPBI_RS15880		septal ring lytic transg	chromosome	I	tB0SQR0	WP_033108072.1	0.554271	M	Cytoplasmic	LIPO	SplI
WP_012390164.1	LEPBI_RS15885		SpoII E family protein	chromosome	I	tB0SQR1	WP_000521950.1	0.631521		CytoplasmicMembrane	NO_SP	TMH
WP_041769908.1	LEPBI_RS15890		CZB domain-containin	chromosome	I	tB0SQR2			T	CytoplasmicMembrane	NO_SP	CYT
WP_012390166.1	LEPBI_RS15895		DUF2147 domain-con	chromosome	I	tB0SQR3	WP_001043223.1	0.5139139500000001		Unknown	SP	Spl
WP_012390167.1	LEPBI_RS15900		dCTP deaminase	chromosome	I	sB0SQR4	WP_000604072.1	0.8381449999999999	F	Cytoplasmic	NO_SP	CYT
WP_012390168.1	LEPBI_RS15905		enoyl-CoA hydratase/	chromosome	I	tB0SQR5	WP_001001943.1	0.58621	I	Cytoplasmic	NO_SP	CYT
WP_041770084.1	LEPBI_RS15910		hypothetical protein	chromosome	I	tB0SQR7	WP_000718925.1	0.44361405000000004		Unknown	LIPO	Spl
WP_012390171.1	LEPBI_RS15915		hypothetical protein	chromosome	I	tB0SQR8				Cytoplasmic	NO_SP	CYT
WP_012390172.1	LEPBI_RS15920		VOC family protein	chromosome	I	tB0SQR9	WP_000587664.1	0.57375		Cytoplasmic	NO_SP	CYT
WP_012390173.1	LEPBI_RS15925		DUF3347 domain-con	chromosome	I	tB0SQS0	WP_000478349.1	0.40802975		Unknown	LIPO	SplI
WP_012390176.1	LEPBI_RS15940		SDR family oxidoredu	chromosome	I	tB0SQS3	WP_000167663.1	0.58671855	R	Cytoplasmic	NO_SP	CYT
WP_187148062.1	LEPBI_RS15960		DUF898 family proteir	chromosome	I	tB0SQS7			S	CytoplasmicMembrane	NO_SP	TMH
WP_012476444.1	LEPBI_RS15965		M48 family metallope	chromosome	I	tB0SQS8			O	Unknown	NO_SP	CYT
WP_012390182.1	LEPBI_RS15970		GDP-mannose 4,6-def	chromosome	I	tB0SQS9	WP_000649925.1	0.5287736999999999	M	Cytoplasmic	NO_SP	CYT
WP_012390183.1	LEPBI_RS15975		hypothetical protein	chromosome	I	tB0SQT0	WP_000389571.1	0.45147000000000004		Cytoplasmic	NO_SP	CYT

WP_012390186.1	LEPBI_RS15990		glycosyltransferase fa	chromosome	I	tBOSQT3	WP_000842678.1	0.4477714		Unknown	NO_SP	CYT	
WP_041769909.1	LEPBI_RS15995		inositol monophosphat	chromosome	I	tBOSQT4	WP_000050899.1	0.559958			NO_SP	CYT	
WP_012476445.1	LEPBI_RS16000		5-bromo-4-chloroindole	chromosome	I	tBOSQT5			G	Cytoplasmic	NO_SP	CYT	
WP_012390189.1	LEPBI_RS16005		toxic anion resistance	chromosome	I	tBOSQT6				Cytoplasmic	NO_SP	TMH	
WP_012390191.1	LEPBI_RS16015		STAS domain-containing	chromosome	I	tBOSQT8			V	Cytoplasmic	NO_SP	CYT	
WP_012390193.1	LEPBI_RS16025		type III pantothenate	chromosome	I	tBOSQU0	WP_000928025.1	0.761635		H	Cytoplasmic	NO_SP	CYT
WP_012390194.1	LEPBI_RS16030		biotin--[acetyl-CoA-car	chromosome	I	tBOSQU1	WP_001181792.1	0.47525940000000005		H	Cytoplasmic	NO_SP	CYT
WP_012476446.1	LEPBI_RS16035		SDR family NAD(P)-de	chromosome	I	tBOSQU2				R	Cytoplasmic	NO_SP	CYT
WP_012390196.1	LEPBI_RS16040	metF	methylenetetrahydrofol	chromosome	I	tBOSQU3	WP_000757856.1	0.50522935		E	Cytoplasmic	NO_SP	CYT
WP_012390203.1	LEPBI_RS16075	prfA	peptide chain release	chromosome	I	sBOSQV0	WP_000567183.1	0.79172775000000001		J	Cytoplasmic	NO_SP	CYT
WP_012390204.1	LEPBI_RS16080		hypothetical protein	chromosome	I	tBOSQV1	WP_000427417.1	0.440167000000000003			Unknown	NO_SP	CYT
WP_012390205.1	LEPBI_RS16085		hypothetical protein	chromosome	I	tBOSQV2	WP_000669757.1	0.39144619999999997			Unknown	LIPO	SpII
WP_012390207.1	LEPBI_RS16095		hypothetical protein	chromosome	I	tBOSQV4					Unknown	NO_SP	CYT
WP_012390208.1	LEPBI_RS16100		NUDIX domain-containing	chromosome	I	tBOSQV5	WP_000033731.1	0.72405165			Cytoplasmic	NO_SP	CYT
WP_012390209.1	LEPBI_RS16105		hypothetical protein	chromosome	I	tBOSQV6					Cytoplasmic	NO_SP	CYT
WP_012390210.1	LEPBI_RS16110		alcohol dehydrogenase	chromosome	I	tBOSQV7	WP_000687497.1	0.63655515000000001		E	Cytoplasmic	NO_SP	CYT
WP_012390213.1	LEPBI_RS16125		hypothetical protein	chromosome	I	tBOSQW0	WP_000529883.1	0.595485			Unknown	NO_SP	CYT
WP_012390214.1	LEPBI_RS16130		alcohol dehydrogenase	chromosome	I	tBOSQW1	WP_002067912.1	0.704055		G	Cytoplasmic	NO_SP	CYT
WP_012390217.1	LEPBI_RS16145		nitronate monooxygenase	chromosome	I	tBOSQW4	WP_001983101.1	0.782725		R	Cytoplasmic	NO_SP	CYT
WP_012390218.1	LEPBI_RS16150		thioredoxin family protein	chromosome	I	tBOSQW5	WP_000949344.1	0.46131625		O	CytoplasmicMembrane	NO_SP	TMH
WP_012390219.1	LEPBI_RS16155		hypothetical protein	chromosome	I	tBOSQW6	WP_001218027.1	0.4918			OuterMembrane	SP	CYT
WP_041769912.1	LEPBI_RS16160		FecR domain-containing	chromosome	I	tBOSQW7	WP_001106967.1	0.459025			Unknown	SP	SpI
WP_012390221.1	LEPBI_RS16165		FAD-dependent thymidyl	chromosome	I	tBOSQW8				F	Cytoplasmic	NO_SP	CYT
WP_187148104.1	LEPBI_RS16170		alpha/beta fold hydro	chromosome	I	tBOSQW9	WP_000929340.1	0.63708			CytoplasmicMembrane	NO_SP	CYT
WP_012390223.1	LEPBI_RS16175		SRPBCC family protein	chromosome	I	tBOSQX0	WP_000697175.1	0.4870698			CytoplasmicMembrane	NO_SP	SpI
WP_012476451.1	LEPBI_RS16180		nuclear transport factor	chromosome	I	tBOSQX1	WP_000833668.1	0.506435			Unknown	NO_SP	CYT
WP_012390225.1	LEPBI_RS16185		rhodanese-like domain	chromosome	I	tBOSQX2					Unknown	NO_SP	CYT
WP_012390226.1	LEPBI_RS16190		phosphoribosyl-AMP	chromosome	I	tBOSQX3				E	Cytoplasmic	NO_SP	CYT
WP_012390228.1	LEPBI_RS16200	metG	methionine--tRNA ligase	chromosome	I	sBOSQX5	WP_001089002.1	0.6723783		J	Cytoplasmic	NO_SP	CYT
WP_187148105.1	LEPBI_RS16205		TerB family tellurite re	chromosome	I	tBOSQX6	WP_001131967.1	0.44126004999999996			Cytoplasmic	NO_SP	CYT
WP_012390230.1	LEPBI_RS16210		zinc-ribbon domain-con	chromosome	I	tBOSQX7					Unknown	NO_SP	SpI
WP_012390232.1	LEPBI_RS16220		TIGR04452 family lipon	chromosome	I	tBOSQX9					CytoplasmicMembrane	LIPO	SpII
WP_012390233.1	LEPBI_RS16225		serine hydrolase	chromosome	I	tBOSQY0					Unknown	LIPO	SpII
WP_012390234.1	LEPBI_RS16230		START domain-containing	chromosome	I	tBOSR86					Unknown	SP	CYT
WP_012390238.1	LEPBI_RS16245		acyl-CoA/acyl-ACP del	chromosome	I	tBOSR90	WP_001274139.1	0.81639855000000001		I	Cytoplasmic	NO_SP	CYT
WP_012390239.1	LEPBI_RS16250		crossover junction en	chromosome	I	tBOSR91	WP_001257915.1	0.55030050000000001		L	Cytoplasmic	NO_SP	CYT
WP_012390241.1	LEPBI_RS16260		TetR/AcrR family tran	chromosome	I	tBOSR93					Cytoplasmic	NO_SP	CYT
WP_012390244.1	LEPBI_RS16275		hypothetical protein	chromosome	I	tBOSR96	WP_000917839.1	0.47639175			Unknown	LIPO	SpII
WP_187148106.1	LEPBI_RS16280		hypothetical protein	chromosome	I		WP_000428739.1	0.65561759999999999			Unknown	NO_SP	CYT
WP_012390246.1	LEPBI_RS16290	sixA	phosphohistidine phos	chromosome	I	tBOSR98	WP_000691324.1	0.5661315		T	Unknown	NO_SP	CYT
WP_012390248.1	LEPBI_RS16300		acylphosphatase	chromosome	I	tBOSRA0	WP_000534971.1	0.75791999999999999		C	Cytoplasmic	NO_SP	CYT
WP_012390249.1	LEPBI_RS16305		aldo/keto reductase	chromosome	I	tBOSRA1	WP_002185292.1	0.80475500000000001		H	Unknown	NO_SP	CYT
WP_012390250.1	LEPBI_RS16310		hypothetical protein	chromosome	I	tBOSRA2					Cytoplasmic	NO_SP	CYT
WP_012390251.1	LEPBI_RS16315		histidine phosphatase	chromosome	I	tBOSRA3	WP_000022300.1	0.545625			Cytoplasmic	NO_SP	CYT

WP_012390252.1	LEPBI_RS16320		hypothetical protein	chromosome	I	tBOSRA4	WP_001153017.1	0.433081599999999996		Unknown	NO_SP	CYT
WP_012390253.1	LEPBI_RS16325		phosphotransferase f2	chromosome	I	tBOSRA5	WP_000995968.1	0.620175599999999999	R	Cytoplasmic	NO_SP	CYT
WP_012390254.1	LEPBI_RS16330		acyl-CoA dehydrogenase	chromosome	I	tBOSRA6	WP_000348045.1	0.760855	I	Cytoplasmic	NO_SP	CYT
WP_041769913.1	LEPBI_RS16345		hypothetical protein	chromosome	I	tBOSRA9	WP_001083103.1	0.461107950000000004		Unknown	SP	Spl
WP_012390258.1	LEPBI_RS16350		hypothetical protein	chromosome	I	tBOSRB0	WP_001192756.1	0.6261504		Cytoplasmic	NO_SP	CYT
WP_012390260.1	LEPBI_RS16360		hypothetical protein	chromosome	I	tBOSRB2	WP_001983891.1	0.66227825000000001		Unknown	NO_SP	CYT
WP_041769914.1	LEPBI_RS16365		carboxypeptidase M3	chromosome	I	tBOSRB3	WP_000252726.1	0.58131120000000001	O	Cytoplasmic	NO_SP	CYT
WP_012390264.1	LEPBI_RS16385		SRPBCC domain-conta	chromosome	I	tBOSRB6			I	Cytoplasmic	NO_SP	CYT
WP_012390266.1	LEPBI_RS16395		alkene reductase	chromosome	I	tBOSRB8			C	Cytoplasmic	NO_SP	CYT
WP_012390268.1	LEPBI_RS16405		hypothetical protein	chromosome	I	tBOSRC0				Cytoplasmic	NO_SP	CYT
WP_012390270.1	LEPBI_RS16415		hypothetical protein	chromosome	I	tBOSRC2				Unknown	SP	Spl
WP_012390271.1	LEPBI_RS16420		pirin family protein	chromosome	I	tBOSRC3			R	Cytoplasmic	NO_SP	CYT
WP_012390272.1	LEPBI_RS16425	ilvD	dihydroxy-acid dehydri	chromosome	I	tBOSRC4	WP_000502718.1	0.588456	E	Cytoplasmic	NO_SP	CYT
WP_012390273.1	LEPBI_RS16430		hypothetical protein	chromosome	I	tBOSRC5				Unknown	SP	CYT
WP_012390274.1	LEPBI_RS16435		TonB-dependent rece	chromosome	I	tBOSRC6	WP_000666312.1	0.497661600000000004		Unknown	SP	Spl
WP_012390277.1	LEPBI_RS16450		class I SAM-dependen	chromosome	I	tBOSRC9	WP_001283365.1	0.50925		Cytoplasmic	NO_SP	CYT
WP_012390278.1	LEPBI_RS16455		M20/M25/M40 family	chromosome	I	tBOSRD0	WP_001104117.1	0.530754899999999999	E	Cytoplasmic	LIPO	SpII
WP_012390279.1	LEPBI_RS16460		ankyrin repeat domai	chromosome	I	tBOSRD1				Unknown	LIPO	SpII
WP_012476456.1	LEPBI_RS16465		prohibitin family prot	chromosome	I	tBOSRD2	WP_001013490.1	0.588144949999999999		Cytoplasmic	LIPO	TMH
WP_012390282.1	LEPBI_RS16475		TonB-dependent rece	chromosome	I	tBOSRD4				OuterMembrane	SP	Spl
WP_012390283.1	LEPBI_RS16480		hypothetical protein	chromosome	I	tBOSRD5				Unknown	LIPO	SpII
WP_012390284.1	LEPBI_RS16485		hypothetical protein	chromosome	I	tBOSRD6	WP_000835560.1	0.489225		Extracellular	LIPO	SpII
WP_012390286.1	LEPBI_RS16495	mltG	endolytic transglycosy	chromosome	I	tBOSRD8	WP_001022114.1	0.7137009	M	Cytoplasmic	NO_SP	Spl
WP_012390287.1	LEPBI_RS16500		UDP-N-acetylmurama	chromosome	I	tBOSRD9	WP_001978935.1	0.2944935	M	Cytoplasmic	NO_SP	CYT
WP_012390288.1	LEPBI_RS16505		Spx/MgsR family RNA	chromosome	I	tBOSRE0	WP_001971937.1	0.6743385	P	Cytoplasmic	NO_SP	CYT
WP_012390289.1	LEPBI_RS16510		efflux RND transporte	chromosome	I	tBOSRE1	WP_000565850.1	0.6680157	P	CytoplasmicMembrane	NO_SP	Spl
WP_012390291.1	LEPBI_RS16520		circularly permuted ty	chromosome	I	tBOSRE3			R	Cytoplasmic	NO_SP	CYT
WP_012390292.1	LEPBI_RS16525		transglutaminase fam	chromosome	I	tBOSRE4			S	Cytoplasmic	NO_SP	CYT
WP_012390293.1	LEPBI_RS16530		alpha-E domain-conta	chromosome	I	tBOSRE5			S	Cytoplasmic	NO_SP	CYT
WP_012390294.1	LEPBI_RS16535		circularly permuted ty	chromosome	I	tBOSRE6			R	Cytoplasmic	NO_SP	CYT
WP_012476457.1	LEPBI_RS16540		SDR family NAD(P)-de	chromosome	I	tBOSRE7				Unknown	NO_SP	CYT
WP_012390296.1	LEPBI_RS16545		YqgE/AlgH family prot	chromosome	I	tBOSRE8	WP_000392362.1	0.631329349999999999	K	Unknown	NO_SP	CYT
WP_012390297.1	LEPBI_RS16550		Gfo/Idh/MocA family	chromosome	I	tBOSRE9	WP_000140212.1	0.7673985	R	Cytoplasmic	NO_SP	CYT
WP_012390298.1	LEPBI_RS16555	dnaJ	molecular chaperone	chromosome	I	sBOSRF0	WP_000004170.1	0.8214624	O	Cytoplasmic	NO_SP	CYT
WP_012390299.1	LEPBI_RS16560	dnaK	molecular chaperone	chromosome	I	sBOSRF1	WP_000031821.1	0.851399999999999999	O	Cytoplasmic	NO_SP	CYT
WP_012390300.1	LEPBI_RS16565	grpE	nucleotide exchange f	chromosome	I	sBOSRF2	WP_000852393.1	0.5351522	O	Cytoplasmic	NO_SP	CYT
WP_012476458.1	LEPBI_RS16570	hrcA	heat-inducible transcr	chromosome	I	tBOSRF3	WP_000366219.1	0.753625	K	Cytoplasmic	NO_SP	CYT
WP_012390302.1	LEPBI_RS16575		GGDEF domain-contai	chromosome	I	tBOSRF4			T	CytoplasmicMembrane	NO_SP	CYT
WP_012390303.1	LEPBI_RS16580		DUF2961 domain-con	chromosome	I	tBOSRF5				Cytoplasmic	NO_SP	CYT
WP_012390306.1	LEPBI_RS16595		alpha-glucosidase	chromosome	I	tBOSRF8	WP_000202103.1	0.448668649999999995	G	Cytoplasmic	NO_SP	CYT
WP_012390308.1	LEPBI_RS16605		efflux RND transporte	chromosome	I	tBOSRG0			M	CytoplasmicMembrane	LIPO	CYT
WP_012390309.1	LEPBI_RS16610		efflux RND transporte	chromosome	I	tBOSRG1			V	CytoplasmicMembrane	NO_SP	TMH
WP_012390310.1	LEPBI_RS16615		efflux transporter outi	chromosome	I	tBOSRG2			M	OuterMembrane	LIPO	CYT
WP_012390312.1	LEPBI_RS16625		hypothetical protein	chromosome	I	tBOSRG4				Unknown	LIPO	SpII

WP_012476462.1	LEPBI_RS16640		OB-fold domain-conta chromosome	I	tBOSRG7	WP_000004301.1	0.429345		Unknown	NO_SP	CYT
WP_012390317.1	LEPBI_RS16650		SH3 domain-containin chromosome	I	tBOSRG9				Unknown	LIPO	SpII
WP_041770094.1	LEPBI_RS16655		BtrH N-terminal doma chromosome	I	tBOSRH0				Cytoplasmic	NO_SP	CYT
WP_012390321.1	LEPBI_RS16670		acetyl-CoA C-acetyltra chromosome	I	tBOSRH3	WP_000063746.1	0.825035	I	Cytoplasmic	NO_SP	CYT
WP_012390323.1	LEPBI_RS16680		NADH-quinone oxidor chromosome	I	sBOSRH5	WP_000537600.1	0.86287	C	Cytoplasmic	NO_SP	CYT
WP_012390324.1	LEPBI_RS16685		(2Fe-2S)-binding prote chromosome	I	tBOSRH6	WP_000238902.1	0.714585	C	Cytoplasmic	NO_SP	CYT
WP_012390325.1	LEPBI_RS16690		response regulator chromosome	I	tBOSRH7	WP_000861511.1	0.48627810000000005	T	Cytoplasmic	NO_SP	CYT
WP_012390326.1	LEPBI_RS16695	aroC	chorismate synthase chromosome	I	sBOSRH8	WP_001141234.1	0.77321509999999999	E	Cytoplasmic	NO_SP	CYT
WP_012390328.1	LEPBI_RS16705		UpxY family transcript chromosome	I	tBOSRI0	WP_000572205.1	0.50791199999999999		Cytoplasmic	NO_SP	CYT
WP_187148107.1	LEPBI_RS16710		KpsF/GutQ family sugi chromosome	I	tBOSRI1	WP_000371240.1	0.70795500000000001	G	Cytoplasmic	NO_SP	CYT
WP_012390330.1	LEPBI_RS16715		type I 3-dehydroquina chromosome	I	tBOSRI2	WP_001076098.1	0.44690325000000003	E	Cytoplasmic	NO_SP	CYT
WP_012390331.1	LEPBI_RS16720		tetratricopeptide repe chromosome	I	tBOSRI3	WP_000885546.1	0.42385		Unknown	SP	SpI
WP_012390332.1	LEPBI_RS16725		GMC family oxidoredt chromosome	I	tBOSRI4	WP_000508949.1	0.78400575	I	Unknown	NO_SP	CYT
WP_012390335.1	LEPBI_RS16740	pepN	aminopeptidase N chromosome	I	tBOSRI7	WP_000339879.1	0.43101999999999996	E	Cytoplasmic	LIPO	CYT
WP_041769916.1	LEPBI_RS16755		glycerophosphodieste chromosome	I	tBOSRJ0	WP_000595809.1	0.63261939999999999	I	Cytoplasmic	LIPO	CYT
WP_012390339.1	LEPBI_RS16765		helix-turn-helix transc chromosome	I	tBOSRJ1				Cytoplasmic	NO_SP	CYT
WP_012390340.1	LEPBI_RS16770	fliG	flagellar motor switch chromosome	I	tBOSRU9	WP_000932791.1	0.95696	N	Cytoplasmic	NO_SP	CYT
WP_012390342.1	LEPBI_RS16780		MBL fold metallo-hydi chromosome	I	tBOSRV1				Unknown	NO_SP	SpI
WP_041769918.1	LEPBI_RS16790		hypothetical protein chromosome	I	tBOSRV3	WP_000871904.1	0.4079878		CytoplasmicMembrane	NO_SP	TMH
WP_012476467.1	LEPBI_RS16805		hypothetical protein chromosome	I	tBOSRV6	WP_001226846.1	0.29320785000000005		Extracellular	LIPO	SpI
WP_041769919.1	LEPBI_RS16810		HmuY family protein chromosome	I	tBOSRV7	WP_001079022.1	0.3685875		Unknown	NO_SP	CYT
WP_012390349.1	LEPBI_RS16815		TonB-dependent rece chromosome	I	tBOSRV8	WP_000449674.1	0.63831820000000001	P	OuterMembrane	SP	SpI
WP_012390353.1	LEPBI_RS16835		ferredoxin--NADP(+) r chromosome	I	tBOSRW2	WP_000805391.1	0.7495187	F	CytoplasmicMembrane	NO_SP	CYT
WP_012390354.1	LEPBI_RS16840		transcriptional coactiv chromosome	I	tBOSRW3	WP_000538229.1	0.70771460000000001		Unknown	NO_SP	CYT
WP_187148065.1	LEPBI_RS16845		VWA domain-containi chromosome	I	tBOSRW4				Cytoplasmic	NO_SP	CYT
WP_041769920.1	LEPBI_RS16855		DEAD/DEAH box helic chromosome	I	tBOSRW6	WP_000393265.1	0.6997914	K	Cytoplasmic	NO_SP	CYT
WP_012390358.1	LEPBI_RS16860		dicarboxylate/amino i chromosome	I	tBOSRW7	WP_001263200.1	0.5196144	C	CytoplasmicMembrane	NO_SP	TMH
WP_012390359.1	LEPBI_RS16865		SGNH/GDSL hydrolase chromosome	I	tBOSRW8				Unknown	LIPO	SpII
WP_012390360.1	LEPBI_RS16870		hypothetical protein chromosome	I	tBOSRW9				OuterMembrane	SP	SpI
WP_012390364.1	LEPBI_RS16895		sodium-translocating chromosome	I	tBOSRX3	WP_001089694.1	0.84220000000000001	C	CytoplasmicMembrane	NO_SP	CYT
WP_012390366.1	LEPBI_RS16905	acs	acetate--CoA ligase chromosome	I	sBOSRX5	WP_001983589.1	0.85166999999999999	I	Cytoplasmic	NO_SP	CYT
WP_012390367.1	LEPBI_RS16910	foIE	GTP cyclohydrolase I F chromosome	I	sBOSRX6	WP_000390685.1	0.85128615	H	Cytoplasmic	NO_SP	CYT
WP_012476470.1	LEPBI_RS16925		WbuC family cupin fol chromosome	I	tBOSRX9	WP_001206947.1	0.5318326		Cytoplasmic	NO_SP	CYT
WP_012476471.1	LEPBI_RS16935		alpha/beta hydrolase chromosome	I	tBOSRY1	WP_001289761.1	0.41497335	H	Unknown	NO_SP	CYT
WP_012390374.1	LEPBI_RS16945		class I SAM-dependen chromosome	I	tBOSRY3	WP_000834071.1	0.4358125	J	Cytoplasmic	NO_SP	CYT
WP_012476473.1	LEPBI_RS16980	dnaX	DNA polymerase III su chromosome	I	tBOSRY5	WP_000929205.1	0.63815895000000001	L	Cytoplasmic	NO_SP	CYT
WP_187148108.1	LEPBI_RS16985		YbaB/Ebfc family nucl chromosome	I	tBOSRY6	WP_000459763.1	0.53859649999999999	K	Unknown	NO_SP	CYT
WP_012390379.1	LEPBI_RS16995		hypothetical protein chromosome	I	tBOSRY8	WP_001282643.1	0.55079919999999999		Unknown	SP	SpI
WP_012390380.1	LEPBI_RS17000		transporter substrate- chromosome	I	tBOSRY9	WP_000462055.1	0.56916	E	Periplasmic	SP	SpI
WP_012390382.1	LEPBI_RS17010	serS	serine--tRNA ligase chromosome	I	sBOSRZ1	WP_000886261.1	0.72544000000000001	J	Cytoplasmic	NO_SP	CYT
WP_012476477.1	LEPBI_RS17015		TatD family hydrolase chromosome	I	tBOSRZ2	WP_000253692.1	0.68367915	N	Cytoplasmic	NO_SP	CYT
WP_012390384.1	LEPBI_RS17020		M23 family metallope chromosome	I	tBOSRZ3	WP_000351651.1	0.719955	M	Unknown	NO_SP	CYT
WP_012390385.1	LEPBI_RS17025		polymer-forming cyto chromosome	I	tBOSRZ4	WP_000246073.1	0.79025265	Z	Cytoplasmic	NO_SP	CYT
WP_012390387.1	LEPBI_RS17035		ATP-binding cassette i chromosome	I	tBOSRZ6			V	CytoplasmicMembrane	NO_SP	SpI

WP_012390388.1	LEPBI_RS17040		ParB/RepB/Spo0J fam chromosome	I	tBOSRZ7	WP_001185518.1	0.6416850000000001	D	Cytoplasmic	NO_SP	CYT
WP_012390389.1	LEPBI_RS17045		ParA family protein chromosome	I	tBOSRZ8	WP_000516556.1	0.7896685499999999	D	CytoplasmicMembrane	NO_SP	CYT
WP_012390390.1	LEPBI_RS17050		ribosomal RNA small s chromosome	I	sBOSRZ9	WP_001153932.1	0.51397875	J	Cytoplasmic	NO_SP	CYT
WP_012390391.1	LEPBI_RS17055		hypothetical protein chromosome	I	tBOSS00	WP_000619331.1	0.43135034999999994		Cytoplasmic	SP	CYT
WP_012390392.1	LEPBI_RS17060	mnmG	tRNA uridine-5-carbox chromosome	I	sBOSS01	WP_000572985.1	0.77175625	J	Cytoplasmic	NO_SP	CYT
WP_012390393.1	LEPBI_RS17065		branched-chain aminoc chromosome	I	tBOSS02	WP_000841027.1	0.75896	E	Cytoplasmic	NO_SP	CYT
WP_012390394.1	LEPBI_RS17070		hypothetical protein chromosome	I	tBOSS03	WP_000834729.1	0.5562859500000001	L	Cytoplasmic	NO_SP	CYT
WP_081431676.1	LEPBI_RS18870		hypothetical protein chromosome	I					Unknown	NO_SP	CYT
WP_015679024.1	LEPBI_RS18950	rpmF	50S ribosomal protein chromosome	I		WP_000290471.1	0.7803100000000001		Cytoplasmic	NO_SP	CYT
WP_012387307.1	LEPBI_RS19095		hypothetical protein chromosome	I	tBOSJ02	WP_001288293.1	0.44511019999999996		Unknown	NO_SP	CYT
WP_167530795.1	LEPBI_RS19115		hypothetical protein chromosome	I					Unknown	LIPO	SpII
WP_012476478.1	LEPBI_RS17080		ParA family protein chromosome	II	tBOSTK5	WP_000637632.1	0.812	D	Unknown	NO_SP	CYT
WP_012476479.1	LEPBI_RS17085		ParB/RepB/Spo0J fam chromosome	II	tBOSTK6	WP_000095801.1	0.6886099999999999	D	Cytoplasmic	NO_SP	CYT
WP_041770179.1	LEPBI_RS17090		helix-turn-helix domain chromosome	II	tBOSTK7	WP_002094852.1	0.49297440000000003		Cytoplasmic	NO_SP	CYT
WP_012476811.1	LEPBI_RS17095		discoidin domain-cont chromosome	II	tBOSTK8	WP_001083720.1	0.5994103500000001		Cytoplasmic	NO_SP	CYT
WP_012476482.1	LEPBI_RS17100		1,4-dihydroxy-6-naph chromosome	II	tBOSTK9	WP_000395994.1	0.6113904	H	Cytoplasmic	NO_SP	CYT
WP_012476483.1	LEPBI_RS17105		hypothetical protein chromosome	II	tBOSTL0				CytoplasmicMembrane	NO_SP	TMH
WP_041770236.1	LEPBI_RS17110		hypothetical protein chromosome	II	tBOSTL1	WP_000755935.1	0.45272979999999996		Cytoplasmic	NO_SP	CYT
WP_012476485.1	LEPBI_RS17115		PAS domain S-box pro chromosome	II	tBOSTL2	WP_000011406.1	0.45594450000000003	T	CytoplasmicMembrane	NO_SP	CYT
WP_012476486.1	LEPBI_RS17120	htpG	molecular chaperone chromosome	II	tBOSTL3	WP_001288005.1	0.73525	O	Cytoplasmic	NO_SP	CYT
WP_012476487.1	LEPBI_RS17125		BatD family protein chromosome	II	tBOSTL4	WP_001079251.1	0.3985611		OuterMembrane	SP	SpI
WP_012476488.1	LEPBI_RS17130		VWA domain-containi chromosome	II	tBOSTL5				Unknown	NO_SP	TMH
WP_012476489.1	LEPBI_RS17135		VWA domain-containi chromosome	II	tBOSTL6	WP_001011139.1	0.5520015		CytoplasmicMembrane	NO_SP	TMH
WP_012476814.1	LEPBI_RS17140		hypothetical protein chromosome	II	tBOSTL7	WP_000744235.1	0.350952		Unknown	SP	CYT
WP_012476491.1	LEPBI_RS17145		DUF58 domain-contai chromosome	II	tBOSTL8	WP_000619592.1	0.350658	S	Cytoplasmic	NO_SP	CYT
WP_187148110.1	LEPBI_RS17150		AAA family ATPase chromosome	II	tBOSTL9	WP_000410299.1	0.659015	R	Cytoplasmic	NO_SP	CYT
WP_012476493.1	LEPBI_RS17155		LIC20035 family adhe: chromosome	II	tBOSTM0	WP_000819152.1	0.48062520000000003		Cytoplasmic	SP	SpII
WP_012476494.1	LEPBI_RS17160		Paal family thioestera chromosome	II	tBOSTM1	WP_000379289.1	0.4497493000000001		Cytoplasmic	NO_SP	CYT
WP_012476495.1	LEPBI_RS17165		alpha/beta hydrolase chromosome	II	tBOSTM2			H	Cytoplasmic	NO_SP	CYT
WP_012476496.1	LEPBI_RS17170		hypothetical protein chromosome	II	tBOSTM3				Cytoplasmic	SP	CYT
WP_187148111.1	LEPBI_RS17180		FAD-dependent oxido chromosome	II	tBOSTM5	WP_000504735.1	0.6963264	C	CytoplasmicMembrane	NO_SP	CYT
WP_012476815.1	LEPBI_RS17190		M48 family metallope chromosome	II	tBOSTM7			R	Cytoplasmic	NO_SP	CYT
WP_012476501.1	LEPBI_RS17195		putative porin chromosome	II	tBOSTM8	WP_001983163.1	0.42690240000000007		OuterMembrane	SP	CYT
WP_049756021.1	LEPBI_RS17200		AAA family ATPase chromosome	II	tBOSTM9	WP_001086265.1	0.6463688	D	Cytoplasmic	NO_SP	CYT
WP_012476503.1	LEPBI_RS17205		ParB/RepB/Spo0J fam chromosome	II	tBOSTN0	WP_001129332.1	0.7415100000000001	D	Cytoplasmic	NO_SP	CYT
WP_012476504.1	LEPBI_RS17210		DUF1569 domain-con chromosome	II	tBOSTN1				Cytoplasmic	NO_SP	CYT
WP_012476505.1	LEPBI_RS17215		NAD(P)H-dependent c chromosome	II	tBOSTN2	WP_000684128.1	0.55		Cytoplasmic	NO_SP	CYT
WP_012476507.1	LEPBI_RS17225		cyclic nucleotide-bind chromosome	II	tBOSTN4	WP_001093846.1	0.714275	T	Unknown	NO_SP	CYT
WP_012476816.1	LEPBI_RS17235		HDOD domain-containi chromosome	II	tBOSTN6			T	Cytoplasmic	NO_SP	CYT
WP_012476512.1	LEPBI_RS17245		STAS domain-containi chromosome	II	tBOSTN9				Cytoplasmic	NO_SP	CYT
WP_004788037.1	LEPBI_RS17250		HU family DNA-bindin chromosome	II	tBOSTP0				Cytoplasmic	NO_SP	CYT
WP_012476513.1	LEPBI_RS17255		hypothetical protein chromosome	II	tBOSTP1	WP_000012417.1	0.3767148		Cytoplasmic	NO_SP	CYT
WP_012476817.1	LEPBI_RS17260		FAD-binding oxidored chromosome	II	tBOSTP2	WP_000500122.1	0.40886520000000004	C	Cytoplasmic	NO_SP	CYT
WP_012476515.1	LEPBI_RS17265		TetR/AcrR family tran: chromosome	II	tBOSTP3				Cytoplasmic	NO_SP	CYT

WP_041770185.1	LEPBI_RS17270		diacylglycerol kinase f chromosome	II	tBOSTP4			I	Cytoplasmic	NO_SP	CYT
WP_012476517.1	LEPBI_RS17275		glycerol-3-phosphate chromosome	II	tBOSTP5	WP_001142835.1	0.5674639	C	Cytoplasmic	NO_SP	CYT
WP_012476518.1	LEPBI_RS17280		thioesterase family pr chromosome	II	tBOSTP6	WP_001972581.1	0.5617260000000001		Cytoplasmic	NO_SP	CYT
WP_012476519.1	LEPBI_RS17285		protein kinase chromosome	II	tBOSTP7	WP_000877311.1	0.640134	O	CytoplasmicMembrane	NO_SP	CYT
WP_012476520.1	LEPBI_RS17290		protein meaA chromosome	II	tBOSTP8	WP_000428541.1	0.8339661	I	Cytoplasmic	NO_SP	CYT
WP_012476521.1	LEPBI_RS17295		hypothetical protein chromosome	II	tBOSTP9	WP_000362811.1	0.425937499999999997		CytoplasmicMembrane	NO_SP	TMH
WP_012476522.1	LEPBI_RS17300		lytic transglycosylase i chromosome	II	tBOSTQ0	WP_000603280.1	0.49653320000000006	M	Periplasmic	NO_SP	CYT
WP_012476523.1	LEPBI_RS17305		response regulator chromosome	II	tBOSTQ1				Cytoplasmic	NO_SP	CYT
WP_012476524.1	LEPBI_RS17310		aspartate ammonia-ly chromosome	II	tBOSTQ2			E	Cytoplasmic	NO_SP	CYT
WP_012476525.1	LEPBI_RS17315		hypothetical protein chromosome	II	tBOSTQ3				Cytoplasmic	SP	Spl
WP_012476526.1	LEPBI_RS17320		SH3 domain-containin chromosome	II	tBOSTQ4				Unknown	LIPO	CYT
WP_012476818.1	LEPBI_RS17325		TIGR04452 family lipo chromosome	II	tBOSTQ5				Periplasmic	LIPO	SplI
WP_012476528.1	LEPBI_RS17330		Spy/CpxP family prote chromosome	II	tBOSTQ6	WP_000060680.1	0.43885900000000005		Cytoplasmic	SP	CYT
WP_012476529.1	LEPBI_RS17335		sigma-70 family RNA f chromosome	II	tBOSTQ7	WP_000988152.1	0.50048955	K	Cytoplasmic	NO_SP	CYT
WP_187148112.1	LEPBI_RS17345		hypothetical protein chromosome	II	tBOSTQ9				Unknown	NO_SP	CYT
WP_012476534.1	LEPBI_RS17360		heavy metal transloca chromosome	II	tBOSTR2			P	CytoplasmicMembrane	NO_SP	CYT
WP_012476535.1	LEPBI_RS17365		FixH family protein chromosome	II	tBOSTR3				Unknown	NO_SP	TMH
WP_012476536.1	LEPBI_RS17370	ccoG	cytochrome c oxidase chromosome	II	tBOSTR4			C	CytoplasmicMembrane	NO_SP	TMH
WP_012476537.1	LEPBI_RS17375		c-type cytochrome chromosome	II	tBOSTR5				Periplasmic	NO_SP	TMH
WP_012476539.1	LEPBI_RS17385	ccoO	cytochrome-c oxidase chromosome	II	tBOSTR7			C	Unknown	NO_SP	CYT
WP_012476540.1	LEPBI_RS17390	ccoN	cytochrome-c oxidase chromosome	II	tBOSTR8			C	CytoplasmicMembrane	NO_SP	TMH
WP_012476541.1	LEPBI_RS17395		hypothetical protein chromosome	II	tBOSTR9	WP_000532389.1	0.50192909999999999		Cytoplasmic	SP	Spl
WP_012476542.1	LEPBI_RS17405		glutamate synthase sl chromosome	II	tBOSTS0			E	Cytoplasmic	NO_SP	CYT
WP_012476543.1	LEPBI_RS17410	gltB	glutamate synthase la chromosome	II	tBOSTS1	WP_000998837.1	0.5255068500000001	E	Unknown	NO_SP	CYT
WP_012476544.1	LEPBI_RS17415		hypothetical protein chromosome	II	tBOSTS2				CytoplasmicMembrane	NO_SP	TMH
WP_012476545.1	LEPBI_RS17420		TPM domain-containin chromosome	II	tBOSTS3			S	CytoplasmicMembrane	SP	Spl
WP_012476547.1	LEPBI_RS17430		DNA-binding protein chromosome	II	tBOSTS5			V	Unknown	NO_SP	CYT
WP_012476548.1	LEPBI_RS17435		shikimate kinase chromosome	II	sBOSTS6	WP_000739193.1	0.5964918	E	Cytoplasmic	NO_SP	CYT
WP_012476549.1	LEPBI_RS17440		HDOD domain-contain chromosome	II	tBOSTS7	WP_000659900.1	0.62311590000000001	T	Unknown	NO_SP	CYT
WP_012476550.1	LEPBI_RS17445		chemotaxis protein Ct chromosome	II	tBOSTS8	WP_000956231.1	0.7171113		Cytoplasmic	NO_SP	CYT
WP_012476551.1	LEPBI_RS17450		TraB/GumN family prc chromosome	II	tBOSTS9	WP_001151299.1	0.65070025	S	CytoplasmicMembrane	NO_SP	CYT
WP_012476553.1	LEPBI_RS17460		four-helix bundle copj chromosome	II	tBOSTT1	WP_000957839.1	0.48841650000000003		Unknown	TAT	Spl
WP_012476554.1	LEPBI_RS17465		hypothetical protein chromosome	II	tBOSTT2				Unknown	NO_SP	CYT
WP_012476555.1	LEPBI_RS17470		hypothetical protein chromosome	II	tBOSTT3	WP_000850434.1	0.340735499999999997		Unknown	SP	CYT
WP_012476556.1	LEPBI_RS17475		UTP--glucose-1-phosp chromosome	II	tBOSTT4	WP_000377734.1	0.6688647	G	Cytoplasmic	NO_SP	CYT
WP_012476558.1	LEPBI_RS17485		fibronectin type III do chromosome	II	tBOSTT6	WP_001221434.1	0.399544199999999996		OuterMembrane	LIPO	Spl
WP_012476559.1	LEPBI_RS17490		energy transducer Tor chromosome	II	tBOSTT7	WP_000776116.1	0.6594425		Unknown	NO_SP	TMH
WP_012476822.1	LEPBI_RS17495		MotA/TolQ/ExbB prot chromosome	II	tBOSTT8	WP_000177702.1	0.65191375	U	CytoplasmicMembrane	NO_SP	CYT
WP_012476561.1	LEPBI_RS17500		hypothetical protein chromosome	II	tBOSTT9	WP_000760152.1	0.5105261		CytoplasmicMembrane	NO_SP	TMH
WP_012476562.1	LEPBI_RS17505		efflux RND transporte chromosome	II	tBOSTU0	WP_001017334.1	0.71387150000000001	V	CytoplasmicMembrane	NO_SP	CYT
WP_012476563.1	LEPBI_RS17510		PilZ domain-containin chromosome	II	tBOSTU1				Cytoplasmic	NO_SP	CYT
WP_012476564.1	LEPBI_RS17515		histidine kinase chromosome	II	tBOSTU2				CytoplasmicMembrane	NO_SP	CYT
WP_012476565.1	LEPBI_RS17520		response regulator chromosome	II	tBOSTU3	WP_000244073.1	0.37466100000000001	T	Cytoplasmic	NO_SP	CYT
WP_012476567.1	LEPBI_RS17530	meaB	methylmalonyl Co-A n chromosome	II	tBOSTU5	WP_000094317.1	0.60826125	O	CytoplasmicMembrane	NO_SP	CYT



WP_012476568.1	LEPBI_RS17535	scpA	methylmalonyl-CoA rr chromosome	II	tBOSTU6	WP_000828548.1	0.8067610500000001	I	Cytoplasmic	NO_SP	CYT
WP_012476569.1	LEPBI_RS17540		methylmalonyl-CoA rr chromosome	II	tBOSTU7	WP_000013232.1	0.4563405	I	Unknown	NO_SP	CYT
WP_041770243.1	LEPBI_RS17545		hypothetical protein chromosome	II	tBOSTU8				Unknown	NO_SP	TMH
WP_012476571.1	LEPBI_RS17550		lysoplasmalogenase chromosome	II	tBOSTU9	WP_000600787.1	0.52044795		CytoplasmicMembrane	NO_SP	CYT
WP_012476572.1	LEPBI_RS17555		ferritin family protein chromosome	II	tBOSTV0	WP_001022430.1	0.4555760000000004		Periplasmic	NO_SP	CYT
WP_012476573.1	LEPBI_RS17560		DUF2505 family prote chromosome	II	tBOSTV1	WP_000875950.1	0.6579801000000001		Cytoplasmic	NO_SP	CYT
WP_049756023.1	LEPBI_RS17565		EamA family transpor chromosome	II	tBOSTV2				CytoplasmicMembrane	NO_SP	TMH
WP_012476575.1	LEPBI_RS17570		RNA polymerase sigm chromosome	II	tBOSTV3			K	Cytoplasmic	NO_SP	CYT
WP_012476576.1	LEPBI_RS17575		hypothetical protein chromosome	II	tBOSTV4				Unknown	NO_SP	CYT
WP_012476577.1	LEPBI_RS17585		hypothetical protein chromosome	II	tBOSTV5				CytoplasmicMembrane	NO_SP	TMH
WP_012476578.1	LEPBI_RS17590		DUF302 domain-cont chromosome	II	tBOSTV6			S	Cytoplasmic	NO_SP	CYT
WP_012476579.1	LEPBI_RS17595		hypothetical protein chromosome	II	tBOSTV7				Unknown	NO_SP	TMH
WP_012476580.1	LEPBI_RS17600	speE	polyamine aminoprop chromosome	II	sBOSTV8	WP_000424716.1	0.7375	E	Cytoplasmic	NO_SP	CYT
WP_187148113.1	LEPBI_RS17605		hypothetical protein chromosome	II	tBOSTV9				OuterMembrane	NO_SP	CYT
WP_012476827.1	LEPBI_RS17610		hypothetical protein chromosome	II	tBOSTW0				Cytoplasmic	LIPO	TMH
WP_012476583.1	LEPBI_RS17615		hypothetical protein chromosome	II	tBOSTW1				Unknown	LIPO	SpI
WP_012476584.1	LEPBI_RS17620	pyrF	orotidine-5'-phosphat chromosome	II	tBOSTW2	WP_002080039.1	0.55918665	F	Cytoplasmic	NO_SP	CYT
WP_012476585.1	LEPBI_RS17625		FAD-dependent oxido chromosome	II	tBOSTW3			R	Cytoplasmic	NO_SP	CYT
WP_012476586.1	LEPBI_RS17630		DUF1365 domain-con chromosome	II	tBOSTW4			S	Unknown	NO_SP	CYT
WP_041770201.1	LEPBI_RS17635		class I SAM-dependen chromosome	II	tBOSTW5			I	Cytoplasmic	NO_SP	CYT
WP_012476588.1	LEPBI_RS17640		SRPBCC domain-cont chromosome	II	tBOSTW6	WP_000450144.1	0.63388215		Unknown	NO_SP	CYT
WP_012476589.1	LEPBI_RS17645		hypothetical protein chromosome	II	tBOSTW7	WP_000422624.1	0.6024942		Unknown	NO_SP	CYT
WP_012476590.1	LEPBI_RS17650		DUF1574 domain-con chromosome	II	tBOSTW8	WP_000837643.1	0.49500495000000005		Unknown	NO_SP	CYT
WP_041770245.1	LEPBI_RS17655		peptidase MA chromosome	II	tBOSTW9				Extracellular	NO_SP	CYT
WP_012476592.1	LEPBI_RS17660		hypothetical protein chromosome	II	tBOSTX0				CytoplasmicMembrane	SP	SpI
WP_012476593.1	LEPBI_RS17665		glycosyltransferase chromosome	II	tBOSTX1			J	Cytoplasmic	NO_SP	CYT
WP_012476594.1	LEPBI_RS17670		NAD-dependent epim chromosome	II	tBOSTX2			M	Cytoplasmic	NO_SP	CYT
WP_187148114.1	LEPBI_RS17675		glycosyltransferase chromosome	II	tBOSTX3				Unknown	NO_SP	CYT
WP_041770247.1	LEPBI_RS17680		hypothetical protein chromosome	II	tBOSTX4	WP_001083737.1	0.4298555		Unknown	NO_SP	TMH
WP_012476597.1	LEPBI_RS17685		EpsG family protein chromosome	II	tBOSTX5	WP_000599986.1	0.5404502499999999		CytoplasmicMembrane	NO_SP	TMH
WP_012476598.1	LEPBI_RS17690		serine protease chromosome	II	tBOSTX6	WP_000944569.1	0.4146868		Cytoplasmic	SP	CYT
WP_041770204.1	LEPBI_RS17695		trypsin-like peptidase chromosome	II	tBOSTX7	WP_000125234.1	0.6057125000000001	O	Periplasmic	SP	SpI
WP_012476835.1	LEPBI_RS17705		adenine phosphoribo: chromosome	II	tBOSTX9	WP_000029425.1	0.7542599999999999	F	Cytoplasmic	NO_SP	CYT
WP_012476602.1	LEPBI_RS17710	htpX	protease HtpX chromosome	II	tBOSTY0	WP_000264281.1	0.7180173	O	CytoplasmicMembrane	NO_SP	TMH
WP_012476603.1	LEPBI_RS17715		permease chromosome	II	tBOSTY1	WP_001075232.1	0.6807521		CytoplasmicMembrane	NO_SP	TMH
WP_012476604.1	LEPBI_RS17720		hypothetical protein chromosome	II	tBOSTY2	WP_000360826.1	0.55128		Cytoplasmic	NO_SP	CYT
WP_012476836.1	LEPBI_RS17725		polysaccharide biosyn chromosome	II	tBOSTY3	WP_000457972.1	0.7313377500000001	M	CytoplasmicMembrane	NO_SP	TMH
WP_012476606.1	LEPBI_RS17730		hypothetical protein chromosome	II	tBOSTY4	WP_002081111.1	0.36334500000000003		Unknown	NO_SP	CYT
WP_012476607.1	LEPBI_RS17735	hrpB	ATP-dependent helica chromosome	II	tBOSTY5			J	Cytoplasmic	NO_SP	CYT
WP_012476608.1	LEPBI_RS17740		methylated-DNA--[prc chromosome	II	tBOSTY6	WP_000020273.1	0.5474182000000001	L	CytoplasmicMembrane	NO_SP	CYT
WP_012476609.1	LEPBI_RS17745		hypothetical protein chromosome	II	tBOSTY7				CytoplasmicMembrane	NO_SP	TMH
WP_012476610.1	LEPBI_RS17750		hypothetical protein chromosome	II	tBOSTY8				Unknown	LIPO	SpII
WP_012476087.1	LEPBI_RS17755		ISNCY-like element IS1 chromosome	II	tBOSTY9				Cytoplasmic	NO_SP	CYT
WP_012476837.1	LEPBI_RS17760		TIGR04452 family lipo chromosome	II	tBOSTZ0				Unknown	LIPO	SpII

WP_012476614.1	LEPBI_RS17765		hypothetical protein	chromosome	II	tBOSTZ2	WP_001240474.1	0.57989685		Cytoplasmic	NO_SP	TMH
WP_012476615.1	LEPBI_RS17770		FecR domain-containi	chromosome	II	tBOSTZ3				Unknown	NO_SP	CYT
WP_081431683.1	LEPBI_RS17775		RNA polymerase sigm	chromosome	II	tBOSTZ4	WP_001971886.1	0.59639	K	Unknown	NO_SP	CYT
WP_012476838.1	LEPBI_RS17780	sthA	Si-specific NAD(P)(+)	chromosome	II	tBOSTZ5			C	Cytoplasmic	NO_SP	CYT
WP_012476618.1	LEPBI_RS17785		HAMP domain-containi	chromosome	II	tBOSTZ6	WP_000179795.1	0.5372112	T	Cytoplasmic	NO_SP	CYT
WP_041770253.1	LEPBI_RS17790		peroxiredoxin	chromosome	II	tBOSTZ7			V	Cytoplasmic	NO_SP	CYT
WP_012476620.1	LEPBI_RS17795		OsmC family protein	chromosome	II	tBOSTZ8			R	Cytoplasmic	NO_SP	CYT
WP_012476839.1	LEPBI_RS17800		DUF547 domain-conta	chromosome	II	tBOSTZ9				Unknown	SP	Spl
WP_012476622.1	LEPBI_RS17805		esterase	chromosome	II	tBOSU00	WP_001191980.1	0.6208176	R	Unknown	NO_SP	CYT
WP_012476623.1	LEPBI_RS17810	dinB	DNA polymerase IV	chromosome	II	tBOSU01	WP_000450032.1	0.6114514	L	Cytoplasmic	NO_SP	CYT
WP_187148109.1	LEPBI_RS17815		SpoIIE family protein	chromosome	II	tBOSU02			T	Cytoplasmic	NO_SP	CYT
WP_012476625.1	LEPBI_RS17820		PAS domain-containin	chromosome	II	tBOSU03			T	CytoplasmicMembrane	NO_SP	CYT
WP_012476840.1	LEPBI_RS17835		ubiquinone/menaquir	chromosome	II	tBOSU06	WP_000012765.1	0.6165082000000001	H	Cytoplasmic	NO_SP	CYT
WP_012476629.1	LEPBI_RS17840		LruC domain-containii	chromosome	II	tBOSU07				Extracellular	LIPO	SplI
WP_012476630.1	LEPBI_RS17845		AMP-binding protein	chromosome	II	tBOSU08			I	Cytoplasmic	NO_SP	CYT
WP_012476631.1	LEPBI_RS17850		PAS domain-containin	chromosome	II	tBOSU09				Unknown	NO_SP	CYT
WP_012476632.1	LEPBI_RS17855		hypothetical protein	chromosome	II	tBOSU10				Unknown	NO_SP	CYT
WP_012476633.1	LEPBI_RS17860		chemotaxis protein	chromosome	II	tBOSU11			T	CytoplasmicMembrane	NO_SP	TMH
WP_012476635.1	LEPBI_RS17870		hypothetical protein	chromosome	II	tBOSU13	WP_000835125.1	0.32199635		CytoplasmicMembrane	NO_SP	TMH
WP_012476636.1	LEPBI_RS17875		TraR/DksA family tran	chromosome	II	tBOSU14	WP_000125527.1	0.6460454	K	Cytoplasmic	NO_SP	CYT
WP_012476637.1	LEPBI_RS17880		bile acid:sodium symf	chromosome	II	tBOSU15	WP_000448522.1	0.5620674999999999	R	CytoplasmicMembrane	NO_SP	TMH
WP_012476639.1	LEPBI_RS17885		aminotransferase clas	chromosome	II	tBOSU17	WP_001190664.1	0.5311355	E	Cytoplasmic	NO_SP	CYT
WP_012476640.1	LEPBI_RS17890	alr	alanine racemase	chromosome	II	tBOSU18	WP_001982425.1	0.5969205	M	Cytoplasmic	NO_SP	CYT
WP_012476641.1	LEPBI_RS17895		alpha/beta hydrolase	chromosome	II	tBOSU19			H	Cytoplasmic	NO_SP	CYT
WP_012476841.1	LEPBI_RS17900		carbon-nitrogen hydr	chromosome	II	tBOSU20	WP_001069019.1	0.3100502	C	Cytoplasmic	NO_SP	CYT
WP_012476842.1	LEPBI_RS17905	argB	acetylglutamate kinas	chromosome	II	tBOSU21	WP_001982628.1	0.7410367999999999	E	Cytoplasmic	NO_SP	CYT
WP_012476644.1	LEPBI_RS17910		SpoIIE family protein	chromosome	II	tBOSU22	WP_000004123.1	0.60152895	T	Cytoplasmic	NO_SP	CYT
WP_012476645.1	LEPBI_RS17915		hypothetical protein	chromosome	II	tBOSU23				Cytoplasmic	NO_SP	CYT
WP_012476646.1	LEPBI_RS17920		efflux RND transporte	chromosome	II	tBOSU24			P	CytoplasmicMembrane	NO_SP	Spl
WP_012476647.1	LEPBI_RS17925		efflux RND transporte	chromosome	II	tBOSU25				Unknown	LIPO	SplI
WP_012476648.1	LEPBI_RS17930		TolC family protein	chromosome	II	tBOSU26				Cytoplasmic	SP	CYT
WP_012476650.1	LEPBI_RS17940		ATP-dependent 6-pho	chromosome	II	tBOSU28	WP_000448293.1	0.77934285	G	Cytoplasmic	NO_SP	CYT
WP_012476651.1	LEPBI_RS17945		hypothetical protein	chromosome	II	tBOSU29	WP_001036162.1	0.4548425		Unknown	SP	Spl
WP_012476652.1	LEPBI_RS17950		energy transducer Tor	chromosome	II	tBOSU30				Cytoplasmic	LIPO	CYT
WP_041770254.1	LEPBI_RS17955		hypothetical protein	chromosome	II	tBOSU31	WP_000075289.1	0.3519585		Unknown	NO_SP	CYT
WP_012476845.1	LEPBI_RS17960	metH	methionine synthase	chromosome	II	tBOSU32	WP_000262613.1	0.7519248	E	Cytoplasmic	NO_SP	CYT
WP_002980754.1	LEPBI_RS17965		4Fe-4S dicluster doma	chromosome	II	tBOSU33	WP_000332230.1	0.6515882999999999		Cytoplasmic	NO_SP	CYT
WP_012476655.1	LEPBI_RS17970		adenosylhomocystein	chromosome	II	tBOSU34	WP_000117570.1	0.8906750000000001	H	Cytoplasmic	NO_SP	CYT
WP_012476656.1	LEPBI_RS17975		metalloregulator ArsR	chromosome	II	tBOSU35	WP_000230180.1	0.7544514499999999	H	Cytoplasmic	NO_SP	CYT
WP_012476657.1	LEPBI_RS17980		methyl-accepting chei	chromosome	II	tBOSU36	WP_000999372.1	0.4158297	T	CytoplasmicMembrane	NO_SP	TMH
WP_012476658.1	LEPBI_RS17985		hypothetical protein	chromosome	II	tBOSU37				Unknown	SP	Spl
WP_012476661.1	LEPBI_RS18000		TIGR04454 family lipo	chromosome	II	tBOSU40				Unknown	LIPO	SplI
WP_012476663.1	LEPBI_RS18010		methyl-accepting chei	chromosome	II	tBOSU42			T	Unknown	NO_SP	CYT
WP_012476664.1	LEPBI_RS18015		methyl-accepting chei	chromosome	II	tBOSU43			T	CytoplasmicMembrane	NO_SP	TMH

WP_041770213.1	LEPBI_RS18020		M61 family metalloprote	II	tBOSU44	WP_000277382.1	0.536256		R	Cytoplasmic	NO_SP	CYT
WP_012476666.1	LEPBI_RS18025		magnesium transport	II	tBOSU45	WP_000821728.1	0.35317924999999994		P	CytoplasmicMembrane	NO_SP	CYT
WP_012476847.1	LEPBI_RS18030		hypothetical protein	II	tBOSU46	WP_000043034.1	0.327617			Cytoplasmic	NO_SP	CYT
WP_012476668.1	LEPBI_RS18035		SDR family oxidoreduc	II	tBOSU47	WP_000172945.1	0.64710719999999999		I	Cytoplasmic	NO_SP	CYT
WP_012476669.1	LEPBI_RS18040		SDR family oxidoreduc	II	tBOSU48	WP_000093663.1	0.43153320000000006			Unknown	NO_SP	CYT
WP_012476670.1	LEPBI_RS18045	mtnB	methylthioribulose 1-	II	sBOSU49	WP_000111953.1	0.42801779999999999		E	Cytoplasmic	NO_SP	CYT
WP_012476671.1	LEPBI_RS18050	efp	elongation factor P	II	sBOSU50	WP_000172195.1	0.84841499999999999		J	Cytoplasmic	NO_SP	CYT
WP_012476672.1	LEPBI_RS18055		KamA family radical S	II	tBOSU51	WP_000103002.1	0.62726399999999999		E	Cytoplasmic	NO_SP	CYT
WP_012476673.1	LEPBI_RS18060		hypothetical protein	II	tBOSU52	WP_000779912.1	0.30556125			Unknown	LIPO	SpII
WP_012476675.1	LEPBI_RS18070		hypothetical protein	II	tBOSU54	WP_001031000.1	0.41965959999999997			Cytoplasmic	NO_SP	CYT
WP_012476676.1	LEPBI_RS18075	msrB	peptide-methionine (f	II	tBOSU55				O	Cytoplasmic	LIPO	SpI
WP_012476677.1	LEPBI_RS18080		GAF domain-contains	II	tBOSU56	WP_001098064.1	0.441264		T	CytoplasmicMembrane	NO_SP	CYT
WP_012476849.1	LEPBI_RS18085		DEAD/DEAH box helic	II	tBOSU57				L	Cytoplasmic	NO_SP	CYT
WP_012476679.1	LEPBI_RS18090		class I SAM-dependen	II	tBOSU58				I	Cytoplasmic	NO_SP	CYT
WP_012476680.1	LEPBI_RS18095		DUF1295 domain-con	II	tBOSU59				R	CytoplasmicMembrane	NO_SP	TMH
WP_012476681.1	LEPBI_RS18100		SDR family NAD(P)-de	II	tBOSU60	WP_001069860.1	0.5571225		I	Cytoplasmic	NO_SP	CYT
WP_012476850.1	LEPBI_RS18105		NAD(P)-dependent alk	II	tBOSU61	WP_000870126.1	0.68856479999999999		C	Cytoplasmic	NO_SP	CYT
WP_012476683.1	LEPBI_RS18110		YdcF family protein	II	tBOSU62					Cytoplasmic	NO_SP	CYT
WP_012476688.1	LEPBI_RS18125		SH3 domain-contains	II	tBOSU67					Unknown	LIPO	SpII
WP_012476690.1	LEPBI_RS18135		alginate export famil	II	tBOSU69	WP_000686593.1	0.528011			OuterMembrane	SP	SpI
WP_012476691.1	LEPBI_RS18145		ankyrin repeat domai	II	tBOSU70					Cytoplasmic	LIPO	SpII
WP_012476694.1	LEPBI_RS18150		hypothetical protein	II	tBOSU73					Unknown	LIPO	CYT
WP_012476696.1	LEPBI_RS18160		SH3 domain-contains	II	tBOSU75					Unknown	SP	SpI
WP_012476697.1	LEPBI_RS18165		hypothetical protein	II	tBOSU76					Cytoplasmic	SP	CYT
WP_012476698.1	LEPBI_RS18170		hypothetical protein	II	tBOSU77					Unknown	LIPO	SpII
WP_012476699.1	LEPBI_RS18175		hypothetical protein	II	tBOSU78					Unknown	LIPO	SpII
WP_012476701.1	LEPBI_RS18185		ZIP family metal tran	II	tBOSU80				P	CytoplasmicMembrane	NO_SP	TMH
WP_012476853.1	LEPBI_RS18190		hypothetical protein	II	tBOSU81					CytoplasmicMembrane	SP	SpI
WP_012476703.1	LEPBI_RS18195		hypothetical protein	II	tBOSU82					Unknown	SP	SpI
WP_012476704.1	LEPBI_RS18200		elongation factor P--(f	II	tBOSU83	WP_002142465.1	0.52147680000000001		J	Cytoplasmic	NO_SP	CYT
WP_012476854.1	LEPBI_RS18205		hypothetical protein	II	tBOSU84					Cytoplasmic	NO_SP	CYT
WP_012476706.1	LEPBI_RS18210		DUF4279 domain-con	II	tBOSU85	WP_000070243.1	0.4279773			Unknown	NO_SP	CYT
WP_012476707.1	LEPBI_RS18215		response regulator trc	II	tBOSU86	WP_000849259.1	0.90666		T	Cytoplasmic	NO_SP	CYT
WP_041770226.1	LEPBI_RS18220		DUF883 family protei	II						Unknown	NO_SP	CYT
WP_012476711.1	LEPBI_RS18235		divalent-cation tolera	II	tBOSU90				P	Cytoplasmic	NO_SP	CYT
WP_012476712.1	LEPBI_RS18240		winged helix-turn-heli	II	tBOSU91					Unknown	NO_SP	CYT
WP_041770259.1	LEPBI_RS18245		SRPBCC domain-conta	II	tBOSU92					Cytoplasmic	NO_SP	CYT
WP_041770228.1	LEPBI_RS18250		YdeI/OmpD-associate	II	tBOSU93				S	Unknown	NO_SP	CYT
WP_012476856.1	LEPBI_RS18260		nicotinamide mononu	II	tBOSU95				H	CytoplasmicMembrane	NO_SP	TMH
WP_012476717.1	LEPBI_RS18265		class I SAM-dependen	II	tBOSU96	WP_000668264.1	0.5310326			Cytoplasmic	NO_SP	CYT
WP_187148115.1	LEPBI_RS18270		hypothetical protein	II	tBOSU97					Cytoplasmic	NO_SP	CYT
WP_012476719.1	LEPBI_RS18275		aconitate hydratase	II	tBOSU98	WP_000863312.1	0.80825085		C	Cytoplasmic	NO_SP	CYT
WP_041770260.1	LEPBI_RS18280		curli production assen	II	tBOSU99					Cytoplasmic	LIPO	TMH
WP_012476721.1	LEPBI_RS18285		hypothetical protein	II	tBOSUA0					Unknown	NO_SP	SpI

WP_012476722.1	LEPBI_RS18290	queA	tRNA preQ1(34) S-ade	chromosome	II	tBOSUA1	WP_000897626.1	0.57948285	J	Cytoplasmic	NO_SP	CYT
WP_012476857.1	LEPBI_RS18300		glycosyltransferase fa	chromosome	II	tBOSUA3	WP_001122447.1	0.53235525	M	Cytoplasmic	NO_SP	CYT
WP_012476725.1	LEPBI_RS18305		hypothetical protein	chromosome	II	tBOSUA4	WP_000812265.1	0.28875		CytoplasmicMembrane	NO_SP	CYT
WP_012476726.1	LEPBI_RS18310		hypothetical protein	chromosome	II	tBOSUA5	WP_000632699.1	0.5073165000000001		CytoplasmicMembrane	NO_SP	SpI
WP_012476727.1	LEPBI_RS18315		MBOAT family proteir	chromosome	II	tBOSUA6	WP_000898540.1	0.684365	M	CytoplasmicMembrane	NO_SP	TMH
WP_012476728.1	LEPBI_RS18320		hypothetical protein	chromosome	II	tBOSUA7	WP_000666150.1	0.4968528		Cytoplasmic	NO_SP	CYT
WP_012476729.1	LEPBI_RS18325		nucleotide pyrophosp	chromosome	II	tBOSUA8	WP_001004759.1	0.7481123999999999		Unknown	NO_SP	CYT
WP_012476730.1	LEPBI_RS18330		hypothetical protein	chromosome	II	tBOSUA9				Cytoplasmic	NO_SP	CYT
WP_012476731.1	LEPBI_RS18335		hypothetical protein	chromosome	II	tBOSUB0				Unknown	LIPO	CYT
WP_012476858.1	LEPBI_RS18340		kelch-like protein	chromosome	II	tBOSUB1				Unknown	LIPO	SpII
WP_012476859.1	LEPBI_RS18345		kelch repeat-containir	chromosome	II	tBOSUB2				Unknown	SP	SpII
WP_012476734.1	LEPBI_RS18350		caspace family proteir	chromosome	II	tBOSUB3				CytoplasmicMembrane	SP	SpI
WP_012476735.1	LEPBI_RS18355		chemotaxis protein	chromosome	II	tBOSUB4			T	CytoplasmicMembrane	NO_SP	TMH
WP_012476736.1	LEPBI_RS18360		pirin family protein	chromosome	II	tBOSUB5			R	Cytoplasmic	NO_SP	CYT
WP_012476738.1	LEPBI_RS18365		PDZ domain-containir	chromosome	II	tBOSUB7			O	CytoplasmicMembrane	LIPO	CYT
WP_012476739.1	LEPBI_RS18370		carbonic anhydrase	chromosome	II	tBOSUB8			P	Cytoplasmic	SP	SpI
WP_012476740.1	LEPBI_RS18375		sodium-dependent bi	chromosome	II	tBOSUB9			S	CytoplasmicMembrane	NO_SP	TMH
WP_041770232.1	LEPBI_RS18380		hypothetical protein	chromosome	II	tBOSUC0				Unknown	NO_SP	CYT
WP_012476742.1	LEPBI_RS18385		BamA/TamA family o	chromosome	II	tBOSUC1	WP_001079689.1	0.5219182		OuterMembrane	SP	CYT
WP_012476743.1	LEPBI_RS18390	pyk	pyruvate kinase	chromosome	II	tBOSUC2	WP_000834388.1	0.776784	G	Cytoplasmic	NO_SP	CYT
WP_012476744.1	LEPBI_RS18395		hypothetical protein	chromosome	II	tBOSUC3	WP_000892881.1	0.5217		Cytoplasmic	NO_SP	CYT
WP_012476745.1	LEPBI_RS18400	asd	aspartate-semialdehy	chromosome	II	tBOSUC4	WP_000092003.1	0.8235612	E	Cytoplasmic	NO_SP	CYT
WP_012476746.1	LEPBI_RS18405		hypothetical protein	chromosome	II	tBOSUC5	WP_000057258.1	0.5346709500000001		Unknown	NO_SP	TMH
WP_012476747.1	LEPBI_RS18410		MBOAT family proteir	chromosome	II	tBOSUC6	WP_002146066.1	0.5146054999999999	M	CytoplasmicMembrane	NO_SP	TMH
WP_012476750.1	LEPBI_RS18420		hypothetical protein	chromosome	II	tBOSUC9	WP_001968786.1	0.6501328000000001		Cytoplasmic	NO_SP	CYT
WP_041770235.1	LEPBI_RS18425		transcriptional regulat	chromosome	II	tBOSUD0	WP_000931504.1	0.420641		Unknown	NO_SP	CYT
WP_012476510.1	LEPBI_RS18990		hypothetical protein	chromosome	II	tBOSTN7	WP_000395725.1	0.4319704		Unknown	SP	SpI
WP_081431684.1	LEPBI_RS18995	rpmG	50S ribosomal protein	chromosome	II		WP_001206796.1	0.712975		Unknown	NO_SP	CYT
WP_081431686.1	LEPBI_RS19005		hypothetical protein	chromosome	II		WP_000852544.1	0.788715		Unknown	NO_SP	CYT
WP_012476748.1	LEPBI_RS19010		hypothetical protein	chromosome	II	tBOSUC7	WP_000157338.1	0.5502576		Unknown	NO_SP	CYT
WP_012476752.1	LEPBI_RS18430		ParA family protein	plasmid	p74	tBOSUD1			D	Cytoplasmic	NO_SP	CYT
WP_012476753.1	LEPBI_RS18435		ParB/RepB/SpoOJ fam	plasmid	p74	tBOSUD2			D	Cytoplasmic	NO_SP	CYT
WP_041770281.1	LEPBI_RS18445		helix-turn-helix domai	plasmid	p74	tBOSUD3				Unknown	NO_SP	CYT
WP_012476755.1	LEPBI_RS18450		hypothetical protein	plasmid	p74	tBOSUD4				Unknown	NO_SP	CYT
WP_012476756.1	LEPBI_RS18455		TetR/AcrR family tran	plasmid	p74	tBOSUD5				Cytoplasmic	NO_SP	CYT
WP_012476757.1	LEPBI_RS18460		Paal family thioestera	plasmid	p74	tBOSUD6	WP_000116457.1	0.3890197		CytoplasmicMembrane	NO_SP	CYT
WP_012476863.1	LEPBI_RS18465		TetR/AcrR family tran	plasmid	p74	tBOSUD7				Cytoplasmic	NO_SP	CYT
WP_012476864.1	LEPBI_RS18470		pyrimidine/purine nu	plasmid	p74	tBOSUD8	WP_000077234.1	0.6780396999999999	F	Unknown	NO_SP	CYT
WP_012476865.1	LEPBI_RS18475		YegP family protein	plasmid	p74	tBOSUD9			S	Unknown	NO_SP	CYT
WP_012476761.1	LEPBI_RS18480		SpoIIE family protein	plasmid	p74	tBOSUE0			T	CytoplasmicMembrane	LIPO	SpII
WP_012476762.1	LEPBI_RS18485		histidine kinase	plasmid	p74	tBOSUE1			T	CytoplasmicMembrane	NO_SP	TMH
WP_012476763.1	LEPBI_RS18490		hemin-degrading fact	plasmid	p74	tBOSUE2			P	Cytoplasmic	NO_SP	CYT
WP_012476764.1	LEPBI_RS18495		heme ABC transport	plasmid	p74	tBOSUE3			P	CytoplasmicMembrane	NO_SP	CYT
WP_012476765.1	LEPBI_RS18500		iron ABC transporter	plasmid	p74	tBOSUE4			P	CytoplasmicMembrane	NO_SP	TMH

WP_012476766.1	LEPBI_RS18505		ABC transporter subst	plasmid	p74	tBOSUE5			P	Unknown	NO_SP	CYT
WP_012476767.1	LEPBI_RS18510		hypothetical protein	plasmid	p74	tBOSUE6				Unknown	LIPO	SpII
WP_012476768.1	LEPBI_RS18515		HmuY family protein	plasmid	p74	tBOSUE7				Extracellular	NO_SP	CYT
WP_081431688.1	LEPBI_RS18520		TonB-dependent rece	plasmid	p74	tBOSUE8			H	OuterMembrane	SP	CYT
WP_012476770.1	LEPBI_RS18525	recD	exodeoxyribonuclease	plasmid	p74	tBOSUE9	WP_000503851.1	0.46734825	L	Cytoplasmic	NO_SP	CYT
WP_012476771.1	LEPBI_RS18530		UvrD-helicase domain	plasmid	p74	tBOSUF0	WP_001103176.1	0.52277665	L	Cytoplasmic	NO_SP	CYT
WP_012476773.1	LEPBI_RS18540		alpha/beta hydrolase	plasmid	p74	tBOSUF2				CytoplasmicMembrane	LIPO	SpII
WP_041770288.1	LEPBI_RS18545		AraC family transcript	plasmid	p74	tBOSUF3				CytoplasmicMembrane	NO_SP	TMH
WP_012476775.1	LEPBI_RS18550		hypothetical protein	plasmid	p74	tBOSUF4				Cytoplasmic	NO_SP	CYT
WP_012476776.1	LEPBI_RS18555		hypothetical protein	plasmid	p74	tBOSUF5				Unknown	NO_SP	CYT
WP_012476777.1	LEPBI_RS18560		DUF1738 domain-con	plasmid	p74	tBOSUF6			L	Cytoplasmic	NO_SP	CYT
WP_012476869.1	LEPBI_RS18565		ISNCY-like element ISl	plasmid	p74	tBOSUF7				Cytoplasmic	NO_SP	CYT
WP_012476779.1	LEPBI_RS18570		hypothetical protein	plasmid	p74	tBOSUF8				Unknown	NO_SP	CYT
WP_012476870.1	LEPBI_RS18575		hypothetical protein	plasmid	p74	tBOSUF9				Unknown	SP	SpI
WP_143708659.1	LEPBI_RS18580		hypothetical protein	plasmid	p74	tBOSUG0				Cytoplasmic	NO_SP	CYT
WP_012476872.1	LEPBI_RS18585		phage Gp37/Gp68 fan	plasmid	p74	tBOSUG1	WP_000501018.1	0.5482847999999999	X	Cytoplasmic	NO_SP	CYT
WP_012476783.1	LEPBI_RS18590	tcmP	three-Cys-motif partn	plasmid	p74	tBOSUG2				Cytoplasmic	NO_SP	CYT
WP_012476784.1	LEPBI_RS18595		DEAD/DEAH box helic	plasmid	p74	tBOSUG3			R	Cytoplasmic	NO_SP	CYT
WP_012476787.1	LEPBI_RS18605		hypothetical protein	plasmid	p74	tBOSUG6				Unknown	NO_SP	CYT
WP_012476788.1	LEPBI_RS18610		hypothetical protein	plasmid	p74	tBOSUG7				Cytoplasmic	NO_SP	CYT
WP_012476789.1	LEPBI_RS18615		HEAT repeat domain- $\alpha$	plasmid	p74	tBOSUG8				Cytoplasmic	SP	CYT
WP_012476790.1	LEPBI_RS18620		hypothetical protein	plasmid	p74	tBOSUG9				CytoplasmicMembrane	LIPO	SpII
WP_012476791.1	LEPBI_RS18625		DUF167 domain-cont	plasmid	p74	tBOSUH0				Unknown	NO_SP	CYT
WP_012476873.1	LEPBI_RS18630		ABC transporter ATP-t	plasmid	p74	tBOSUH1			M	CytoplasmicMembrane	NO_SP	CYT
WP_012476793.1	LEPBI_RS18635		FtsX-like permease fa	plasmid	p74	tBOSUH2				CytoplasmicMembrane	NO_SP	CYT
WP_012476794.1	LEPBI_RS18640		efflux RND transporte	plasmid	p74	tBOSUH3				Cytoplasmic	NO_SP	CYT
WP_041770303.1	LEPBI_RS18645		PAS domain S-box pro	plasmid	p74	tBOSUH4			T	CytoplasmicMembrane	NO_SP	TMH
WP_012476796.1	LEPBI_RS18650		TetR/AcrR family tran	plasmid	p74	tBOSUH5				Cytoplasmic	NO_SP	CYT
WP_012476797.1	LEPBI_RS18655		dihydrofolate reducta	plasmid	p74	tBOSUH6			H	Cytoplasmic	NO_SP	CYT
WP_012476798.1	LEPBI_RS18660		type II toxin-antitoxin	plasmid	p74	tBOSUH7				Unknown	NO_SP	CYT
WP_012476799.1	LEPBI_RS18665		PIN domain-containin	plasmid	p74	tBOSUH8				Unknown	NO_SP	CYT
WP_012476800.1	LEPBI_RS18670		RNA methyltransferas	plasmid	p74	tBOSUH9			J	Cytoplasmic	NO_SP	CYT
WP_012476801.1	LEPBI_RS18675		serine/threonine prot	plasmid	p74	tBOSUI0	WP_000753043.1	0.5204727	T	Cytoplasmic	NO_SP	CYT
WP_012476802.1	LEPBI_RS18680		diguanylate cyclase	plasmid	p74	tBOSUI1	WP_000377275.1	0.5196629500000001	T	Cytoplasmic	NO_SP	CYT
WP_012476803.1	LEPBI_RS18685		hypothetical protein	plasmid	p74	tBOSUI2				CytoplasmicMembrane	LIPO	SpII
WP_012476804.1	LEPBI_RS18690		hypothetical protein	plasmid	p74	tBOSUI3				Unknown	LIPO	CYT
WP_012476805.1	LEPBI_RS18695		glucan biosynthesis pr	plasmid	p74	tBOSUI4			M	Unknown	NO_SP	CYT
WP_012476875.1	LEPBI_RS18700		hypothetical protein	plasmid	p74	tBOSUI5				CytoplasmicMembrane	NO_SP	CYT
WP_012476807.1	LEPBI_RS18705	mdoH	glucans biosynthesis g	plasmid	p74	tBOSUI6			M	CytoplasmicMembrane	NO_SP	TMH
WP_012476808.1	LEPBI_RS18710		alpha/beta fold hydro	plasmid	p74	tBOSUI7	WP_000625202.1	0.49372559999999993	R	Cytoplasmic	NO_SP	CYT
WP_012476809.1	LEPBI_RS18715		hypothetical protein	plasmid	p74	tBOSUI8				Unknown	LIPO	SpII
WP_012476876.1	LEPBI_RS18720		helix-turn-helix domai	plasmid	p74	tBOSUI9				Cytoplasmic	NO_SP	CYT

**Table S2. *L. interrogans* proteins (1,109) classified into low conserved (543) in *L. biflexa* and specific (566) in pathogenic strain**

ID NCBI	ID UniProt	C-values	Protein
WP_000004000.1	Q72RJ2	0.5	low conserved
WP_000008630.1	Q75FW5	0.5	low conserved
WP_000010969.1	Q72NT1	0.5	low conserved
WP_000011406.1	Q75FE7	0.5	low conserved
WP_000013232.1	Q75F11	0.5	low conserved
WP_000014283.1	Q72PC5	0.5	low conserved
WP_000017889.1	Q72R74	0.5	low conserved
WP_000018492.1	Q72SB6	0.5	low conserved
WP_000020273.1	Q72LZ1	0.5	low conserved
WP_000022300.1	Q72U60	0.5	low conserved
WP_000033675.1	Q72U90	0.5	low conserved
WP_000039575.1	Q72TA9	0.5	low conserved
WP_000047876.1	Q72U64	0.5	low conserved
WP_000050531.1	Q75FN4	0.5	low conserved
WP_000050593.1	Q72VR8	0.5	low conserved
WP_000054119.1	Q72M88	0.5	low conserved
WP_000054706.1	Q72QN3	0.5	low conserved
WP_000061045.1	Q72M58	0.5	low conserved
WP_000066266.1	Q72RP3	0.5	low conserved
WP_000068280.1	Q72T44	0.5	low conserved
WP_000086813.1	Q75G06	0.5	low conserved
WP_000088543.1	Q72M23	0.5	low conserved
WP_000088841.1	Q72M52	0.5	low conserved
WP_000095033.1	Q72RF9	0.5	low conserved
WP_000099422.1	Q72QY5	0.5	low conserved
WP_000134554.1	Q72PK4	0.5	low conserved
WP_000135393.1	Q72PS1	0.5	low conserved
WP_000141650.1	Q72RB0	0.5	low conserved
WP_000141824.1	Q72MF6	0.5	low conserved
WP_000143821.1	Q72Q66	0.5	low conserved
WP_000143898.1	Q72M12	0.5	low conserved
WP_000145205.1	Q72W84	0.5	low conserved
WP_000155537.1	Q72W21	0.5	low conserved
WP_000165932.1	Q72Q91	0.5	low conserved
WP_000166979.1	Q72R97	0.5	low conserved
WP_000174861.1	Q72T78	0.5	low conserved
WP_000176746.1	Q72T71	0.5	low conserved
WP_000180222.1	Q72QA1	0.5	low conserved
WP_000184345.1	Q72UN9	0.5	low conserved
WP_000184524.1	Q72TE0	0.5	low conserved
WP_000185977.1	Q72R18	0.5	low conserved
WP_000188441.1	Q72TB1	0.5	low conserved
WP_000219378.1	Q72RX7	0.5	low conserved
WP_000230450.1	Q72RZ8	0.5	low conserved
WP_000242794.1	Q72RG1	0.5	low conserved
WP_000254988.1	Q72Q08	0.5	low conserved
WP_000257883.1	Q72RG6	0.5	low conserved
WP_000264232.1	Q72PN9	0.5	low conserved
WP_000277167.1	Q72MB2	0.5	low conserved
WP_000277382.1	Q75FT9	0.5	low conserved
WP_000291493.1	Q72NY5	0.5	low conserved
WP_000332925.1	Q72PI4	0.5	low conserved
WP_000333575.1	Q72U93	0.5	low conserved
WP_000339988.1	Q72W03	0.5	low conserved
WP_000348938.1	Q72PG6	0.5	low conserved
WP_000358377.1	Q72S36	0.5	low conserved
WP_000365849.1	Q72PL2	0.5	low conserved
WP_000365940.1	Q72S62	0.5	low conserved

WP_000366324.1	Q72MF1	0.5	low conserved
WP_000367570.1	Q75FV5	0.5	low conserved
WP_000377275.1	Q72SD9	0.5	low conserved
WP_000377539.1	Q72R85	0.5	low conserved
WP_000384982.1	Q72SG7	0.5	low conserved
WP_000388230.1	Q72UR6	0.5	low conserved
WP_000389571.1	Q72VU4	0.5	low conserved
WP_000391163.1	Q72LY1	0.5	low conserved
WP_000393930.1	Q72MK6	0.5	low conserved
WP_000402080.1	Q72S59	0.5	low conserved
WP_000420355.1	Q72WA7	0.5	low conserved
WP_000423512.1	Q72ME8	0.5	low conserved
WP_000433740.1	Q72V17	0.5	low conserved
WP_000435437.1	Q72MA3	0.5	low conserved
WP_000444199.1	Q72TG0	0.5	low conserved
WP_000444207.1	Q72W86	0.5	low conserved
WP_000445616.1	P62472	0.5	low conserved
WP_000446221.1	Q72VZ2	0.5	low conserved
WP_000447930.1	Q72R31	0.5	low conserved
WP_000453665.1	Q72V86	0.5	low conserved
WP_000455556.1	Q72VM7	0.5	low conserved
WP_000455718.1	Q72N44	0.5	low conserved
WP_000457083.1	Q72PW8	0.5	low conserved
WP_000459763.1	Q72LS6	0.5	low conserved
WP_000470536.1	Q72RK9	0.5	low conserved
WP_000471275.1	Q72S09	0.5	low conserved
WP_000475904.1	Q72QH2	0.5	low conserved
WP_000479265.1	Q72US6	0.5	low conserved
WP_000485070.1	Q72RY6	0.5	low conserved
WP_000487747.1	Q72PN5	0.5	low conserved
WP_000488503.1	Q72VI3	0.5	low conserved
WP_000490756.1	Q72NC6	0.5	low conserved
WP_000492446.1	Q75FM6	0.5	low conserved
WP_000499591.1	Q75G03	0.5	low conserved
WP_000503851.1	Q72NZZ	0.5	low conserved
WP_000510657.1	Q72S86	0.5	low conserved
WP_000512778.1	Q72LY7	0.5	low conserved
WP_000523717.1	Q72SX5	0.5	low conserved
WP_000528391.1	Q75FK2	0.5	low conserved
WP_000531352.1	Q72QT5	0.5	low conserved
WP_000532389.1	Q75FZ9	0.5	low conserved
WP_000545443.1	Q72NU9	0.5	low conserved
WP_000572205.1	Q72W96	0.5	low conserved
WP_000582255.1	Q72SH0	0.5	low conserved
WP_000586914.1	Q72Q16	0.5	low conserved
WP_000599986.1	Q75FN7	0.5	low conserved
WP_000604091.1	Q72TV4	0.5	low conserved
WP_000604760.1	Q72VH1	0.5	low conserved
WP_000610519.1	Q72WC6	0.5	low conserved
WP_000612752.1	Q72S71	0.5	low conserved
WP_000615876.1	Q72TF5	0.5	low conserved
WP_000616634.1	Q72W07	0.5	low conserved
WP_000621271.1	Q72RV6	0.5	low conserved
WP_000621805.1	Q72RB1	0.5	low conserved
WP_000623631.1	Q72TE7	0.5	low conserved
WP_000625202.1	Q72MW2	0.5	low conserved
WP_000625234.1	Q72V75	0.5	low conserved
WP_000626110.1	Q72M81	0.5	low conserved
WP_000627565.1	Q72UD1	0.5	low conserved
WP_000628885.1	Q72QX6	0.5	low conserved
WP_000638432.1	Q72RG7	0.5	low conserved

WP_000640630.1	Q72UX8	0.5	low conserved
WP_000646914.1	Q72VV2	0.5	low conserved
WP_000649925.1	Q72VU3	0.5	low conserved
WP_000651714.1	Q72RG3	0.5	low conserved
WP_000656232.1	Q72SP5	0.5	low conserved
WP_000657518.1	Q72RR0	0.5	low conserved
WP_000657852.1	Q72P28	0.5	low conserved
WP_000658622.1	Q72VU6	0.5	low conserved
WP_000662272.1	Q72UA2	0.5	low conserved
WP_000664912.1	Q72M55	0.5	low conserved
WP_000666150.1	Q75FL7	0.5	low conserved
WP_000668264.1	Q75FX1	0.5	low conserved
WP_000669547.1	Q72UY4	0.5	low conserved
WP_000671558.1	Q72NP4	0.5	low conserved
WP_000671644.1	Q72NB2	0.5	low conserved
WP_000675685.1	Q72SB0	0.5	low conserved
WP_000675807.1	Q72QN4	0.5	low conserved
WP_000678902.1	Q72MY9	0.5	low conserved
WP_000684121.1	Q72Q82	0.5	low conserved
WP_000684307.1	Q72N62	0.5	low conserved
WP_000687885.1	Q72P41	0.5	low conserved
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WP_000680449.1	Q72NK0	0.3	low conserved
WP_000733128.1	Q72PI2	0.3	low conserved
WP_000742170.1	Q72UC8	0.3	low conserved
WP_000779912.1	Q75FF9	0.3	low conserved
WP_000812265.1	Q75FM0	0.3	low conserved
WP_000821095.1	Q72VJ5	0.3	low conserved
WP_000832927.1	Q72M77	0.3	low conserved
WP_000836305.1	Q72U95	0.3	low conserved
WP_000850434.1	Q75G22	0.3	low conserved
WP_000896013.1	Q72U86	0.3	low conserved
WP_000945708.1	Q72WC5	0.3	low conserved
WP_001069019.1	Q72VV3	0.3	low conserved
WP_001095794.1	Q75FM2	0.3	low conserved
WP_001100379.1	Q72PN8	0.3	low conserved
WP_001104455.1	Q72UB9	0.3	low conserved
WP_001119768.1	Q72N12	0.3	low conserved
WP_001129541.1	Q72Q64	0.3	low conserved
WP_001202539.1	Q72R36	0.3	low conserved
WP_001226846.1	Q75FM9	0.3	low conserved
WP_001250026.1	Q72PU0	0.3	low conserved
WP_001281703.1	Q72RT2	0.3	low conserved
WP_001978935.1	Q72MQ5	0.3	low conserved
WP_002070138.1	Q72VH9	0.3	low conserved
WP_011172165.1	Q72T06	0.3	low conserved
WP_000394962.1	Q72RT6	0.2	low conserved
WP_000002712.1	Q72Q65	—	specific
WP_000007034.1	Q75G09	—	specific
WP_000007538.1	Q72QG7	—	specific

WP_000007746.1	Q72QV0	—	specific
WP_000010627.1	Q72PH0	—	specific
WP_000013299.1	Q72MS5	—	specific
WP_000013893.1	Q72UM8	—	specific
WP_000014613.1	Q72PZ2	—	specific
WP_000017270.1	Q72P71	—	specific
WP_000017970.1	Q72M82	—	specific
WP_000018463.1	Q72PK2	—	specific
WP_000026697.1	Q72UI9	—	specific
WP_000028195.1	Q72PY6	—	specific
WP_000032804.1	Q72S88	—	specific
WP_000033195.1	Q72W24	—	specific
WP_000033739.1	Q72LZ8	—	specific
WP_000040881.1	Q72MF4	—	specific
WP_000041838.1	Q72P23	—	specific
WP_000042605.1	Q72R02	—	specific
WP_000045337.1	Q72VY4	—	specific
WP_000045629.1	Q72UJ5	—	specific
WP_000050431.1	Q72QH9	—	specific
WP_000051773.1	Q72T39	—	specific
WP_000052101.1	Q72TT1	—	specific
WP_000052874.1	Q72RH5	—	specific
WP_000053472.1	Q72RM9	—	specific
WP_000053804.1	Q72VK2	—	specific
WP_000054152.1	Q75FF5	—	specific
WP_000054457.1	Q72NF6	—	specific
WP_000058820.1	Q72UM2	—	specific
WP_000060053.1	Q72T25	—	specific
WP_000076448.1	Q75FY1	—	specific
WP_000076961.1	Q72NU2	—	specific
WP_000080465.1	Q75FY3	—	specific
WP_000082164.1	Q72MK0	—	specific
WP_000083101.1	Q72TT6	—	specific
WP_000085100.1	Q72R28	—	specific
WP_000087787.1	Q72VD4	—	specific
WP_000088214.1	Q72QS7	—	specific
WP_000098500.1	P62392	—	specific
WP_000102691.1	Q75G30	—	specific
WP_000103483.1	Q72VX0	—	specific
WP_000118553.1	Q72MI3	—	specific
WP_000119461.1	Q72M91	—	specific
WP_000126723.1	Q72TU8	—	specific
WP_000129836.1	Q72PZ4	—	specific
WP_000132016.1	Q72QD5	—	specific
WP_000132506.1	Q72QA5	—	specific
WP_000135118.1	Q72MX3	—	specific
WP_000135500.1	Q72SA2	—	specific
WP_000141537.1	Q72TT8	—	specific
WP_000141840.1	Q72VH5	—	specific
WP_000142586.1	Q72ST4	—	specific
WP_000147223.1	Q72VH6	—	specific
WP_000147970.1	Q72UM5	—	specific
WP_000149359.1	Q72P72	—	specific
WP_000160087.1	Q75FP9	—	specific
WP_000171192.1	Q72P69	—	specific
WP_000172726.1	Q72MQ6	—	specific
WP_000173137.1	Q72SS6	—	specific
WP_000180853.1	Q72T93	—	specific
WP_000183410.1	Q72N57	—	specific
WP_000186016.1	Q72U58	—	specific
WP_000194186.1	Q72RV4	—	specific

WP_000199612.1	Q72TT5	—	specific
WP_000201659.1	Q72SI4	—	specific
WP_000202830.1	Q72QE6	—	specific
WP_000202854.1	Q72SF1	—	specific
WP_000207444.1	Q72QZ7	—	specific
WP_000224794.1	Q72P81	—	specific
WP_000230454.1	Q72N09	—	specific
WP_000234636.1	Q72LW3	—	specific
WP_000250738.1	Q72VZ7	—	specific
WP_000253510.1	Q72V29	—	specific
WP_000257955.1	Q72P74	—	specific
WP_000273657.1	Q72P31	—	specific
WP_000282526.1	Q72PT7	—	specific
WP_000284396.1	Q72VK3	—	specific
WP_000286838.1	Q72QT7	—	specific
WP_000289498.1	Q72QH6	—	specific
WP_000291460.1	Q72NV3	—	specific
WP_000291894.1	Q72PE0	—	specific
WP_000332802.1	Q72ST6	—	specific
WP_000337318.1	Q72VN7	—	specific
WP_000342713.1	Q72QB7	—	specific
WP_000344487.1	Q72QC6	—	specific
WP_000345313.1	Q72SG2	—	specific
WP_000346036.1	Q72QE4	—	specific
WP_000346055.1	Q72N26	—	specific
WP_000348685.1	Q72WB0	—	specific
WP_000355766.1	Q72MN1	—	specific
WP_000359684.1	Q72VV9	—	specific
WP_000359691.1	Q72VV7	—	specific
WP_000360484.1	Q72PZ8	—	specific
WP_000365024.1	Q72PC1	—	specific
WP_000365439.1	Q72S99	—	specific
WP_000367388.1	Q72P49	—	specific
WP_000371344.1	Q72TT2	—	specific
WP_000372769.1	Q72MV6	—	specific
WP_000372824.1	Q72QS6	—	specific
WP_000377029.1	Q72VS0	—	specific
WP_000389641.1	Q72NX3	—	specific
WP_000389996.1	Q72U26	—	specific
WP_000391357.1	Q72N59	—	specific
WP_000392377.1	Q75FR7	—	specific
WP_000393747.1	Q72PZ7	—	specific
WP_000409183.1	Q75FV3	—	specific
WP_000412038.1	Q72VW0	—	specific
WP_000412073.1	Q72UL4	—	specific
WP_000412628.1	Q72MV0	—	specific
WP_000414123.1	Q72PZ3	—	specific
WP_000416252.1	Q72RJ8	—	specific
WP_000421034.1	Q72PB8	—	specific
WP_000425207.1	Q72S83	—	specific
WP_000426795.1	Q72N37	—	specific
WP_000429218.1	Q72SF0	—	specific
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WP_000435433.1	Q72PY8	—	specific
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WP_000444619.1	Q72PY9	—	specific
WP_000445974.1	Q72RN9	—	specific
WP_000445979.1	Q72VX5	—	specific
WP_000447937.1	Q72PU6	—	specific



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WP_000449386.1	Q72TH6	—	specific
WP_000450441.1	Q75FS3	—	specific
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WP_000460443.1	Q72MF2	—	specific
WP_000465279.1	Q72P27	—	specific
WP_000465640.1	Q75FP6	—	specific
WP_000468940.1	Q72ME1	—	specific
WP_000471762.1	Q72SE3	—	specific
WP_000472806.1	Q72TK9	—	specific
WP_000472812.1	Q72R05	—	specific
WP_000479982.1	Q72QB9	—	specific
WP_000483735.1	Q72TN2	—	specific
WP_000486431.1	Q72RU6	—	specific
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WP_000487353.1	Q72RX6	—	specific
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WP_000488902.1	Q72S63	—	specific
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WP_000492789.1	Q72SV1	—	specific
WP_000497855.1	Q72VW5	—	specific
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WP_000502132.1	Q72NE1	—	specific
WP_000505755.1	Q72ST0	—	specific
WP_000508128.1	Q72TK7	—	specific
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WP_000516668.1	Q72UV6	—	specific
WP_000517242.1	Q72QC2	—	specific
WP_000517492.1	Q72R99	—	specific
WP_000528830.1	Q72PX8	—	specific
WP_000529175.1	Q72M37	—	specific
WP_000536762.1	Q72S89	—	specific
WP_000539242.1	Q72T99	—	specific
WP_000539780.1	Q72PY5	—	specific
WP_000547427.1	Q72QF1	—	specific
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WP_000559149.1	Q72QW5	—	specific
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WP_000568675.1	Q72SE4	—	specific
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WP_000569939.1	Q72NE6	—	specific
WP_000570103.1	Q72PK1	—	specific
WP_000570492.1	Q72SD6	—	specific
WP_000570772.1	Q72N64	—	specific
WP_000579813.1	Q72QD3	—	specific
WP_000579997.1	Q72P68	—	specific
WP_000581337.1	Q72QS8	—	specific
WP_000582618.1	Q72QE3	—	specific
WP_000583389.1	Q72QH0	—	specific
WP_000588682.1	Q72TM4	—	specific
WP_000588742.1	Q72TA8	—	specific
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WP_000594767.1	Q72QP6	—	specific
WP_000595826.1	Q75FM4	—	specific
WP_000600052.1	Q75FT4	—	specific
WP_000600224.1	Q72W35	—	specific
WP_000600889.1	Q72QD6	—	specific
WP_000602773.1	Q72Q99	—	specific
WP_000604355.1	Q72Q32	—	specific
WP_000604524.1	Q72QA8	—	specific
WP_000604736.1	Q72PG5	—	specific

WP_000608295.1	Q72QB5	—	specific
WP_000608695.1	Q72P45	—	specific
WP_000610939.1	Q72RN6	—	specific
WP_000611594.1	Q72QC3	—	specific
WP_000612797.1	Q72QB2	—	specific
WP_000614734.1	Q72P73	—	specific
WP_000615085.1	Q72MJ9	—	specific
WP_000615236.1	Q72RB4	—	specific
WP_000615647.1	Q72R21	—	specific
WP_000615986.1	Q72PQ3	—	specific
WP_000619739.1	Q72MY1	—	specific
WP_000620240.1	Q72VC9	—	specific
WP_000620271.1	Q72WB3	—	specific
WP_000620895.1	Q72LY6	—	specific
WP_000620907.1	Q72SP3	—	specific
WP_000622941.1	Q72V95	—	specific
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WP_000626203.1	Q72LV0	—	specific
WP_000627663.1	Q72RL7	—	specific
WP_000629003.1	Q72P44	—	specific
WP_000636852.1	Q72PZ6	—	specific
WP_000639029.1	Q72SB9	—	specific
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WP_000653315.1	Q72TW2	—	specific
WP_000653730.1	Q72SX0	—	specific
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WP_000656510.1	Q72UL7	—	specific
WP_000657656.1	Q72P67	—	specific
WP_000661932.1	Q72QF8	—	specific
WP_000662440.1	Q72WC0	—	specific
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WP_000666973.1	Q72SP9	—	specific
WP_000667710.1	Q72QZ2	—	specific
WP_000667978.1	Q72SQ5	—	specific
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WP_000669336.1	Q72MY3	—	specific
WP_000670472.1	Q72VX4	—	specific
WP_000670745.1	Q72VI1	—	specific
WP_000671777.1	Q72LZ6	—	specific
WP_000672059.1	Q72SV8	—	specific
WP_000672221.1	Q72V90	—	specific
WP_000672464.1	Q72MA0	—	specific
WP_000672495.1	Q72MY0	—	specific
WP_000674082.1	Q72UZ1	—	specific
WP_000676196.1	Q72P70	—	specific
WP_000676629.1	Q75FX7	—	specific
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WP_000686571.1	Q72QH5	—	specific
WP_000687983.1	Q72VC1	—	specific
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WP_000688790.1	Q72R87	—	specific
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WP_000689751.1	Q72TK2	—	specific
WP_000692782.1	Q72MH1	—	specific
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WP_000701955.1	Q75G15	—	specific
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WP_000703334.1	Q72WA9	—	specific
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WP_000715695.1	Q75FQ5	—	specific
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WP_000719850.1	Q72R62	—	specific
WP_000720585.1	Q72NLO	—	specific
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WP_000760133.1	Q75G13	—	specific
WP_000764096.1	Q72VW4	—	specific
WP_000768559.1	Q72R46	—	specific
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WP_000791177.1	Q72TM9	—	specific
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WP_000792403.1	Q72VB4	—	specific
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WP_000796757.1	Q72SX6	—	specific

WP_000797254.1	Q72SX2	—	specific
WP_000799620.1	Q72UJ3	—	specific
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WP_000809416.1	Q72VC5	—	specific
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WP_000809732.1	Q75FY9	—	specific
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WP_000859768.1	Q72Q74	—	specific
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WP_000869875.1	Q72W69	—	specific
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WP_000875567.1	Q72VD2	—	specific
WP_000876106.1	Q72QI1	—	specific
WP_000876506.1	Q72QA4	—	specific
WP_000879539.1	Q72VQ2	—	specific
WP_000884059.1	Q72QA9	—	specific
WP_000889664.1	Q72SE6	—	specific
WP_000891790.1	Q72V63	—	specific
WP_000895907.1	Q72R42	—	specific
WP_000902962.1	Q72R69	—	specific
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WP_000910559.1	Q72W39	—	specific
WP_000910567.1	Q72PQ4	—	specific

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WP_000913842.1	Q72UF1	—	specific
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WP_000925584.1	Q75FJ2	—	specific
WP_000928001.1	Q72W06	—	specific
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WP_000932549.1	Q72TI6	—	specific
WP_000947844.1	Q72QD7	—	specific
WP_000947957.1	Q72P43	—	specific
WP_000948326.1	Q72US9	—	specific
WP_000949351.1	Q72Q50	—	specific
WP_000950355.1	Q72V99	—	specific
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WP_000959560.1	Q72MN8	—	specific
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WP_000979383.1	Q72SH9	—	specific
WP_000990862.1	Q72P63	—	specific
WP_000992621.1	Q75FF4	—	specific
WP_000993325.1	Q72UJ4	—	specific
WP_000997772.1	Q72NN1	—	specific
WP_000999239.1	Q75FQ1	—	specific
WP_000999362.1	Q72NJ8	—	specific
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WP_001011107.1	Q72TC3	—	specific
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WP_001014491.1	Q72MY4	—	specific
WP_001015422.1	Q72QC4	—	specific
WP_001015698.1	Q72VY2	—	specific
WP_001016431.1	Q72P01	—	specific
WP_001019268.1	Q72NS4	—	specific
WP_001019283.1	Q72RV2	—	specific
WP_001022069.1	Q75FQ8	—	specific
WP_001022640.1	Q72QF7	—	specific
WP_001024049.1	Q72SA3	—	specific
WP_001024125.1	Q72QH3	—	specific
WP_001028883.1	Q72QX3	—	specific
WP_001029784.1	Q75FT5	—	specific
WP_001033987.1	Q72U27	—	specific
WP_001038641.1	Q72VZ8	—	specific
WP_001038648.1	Q72QV3	—	specific
WP_001040162.1	Q72SZ1	—	specific
WP_001045300.1	Q72QG3	—	specific
WP_001045809.1	Q72RN7	—	specific
WP_001046757.1	Q72QE5	—	specific
WP_001049247.1	Q75FI8	—	specific
WP_001049451.1	Q72P94	—	specific
WP_001049563.1	Q72UE4	—	specific
WP_001050075.1	Q72NT9	—	specific

WP_001050103.1	Q72T50	—	specific
WP_001050790.1	Q72MA2	—	specific
WP_001051299.1	Q72T59	—	specific
WP_001052315.1	Q72QD4	—	specific
WP_001052498.1	Q72LW2	—	specific
WP_001052514.1	Q72VW2	—	specific
WP_001053431.1	Q72N43	—	specific
WP_001053462.1	Q72MV9	—	specific
WP_001054050.1	Q72VS1	—	specific
WP_001054393.1	Q75FY4	—	specific
WP_001057349.1	Q72UJ6	—	specific
WP_001060301.1	Q72M93	—	specific
WP_001066610.1	Q72MI6	—	specific
WP_001067557.1	Q72QB3	—	specific
WP_001067923.1	Q72QV8	—	specific
WP_001068355.1	Q75FJ6	—	specific
WP_001068357.1	Q72MZ7	—	specific
WP_001068401.1	Q72TM3	—	specific
WP_001068465.1	Q72QQ0	—	specific
WP_001068672.1	Q72VW8	—	specific
WP_001070328.1	Q72MC0	—	specific
WP_001071214.1	Q72U29	—	specific
WP_001071872.1	Q72P02	—	specific
WP_001074432.1	Q72VS7	—	specific
WP_001075122.1	Q72UK2	—	specific
WP_001077104.1	Q72T18	—	specific
WP_001078557.1	Q72TM6	—	specific
WP_001081287.1	Q72U47	—	specific
WP_001081432.1	Q72VQ5	—	specific
WP_001082704.1	Q72S01	—	specific
WP_001084413.1	Q72T58	—	specific
WP_001084676.1	Q72QI0	—	specific
WP_001085583.1	Q75FD4	—	specific
WP_001087205.1	Q72PX6	—	specific
WP_001087680.1	Q72U69	—	specific
WP_001088078.1	Q72UJ0	—	specific
WP_001088866.1	Q72QC1	—	specific
WP_001089511.1	Q72QZ4	—	specific
WP_001089660.1	Q72QR6	—	specific
WP_001095358.1	Q72UW1	—	specific
WP_001097652.1	Q72T01	—	specific
WP_001104042.1	Q75FD5	—	specific
WP_001104074.1	Q72PF6	—	specific
WP_001105364.1	Q72RV3	—	specific
WP_001106690.1	Q72P76	—	specific
WP_001106774.1	Q72QC9	—	specific
WP_001109419.1	Q72NS0	—	specific
WP_001110347.1	Q72TS0	—	specific
WP_001110981.1	Q72NF7	—	specific
WP_001111376.1	Q72Q80	—	specific
WP_001114267.1	Q72QJ2	—	specific
WP_001124477.1	Q72RR6	—	specific
WP_001128566.1	Q72LZ9	—	specific
WP_001131807.1	Q72S02	—	specific
WP_001136112.1	Q72PS5	—	specific
WP_001148175.1	Q72UT9	—	specific
WP_001151672.1	Q72NU0	—	specific
WP_001153181.1	Q72MV2	—	specific
WP_001153324.1	Q72QJ8	—	specific
WP_001155666.1	Q72PU5	—	specific
WP_001156166.1	Q72M45	—	specific

WP_001158622.1	Q72LW5	—	specific
WP_001159758.1	Q72QI7	—	specific
WP_001162965.1	Q72VW9	—	specific
WP_001165798.1	Q72ST5	—	specific
WP_001166217.1	Q72NK7	—	specific
WP_001166258.1	Q72QX5	—	specific
WP_001169645.1	Q72NQ2	—	specific
WP_001173226.1	Q72P75	—	specific
WP_001173977.1	Q72QS2	—	specific
WP_001177543.1	Q72T21	—	specific
WP_001178919.1	Q72PE8	—	specific
WP_001183580.1	Q72MJ7	—	specific
WP_001186638.1	Q72TD0	—	specific
WP_001188705.1	Q72M95	—	specific
WP_001198107.1	Q72QB4	—	specific
WP_001200973.1	Q72W13	—	specific
WP_001205041.1	Q72W10	—	specific
WP_001206409.1	Q72QD2	—	specific
WP_001208364.1	Q72UP0	—	specific
WP_001208436.1	Q72ND2	—	specific
WP_001211392.1	Q75FI9	—	specific
WP_001211616.1	Q72MK1	—	specific
WP_001213235.1	Q72Q68	—	specific
WP_001221057.1	Q72UE6	—	specific
WP_001221130.1	Q72QP2	—	specific
WP_001222829.1	Q72VX2	—	specific
WP_001224416.1	Q72UZ6	—	specific
WP_001225709.1	Q72M16	—	specific
WP_001226991.1	Q72U30	—	specific
WP_001227922.1	Q72SS9	—	specific
WP_001228945.1	Q72N71	—	specific
WP_001232731.1	Q75FS2	—	specific
WP_001243368.1	Q72VN8	—	specific
WP_001244016.1	Q75FV4	—	specific
WP_001244256.1	Q72UK0	—	specific
WP_001245964.1	Q72N74	—	specific
WP_001246618.1	Q72QB8	—	specific
WP_001250524.1	Q72Q37	—	specific
WP_001253389.1	Q72M30	—	specific
WP_001253849.1	Q72MX9	—	specific
WP_001256841.1	Q72UR1	—	specific
WP_001258732.1	Q72W43	—	specific
WP_001273884.1	Q72U72	—	specific
WP_001276053.1	Q72P61	—	specific
WP_001281681.1	Q75FD8	—	specific
WP_001283178.1	Q75FT8	—	specific
WP_001284494.1	Q72PNO	—	specific
WP_001288326.1	Q72VE7	—	specific
WP_001289449.1	Q72QW0	—	specific
WP_001290019.1	Q72VJ7	—	specific
WP_001291837.1	Q72M63	—	specific
WP_001292110.1	Q75FT3	—	specific
WP_001967625.1	Q72Q35	—	specific
WP_001968824.1	Q75FY2	—	specific
WP_001972941.1	Q72LV8	—	specific
WP_001973894.1	Q72UV9	—	specific
WP_001974506.1	Q72T24	—	specific
WP_001974549.1	Q72T23	—	specific
WP_001978622.1	Q72VU0	—	specific
WP_001982416.1	Q72N06	—	specific
WP_001982901.1	Q75FL5	—	specific

WP_001984210.1	Q72R76	—	specific
WP_001984564.1	Q72W45	—	specific
WP_001987099.1	Q72VF7	—	specific
WP_002080824.1	Q72PQ9	—	specific
WP_002082140.1	Q72QE8	—	specific
WP_002082862.1	Q72P32	—	specific
WP_002093809.1	G1UB65	—	specific
WP_002144337.1	Q72TC4	—	specific
WP_002145819.1	Q72U65	—	specific
WP_002146465.1	Q72QM6	—	specific
WP_011172234.1	Q72R88	—	specific
WP_011172385.1	Q72MI9	—	specific
WP_025176935.1	Q72ST9	—	specific
WP_033108136.1	Q72TT9	—	specific



**Table S3. Protein features of *L. interrogans* (182) that are low conserved in *L. biflexa***

ID Gene	ID UniProt	c-values	SignalP	LipoP	Psortb	CELLO	COG	SMART
LIC_13100	Q72MU2	0.5	—	—	CP		R	Epimerase / DUF1731
LIC_12994	Q72N44	0.5	—	—	CP		—	DUF1577
LIC_12928	Q72NA8	0.5	—	—	CP		—	Lactamase_B
LIC_12707	Q72NX1	0.5	—	—	CP		—	DUF150
LIC_12546	Q72PC5	0.5	—	—	CP		—	DUF1577
LIC_12211	Q72QA1	0.5	—	—	CP		O	HSP20
LIC_11920	Q72R31	0.5	—	—	CP		—	DUF1577
LIC_11731	Q72RL4	0.5	—	—	CP		O	FKBP_C
LIC_11553	Q72S33	0.5	—	—	CP		M	PASTA
LIC_10925	Q72TU1	0.5	—	—	CP		—	Lactamase_B
LIC_10768	Q72U93	0.5	SPI	—	CP		R	Peptidase_M16 / Peptidase_M16_C
LIC_10581	Q72US6	0.5	—	—	CP		E	Peptidase_C26 / GATase
LIC_10134	Q72W07	0.5	—	—	CP		—	DUF3095
LIC_10053	Q72W84	0.5	—	—	CP		—	TPR
LIC_20092	Q75FT9	0.5	—	—	CP		R	Peptidase_M61
LIC_12482	Q72PI9	0.5	—	—	CMP		T	HAMP / MA
LIC_12433	Q72PN5	0.5	—	—	CMP		M	DUF229 / Sulfatase
LIC_12289	Q72Q25	0.5	SPII	SPII	CMP		—	TRL
LIC_11753	Q72RJ2	0.5	—	—	CMP		—	Wzy_C
LIC_11691	Q72RQ3	0.5	—	—	CMP		T	MA
LIC_11329	Q72SP6	0.5	—	—	CMP		—	Virul_fac_BrkB
LIC_11060	Q72TG1	0.5	—	—	CMP		S	DUF389
LIC_10815	Q72U49	0.5	—	—	CMP		M	DUF218
LIC_10115	Q72W26	0.5	—	SPI	CMP		—	VKc / DSBA / Thioredoxin_4
LIC_11851	Q72R97	0.5	SPI	—	OMP		—	—
LIC_10050	Q72W87	0.5	SPI	SPI	OMP		M	PD40 / OmpA
LIC_12401	Q72PR6	0.5	SPII	—	EP		—	LRR
LIC_10920	Q72TU6	0.5	SPII	SPII	EP		—	—
LIC_12700	Q72NX8	0.5	—	—	—	CP	R	Peptidase_M16 / Peptidase_M16_C
LIC_11948	Q72R04	0.5	—	—	—	CP	—	DUF4416
LIC_11149	Q72T72	0.5	SPI	SPI	—	CP	M	Peptidase_M23
LIC_20034	Q75G31	0.5	—	—	—	CP	—	DUF1574
LIC_10064	Q72W73	0.5	SPI	SPI	—	PP	—	DUF2147
LIC_13363	Q72M28	0.5	SPI	SPI	—	OMP	—	—
LIC_13341	Q72M50	0.5	SPII	—	—	OMP	—	—
LIC_12730	Q72NU9	0.5	SPI	SPI	—	OMP	—	NHL
LIC_12708	Q72NX0	0.5	SPII	SPI	—	OMP	—	—
LIC_12693	Q72NY5	0.5	SPI	SPI	—	OMP	M	OEP
LIC_12396	Q72PS1	0.5	—	—	—	OMP	—	—
LIC_12373	Q72PU4	0.5	SPI	—	—	OMP	—	—
LIC_10486	Q72V17	0.5	—	—	—	OMP	—	—
LIC_10314	Q72VI3	0.5	SPI	SPI	—	OMP	—	Borrelia_P83
LIC_10123	Q72W18	0.5	SPII	SPII	—	OMP	—	FecR
LIC_13050	Q72MY9	0.5	SPI	SPI	—	EP	—	—
LIC_12487	Q72PI4	0.5	—	—	—	EP	—	—
LIC_12227	Q72Q85	0.5	SPI	SPI	—	EP	—	DUF3015
LIC_10973	Q72TP4	0.5	SPI	SPI	—	EP	—	Porin_OmpL1
LIC_10281	Q72VL6	0.5	—	—	—	EP	—	AHSA1
LIC_20035	Q75G29	0.5	SPII	SPII	—	EP	—	MORN_2
LIC_13333	Q72M58	0.5	SPII	—	—	—	—	—
LIC_12333	Q72PY4	0.5	SPI	—	—	—	—	—
LIC_12307	Q72Q08	0.5	SPI	SPI	—	—	—	OEP
LIC_11990	Q72QW8	0.5	—	—	—	—	—	TPR
LIC_11653	Q72RT7	0.5	SPI	SPI	—	—	—	—
LIC_11227	Q72SZ5	0.5	SPI	SPI	—	—	—	FecR

LIC_10592	Q72UR5	0.5	SPI	—	—	—	M	OmpA
LIC_10434	Q72V68	0.5	SPI	SPI	—	—	—	—
LIC_10421	Q72V80	0.5	SPI	SPI	—	—	—	—
LIC_13212	Q72MH5	0.5	SPI	—	CP	—	—	—
LIC_12230	Q72Q82	0.5	SPI	—	CP	—	—	—
LIC_12075	Q72QN8	0.5	SPI	SPI	CP	—	—	—
LIC_11874	Q72R74	0.5	SPII	—	CP	—	—	—
LIC_11837	Q72RB1	0.5	SPI	—	CP	—	—	—
LIC_11711	Q72RN4	0.5	SPII	SPII	CP	—	—	—
LIC_11468	Q72SB6	0.5	SPII	SPII	CP	—	—	—
LIC_10011	Q72WC6	0.5	SPII	SPII	PP	—	—	—
LIC_11695	Q72RP9	0.5	SPII	SPII	—	CP	—	—
LIC_11456	Q72SC8	0.5	SPII	SPII	—	CP	—	—
LIC_10879	Q72TY5	0.5	SPII	SPII	—	PP	—	—
LIC_13453	Q72MJ2	0.4	SPI	—	CP	M	Peptidase_M23	
LIC_13182	Q72ML1	0.4	—	—	CP	I	GDPD	
LIC_12719	Q72NV9	0.4	—	—	CP	—	TPR_11	
LIC_12591	Q72P84	0.4	—	—	CP	E	Peptidase_M1 / ERAP1_C	
LIC_12210	Q72QA2	0.4	—	—	CP	O	HSP20	
LIC_11741	Q72RK4	0.4	—	—	CP	R	PmbA_TldD	
LIC_11740	Q72RK5	0.4	—	—	CP	R	PmbA_TldD	
LIC_11543	Q72S43	0.4	SPII	SPI	CP	—	OstA	
LIC_11008	Q72TL0	0.4	SPI	—	CP	—	Peptidase_M23	
LIC_10769	Q72U92	0.4	—	—	CP	R	Peptidase_M16_C	
LIC_10721	Q72UD6	0.4	SPI	—	CP	—	Peptidase_23	
LIC_10615	Q72UP2	0.4	—	—	CP	—	TPR_8	
LIC_10599	Q72UQ8	0.4	SPII	SPII	CP	—	DUF4349	
LIC_10425	Q72V76	0.4	—	—	CP	K	WYL	
LIC_10419	Q72V82	0.4	—	—	CP	—	WYL	
LIC_10254	Q72VP2	0.4	—	—	CP	—	CBS	
LIC_10218	Q72VS8	0.4	SPII	SPII	CP	—	MORN_2	
LIC_10049	Q72W88	0.4	—	—	CP	—	DUF1577	
LIC_10038	Q72W99	0.4	SPI	SPI	CP	—	TPR / ANAPC3 / TPR_16 / SEL1	
LIC_10032	Q72WA5	0.4	—	—	CP	O	HSP33	
LIC_20273	Q75FC1	0.4	—	—	CP	—	HTH_8	
LIC_20253	Q75FE1	0.4	—	—	CP	—	DUF4279	
LIC_20147	Q75FN5	0.4	—	—	CP	P	FUR	
LIC_20144	Q75FN8	0.4	SPI	SPI	CP	—	PDZ	
LIC_12390	Q72PS7	0.4	—	—	CMP	H	ABC1	
LIC_12114	Q72QJ9	0.4	—	—	CMP	M	PGA_cap	
LIC_12086	Q72QM7	0.4	—	—	CMP	—	Peptidase_S24	
LIC_11176	Q72T45	0.4	—	—	CMP	—	Rhomboid	
LIC_10792	Q72U70	0.4	—	SPI	CMP	—	Acyl_transf_3	
LIC_10285	Q72VL2	0.4	—	—	CMP	M	Acyl_transf_3	
LIC_10043	Q72W94	0.4	—	—	CMP	T	PAS / PAC / MA	
LIC_11959	Q72QZ3	0.4	SPI	SPI	OMP	—	—	
LIC_11436	Q72SE7	0.4	—	—	OMP	—	FecR	
LIC_11366	Q72SL3	0.4	SPI	SPI	OMP	—	—	
LIC_11026	Q72TJ5	0.4	—	—	OMP	—	—	
LIC_11003	Q72TL5	0.4	SPII	SPII	OMP	—	DUF4398 / LysM	
LIC_20250	Q75FE4	0.4	—	—	OMP	M	OmpA	
LIC_20197	Q75FI7	0.4	SPI	SPI	OMP	—	Peptidase_C39_2 / Peptidase_C1 / FN3	
LIC_12337	Q72PY0	0.4	—	SPI	EP	—	—	
LIC_11463	Q72SC1	0.4	SPII	—	EP	—	DUF676 / LCAT / PGAP1	
LIC_12643	Q72P33	0.4	—	—	—	CP	DUF1801	
LIC_11670	Q72RS2	0.4	SPI	SPI	—	CP	TPR	
LIC_12287	Q72Q27	0.4	SPI	SPI	—	PP	TRL	
LIC_13434	Q72LV9	0.4	SPII	SPII	—	OMP	Peptidase_M43	

LIC_13359	Q72M32	0.4	SPI	—	—	OMP	—	VWA
LIC_13272	Q72MB6	0.4	—	—	—	OMP	—	—
LIC_13065	Q72MX4	0.4	—	—	—	OMP	—	DUF2804
LIC_12805	Q72NM7	0.4	—	—	—	OMP	—	—
LIC_12499	Q72PH2	0.4	SPI	SPI	—	OMP	—	—
LIC_12253	Q72Q60	0.4	SPII	—	—	OMP	—	DUF1566
LIC_12225	Q72Q87	0.4	SPI	SPI	—	OMP	—	DUF4105
LIC_12030	Q72QS9	0.4	SPII	SPII	—	OMP	—	DUF676 / LCAT / PGAP1
LIC_11988	Q72QX0	0.4	—	—	—	OMP	—	—
LIC_11823	Q72RC3	0.4	SPI	SPI	—	OMP	—	VWA / FHA
LIC_11739	Q72RK6	0.4	—	—	—	OMP	R	MG1 / A2M_N / A2M_N_2 / A2M
LIC_11718	Q72RM7	0.4	—	—	—	OMP	O	Peptidase_S49
LIC_11489	Q72S95	0.4	—	—	—	OMP	—	—
LIC_11111	Q72TB0	0.4	SPI	SPI	—	OMP	—	PDZ
LIC_11028	Q72TJ3	0.4	SPI	SPI	—	OMP	U	PD40 / TPR
LIC_10772	Q72U89	0.4	SPI	SPI	—	OMP	—	—
LIC_10125	Q72W16	0.4	SPII	SPII	—	OMP	—	TPR
LIC_10124	Q72W17	0.4	SPII	SPII	—	OMP	—	—
LIC_10104	Q72W36	0.4	—	—	—	OMP	—	—
LIC_10026	Q72WB1	0.4	SPII	SPII	—	OMP	—	—
LIC_20043	Q75FY8	0.4	SPI	SPI	—	OMP	—	BatD
LIC_11935	Q72R17	0.4	SPI	SPI	—	EP	—	BBP2
LIC_11696	Q72RP8	0.4	SPII	SPII	—	EP	—	—
LIC_11089	Q72TD2	0.4	SPI	SPII	—	EP	—	—
LIC_10067	Q72W70	0.4	—	—	—	EP	—	TIG
LIC_13410	Q72LY3	0.4	SPII	SPII	—	—	—	—
LIC_13338	Q72M53	0.4	SPII	SPII	—	—	—	—
LIC_13259	Q72MC9	0.4	SPII	SPII	—	—	—	DUF3347
LIC_12784	Q72NP8	0.4	SPI	—	—	—	—	—
LIC_12734	Q72NU5	0.4	SPI	SPI	—	—	—	—
LIC_12493	Q72PH8	0.4	—	—	—	—	—	DUF3332
LIC_12231	Q72Q81	0.4	SPI	SPII	—	—	—	—
LIC_11671	Q72RS1	0.4	SPII	SPII	—	—	—	—
LIC_11027	Q72TJ4	0.4	SPII	SPII	—	—	—	—
LIC_20112	Q75FR9	0.4	SPI	SPI	—	—	—	FecR
LIC_13144	Q72MP9	0.4	SPII	SPI	CP	—	—	—
LIC_12936	Q72NA0	0.4	SPI	—	CP	—	—	—
LIC_12096	Q72QL7	0.4	SPI	—	CP	—	—	—
LIC_11789	Q72RF6	0.4	SPI	—	CP	—	—	—
LIC_11567	Q72S20	0.4	SPII	SPII	CP	—	—	—
LIC_10230	Q72VR6	0.4	SPII	—	CMP	—	—	—
LIC_20016	Q75FZ9	0.4	SPI	SPI	CMP	—	—	—
LIC_13123	Q72MR9	0.4	SPI	—	—	CP	—	—
LIC_12399	Q72PR8	0.4	SPII	SPII	—	CP	—	—
LIC_12020	Q72QT9	0.4	SPI	SPI	—	CP	—	—
LIC_10765	Q72U96	0.4	SPI	SPI	—	CP	—	—
LIC_20045	Q75FY6	0.4	SPI	—	—	CP	—	—
LIC_11625	Q72RW3	0.4	SPI	SPI	—	PP	—	—
LIC_12587	Q72P88	0.4	SPII	SPII	CP	—	—	—
LIC_13313	Q72M77	0.3	—	SPI	CP	—	—	DUF4340
LIC_12834	Q72NK0	0.3	SPII	—	CP	—	G	Lactamase_B_2 / Lactamase_B_3
LIC_12576	Q72P99	0.3	—	—	CP	—	—	SH3b
LIC_12377	Q72PU0	0.3	SPI	SPI	CMP	—	M	PGA_cap
LIC_11216	Q72T06	0.3	—	SPI	CMP	—	T	4HB_MCP_1 / TarH / MA
LIC_10731	Q72UC8	0.3	SPII	SPII	CMP	—	V	Beta-lactamase
LIC_12731	Q72NU8	0.3	SPI	SPI	—	OMP	—	—
LIC_11883	Q72R65	0.3	—	—	—	OMP	—	—
LIC_11435	Q72SE8	0.3	SPI	SPI	—	OMP	—	—

LIC_10318	Q72VH9	0.3	SPI	—	—	OMP	—	FN3
LIC_10012	Q72WC5	0.3	SPI	—	—	OMP	—	VWA
LIC_20231	Q75FF9	0.3	SPII	—	—	OMP	—	—
LIC_20087	Q75FU4	0.3	SPI	SPI	—	OMP	—	—
LIC_20153	Q75FM9	0.3	SPII	SPII	—	EP	—	—
LIC_12262	Q72Q51	0.3	SPI	—	—	—	—	—
LIC_10767	Q72U94	0.3	SPI	—	—	—	—	—
LIC_10766	Q72U95	0.3	SPI	SPII	—	—	—	—
LIC_10302	Q72VJ5	0.3	SPI	SPI	—	—	—	TPR
LIC_20200	Q75G22	0.3	SPI	SPI	—	—	—	—
LIC_13023	Q72N15	0.3	—	SPI	CP	—	—	—

**Table S4. Features of proteins that are specific (176) of *L. interrogans***

ID Gene	ID UniProt	SignalP	LipoP	Psortb	CELLO	COG	SMART
LIC_13407	Q72LY6	—	—	CP	—	—	AHSA1
LIC_13295	Q72M93	—	—	CP	—	J	A1pp
LIC_13236	Q72MF2	—	—	CP	—	—	ANK
LIC_13233	Q72MF4	—	—	CP	—	—	DUF2889
LIC_13117	Q72MS5	—	—	CP	—	—	Fer4_13 / Lactamase_B
LIC_13058	Q72MY1	SPI	—	CP	—	—	DUF5329
LIC_13001	Q72N37	—	SPI	CP	—	—	DUF3604
LIC_12756	Q72NS3	—	—	CP	—	—	FecR
LIC_12726	Q72NV3	SPI	SPI	CP	—	R	DUF4015
LIC_12675	Q72P02	—	—	CP	—	—	DUF4303
LIC_12649	Q72P27	SPI	SPI	CP	—	—	DUF1375
LIC_12604	Q72P72	—	—	CP	—	—	DUF3751
LIC_12523	Q72PE8	—	—	CP	—	—	DUF2236
LIC_12468	Q72PK3	—	—	CP	—	—	TPR_8/ TPR_2
LIC_12393	Q72PS4	SPI	—	CP	—	—	ANK
LIC_12115	Q72QJ8	—	—	CP	—	—	ANK
LIC_12022	Q72QT7	—	—	CP	—	—	DUF1176
LIC_11983	Q72QX5	—	—	CP	—	S	MORN
LIC_11958	Q72QZ4	SPI	SPI	CP	—	—	HEAT_2
LIC_11879	Q72R69	—	—	CP	—	S	DUF2461
LIC_11834	Q72RB4	SPII	SPII	CP	—	—	FecR
LIC_11770	Q72RH5	—	—	CP	—	P	Cu-oxidase_4
LIC_11163	Q72T58	—	—	CP	—	—	DUF1963
LIC_11046	Q72TH5	SPI	—	CP	—	—	SH3b
LIC_10983	Q72TN4	SPII	SPII	CP	—	—	Zn_pept
LIC_10918	Q72TU8	—	—	CP	—	I	AHSA1
LIC_10793	Q72U69	SPII	SPII	CP	—	—	Lactonase
LIC_10663	Q72UJ4	—	—	CP	—	I	AHSA1
LIC_10661	Q72UJ6	—	—	CP	—	I	AHSA1
LIC_10596	Q72UR1	SPII	—	CP	—	—	TPR
LIC_10578	Q72US9	SPI	SPI	CP	—	—	HEAT_2
LIC_10406	Q72V95	SPI	—	CP	—	—	HEAT_2
LIC_10387	Q72VB4	—	—	CP	—	—	FecR
LIC_10143	Q72VZ8	—	—	CP	—	—	DUF433
LIC_10117	Q72W24	—	—	CP	—	S	DUF885
LIC_10004	Q72WD3	—	—	CP	—	—	DUF721
LIC_20158	Q75FM4	—	—	CP	—	O	AAA_32 / Lon_C
LIC_20114	Q75FR7	—	—	CP	—	—	FecR
LIC_20042	Q75FY9	SPI	SPI	CP	—	—	TPR
LIC_13394	Q72LZ9	—	—	CMP	—	T	MA
LIC_13364	Q72M27	—	—	CMP	—	—	Abi
LIC_13201	Q72MI6	—	—	CMP	—	R	CYCc / AAA_16 / TPR
LIC_13066	Q72MX3	SPII	—	CMP	—	—	SBBP
LIC_13056	Q72MY3	SPII	SPII	CMP	—	N	OmpA
LIC_13012	Q72N26	—	—	CMP	—	—	DUF2339
LIC_11523	Q72S63	—	—	CMP	—	T	PAS / HAMP / MA
LIC_11501	Q72S83	—	—	CMP	—	—	DUF350

LIC_11290	Q72ST4	—	—	CMP	—	DUF445
LIC_10376	Q72VC5	SPI	—	CMP	—	ANK
LIC_11903	Q72R46	SPI	SPI	PP	—	Big_5
LIC_13247	Q72ME1	SPI	SPI	OMP	—	—
LIC_13238	Q72MF0	SPI	—	OMP	—	—
LIC_12645	Q72P31	SPI	—	OMP	—	—
LIC_10713	Q72UE4	SPII	SPII	OMP	S	Peptidase_M75
LIC_10711	Q72UE6	SPI	—	OMP	—	Peptidase_M75
LIC_10439	Q72V63	—	—	OMP	—	DUF4178
LIC_10017	Q72WC0	—	—	OMP	—	—
LIC_13198	Q72MI9	SPII	SPI	EP	—	—
LIC_12901	Q72ND3	—	—	EP	K	WGR / DUF4132 / LRR
LIC_12759	Q72NS0	SPI	—	EP	—	LRR
LIC_12601	Q72P75	—	—	EP	—	—
LIC_12539	Q72PD2	SPI	SPI	EP	—	—
LIC_11098	Q72TC3	SPI	SPI	EP	K	LRR
LIC_11097	Q72TC4	SPI	—	EP	K	LRR
LIC_11051	Q72TH0	—	—	EP	—	WGR / LRR
LIC_10828	Q72U36	SPI	—	EP	K	LRR
LIC_20172	Q75FL0	SPII	SPII	EP	—	DUF4842
LIC_12326	Q72PY9	—	—	—	CP	DUF1987
LIC_12005	Q72QV3	—	—	—	CP	DUF4375
LIC_11403	Q72SH9	—	—	—	CP	FeoA
LIC_10664	Q72UJ3	—	—	—	CP	I AHSA1
LIC_10128	Q72W13	—	—	—	CP	PilZ
LIC_11441	Q72SE2	SPI	—	—	PP	DUF3347
LIC_11352	Q72SM7	SPII	SPII	—	PP	LipL32
LIC_11035	Q72TI6	SPI	SPI	—	PP	DUF4087
LIC_13435	Q72LV8	SPI	SPI	—	OMP	—
LIC_13361	Q72M30	SPI	SPI	—	OMP	DUF4140 / DUF4139
LIC_13360	Q72M31	—	—	—	OMP	DUF4140 / DUF4139
LIC_13293	Q72M95	SPI	SPI	—	OMP	Peptidase_M48
LIC_13089	Q72MV0	SPI	SPI	—	OMP	—
LIC_13078	Q72MW1	SPI	—	—	OMP	—
LIC_13070	Q72MW9	SPI	SPI	—	OMP	—
LIC_13055	Q72MY4	SPI	—	—	OMP	—
LIC_13032	Q72N06	—	—	—	OMP	—
LIC_12615	Q72P61	—	—	—	OMP	DUF3383
LIC_12608	Q72P68	—	—	—	OMP	—
LIC_12170	Q72QE2	—	—	—	OMP	—
LIC_12067	Q72QP6	SPI	SPI	—	OMP	—
LIC_12033	Q72QS6	—	—	—	OMP	ANK
LIC_11612	Q72RX6	SPI	SPI	—	OMP	—
LIC_11399	Q72SI3	SPI	—	—	OMP	F5_F8_type_C / Peptidase_M23
LIC_11334	Q72SP3	SPI	SPI	—	OMP	S SIMPL
LIC_11320	Q72SQ5	SPI	—	—	OMP	—
LIC_11264	Q72SV8	SPI	—	—	OMP	—
LIC_11009	Q72TK9	SPI	SPI	—	OMP	—
LIC_10968	Q72TP9	SPII	SPI	—	OMP	—
LIC_10902	Q72TW2	—	—	—	OMP	FecR

LIC_10547	Q72UW0	SPII	—	—	OMP	—	—
LIC_10258	Q72VN8	SPI	—	—	OMP	—	OmpA
LIC_10189	Q72VV7	—	—	—	OMP	—	—
LIC_10187	Q72VV9	—	—	—	OMP	—	—
LIC_10105	Q72W35	—	—	—	OMP	—	—
LIC_20185	Q75FJ7	SPII	SPII	—	OMP	—	FecR
LIC_20036	Q75G30	—	—	—	OMP	—	—
LIC_10465	G1UB65	SPII	SPII	—	EP	—	BID_2
LIC_13354	Q72M37	—	—	—	EP	—	—
LIC_13060	Q72MX9	SPII	SPII	—	EP	—	—
LIC_12602	Q72P74	—	—	—	EP	—	—
LIC_12339	Q72PX8	SPI	SPI	—	EP	—	DUF1561
LIC_12208	Q72QA4	SPII	—	—	EP	—	SBBP
LIC_10706	Q72UF1	SPII	—	—	EP	—	—
LIC_10705	Q72UF2	SPI	—	—	EP	—	—
LIC_10464	Q72V39	SPII	SPII	—	EP	—	BID_2
LIC_10280	Q72VL7	SPI	SPI	—	EP	—	—
LIC_13436	Q72LV7	SPI	SPI	—	—	—	—
LIC_13249	Q72MD9	—	—	—	—	—	Imm26
LIC_13216	Q72MH1	SPI	—	—	—	—	—
LIC_13059	Q72MY0	SPII	SPII	—	—	—	—
LIC_12963	Q72N74	SPI	—	—	—	—	DUF1561
LIC_12581	Q72P94	—	—	—	—	—	AHSA1
LIC_12372	Q72PU5	—	—	—	—	—	ANK
LIC_12341	Q72PX6	SPI	SPI	—	—	—	—
LIC_11966	Q72QY9	SPII	SPII	—	—	—	—
LIC_11486	Q72S98	SPI	SPI	—	—	—	TPR_8
LIC_11481	Q72SA3	SPII	SPII	—	—	—	—
LIC_11388	Q72SJ4	SPII	SPI	—	—	—	—
LIC_11158	Q72T63	—	—	—	—	—	FUR
LIC_11122	Q72T99	SPII	SPII	—	—	—	FecR
LIC_11059	Q72TG2	—	—	—	—	—	DUF736
LIC_10797	Q72U67	SPII	SPII	—	—	—	—
LIC_10655	Q72UK2	SPI	—	—	—	—	—
LIC_10520	Q72UY3	SPI	SPI	—	—	—	—
LIC_10411	Q72V90	SPI	SPI	—	—	—	HEAT_2
LIC_10371	Q72VC9	SPII	—	—	—	—	SBBP
LIC_10368	Q72VD2	SPII	SPII	—	—	—	—
LIC_10211	Q72VT5	SPII	SPII	—	—	—	—
LIC_10095	Q72W45	SPI	SPI	—	—	—	—
LIC_10028	Q72WA9	SPII	SPII	—	—	—	—
LIC_10009	Q72WC8	SPII	SPII	—	—	—	—
LIC_20196	Q75FI8	SPI	SPI	—	—	—	—
LIC_20167	Q75FL5	—	—	—	—	—	DUF1574
LIC_20047	Q75FY4	SPII	SPI	—	—	R	DUF839
LIC_20029	Q75G15	—	SPI	—	—	—	—
LIC_13351	Q72M40	SPII	SPII	CP	—	—	—
LIC_13286	Q72MA2	SPI	—	CP	—	—	—
LIC_13204	Q72MI3	SPI	SPI	CP	—	—	—
LIC_12895	Q72ND9	SPII	SPII	CP	—	—	—

LIC_12667	Q72P10	SPII	SPII	CP		—	—
LIC_12353	Q72PW4	SPII	SPII	CP		—	—
LIC_12263	Q72Q50	SPI	SPI	CP		—	—
LIC_11947	Q72R05	SPII	—	CP		—	—
LIC_11299	Q72SS6	SPII	SPII	CP		—	—
LIC_11171	Q72T50	SPI	—	CP		—	—
LIC_11113	Q72TA8	SPI	SPI	CP		—	—
LIC_10985	Q72TN2	SPII	SPII	CP		—	—
LIC_10512	Q72UZ1	SPI	SPI	CP		—	—
LIC_10508	Q72UZ5	SPII	SPII	CP		—	—
LIC_10507	Q72UZ6	SPII	SPII	CP		—	—
LIC_10402	Q72V99	SPII	—	CP		—	—
LIC_13268	Q72MC0	SPI	SPI	CMP		—	—
LIC_13151	Q72MP2	SPII	SPII	CMP		—	—
LIC_12669	Q72P08	SPI	SPI	CMP		—	—
LIC_11271	Q72SV1	SPI	SPI	CMP		—	—
LIC_20109	Q75FS2	SPI	—	CMP		—	—
LIC_12966	Q72N71	SPII	SPII	—	CP	—	—
LIC_12824	Q72NL0	SPI	—	—	CP	—	—
LIC_12238	Q72Q74	SPII	SPII	—	CP	—	—
LIC_11960	Q72QZ2	SPI	SPI	—	CP	—	—
LIC_11288	Q72ST6	SPII	SPII	—	CP	—	—
LIC_10672	Q72UI5	SPI	SPI	—	CP	—	—
LIC_10316	Q72VI1	—	SPI	—	CP	—	—
LIC_10301	Q72VJ6	SPII	SPII	—	CP	—	—
LIC_10236	Q72VR0	SPI	—	—	CP	—	—
LIC_12893	Q72NE1	SPI	SPI	—	PP	—	—
LIC_12561	Q72PB1	SPI	SPI	—	PP	—	—
LIC_10683	Q72UH4	SPI	SPI	—	PP	—	—



**Table S5. Proteins of *L. interrogans* containing peptidase domains**

ID Gene	ID UniProt	<i>c-values</i>	COG	SignalP	LipoP	PSORT	CELLO	SMART
LIC_10581	Q72US6	0.5	E	—	—	CP		Peptidase_C26 / GATase
LIC_10768	Q72U93	0.5	R	SPI	—	CP		Peptidase_M16
LIC_11149	Q72T72	0.5	M	SPI	SPI	—	CP	Peptidase_M23
LIC_12700	Q72NX8	0.5	R	—	—	—	CP	Peptidase_M16
LIC_13491	Q72LR2	0.5	E	—	SPI	CP		Peptidase_M20 / M20_dimer
LIC_20092	Q75FT9	0.5	R	—	—	CP		Peptidase_M61
LIC_10721	Q72UD6	0.4	—	SPI	—	CP		Peptidase_M23
LIC_10769	Q72U92	0.4	R	—	—	CP		Peptidase_M16
LIC_11008	Q72TL0	0.4	—	SPI	—	CP		Peptidase_M23
LIC_11718	Q72RM7	0.4	O	—	—	—	OMP	Peptidase_S49
LIC_12086	Q72QM7	0.4	—	—	—	CMP		Peptidase_S26
LIC_12591	Q72P84	0.4	E	—	—	CP		Peptidase_M1 / ERAP1
LIC_13434	Q72LV9	0.4	—	SPII	SPII	—	OMP	Peptidase_M43
LIC_13453	Q72MJ2	0.4	M	SPI	—	CP		Peptidase_M23
LIC_20197	Q75FI7	0.4	—	SPI	SPI	OMP		Peptidase_C39 / Peptidase_C1 / FN3
LIC_10711	Q72UE6	—	—	SPI	—	OMP		Peptidase_M75
LIC_10713	Q72UE4	—	S	SPII	SPII	OMP		Peptidase_M75
LIC_11399	Q72SI3	—	—	SPI	—	—	OMP	F5_F8_type_C / Peptidase_M23
LIC_13293	Q72M95	—	—	SPI	SPI	—	OMP	Peptidase_M48

**Table S6. Proteins of *L. interrogans* containing Leucine-rich repeats (LRR) motifs**

<b>ID Gene</b>	<b>ID UniProt</b>	<b><i>c-values</i></b>	<b>COG</b>	<b>SignalP</b>	<b>LipoP</b>	<b>PSORT</b>	<b>CELLO</b>	<b>SMART</b>
LIC_12401	Q72PR6	0.5	—	SPII	—	EP		LRR_8
LIC_10828	Q72U36	—	K	SPI	—	EP		LRR_8
LIC_11051	Q72TH0	—	—	—	—	EP		WGR / LRR_8
LIC_11097	Q72TC4	—	K	SPI	—	EP		LRR_8
LIC_11098	Q72TC3	—	K	SPI	SPI	EP		LRR_8
LIC_12759	Q72NS0	—	—	SPI	—	EP		LRR_8
LIC_12901	Q72ND3	—	K	—	—	EP		WGR / DUF4132 / LRR_8

**Table S7. Proteins of *L. interrogans* containing Tetratricopeptide repeats (TPR) motifs**

<b>ID Gene</b>	<b>ID UniProt</b>	<b>c-values</b>	<b>COG</b>	<b>SignalP</b>	<b>LipoP</b>	<b>PSORT</b>	<b>CELLO</b>	<b>SMART</b>
LIC_10053	Q72W84	0.5	—	—	—	CP	—	TPR
LIC_11990	Q72QW8	0.5	—	—	—	—	—	TPR
LIC_10038	Q72W99	0.4	—	SPI	SPI	CP	—	TPR / SEL1
LIC_10125	Q72W16	0.4	—	SPII	SPII	—	OMP	TPR
LIC_10615	Q72UP2	0.4	—	—	—	CP	—	TPR_8
LIC_11028	Q72TJ3	0.4	U	SPI	SPI	—	OMP	PD40 / TPR
LIC_11670	Q72RS2	0.4	—	SPI	SPI	—	CP	TPR
LIC_12719	Q72NV9	0.4	—	—	—	CP	—	TPR_11
LIC_10302	Q72VJ5	0.3	—	SPI	SPI	—	—	TPR

**Table S8. Proteins of *L. interrogans* containing Ankyrin repeats (ANK) motifs**

<b>ID Gene</b>	<b>ID UniProt</b>	<b><i>c-values</i></b>	<b>COG</b>	<b>SignalP</b>	<b>LipoP</b>	<b>PSORT</b>	<b>CELLO</b>	<b>SMART</b>
LIC_10376	Q72VC5	—	—	SPI	—	CMP		ANK
LIC_12033	Q72QS6	—	—	—	—	—	OMP	ANK_2
LIC_12115	Q72QJ8	—	—	—	—	CP		ANK_2
LIC_12372	Q72PU5	—	—	—	—	—	—	ANK_2 / ANK_5
LIC_12393	Q72PS4	—	—	SPI	—	CP		ANK
LIC_13236	Q72MF2	—	—	—	—	CP		ANK_2