Supplemental Table 2. List of all identified and predicted Lc705 proteins obtained with high-confidence identification and less-stringent search criteria. Relevant information related to protein/gene functions, protein conservation, physiochemical characters, subcellular location, presence of adhesive domains is based on previous comparative genomics study by Kankainen et al. (2009). Cellular location signals found in the proteins sequence: transmembrane (TMHMM), integral membrane protein (IMP), C-terminal lysin motif mediating non-covalent attachment to peptidoglycan (LysM), sortase-mediated covalent attachment to peptidoglycan (LPxTG motif), repeated Gly-Trp dipeptide modules that anchor the protein to lipotheicoic acids of the cell wall (GW).

Proteins identified with less-stingent search criteria	+	[ms] < 50 (p < 0.05) in Lc705 and [ms] > 50 (p < 0.05) in GG
	+	[ms] < 50 (p < 0.05) in Lc705 and GG

Locus	Gene	Start coord	End coord	Length (amino acids)	pI	MW	Strand	Blannotator	Blast annotation	ERGO annotation	INTERPRO	COG	Homolog in GG	Adhesion-associated domains	Cellular location	#TMHMM	Glucosidase	Phage proteins	EPS synthesis	Signal transduction	Regulator	Protease	Identified by GeLC-MS/MS
LC_00001	dnaA	1	1350	449	5,36	50754	+	Chromosomal replication initiator protein dnaA	bacterial chromosomal replication initiator protei	Chromosomal replication initiator protein dnaA	Bacterial chromosomal replication initiator prote	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00002	dnaN	1524	2663	379	4,4	41440	+	DNA polymerase III, beta subunit	DNA-directed DNA polymerase III beta subunit	DNA polymerase III, beta chain (EC 2.7.7.7)	DNA polymerase III, beta chain	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00003	null	2954	2772	60	10,11	6849	-	putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00004	yyaA	3529	3741	70	7,53	7612	+	S4 domain protein YaaA	RNA-binding S4 domain protein	Hypothetical cytosolic protein	RNA-binding S4|S4 region, YaaA	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00005	recF	3738	4856	372	8,59	41842	+	DNA replication and repair protein recF	DNA replication and repair protein recF	DNA replication and repair protein recF	RecF protein|SMC protein, N-terminal	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00006	gyrB	4888	6849	653	6,26	72473	+	DNA gyrase subunit B	DNA gyrase B subunit, DNA topoisomerase (A'	DNA gyrase subunit B (EC 5.99.1.3)	DNA topoisomerase, type IIA, subunit B|DNA t	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00007	gyrA	6912	9524	870	5,52	96605	+	DNA gyrase subunit A	DNA gyrase subunit A (EC 5.99.1.3)	DNA gyrase subunit A (EC 5.99.1.3)	DNA topoisomerase, type IIA, subunit A or C-te	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00008	null	9742	9843	33	6,62	3689	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	Single-strand binding protein/Primosomal replic	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00009	null	10220	10447	75	4,54	7387	+	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00010	coaC	10542	11054	170	6,1	19494	+	Pediocin PapC-like protein	pediocin PA-1 biosynthesis protein pedC (Pedic	Pediocin PapC-like protein	Glutaredoxin|Thioredoxin fold|Thioredoxin-like f	OC	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00011	ssb	11378	11809	143	5,94	15701	+	Single-stranded DNA-binding protein	phage single-strand DNA binding protein (SSB	Single-strand DNA binding protein	Single-strand binding protein/Primosomal replic	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-
LC_00012	rpsF	11936	12232	98	4,79	11573	+	SSU/30S ribosomal protein S6P	SSU ribosomal protein S6P	SSU ribosomal protein S6P	Ribosomal protein S6|Translation elongation fac	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00013	null	12262	12852	196	4,91	20906	+	Single-stranded DNA-binding protein	prophage LambdaSa2, single-strand DNA-bindi	Single-strand DNA binding protein	Single-strand binding protein/Primosomal replic	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+
LC_00014	rpsR	12944	13180	78	11,88	9128	+	SSU/30S ribosomal protein S18P	30S ribosomal protein S18P (BS21) (BS19)	SSU ribosomal protein S18P	Ribosomal protein S18	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00015	yraA	13979	13473	168	4,67	18393	-	Intracellular protease, PfpI family	intracellular protease, PfpI family	Hypothetical cytosolic protein	ThiJ/PfpI|Peptidase C56, PfpI	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00016	cydA	14290	15768	492	9,47	54640	+	Cytochrome d ubiquinol oxidase subunit I	cytochrome BD ubiquinol oxidase subunit I	Cytochrome d ubiquinol oxidase subunit I (EC	Cytochrome bd ubiquinol oxidase, subunit I	C	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_00017	null	15761	16780	339	10,17	37616	+	Cytochrome d ubiquinol oxidase subunit II	cytochrome d ubiquinol oxidase, subunit II	Cytochrome d ubiquinol oxidase subunit I (EC	Cytochrome bd ubiquinol oxidase, subunit II	C	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_00018	null	16820	17014	64	10,83	7527	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00019	null	17518	17093	141	7,07	16067	-	Putative protein without homology	predicted ORF	CAAX amino terminal protease family	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	protease	-
LC_00020	null	18365	19042	225	9,83	25498	+	Abortive infection protein	membrane protease, CAAX family	CAAX amino terminal protease family	Abortive infection protein	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	protease	-
LC_00021	null	20070	19318	250	8,93	28226	-	ABC transporter, permease protein	predicted ORF	ABC transporter permease protein	ABC-2 type transporter|ABC-2 transporter	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00022	null	21001	20093	302	9,67	34110	-	ABC transporter, ATPase component	predicted ORF	Sodium export ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00023	amt	21739	22824	361	8,36	38750	+	Ammonium transporter family protein	ammonium transporter (Amt) family protein	Ammonium transporter	Ammonium transporter|Rh-like protein/ammoni	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_00024	null	22842	23951	369	4,88	40811	+	Monooxygenase	FAD-dependent pyridine nucleotide-disulphide (	Oxidoreductase (EC 1.1.1.-)	Pyridine nucleotide-disulphide oxidoreductase, (	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00025	isp2	25419	24169	416	7,7	42586	-	Surface antigen	surface antigen, p40	Putative secreted antigen GbpB/SagA, putativ	Cysteine, histidine-dependent amidohydrolase/p	M	Yes	-	Sec	tmhmm:0	-	-	-	-	-	protease	+
LC_00026	null	28195	25622	857	10,81	93420	-	ABC transporter, antimicrobial peptide transpo	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein	Protein of unknown function DUF214, permease	null	Yes	-	LPxTG	tmhmm:8	-	-	-	-	-	-	+
LC_00027	abc	28906	28205	233	5,95	25430	-	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00028	null	29079	29630	183	7,59	20849	+	Transcriptional regulator, TetR family	transcriptional regulator	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00029	null	29676	30482	268	5,56	29744	+	Hydrolase	hydrolase, HAD superfamily, Cof family	Hydrolase (HAD superfamily)	Cof protein|HAD-superfamily hydrolase, subfam	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00030	null	30503	30811	102	11,15	11355	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00031	null	31760	30987	257	10,55	26914	-	Permease	permease	Hypothetical membrane spanning protein	Protein of unknown function DUF81	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-
LC_00032	null	31930	32529	199	8,99	22551	+	Conserved integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF1211	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00033	thgA1	32782	33384	200	6,67	22038	+	Maltose O-acetyltransferase	galactoside O-acetyltransferase, GAT, (Thiogal	Galactoside O-acetyltransferase (EC 2.3.1.18	Bacterial transferase hexapeptide repeat[Trimer	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00034	null	33729	33391	112	9,98	12672	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00035	pepD	34007	35449	480	4,53	53713	+	Dipeptidase A	dipeptidase A. Cysteine peptidase. MEROPS fa	Dipeptidase A (EC 3.4.13.-)	Peptidase C69, dipeptidase A	C	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00036	map	35604	36233	209	8,33	23344	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Integral membrane protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00037	null	36665	37198	177	9,75	20326	+	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00038	null	37829	38155	108	9,71	12393	+	Putative protein without homology	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00039	ykuG	41556	39229	775	4,52	84202	-	YkuG protein	YkuG protein	not_predicted_by_ERGO	Peptidoglycan-binding domain 1|Peptidoglycan	null	No	peptidoglucar	-	tmhmm:0	-	-	-	-	-	-	+
LC_00040	yqfD	41900	42610	236	7,16	25278	+	Branched-chain amino acid transport protein a	branched-chain amino acid transporter, AzlC fa	Branched-chain amino acid transport protein a	AzlC-like	E	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00041	null	42597	42926	109	11,04	11824	+	Branched-chain amino acid transport protein a	conserved hypothetical protein (integral membr	Branched-chain amino acid transport protein a	Branched-chain amino acid transport	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00042	uidA	43188	44987	599	5,32	68141	+	Beta-glucuronidase (GH2)	beta-glucuronidase GUSPlus-His6	Beta-glucuronidase (EC 3.2.1.31)	Glycoside hydrolase, family 2|Glycoside hydrola	G	Yes	-	-	tmhmm:0	LC00042	-	-	-	-	-	+
LC_00043	null	45422	49900	1492	5,67	160641	+	Glycoside hydrolase, family 59/fibronectin type	conserved hypothetical protein	Cell wall-associated glycosyl hydrolase	Glycoside hydrolase, family 59|Galactose-bindir	null	Yes	fibronectin	LPxTG	tmhmm:2	LC00043	-	-	-	-	-	+
LC_00044	eda-1	50880	50230	216	4,82	22405	-	2-dehydro-3-deoxyphosphogluconate aldolase	2-dehydro-3-deoxyphosphogluconate aldolase/4	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.1	KDPG and KHG aldolase|Aldolase-type TIM ba	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00045	kdgK	51925	50954	323	6,52	34181	-	2-dehydro-3-deoxygluconokinase	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)	2-dehydro-3-deoxygluconokinase (EC 2.7.1.4	PfkB	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00046	uxaC	53383	51950	477	5,04	54954	-	Uronate isomerase	uronate isomerase (Glucuronate isomerase) (Us	Uronate isomerase (EC 5.3.1.12)	Glucuronate isomerase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00047	uxuA	54468	53383	361	4,96	41740	-	Mannonate dehydratase	D-mannonate dehydratase (EC 4.2.1.8)	Mannonate dehydratase (EC 4.2.1.8)	Mannonate dehydratase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00048	uxuB	56106	54472	544	5,16	60105	-	Mannitol dehydrogenase domain protein	fructuronate reductase (EC 1.1.1.57) /Mannitol-	Fructuronate reductase (EC 1.1.1.57)	6-phosphogluconate dehydrogenase, C-termina	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00049	null	57884	56307	525	5,04	58143	-	O-Glycosyl hydrolase	O-glycosyl hydrolase	not_predicted_by_ERGO	Glycoside hydrolase, family 30|Glycoside hydro	null	No	invasin	-	tmhmm:0	LC00049	-	-	-	-	-	+
LC_00050	null	59227	57932	431	10,07	45942	-	Transporter, major facilitator superfamily MFS	melibiose:Na(+) transport protein	Transporter, MFS superfamily	Major facilitator superfamily|Major facilitator sup	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00051	kdgR	59631	60332	233	5,31	26895	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|GntR, C	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00052	kdgK	60400	61419	339	5,17	36810	+	2-dehydro-3-deoxygluconokinase	2-dehydro-3- deoxygluconokinase (Ec 2.7.1.45)	2-dehydro-3-deoxygluconokinase (EC 2.7.1.4	PfkB	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00053	null	61451	63970	839	5,11	92883	+	Galactosidase (GH59)	conserved hypothetical protein	Cell wall-associated glycosyl hydrolase	Glycoside hydrolase, family 59|Concanavalin A-	null	Yes	-	-	tmhmm:0	LC00053	-	-	-	-	-	+
LC_00054	null	64294	64623	109	8,75	12362	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00055	null	64802	65167	121	6,51	13404	+	FMN-binding protein	pyridoxamine 5'-phosphate oxidase-related, FMI	FMN-binding protein	FMN-binding split barrel, related|Pyridoxamine !	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00056	ypiB	66756	65386	456	10,43	49149	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-
LC_00057	null	68247	67078	389	10,19	43825	-	Alpha/beta hydrolase fold-3	alpha/beta acetyl-hydrolase fold-3	Esterase (EC 3.1.1.-)	Alpha/beta hydrolase fold-3	I	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00058	null	68411	68965	184	9,58	20909	+	Transcriptional regulator, TetR family	predicted ORF	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	IMP	tmhmm:1	-	-	-	-	regulator	-	-
LC_00059	null	69195	69569	124	7,6	14680	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00060	null	73010	69762	1082	10,32	115086	-	Conserved membrane protein	membrane protein, MmpL family	Transporter, MMPL family	Sterol-sensing 5TM box|MMPL	R	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_00061	null	73609	73007	200	6,11	22221	-	Transcriptional regulator, TetR family	transcriptional regulator	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+

LC_00062	null	74358	73816	180	10,07	18921	-	Conserved protein	predicted ORF	Hypothetical membrane spanning protein	Protein of unknown function DUF81	R	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00063	null	75851	74520	443	6,31	48262	-	Amidohydrolase domain protein	conserved hypothetical protein	Chlorohydrolase/deaminase family protein	Amidohydrolase 1|Metal-dependent hydrolase, (	FR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00064	null	76298	75852	148	10,33	15488	-	Conserved protein	conserved protein	Hypothetical protein	no annotation	R	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00065	null	77140	76298	280	10	29779	-	Conserved protein	conserved protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-
LC_00066	null	77706	77464	80	10,36	8704	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	Nterm	tmhmm:0	-	-	-	-	-	-	-
LC_00067	opuD	78646	77984	220	10,04	23300	-	Binding-protein-dependent transport systems i	glycine betaine/carnitine/choline ABC transporte	Glycine betaine/carnitine/choline transport sys	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00068	opuCc	79575	78646	309	9,72	34742	-	ABC transporter, glycine betaine/carnitine/cho	glycine betaine/choline/L-proline ABC transporte	Glycine betaine/carnitine/choline-binding prote	Substrate-binding region of ABC-type glycine b	M	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+
LC_00069	opuCb	80216	79587	209	6,52	22341	-	Binding-protein-dependent transport systems i	glycine betaine/carnitine/choline ABC transporte	Glycine betaine/carnitine/choline transport sys	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00070	opuA	81466	80219	415	5,15	46408	-	ABC transporter, Glycine betaine/L-proline tra	glycine betaine/carnitine/choline/proline ABC tra	Glycine betaine/carnitine/choline transport ATI	Cystathionine-beta-synthase|ABC transporter re	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00071	cadA	81692	83548	618	9,77	65179	+	Cation transport ATPase	cation transport ATPase, P-type	Lead, cadmium, zinc and mercury transporting	Cof protein|ATPase, P-type, K/Mg/Cd/Cu/Zn/Na	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00072	copZ	83568	83795	75	9,26	7982	+	Copper chaperone	metal binding protein (copper chaperone CopZ)	Heavy metal binding protein	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-t	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00073	dpsB	84132	84710	192	4,65	21216	+	DNA-binding ferritin-like protein (Oxidative dar	DNA-binding ferritin-like protein (oxidative dama	Non-specific DNA-binding protein Dps / Iron-b	Actin-binding, actinin-type|Ferritin/ribonucleotid	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00074	rcfA	84763	85422	219	5,62	24064	+	Transcriptional regulator, crp family	transcriptional regulator, Flp/Fnr/Crp family	Transcription regulator, crp family	Cyclic nucleotide-binding|Bacterial regulatory pr	T	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00075	null	85764	85501	87	10,19	9849	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00076	null	86724	85843	293	8,63	32717	-	Metal-dependent membrane protease	metal-dependent membrane protease	CAAX amino terminal protease family	Abortive infection protein	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	protease	-
LC_00077	frvB	86989	88482	497	9,41	52583	+	PTS system, IICB component	PTS system, fructose-specific IIBC component	PTS system, mannose-specific IIAB compone	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_00078	frvA	88525	88983	152	6,68	17189	+	PTS system, IIA component	PTS system, fructose/mannitol IIA component	PTS system, mannose-specific IIAB compone	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00079	null	88991	91612	873	5,66	99616	+	Alpha-mannosidase (GH38)	alpha-mannosidase	Alpha-mannosidase (EC 3.2.1.24)	Glycoside hydrolase, family 38|Glycoside hydro	G	Yes	-	-	tmhmm:0	LC00079	-	-	-	-	-	+
LC_00080	null	91624	92415	263	7,34	29753	+	Putative protein without homology	predicted ORF	Transcriptional regulator, RpiR family	Helix-turn-helix protein RpiR|Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00081	celG	92426	93694	422	6,27	48406	+	Beta-glucosidase (GH1)	6-phospho-beta-glucosidase, glycoside hydrola	Beta-glucosidase (EC 3.2.1.21)	Glycoside hydrolase, family 1|Glycoside hydrola	G	Yes	-	-	tmhmm:0	LC00081	-	-	-	-	-	-
LC_00082	null	93684	93797	37	11,11	4299	+	Putative protein without homology	beta-glucosidase/6-phospho-beta-glucosidase/t	not_predicted_by_ERGO	no annotation	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00083	ypbG	93807	94682	291	5,86	31898	+	ROK family protein	ROK family protein	Glucokinase (EC 2.7.1.2) / transcription regula	ROK	KG	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00084	null	94928	95101	57	10,55	6689	+	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00085	trpA	96136	95327	269	6,14	28953	-	Tryptophan synthase alpha chain	tryptophan synthase alpha chain, trpA	Tryptophan synthase alpha chain (EC 4.2.1.20	Tryptophan synthase, alpha chain|Ribulose-phc	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00086	trpB	97349	96129	406	5,04	43484	-	Tryptophan synthase beta chain	tryptophan synthase beta chain	Tryptophan synthase beta chain (EC 4.2.1.20)	Pyridoxal-5'-phosphate-dependent enzyme, beta	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00087	trpF	97932	97333	199	6,65	21546	-	N-(5'-phosphoribosyl)anthranilate isomerase	N-(5'-phosphoribosyl)anthranilate isomerase (PI	N-(5'-phosphoribosyl)anthranilate isomerase (I	N-(5'phosphoribosyl)anthranilate isomerase (PF	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00088	trpC	98715	97936	259	9,83	28730	-	Indole-3-glycerol phosphate synthase	strongly similar to indole-3-glycerol phosphate s	Indole-3-glycerol phosphate synthase (EC 4.1	Indole-3-glycerol phosphate synthase, central re	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00089	trpD	99737	98712	341	5,38	36405	-	Anthranilate phosphoribosyltransferase	anthranilate phosphoribosyltransferase, TrpD	Anthranilate phosphoribosyltransferase (EC 2.	Glycosyl transferase, family 3|Anthranilate phos	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00090	null	99834	99718	38	10,71	4801	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00091	null	102153	100327	608	10,59	64798	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Tetracycline resistance protein TetB|Drug resis	GEPF	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	-
LC_00092	null	102311	102916	201	6,52	23257	+	Transcriptional regulator, TetR family	transcriptional regulator	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00093	null	103629	102925	234	10,86	25693	-	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_00094	null	105182	103941	413	9,11	46038	-	ABC transporter	predicted ORF	ABC transporter	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00095	null	106101	105187	304	11,02	35296	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00096	null	106784	106098	228	8,78	25582	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00097	null	107054	107935	293	4,85	33629	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	not_predicted_by_ERGO	Helix-turn-helix type 3|Transcriptional activator f	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00098	rmlC	108554	109144	196	6,13	21635	+	dTDP-4-dehydrorhamnose 3,5-epimerase	dTDP-4-dehydrorhamnose 3,5-epimerase or rel	dTDP-4-dehydrorhamnose 3,5-epimerase (EC	dTDP-4-dehydrorhamnose 3,5-epimerase relate	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00099	dapB	110051	109284	255	6,31	27234	-	Dihydrodipicolinate reductase	Dihydrodipicolinate reductase (DHPR)	Dihydrodipicolinate reductase (EC 1.3.1.26)	Dihydrodipicolinate reductase|Dihydrodipicolina	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00100	dapA2	110953	110048	301	5,76	32339	-	Dihydrodipicolinate synthase	Dihydrodipicolinate synthase/N-acetylneuramin	Dihydrodipicolinate synthase (EC 4.2.1.52)	Dihydrodipicolinate synthetase|Dihydrodipicolina	EM	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00101	null	111262	111083	59	10,84	6161	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00102	dapE	112429	111278	383	5,94	41783	-	Peptidase, M20/M25/M40 family	metal-dependent amidase/aminoacylase/carbox	Putative N-acetyldiaminopimelate deacetylase	Peptidase M20|Peptidase M20D, amidohydrola	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00103	dapD	113140	112436	234	7,8	24211	-	2,3,4,5-tetrahydropyridine-2-carboxylate N-suc	tetrahydrodipicolinate N-succinyltransferase	Tetrahydrodipicolinate N-acetyltransferase (E(	Bacterial transferase hexapeptide repeat|Trimer	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00104	lysA	114493	113150	447	5,87	48107	-	Diaminopimelate decarboxylase	lysine biosynthesis diaminopimelate decarboxyl	Diaminopimelate decarboxylase (EC 4.1.1.20)	Orn/DAP/Arg decarboxylase 2|Diaminopimelate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00105	thrA	115459	116838	459	6,15	50147	+	Aspartokinase	aspartate kinase region	Aspartokinase (EC 2.7.2.4)	Aspartate/glutamate/uridylate kinase|Aspartate l	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00106	dapF	116841	117848	335	5,33	35770	+	Diaminopimelate epimerase	diaminopimelate epimerase (DAP epimerase)	Diaminopimelate epimerase (EC 5.1.1.7)	Diaminopimelate epimerase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00107	asd	117856	118914	352	4,99	37960	+	Aspartate-semialdehyde dehydrogenase	Aspartate-semialdehyde dehydrogenase, USG-	Aspartate-semialdehyde dehydrogenase (EC :	Semialdehyde dehydrogenase, NAD - binding|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00108	null	119130	119507	125	10,95	13682	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_00109	null	119676	120089	137	5,85	15590	+	ADP-ribose pyrophosphatase	ADP-ribose pyrophosphatase	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00110	null	120082	120960	292	10,69	31733	+	Permease of the drug/metabolite transporter (I	permease of the drug/metabolite transporter (DI	Transporter	Protein of unknown function DUF6, transmemb	GER	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_00111	null	122252	121518	244	10,97	28492	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_00112	null	122663	123190	175	10,86	20073	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00113	null	123325	123951	208	9,89	24247	+	Transposase, IS4 family protein	transposase, DDE domain	Transposase	Transposase, IS4-like|Polynucleotidyl transfera	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00114	null	124928	124287	213	9,4	24220	-	Transcriptional regulator, TetR family	transcriptional regulator	not_predicted_by_ERGO	Bacterial regulatory protein, TetR|Tetracycline r	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00115	null	126121	125165	318	10,36	34755	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	ABC-2 type transporter	V	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00116	null	126864	126124	246	8,72	27678	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	ABC-2 type transporter	V	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00117	sagG	127813	126878	311	6,73	34261	-	ABC transporter, ATPase component	multidrug ABC transporter, ATPase component	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00118	yybT	128137	130143	668	4,77	74742	+	Phosphoesterase, DHH family protein	signaling protein (consists of PAS, a modified G	Phosphoesterase, DHH family protein	GGDEF|Phosphoesterase, RecJ-like|Phosphoe	R	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_00119	rplI	130160	130615	151	10,57	16917	+	LSU/50S ribosomal protein L9P	50S ribosomal protein L9 (BL17)	LSU ribosomal protein L9P	Ribosomal protein L9|Ribosomal protein L9 N-te	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00120	dnaC	131199	132584	461	4,32	51302	+	Replicative DNA helicase	primary replicative DNA helicase	Replicative DNA helicase (EC 3.6.1.-)	DnaB helicase|DnaB-like helicase, N-terminal|D	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00121	null	132647	133810	387	4,35	43591	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00122	pts	135923	133932	663	7,01	68575	-	PTS system, sucrose-specific IIABC compone	PTS system, sucrose-specific IIBC component	PTS system, sucrose-specific IIABC compone	Phosphotransferase system, sugar-specific per	G	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_00123	murQ	136842	135910	310	5,63	32529	-	N-acetylmuramic acid 6-phosphate etherase	N-acetylmuramic acid 6-phosphate etherase (M	Glucokinase regulatory protein	Regulator of chromosome condensation, RCC1	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00124	yleB	137945	136899	348	6,7	38318	-	Outer surface protein	outer surface protein	outer surface protein	Peptidyl-prolyl cis-trans isomerase, cyclophilin-t	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00125	null	139021	138152	289	8,37	31972	-	Transcriptional regulator, RpiR family	transcriptional regulator, helix-turn-helix protein	Transcriptional regulator, RpiR family	Helix-turn-helix protein RpiR|Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00126	null	139734	139129	201	7,63	22463	-	Transcriptional regulator, TetR family	predicted ORF	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00127	psaA	140030	140734	234	4,94	25616	+	ABC transporter, ATPase component	amino acid ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00128	ileS	140745	144050	1101	10,02	122916	+	ABC transporter permease protein	efflux ABC transporter, permease component	ABC transporter permease protein	Protein of unknown function DUF214, permase	V	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_00129	null	144242	145297	351	7,3	39969	+	Metal-dependent hydrolase	metal-dependent hydrolase	metal-dependent hydrolase	Amidohydrolase 2	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00130	purA	145512	146804	430	6,03	47137	+	Adenylosuccinate synthetase	adenylosuccinate synthetase (IMP--aspartate lig	Adenylosuccinate synthetase (EC 6.3.4.4)	Adenylosuccinate synthetase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+

LC_00131	null	147069	146818	83	12,25	9080	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00132	null	147036	147209	57	10,82	6552	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00133	cadA	147253	149151	632	6,37	67149	+	Heavy metal-transporting ATPase	ATPase, E1-E2 type:Heavy metal-(Cd/Co/Hg/P	Lead, cadmium, zinc and mercury transporting	Cof protein|H+ transporting ATPase, proton pur	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00134	yozA	149247	149591	114	5,89	12687	+	Transcriptional regulator, ArsR family	transcriptional regulator, ArsR family	Cadmium efflux system accessory protein	Bacterial regulatory protein, ArsR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00135	null	149944	151158	404	10,11	44433	+	Transporter, major facilitator superfamily MFS	permease, MDR related, probably tetracycline r	Tetracycline resistance protein	Major facilitator superfamily MFS_1	GEPF	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_00136	null	151388	152509	373	8,34	41812	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00137	null	152558	152773	71	9,07	8377	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00138	CcmA9	152770	153699	309	10,02	33696	+	ABC transporter, ATPase component	multidrug ABC transporter, ATPase component	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00139	null	153696	154457	253	10,07	27929	+	ABC transporter, permease protein	ABC transporter, permease component, membr	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00140	nrdD	154742	156925	727	8,14	82599	+	Anaerobic ribonucleoside-triphosphate reducta	anaerobic ribonucleoside-triphosphate reductas	Anaerobic ribonucleoside-triphosphate reducta	Formate C-acetyltransferase glycine radical|ATI	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00141	null	157108	157332	74	9,92	8585	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00142	null	157511	157807	98	9,92	11494	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00143	null	158429	157821	202	9,79	22818	-	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional repressor	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	IMP	tmhmm:4	-	-	-	-	regulator	-	-
LC_00144	yveB	160020	159040	326	9,43	36335	-	Membrane-associated phospholipid phosphata	membrane-associated phospholipid phosphatas	putative phosphatases	Phosphoesterase, PA-phosphatase related|Acid	I	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00145	null	161197	160121	358	5,97	40510	-	MccC family protein	microcin C7 resistance MccF/MccC related pro	Muramoyltetrapeptide carboxypeptidase (EC 3	Peptidase S66, LD-carboxypeptidase A	V	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00146	null	161455	161706	83	8,1	8998	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00147	ddl2	162918	161836	360	5,09	39250	-	D-alanine--D-alanine ligase	D-alanine-D-alanine ligase related ATP-grasp e	D-alanine--D-alanine ligase (EC 6.3.2.4)	D-alanine--D-alanine ligase/VANA/B/C|D-alanin	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00148	null	163208	163474	88	11,11	9157	+	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00149	null	164548	163904	214	10,33	23595	-	Conserved protein	predicted ORF	Transporter	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00150	null	165987	164566	473	10,54	49814	-	Transporter, major facilitator superfamily MFS	predicted ORF	Multidrug resistance protein B	Tetracycline resistance protein TetB|Drug resis	GEPF	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	-
LC_00151	null	166557	166051	168	9,64	18962	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00152	phoR	167751	166684	355	6,44	39402	-	Two component sensor transduction histidine	two-component sensor histidine kinase	Phosphate regulon sensor protein phoR (EC 2	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	-
LC_00153	phoP	168422	167748	224	4,93	25416	-	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+
LC_00154	ogt	168626	169117	163	9,93	18397	+	Methylated DNA-protein cysteine methyltransf	methylated-DNA--protein-cysteine methyltransfe	O6-methylguanine-DNA methyltransferase (E	Methylated-DNA-[protein]-cysteine S-methyltrar	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00155	ldhD	169223	170224	333	5,56	37130	+	D-lactate dehydrogenase	D-2-hydroxyisocaproate dehydrogenase	D-2-hydroxyisocaproate dehydrogenase (EC 1	D-isomer specific 2-hydroxyacid dehydrogenase	CHR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00156	pts	170506	170820	104	5,18	11334	+	PTS system, cellobiose-specific IIB componer	PTS system, cellobiose-specific IIB component	PTS system, cellobiose-specific IIB componer	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_00157	pts	170830	171153	107	5,98	11728	+	PTS system, cellobiose-specific IIA componer	PTS system, cellobiose-specific IIA component	PTS system, cellobiose-specific IIA componer	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00158	null	171173	171667	164	10,64	18835	+	PTS system, cellobiose-specific IIC componer	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00159	pts	171690	173054	454	9,35	49298	+	PTS system, IIC component	PTS system, lactose/cellobiose/lichenan/oligosa	PTS system, cellobiose-specific IIC componer	Peptidase, cysteine peptidase active site|Phosp	G	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00160	bglA	173100	174536	478	5,13	54729	+	6-phospho-beta-glucosidase (GH1)	beta-glucosidase/6-phospho-beta-glucosidase/t	6-phospho-beta-glucosidase (EC 3.2.1.86)	Glycoside hydrolase, family 1|Glycoside hydrola	G	Yes	-	-	tmhmm:0	LC00160	-	-	-	-	-	-
LC_00161	null	174759	175496	245	8,86	27413	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00162	null	175866	175570	98	9,66	10833	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00163	null	176280	175912	122	10,02	13277	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function DUF1304	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00164	null	176672	176322	116	11,94	13109	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	Protein of unknown function DUF1516	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00165	pbuO	176866	178323	485	6,68	50856	+	Xanthine/uracil permease family protein	xanthine/uracil/vitamin C permease family	Guanine-hypoxanthine permease	Xanthine/uracil/vitamin C permease	R	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_00166	null	178459	178782	107	5,96	11860	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	Domain of unknown function DUF1791	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00167	yaiA	179835	178858	325	4,88	36830	-	Glyoxalase family protein	dioxygenase/glyoxalase / Lactoylglutathione lya	Glyoxalase family protein	Glyoxalase/bleomycin resistance protein/dioxyge	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00168	null	180026	180322	98	6,73	10656	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00169	null	181069	180494	191	8,44	22221	-	Alanine acetyl transferase	conserved hypothetical protein	Ribosomal-protein-alanine acetyltransferase (E	no annotation	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00170	null	181565	183514	649	9,15	70293	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00171	null	183529	183849	106	4,7	11778	+	Conserved extracellular protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-
LC_00172	yqcC	183852	184658	268	5,08	28475	+	Cell surface protein	cell surface protein	Hypothetical exported protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_00173	ynjC	184800	185879	359	10,38	39517	+	Cell surface protein	cell surface protein	Hypothetical protein	Sugar transporter superfamily|Protein of unkno	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-
LC_00174	null	185960	186181	73	10,85	8392	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00175	null	186192	187655	487	6,03	56166	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00176	null	187848	188834	328	10,41	36090	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function DUF805	null	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+
LC_00177	null	189244	188918	108	6,52	12237	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	Concanavalin A-like lectin/glucanase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00178	cshA2	189537	190883	448	7,82	49942	+	AAA ATPase	recombination factor protein RarA	ATPase, AAA family	AAA+ ATPase, core|AAA ATPase, core	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00179	ack2	191159	192349	396	4,67	43235	+	Acetate kinase	acetate kinase	Acetate kinase (EC 2.7.2.1)	Acetate and butyrate kinase|Acetate kinase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00180	null	193248	192496	250	8,41	27909	-	Transcriptional regulator, DeoR family	transcriptional regulator, DeoR family	Transcriptional regulator, DeoR family	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00181	null	193415	194911	498	5,56	55210	+	Xylulokinase	xylose kinase	Xylulose kinase (EC 2.7.1.17)	Carbohydrate kinase, FGGY|Small acid-soluble	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00182	agaY	194923	195792	289	5,12	32170	+	Fructose-bisphosphate aldolase	fructose/tagatose bisphosphate aldolase	Fructose-biphosphate aldolase class-II family	Ketose-bisphosphate aldolase, class-II|Aldolase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00183	ulaA	195904	197241	445	9,95	47293	+	PTS system, ascorbate-specific IIC componer	PTS system, ascorbate-specific IIC component	Putative transport protein sgaT	Putative sugar-specific permease, SgaT/UlaA	S	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00184	null	198211	197387	274	6,68	31009	-	Diadenosine tetraphosphatase related serine/t	Diadenosine tetraphosphatase related serine/thr	Serine/threonine protein phosphatase (EC 3.1	Metallophosphoesterase	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00185	null	198369	199088	239	8,72	27682	+	Similar to endonuclease III	DNA-3-methyladenine glycosylase III / Endonuc	Endonuclease III (EC 4.2.99.18)	HhH-GPD|DNA glycosylase	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00186	null	200551	199103	482	9,8	52159	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	+
LC_00187	null	201303	200635	222	8	25456	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00188	null	201716	201333	127	7,86	14393	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00189	null	202761	201961	266	9,6	29620	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00190	null	203277	202783	164	10,24	18985	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00191	abc	203914	203270	214	9,36	23717	-	ABC transporter, ATPase component	antibiotic ABC transporter, ATPase component	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00192	null	204495	204322	57	6,5	6345	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00193	null	204655	204509	48	8,47	5272	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00194	xpkA	204916	207297	793	5,48	89600	+	Phosphoketolase	xylulose-5-phosphate phosphoketolase	Xylulose-5-phosphate (EC 4.1.2.9) / Fructose-	D-xylulose 5-phosphate/D-fructose 6-phosphate	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00195	oppA	207605	209227	540	9,97	59853	+	ABC transporter, oligopeptide-binding protein	oligopeptide ABC transporter, oligopeptide-bind	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_00196	null	209838	210626	262	10,1	28895	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00197	null	210768	211334	188	10,35	20912	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00198	null	211341	212075	244	9,79	27821	+	Phosphotransferase system, mannose/fructos	predicted ORF	ABC transporter ATP-binding protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00199	abc	212056	212724	222	5,07	24450	+	ABC transporter, ATPase component	lantibiotic ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-

LC_00200	null	212727	213200	157	11,58	18192	+	Conserved protein	conserved hypothetical protein	ABC transporter ATP-binding protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00201	null	213254	213721	155	5,2	17508	+	Phosphohydrolase, MutT/nudix family	NUDIX family hydrolase	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00202	null	213864	214997	377	5,84	41825	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00203	null	216916	215078	612	6,73	68767	-	FAD(NAD)-dependent oxidoreductase	FAD(NAD)-dependent oxidoreductase	Hypothetical cytosolic protein	no annotation	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00204	nox5	217064	218425	453	6,16	49513	+	NADH oxidase	H2O-forming NADH oxidase	NADH oxidase H2O-forming (EC 1.6.-.-)	Pyridine nucleotide-disulphide oxidoreductase, (	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00205	null	218436	219068	210	9,16	23753	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_00206	null	219217	219065	50	10,04	5543	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:0	-	-	-	-	-	-	-
LC_00207	null	219427	220623	398	9,09	43376	+	Beta-propeller domains of methanol dehydroge	beta-propeller domains of methanol dehydrogen	Hypothetical membrane spanning protein	Histidine acid phosphatase|Protein of unknown	R	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_00208	yxaA	220737	221579	280	10,24	29119	+	Permease	permease	Hypothetical membrane spanning protein	Protein of unknown function DUF81	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_00209	ywjH	221579	221953	124	8,89	13332	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane associated protein	Protein of unknown function DUF1634	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00210	null	222278	222072	68	6,68	7841	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00211	null	222964	222575	129	10,39	15089	-	Putative protein without homology	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	Nterm/Cter	tmhmm:2	-	-	-	-	-	-	-
LC_00212	null	223200	223505	101	5,17	11954	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00213	fldA	223585	224052	155	4,62	17145	+	Flavodoxin	flavodoxin/nitric oxide synthase	Flavodoxin	Flavodoxin/nitric oxide synthase|Flavodoxin	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00214	null	224099	224341	80	5,01	8718	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00215	null	224338	224532	64	9,93	7050	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00216	null	224502	224657	51	12,08	5637	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00217	null	225308	224622	228	6,43	24405	-	2-hydroxyacid dehydrogenase	D-isomer specific 2-hydroxyacid dehydrogenas	Glyoxylate reductase (NADP+) (EC 1.1.1.79) ,	D-isomer specific 2-hydroxyacid dehydrogenas	CHR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00218	null	225583	225374	69	9,77	7219	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00219	null	225796	226197	133	4,92	14708	+	Pyridoxine 5'-phosphate oxidase V related favi	pyridoxine 5'-phosphate oxidase V related favin	Hypothetical cytosolic protein	FMN-binding split barrel, related|Pyridoxamine 5	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00220	ydaS	226442	226696	84	11,38	8657	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Integral membrane protein	Transglycosylase-associated protein	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00221	null	226710	227249	179	11,02	19814	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00222	null	227351	227548	65	10,63	7172	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00223	asp1	227614	227967	117	4,48	13055	+	Alkaline shock protein	general stress protein, gls24 protein / alkaline sl	General stress protein, Gls24 family	Protein of unknown function DUF322	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00224	asp2	228125	228550	141	4,49	15559	+	Alkaline shock protein	alkaline shock protein 23	General stress protein, Gls24 family	Protein of unknown function DUF322	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00225	null	229277	228621	218	6,06	25591	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)	Haloacid dehalogenase-like hydrolase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00226	null	229494	230174	226	10,47	24686	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Permease	Protein of unknown function DUF969	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00227	null	230171	231088	305	10,08	31370	+	Putative protein without homology	conserved hypothetical protein (transmembrane	Permease	Protein kinase|Protein of unknown function DUI	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_00228	pcp	231104	231751	215	5,13	23504	+	Pyrrolidone-carboxylate peptidase	pyrrolidone-carboxylate peptidase (5-oxoprolyl-p	Pyrrolidone-carboxylate peptidase (EC 3.4.19.	Peptidase C15, pyroglutamyl peptidase I	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00229	null	231906	232526	206	6,36	21566	+	NADP oxidoreductase coenzyme F420-depen	NADP oxidoreductase coenzyme F420-dependi	Oxidoreductase (EC 1.1.1.-)	NADP oxidoreductase, coenzyme F420-dependi	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00230	null	232569	232721	50	10	5804	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00231	cobQ	233528	232854	224	6,52	25129	-	Glutamine amidotransferase	CobB/CobQ-like glutamine amidotransferase dc	CobB/CobQ-like glutamine amidotransferase (	CobB/CobQ-like glutamine amidotransferase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00232	null	234088	233708	126	4,24	15183	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00233	gidB	234627	235358	243	8,24	26466	+	Ribosomal RNA small subunit methyltransfera	methyltransferase gidB (glucose-inhibited divisi	Methyltransferase gidB (EC 2.1.-.-)	Glucose inhibited division protein	M	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	+
LC_00234	parB1	235362	236189	275	9,82	31088	+	Nucleoid occlusion protein	chromosome partitioning protein (stage 0 sporu	Chromosome partitioning protein parB	ParB-like nuclease|ParB-like partition protein	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00235	parA	236199	236966	255	5,11	27645	+	Chromosome partitioning protein ParA	chromosome partitioning ATPase, ParA family /	Chromosome partitioning protein parA	Cobyrinic acid a,c-diamide synthase	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00236	parB2	236956	237828	290	9,99	32516	+	ParB-like partition protein	Spo0J-like protein, ParB-like nuclease domain	Spo0J-like protein	ParB-like nuclease|ParB-like partition protein	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00237	null	237855	238046	63	9,94	7342	+	Conserved domain protein	translation-associated GTPase	Hypothetical cytosolic protein	Protein of unknown function DUF951, bacterial	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00238	ychF	238069	239175	368	4,64	40320	+	GTP-binding protein YchF	translation-associated GTPase	GTP-binding protein, probable translation fact	GTP-binding protein, HSR1-related|Conserved	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00239	null	239233	240021	262	9,43	29083	+	Conserved membrane protein	conserved hypothetical protein (membrane-bou	Hypothetical membrane spanning protein	Membrane protein of unknown function UCP03:	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00240	guaB	240414	241901	495	5,99	52619	+	Inosine-5'-monophosphate dehydrogenase	inosine-5'-monophosphate dehydrogenase (IMF	Inosine-5'-monophosphate dehydrogenase (E(	Cystathionine-beta-synthase|IMP dehydrogenas	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00241	null	242225	241911	104	12,02	11174	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00242	null	242935	242246	229	10,69	26023	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00243	rrp31	243079	243765	228	4,64	25514	+	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+
LC_00244	hpk31	243769	244959	396	7,27	44723	+	Two component sensor transduction histidine	two-component system, sensor histidine kinase	Two component system histidine kinase (EC 2	ATP-binding region, ATPase-like|Histidine kina	null	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	+
LC_00245	dacA	244956	246266	436	10,17	46901	+	D-alanyl-D-alanine carboxypeptidase	D-alanyl-D-alanine carboxypeptidase (penicillin-	D-alanyl-D-alanine serine-type carboxypeptida	Peptidase S11, D-alanyl-D-alanine carboxypept	M	Yes	-	Sec	tmhmm:1	-	-	-	-	-	protease	+
LC_00246	null	246586	246317	89	11,96	9760	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00247	greA	246631	247128	165	5,61	17747	+	Transcription elongation factor	transcription elongation factor greA 1 (transcripl	Transcription elongation factor greB	Transcription elongation factor, GreA/GreB regi	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00248	murE	247326	248879	517	6,52	56715	+	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--l	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-	Cytoplasmic peptidoglycan synthetases, C-term	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00249	racD	248885	249637	250	6,17	28415	+	Aspartate racemase	aspartate racemase (5.1.1.13)	Aspartate racemase (EC 5.1.1.13)	Asp/Glu racemase|Aspartate racemase	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00250	ycgG	249784	250644	286	6,37	31598	+	Oxidoreductase, aldo/keto reductase family	aldo/keto reductase of diketogulonate reductase	Aldo/keto reductase family	Aldo/keto reductase	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00251	iolR	251595	250801	264	9,16	29287	-	Transcriptional regulator, DeoR family	transcriptional regulator, DeoR family, iolR	DNA-binding protein iolR	Bacterial regulatory protein, DeoR N-terminal|Ba	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00252	iolT	252019	253506	495	10,75	53851	+	Transporter, major facilitator superfamily MFS	sugar transporter, MFS superfamily protein, ma	Myo-inositol transporter	Sugar transporter|General substrate transporter	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00253	iolA	253900	255375	491	5,5	53493	+	Methylmalonate-semialdehyde dehydrogenase	methylmalonate semialdehyde dehydrogenase	Malonate-semialdehyde dehydrogenase (acety	Aldehyde dehydrogenase|Methylmalonate-semi	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00254	iolB	255409	256224	271	6,12	30754	+	Myo-inositol catabolism IolB domain protein	iolB protein	IolB protein	Myo-inositol catabolism IolB region|Cupin, RmlC	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00255	iolC	256274	257248	324	4,79	35347	+	5-dehydro-2-deoxygluconokinase	iolC protein	5-dehydro-2-deoxygluconokinase (EC 2.7.1.92	Carbohydrate kinase, PfkB|PfkB	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00256	iolD	257265	259211	648	5,09	70598	+	Myo-inositol catabolism protein IolD	myo-inositol catabolism (acetolactate synthase)	IOLD PROTEIN	TPP-binding enzymes|Thiamine pyrophosphate	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00257	iolG1	259242	260282	346	4,83	38082	+	Myo-inositol 2-dehydrogenase	oxidoreductase, myo-inositol 2-dehydrogenase (	Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	Oxidoreductase, N-terminal|Oxidoreductase, C-	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00258	iolG2	260323	261375	350	4,86	38272	+	Myo-inositol 2-dehydrogenase	myo-inositol dehydrogenase	Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	Oxidoreductase, N-terminal|Oxidoreductase, C-	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00259	iolE	261368	262273	301	5,64	34164	+	Myo-inosose dehydratase	Myo-inositol catabolism protein IolE (2-keto-myc	IOLE protein	Xylose isomerase-like TIM barrel	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00260	iolJ	262303	263175	290	6,85	30944	+	Fructose-bisphosphate aldolase	fructose-bisphosphate aldolase 2	Fructose-bisphosphate aldolase (EC 4.1.2.13)	Ketose-bisphosphate aldolase, class-II|Aldolase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00261	iolK	263272	263661	129	5,56	14738	+	4-oxalocrotonate tautomerase	4-oxalocrotonate tautomerase	Tautomerase family protein	4-oxalocrotonate tautomerase|Tautomerase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00262	null	263931	264818	295	5,18	33349	+	Xylose isomerase domain protein TIM barrel	xylose isomerase/epimerase domain protein TIM	Hypothetical protein	Xylose isomerase-like TIM barrel	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00263	iolH	264815	265687	290	5,36	33463	+	IolH	xylose isomerase domain protein TIM barrel, Pn	IOLH protein	Xylose isomerase-like TIM barrel	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00264	gntR	266660	265818	280	7,19	30419	-	Transcriptional regulator, RpiR family	gluconate operon transcriptional regulator, RpiR	Transcriptional regulator, RpiR family	Helix-turn-helix protein RpiR|Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00265	gnd1	266943	267851	302	5,29	32274	+	6-phosphogluconate dehydrogenase	6-phosphogluconate dehydrogenase-like protei	6-phosphogluconate dehydrogenase (EC 1.1.1.	6-phosphogluconate dehydrogenase related prc	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00266	gntK	268033	269601	522	5,3	57078	+	Gluconate kinase	gluconate kinase (2-dehydro-3-deoxygluconokin	Gluconokinase (EC 2.7.1.12)	Carbohydrate kinase, FGGY|Gluconate kinase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00267	null	269767	269919	50	11,97	5390	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00268	gntP	270178	271530	450	9,71	46764	+	Gluconate transporter	high-affinity H+/gluconate symporter permease	Gluconate permease	Gluconate transporter	GE	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-

LC_00269	null	271663	272007	114	5,91	12822	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00270	znuC	272172	272891	239	6,64	27018	+	ABC transporter, ATPase component	Mn2+/Zn2+ ABC transporter, ATPase compone	Manganese transport system ATP-binding prc	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00271	null	272888	273685	265	9,84	28442	+	ABC transporter, Mn2+/Zn2+ transporter perm	Mn2+/Zn2+ ABC transporter, permease compo	Manganese transport system membrane prote	ABC-3	P	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_00272	null	274646	273798	282	6,55	31861	-	Ser/Thr protein phosphatase family	Diadenosine tetraphosphatase related serine/th	Bis(5'-nucleosyl)-tetraphosphatase (symmetric	Metallophosphoesterase|Phosphoesterase MJ0	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00273	mmsB	275515	274643	290	7,08	30382	-	3-hydroxyisobutyrate dehydrogenase	3-hydroxyisobutyrate dehydrogenase related bel	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.	Aminotransferase, class-II|Hydroxyacid dehydr	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00274	pepF1	277320	275521	599	5,44	67221	-	Oligoendopeptidase F	oligoendopeptidase F1. Metallo peptidase. MER	Oligoendopeptidase F (EC 3.4.24.-)	Peptidase M3A and M3B, thimet/oligopeptidase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00275	lytR	277449	278543	364	10,06	40272	+	Transcriptional regulator, LytR family	transcriptional regulator, LytR family	Transcriptional regulator, LytR family	Cell envelope-related transcriptional attenuator	K	Yes	-	Sec	tmhmm:1	-	-	-	-	regulator	-	+	
LC_00276	null	278549	278701	50	10,33	5774	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00277	brnQ	280031	278652	459	10,33	49056	-	Branched-chain amino acid transport protein	branched-chain amino acid permease	Branched-chain amino acid transport system (	Branched-chain amino acid transport system II	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_00278	null	281372	280683	229	4,71	23601	-	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00279	fcsR	282059	282817	252	9,82	28244	+	Transcriptional regulator, DeoR family	transcriptional repressor of sugar metabolism, C	Transcriptional regulator, DeoR family	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00280	null	282901	283683	260	9,73	30134	+	Glycosyl transferase, group 2	glycosyltransferase related enzyme	Glycosyltransferase involved in cell wall bioger	Glycosyl transferase, family 2	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00281	null	283702	284439	245	10,05	28114	+	Integral membrane protein	conserved hypothetical protein (integral membra	Integral membrane protein	Protein of unknown function DUF975	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_00282	null	284536	284868	110	5,86	12387	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00283	sipT	285597	284998	199	10,57	22767	-	Signal peptidase I	signal peptidase I (Leader peptidase I, Spasel)	Signal peptidase I (EC 3.4.21.89)	Peptidase S26A, signal peptidase I|Peptidase S	U	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+	
LC_00284	null	286612	285674	312	4,89	33104	-	ADP-ribosylglycohydrolase	ADP-ribosylglycohydrolase	ADP-ribosylglycohydrolase (EC 3.2.-.-)	ADP-ribosylation/Crystallin J1|ADP-ribosylglycc	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00285	abc	287025	288572	515	5,14	57587	+	ABC transporter, ATPase component	ABC transporter with duplicated ATPase domai	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00286	null	289454	288708	248	6,31	27965	-	Methylase for ubiquinone/menaquinone biosyr	methylase for ubiquinone/menaquinone biosynth	Hypothetical cytosolic protein	Peptidase, cysteine peptidase active site	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00287	null	290252	290067	61	10,44	6799	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00288	null	290203	290406	67	11,84	7290	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00289	null	290677	290360	105	12,08	11621	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00290	null	290856	290662	64	11,31	7429	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00291	null	291541	291143	132	10,4	14921	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	C-type lectin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00292	null	291729	291517	70	8,5	7801	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00293	null	292531	292136	131	8,72	14815	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00294	null	293745	293446	99	11,9	11432	-	Lipoprotein	lipoprotein	not_predicted_by_ERGO	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00295	null	293883	294221	112	11,26	12018	+	Conserved protein	metal-dependent RNase, consists of a metallo-l	not_predicted_by_ERGO	KH, prokaryotic type	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00296	trxA	294863	295183	106	9,49	11769	+	Thioredoxin	thiol-disulfide isomerase and thioredoxins	Thioredoxin	Thioredoxin-related|Thioredoxin fold|Thioredoxi	OC	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00297	labL	295207	295956	249	5,7	27205	+	Threonine/Serine Exporter	conserved hypothetical protein (membrane prot	Threonine/Serine Exporter	Protein of unknown function DUF1212	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_00298	null	295974	296432	152	11,15	16704	+	Threonine/Serine Exporter	conserved hypothetical protein (integral membra	Threonine/Serine Exporter	no annotation	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_00299	livA	297121	298314	397	10,16	41554	+	ABC transporter, branched-chain amino acid-l	high affinity branched-chain amino acid ABC tra	Leucine-, isoleucine-, valine-, threonine-, and a	Leu/Ile/Val-binding protein|Extracellular ligand-b	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_00300	livB	298351	299229	292	9,75	31069	+	ABC transporter, branched-chain amino acid t	high affinity branched-chain amino acid ABC tra	Branched-chain amino acid transport system p	Bacterial inner-membrane translocator	E	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_00301	livC	299234	300184	316	10,13	33394	+	ABC transporter, branched-chain amino acid t	high affinity branched-chain amino acid ABC tra	Branched-chain amino acid transport system p	Bacterial inner-membrane translocator	E	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_00302	livD	300181	300966	261	6,64	28347	+	ABC transporter, branched-chain amino acid t	branched-chain amino acid ABC transporter, A	Branched-chain amino acid transport ATP-bin	ABC transporter related|AAA+ ATPase, core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00303	livE	300959	301675	238	9,8	25210	+	ABC transporter, branched-chain amino acid t	branched-chain amino acid ABC transporter, A	Branched-chain amino acid transport ATP-bin	ABC transporter related|AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00304	mazG	301840	302163	107	4,94	12560	+	Pyrophosphatase	MazG/MagZ nucleotide pyrophosphohydrolase	Hypothetical protein	NTP pyrophosphohydrolase MazG, putative cat	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00305	null	303185	302283	300	9,69	33124	-	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Protein of unknown function DUF915, hydrolas	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00306	pts	304494	303178	438	10,52	48295	-	PTS system, cellobiose-specific IIC componer	PTS system, cellobiose-specific IIC component	PTS system, cellobiose-specific IIC componer	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_00307	deoC	304812	305477	221	4,91	23095	+	Deoxyribose-phosphate aldolase	deoxyribose-phosphate aldolase (Phosphodeox	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	Deoxyribose-phosphate aldolase/phospho-2-del	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00308	deoB	305479	306669	396	4,72	43167	+	Phosphopentomutase	Phosphopentomutase (Phosphodeoxyribomutas	Phosphopentomutase (EC 5.4.2.7)	Alkaline phosphatase|Metalloenzyme|Phosphop	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00309	deoD	306794	307510	238	5,63	25831	+	Purine nucleoside phosphorylase II	Purine nucleoside phosphorylase deoD-type (Pl	Purine nucleoside phosphorylase II (EC 2.4.2.	Nucleoside phosphorylase|Purine nucleoside pl	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00310	null	307701	309182	493	6,96	49323	+	Cell wall-associated glycoside hydrolase (NLP	conserved hypothetical protein (p75)	Cell wall-associated glycosyl hydrolase	NLP/P60 (cell wall hydrolase)	null	Yes	-	Sec	tmhmm:1	LC00310	-	-	-	-	-	+	
LC_00311	nox	310691	309330	453	4,86	49061	-	NADH oxidase	NADH oxidase (NOXase)	NADH oxidase H2O-forming (EC 1.6.-.-)	Pyridine nucleotide-disulphide oxidoreductase, (	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00312	lacE-1	311240	313033	597	6,44	65274	+	PTS system, lactose-specific IIBC component	PTS system, lactose-specific IICB component (	not_predicted_by_ERGO	Phosphotransferase system, EIIC|Phosphotran	G	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_00313	lacT	313090	313956	288	7,29	32881	+	Transcription antiterminator lacT	Transcription antiterminator lacT	not_predicted_by_ERGO	CAT RNA-binding region|PRD	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00314	lacF-1	314057	314422	121	4,43	13402	+	PTS system, lactose-specific IIA component	PTS system, lactose-specific IIA component	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose-	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00315	lacG1	314448	315872	474	5,6	54247	+	6-phospho-beta-galactosidase	beta-glucosidase/6-phospho-beta-glucosidase/t	not_predicted_by_ERGO	Glycoside hydrolase, family 1|6-phospho-beta-g	G	No	-	-	tmhmm:0	LC00315	-	-	-	-	-	+	
LC_00316	null	316779	315931	282	8,71	31356	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00317	null	317456	316776	226	7,65	25515	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00318	srmB	319818	317434	794	6,28	89453	-	ATP-dependent helicase	Rad3-related ATP-dependent DNA and RNA re	Superfamily II DNA and RNA helicase	DEXDc2|Helicase c2|DEAD_2|Helicase superfa	KL	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00319	malE2	320025	321314	429	10,09	46825	+	ABC transporter, sugar transporter periplasmi	sugar ABC transporter, periplasmic component	Sugar-binding protein	Bacterial extracellular solute-binding protein, far	G	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_00320	null	321511	322161	216	10,4	23811	+	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00321	null	322459	324393	644	8,03	71927	+	PTS system, IIAB component	predicted ORF	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00322	frvA	324386	324841	151	5,91	16241	+	PTS system, IIA component	PTS system, IIA component	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00323	FruA	324861	326303	480	7,38	49403	+	PTS system, fructose-specific IIC component	PTS system, fructose IIC component	not_predicted_by_ERGO	Phosphotransferase system, EIIC|Phosphotran	G	No	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_00324	manA	326559	327530	323	6,51	36028	+	Mannose-6-phosphate isomerase	mannose-6-phosphate isomerase (Phosphomar	Mannose-6-phosphate isomerase (EC 5.3.1.8)	Mannose-6-phosphate isomerase, type I|Cupin, G	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00325	gntR	327924	328640	238	6,9	27231	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00326	agaS	328654	329835	393	4,54	42954	+	Tagatose-6-phosphate ketose/aldose isomera	phosphosugar isomerases	Galactosamine-6-phosphate deaminase (isom	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00327	nagA	329912	331072	386	4,84	41532	+	N-acetylglucosamine-6-phosphate deacetylas	N-acetylglucosamine-6-phosphate deacetylase	N-acetylglucosamine-6-phosphate deacetylas	N-acetylglucosamine-6-phosphate deacetylase|	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00328	bgaC	331215	332996	593	5,54	67221	+	Beta-galactosidase (GH35)	glycosyl hydrolase / Beta-galactosidase 3	Beta-galactosidase (EC 3.2.1.23)	Glycoside hydrolase, family 35|Glycoside hydro	G	Yes	-	-	tmhmm:0	LC00328	-	-	-	-	-	+	
LC_00329	pts	333189	333671	160	9,02	17347	+	PTS system, mannose-specific IIB componen	PTS system, IIB component	PTS system, galactosamine-specific IIB comp	Phosphotransferase system, sorbose subfamily	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00330	pts	333684	334598	304	5,57	32010	+	PTS system, mannose-specific IIC componen	PTS system, IIC component	PTS system, galactosamine-specific IIC comp	Phosphotransferase system, sorbose-specific i	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_00331	fbpC	334585	335406	273	10,46	29843	+	PTS system, mannose-specific IID componen	PTS system, IID component	PTS system, galactosamine-specific IID comp	Phosphotransferase system, mannose/fructose	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_00332	pts	335548	335928	126	4,24	13473	+	PTS system, mannose-specific IIA componen	PTS system, mannose/fructose-specific IIA cor	PTS system, N-acetylgalactosamine-specific I	Phosphotransferase system, fructose subfamily	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00333	yohJ	336197	337723	508	6,86	57818	+	Lipopolysaccharide biosynthesis protein	lipopolysaccharide biosynthesis protein / polygly	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Cyclin-like|Proteir	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00334	yohH	337740	339353	537	6,13	61955	+	Poly(Glycerol-phosphate) alpha-glucosyltransf	lipopolysaccharide biosynthesis protein / polygly	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Protein of unknov	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00335	null	339477	340748	423	10,19	48265	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00336	PatB	342084	340888	398	4,97	44686	-	Aminotransferase	aminotransferase, classes I and II	Cystathionine beta-lyase (EC 4.4.1.8)	1-aminocyclopropane-1-carboxylate synthase|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00337	ypdF	343150	342071	359	5,53	38627	-	Aminopeptidase YpdF	peptidase M24	Xaa-Pro dipeptidase (EC 3.4.13.9)	Creatinase|Peptidase M24, catalytic core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-	

LC_00338	null	344583	343258	441	8,82	48282	-	PTS system, IIC component	PTS system, IIC component	PTS system, cellobiose-specific IIC componer	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-	
LC_00339	CelA	344956	344618	112	6,67	12438	-	PTS system, lactose/cellobiose-specific IIB cc	PTS system, lactose/cellobiose IIB component	PTS system, cellobiose-specific IIB componer	Phosphotransferase system, lactose/cellobiose	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00340	ptcA	345340	345023	105	4,52	11588	-	PTS system, lactose/cellobiose-specific IIA cc	PTS system, lactose-specific IIA component	PTS system, cellobiose-specific IIA componer	Phosphotransferase system, lactose/cellobiose	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00341	celM	346464	345424	346	5,87	36937	-	Aminopeptidase	deblocking (glutamyl)aminopeptidase, M42 fami	Aminopeptidase, M42 family (EC 3.4.-.-)	Peptidase M42	G	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-	
LC_00342	null	348242	346449	597	9,7	66688	-	Transcription antiterminator	predicted ORF	Transcription antiterminator, BglG family	Bacterial regulatory protein, DeoR N-terminal|PI	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	+
LC_00343	pepT-2	349876	348647	409	4,86	44581	-	Peptidase T	peptidase T, metallo peptidase, MEROPS famil	Tripeptidase T (EC 3.4.11.4)	ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|F	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00344	oppA	350008	351642	544	10,12	60349	+	ABC transporter, oligopeptide-binding protein	oligopeptide ABC transporter, oligopeptide-bind	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00345	wecD	352374	351730	214	6,3	24139	-	Acetyltransferase	GCN5-related N-acetyltransferase	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00346	null	352752	352540	70	7,77	7750	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00347	null	352688	352843	51	7,25	5527	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_00348	null	353535	353383	50	7,53	5538	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00349	nisT	355142	353586	518	9,51	57829	-	ABC transporter, cobalt transporter ATPase a	multidrug ABC transporter, ATPase/permease (	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core|Al	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00350	null	355761	356450	229	9,3	24870	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	R	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00351	null	356502	357209	235	8,55	26323	+	Peptidase S54, rhomboid	conserved hypothetical protein	not_predicted_by_ERGO	Peptidase S54, rhomboid|Protein kinase-like	R	No	-	IMP	tmhmm:6	-	-	-	-	-	protease	-	
LC_00352	null	357585	358154	189	9,44	20534	+	ABC transporter, cobalt transporter permease	cobalt ABC transporter, permease component	Hydroxymethylpyrimidine transport system per	no annotation	P	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00353	abc	358161	359504	447	10,07	49007	+	ABC transporter, cobalt transporter ATPase c	cobalt or other cation ABC transporter, ATPase	Hydroxymethylpyrimidine transport ATP-bindir	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00354	null	359509	360156	215	10,22	24040	+	ABC transporter, cobalt transporter permease	cobalt ABC transporter, permease component,	Hydroxymethylpyrimidine transport system per	no annotation	P	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00355	tenA	360270	360962	230	6,15	26243	+	Transcriptional activator TenA	transcriptional activator, TENA/THI-4 family	Transcriptional activator tenA	TENA/THI-4 protein	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00356	thiW	360943	361443	166	10,49	17878	+	Hydroxyethylthiazole permease	thiW protein, membrane protein	Hydroxyethylthiazole permease	ThiW	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_00357	null	361494	361982	162	6,35	17589	+	Hydroxyethylthiazole kinase	predicted ORF	Hydroxyethylthiazole kinase (EC 2.7.1.50)	Hydroxyethylthiazole kinase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00358	null	361979	362332	117	7,42	12488	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00359	thiE2	362329	362958	209	5,95	21827	+	Thiamine-phosphate pyrophosphorylase	thiamine-phosphate pyrophosphorylase 2 (TMP	Thiamin-phosphate pyrophosphorylase (EC 2.	Thiamine monophosphate synthase|Thiamine-p	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00360	thiD	362960	363811	283	6,3	29342	+	Phosphomethylpyrimidine kinase	hydroxymethylpyrimidine/phosphomethylpyrimid	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	Phosphomethylpyrimidine kinase type-2|Phospl	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00361	ycaM	364201	365649	482	9,82	53834	+	Amino acid transporter	APC family, amino-acid transporter	Amino acid permease	Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_00362	null	365657	365875	72	9,91	8342	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00363	rbsR	366062	367081	339	10,14	37116	+	Transcriptional regulator, LacI family	transcriptional regulator, LacI family, sugar-bind	Ribose operon repressor	Bacterial regulatory protein, LacI|Periplasmic bi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00364	rbsD	367115	367507	130	5,72	14568	+	D-ribose pyranase	ribose ABC transporter RbsD, auxiliary compon	not_predicted_by_ERGO	RbsD or FucU transport	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00365	rbsA	367672	369174	500	4,9	54990	+	ABC transporter, ribose-transporter ATPase c	ribose ABC transporter, ATPase component, R	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00366	rbsC	369158	370138	326	11,02	33843	+	ABC transporter, ribose-transporter permease	D-ribose ABC transporter, permease componer	not_predicted_by_ERGO	Bacterial inner-membrane translocator	G	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00367	rbsB	370249	371208	319	9,93	33376	+	ABC transporter, periplasmic ribose-binding p	D-ribose ABC-transporter, periplasmic compon	not_predicted_by_ERGO	Periplasmic binding protein/LacI transcriptional	G	No	-	Lipobox	tmhmm:1	-	-	-	-	-	-	-	
LC_00368	rbsK	371306	372247	313	5,1	32485	+	Ribokinase	sugar kinase, ribokinase family protein	Ribokinase (EC 2.7.1.15)	Ribokinase|Carbohydrate kinase, PfkB|PfkB|Rit	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00369	pheT	372654	372352	100	10,17	10960	-	Transcriptional regulator	transcriptional regulator, xre family	Transcriptional regulator	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00370	null	373505	372819	228	9,27	25311	-	Peptidase S54, rhomboid	conserved hypothetical protein	Integral membrane protein (Rhomboid family)	Peptidase S54, rhomboid	null	No	-	IMP	tmhmm:5	-	-	-	-	-	protease	-	
LC_00371	null	374431	374234	65	9,88	7474	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00372	null	374731	374549	60	6,78	7069	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00373	null	375856	375683	57	10,11	6651	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00374	null	376728	375913	271	8,2	31001	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00375	pbp5	378865	376877	662	9,99	70831	-	Penicillin-binding protein 3	cell division protein FtsI/penicillin-binding protei	Beta-lactam-inducible D,D-transpeptidase	Penicillin-binding protein, transpeptidase|Penici	D	Yes	-	Sec	tmhmm:1	-	-	-	-	-	protease	+	
LC_00376	null	379536	379012	174	10,58	20107	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-	
LC_00377	spaF	380161	379526	211	6,98	23280	-	ABC transporter, ribose-transporter ATPase c	lantibiotic ABC transporter, ATPase component	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00378	null	380895	380173	240	10,32	27039	-	Rhodopsin-like GPCR superfamily	predicted ORF	not_predicted_by_ERGO	Rhodopsin-like GPCR superfamily	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00379	null	381572	380892	226	9,18	25219	-	Conserved membrane protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00380	null	382347	381562	261	9,9	28985	-	Conserved membrane protein	conserved hypothetical protein (integral membr	not_predicted_by_ERGO	no annotation	null	No	-	LPxTG	tmhmm:6	-	-	-	-	-	-	-	
LC_00381	null	382978	383508	176	8,23	18759	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Tetracycline resistance protein TetB|Major facili	GEPF	No	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_00382	null	383492	384367	291	11,63	31389	+	Transporter, major facilitator superfamily MFS	predicted ORF	Tetracenomycin C resistance and export prote	Major facilitator superfamily|Major facilitator sup	GEPF	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_00383	null	384343	384777	144	7,68	16218	+	Transcriptional regulator, MarR family	transcriptional regulator, MarR family	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00384	null	384774	385334	186	7,9	21401	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00385	null	385517	385732	71	4,26	8069	+	Putative protein without homology	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00386	sgcA	386270	388366	698	6,44	79058	+	PTS system, IIA component	PTS system, mannitol IIA component / transcrip	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00387	null	388367	388678	103	4,45	11250	+	PTS system, IIB component	PTS system, lactose/cellobiose/mannitol/galacti	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00388	ulaA	388712	389998	428	10,09	45282	+	PTS system, IIC component	PTS system, ascorbate-specific IIC component	not_predicted_by_ERGO	Putative sugar-specific permease, SgaT/UlaA	S	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_00389	null	390015	390437	140	5,32	15603	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	D	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00390	null	390459	391319	286	5,74	31603	+	Fructose-bisphosphate aldolase	Fructose/tagatose/ketose bisphosphate aldolase	not_predicted_by_ERGO	Ketose-bisphosphate aldolase, class-II|Aldolase	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00391	null	391338	391973	211	6,75	24541	+	Kinase	kinase	not_predicted_by_ERGO	AAA+ ATPase, core	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00392	rihC	392450	393385	311	7,06	33144	+	Inosine-uridine preferring nucleoside hydrolase	Inosine-uridine nucleoside N-ribohydrolase	not_predicted_by_ERGO	Inosine/uridine-preferring nucleoside hydrolase	F	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00393	dcuC	393397	394803	468	9,92	49623	+	C4-dicarboxylate transporter	cryptic C4-dicarboxylate transporter DcuD	not_predicted_by_ERGO	C4-dicarboxylate anaerobic carrier	C	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_00394	null	394819	395316	165	8,14	19537	+	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family	not_predicted_by_ERGO	GCN5-related N-acetyltransferase	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00395	null	395358	396098	246	6,37	27981	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	not_predicted_by_ERGO	Bacterial regulatory protein GntR, HTH|Winged	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00396	null	396309	397106	265	5,68	28405	+	Aldolase, DeoC/FbaB family protein	predicted ORF	not_predicted_by_ERGO	Deoxyribose-phosphate aldolase/phospho-2-del	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00397	null	397166	397729	187	9,26	20788	+	Glycerol uptake operon antiterminator	predicted ORF	not_predicted_by_ERGO	Glycerol-3-phosphate responsive antiterminator	K	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00398	lyx	397763	399292	509	6,89	57134	+	L-xylulose kinase	L-xylulose kinase, cryptic	not_predicted_by_ERGO	Carbohydrate kinase, FGGY	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00399	fabG	399326	400090	254	9,23	27405	+	3-oxoacyl-[acyl-carrier-protein] reductase	beta-ketoacyl-acyl carrier protein reductase	not_predicted_by_ERGO	Short-chain dehydrogenase/reductase SDR|Glu	IQR	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00400	serA-like	400111	401109	332	5,69	36692	+	D-isomer specific 2-hydroxyacid dehydrogenas	D-isomer specific 2-hydroxyacid dehydrogenase	not_predicted_by_ERGO	D-isomer specific 2-hydroxyacid dehydrogenase	HE	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00401	pts	401142	402401	419	10,19	45631	+	PTS system, galactitol-specific IIC componen	PTS system, galactitol-specific EIIC componen	PTS system, galactitol-specific IIC componen	Phosphotransferase system, galactitol-specific	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_00402	null	402662	404530	622	6,69	71252	+	Transcriptional antiterminator, BglG family	predicted ORF	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00403	fba	404520	405386	288	5,18	31479	+	Fructose-bisphosphate aldolase	fructose-bisphosphate aldolase, class II family	not_predicted_by_ERGO	Ketose-bisphosphate aldolase, class-II|Aldolase	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00404	fruA	405426	407369	647	8,73	69396	+	PTS system, fructose-specific, IIABC compor	PTS system, fructose-specific IIABC componer	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	G	No	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_00405	sorE	408893	407655	412	4,83	45287	-	L-sorbose 1-phosphate reductase	L-sorbose-1-phosphate reductase	not_predicted_by_ERGO	Alcohol dehydrogenase superfamily, zinc-conta	ER	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00406	sorR	409970	409023	315	9,58	34620	-	Rranscriptional regulator, sorbitol operon regul	transcriptional regulator, SorR, sorbitol operon r	not_predicted_by_ERGO	Putative sugar-binding region|Homeodomain-lik	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-	

LC_00407	sorF	410115	410915	266	9,65	28391	+	Sorbitol-6-phosphate 2-dehydrogenase	D-sorbitol 6-phosphate 2-dehydrogenase	not_predicted_by_ERGO	Short-chain dehydrogenase/reductase SDR|Gl	IQR	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00408	sorA	410950	411366	138	5,19	14922	+	PTS system, sorbose-specific IIA component	PTS system, sorbose IIA component	not_predicted_by_ERGO	Phosphotransferase system, fructose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00409	sorB	411366	411860	164	9,95	18244	+	PTS system, sorbose-specific IIB component	PTS system, sorbose IIB component	not_predicted_by_ERGO	Phosphotransferase system, sorbose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00410	sorC	411874	412707	277	4,73	29107	+	PTS system, sorbose-specific IIC component	PTS system, mannose-specific IIC component	not_predicted_by_ERGO	Phosphotransferase system, sorbose-specific I	G	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00411	sorD	412726	413574	282	10,2	30782	+	PTS system, sorbose-specific IID component	PTS system, mannose/fructose/sorbose IID co	not_predicted_by_ERGO	Phosphotransferase system, mannose/fructose	G	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00412	sorG	413763	414662	299	4,97	32930	+	D-fructose-1,6-biphosphate aldolase	D-fructose-1,6-biphosphate aldolase, class II fa	not_predicted_by_ERGO	Ketose-bisphosphate aldolase, class-II|Aldolase	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00413	null	416279	414795	494	9,83	53874	-	Sodium-dependent dicarboxylate transporter s	predicted ORF	not_predicted_by_ERGO	Divalent ion symporter	P	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00414	null	417558	416281	425	8,09	46758	-	FAD dependent oxidoreductase	predicted ORF	not_predicted_by_ERGO	FAD dependent oxidoreductase	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00415	null	417704	418597	297	5,2	33880	+	Transcriptional regulator, LysR family	predicted ORF	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR|LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+
LC_00416	ilvH	418877	419713	278	5,93	30522	+	DNA-directed RNA polymerase subunit delta	DNA-directed RNA polymerase subunit delta	GTP-binding protein	Protein of unknown function DUF62	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00417	null	419796	420356	186	10,5	20192	+	Cobalt transport protein cbiQ	conserved hypothetical protein (integral membr	Cobalt transport protein cbiQ	Protein of unknown function DUF1393	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00418	ykoD	420358	422058	566	5,22	61660	+	ABC transporter, cobalt transporter eATPase	ABC transporter, ATPase component	Cobalt transport ATP-binding protein cbiO	ABC transporter related|AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00419	sdcBB	422055	422891	278	10,35	31543	+	Cobalt transport protein cbiQ	nickel/cobalt uptake ABC transporter, permeas	Cobalt transport protein cbiQ	Cobalt transport protein	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00420	null	424038	423016	340	9,31	37029	-	Transcription regulator, LacI family	periplasmic binding protein / LacI transcriptiona	not_predicted_by_ERGO	Bacterial regulatory protein, LacI|Periplasmic bi	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+
LC_00421	null	425496	424132	454	9,64	49812	-	Transporter, major facilitator superfamily MFS	permease, integral membrane transport protein	not_predicted_by_ERGO	Major facilitator superfamily MFS_1	GEPF	No	-	LPxTG	tmhmm:12	-	-	-	-	-	-	-
LC_00422	null	425868	425530	112	6,24	12923	-	Glycosyl hydrolase, group 13	predicted ORF	not_predicted_by_ERGO	Glycosyl hydrolase, family 13, all-beta|Glycosid	null	No	-	-	tmhmm:0	LC00422	-	-	-	-	-	-
LC_00423	null	427205	425865	446	5,67	51687	-	Alpha-glucosidase (GH13)	oligo-1,6-glucosidase	not_predicted_by_ERGO	Glycosyl hydrolase, family 13, catalytic region|G	G	No	fibronectin	-	tmhmm:0	LC00423	-	-	-	-	-	-
LC_00424	frdC	427616	429139	507	10,4	53953	+	Fumarate reductase flavoprotein subunit	fumarate reductase, flavoprotein subunit precur	not_predicted_by_ERGO	Fumarate reductase/succinate dehydrogenase f	C	No	-	Lipobox	tmhmm:1	-	-	-	-	-	-	-
LC_00425	null	430051	429305	248	4,64	27195	-	Class II aldolase/adducin domain protein	class II sugas phosphate aldolase/adducin, N-t	not_predicted_by_ERGO	Class II aldolase/adducin, N-terminal	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00426	pts	431744	430359	461	9,94	49891	-	PTS system, galactitol-specific IIC component	PTS system, galactitol-specific IIC component	not_predicted_by_ERGO	Phosphotransferase system, galactitol-specific	G	No	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_00427	null	432100	431771	109	4,16	11590	-	PTS system, galactitol-specific IIB component	PTS system, galactitol specific IIB component	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose-	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00428	null	432586	432113	157	6,11	18009	-	PTS system, galactitol-specific IIA component	PTS system, (likely galactitol) IIA component	PTS system, galactitol-specific IIA component	Phosphotransferase system, phosphoenolpyru	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00429	lacR.1	432842	433594	250	10,19	27835	+	Lactose phosphotransferase system represso	PTS system, lactose specific repressor protein,	Lactose phosphotransferase system represso	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	IMP	tmhmm:1	-	-	-	-	-	regulator	-	+
LC_00430	lacC	433600	434592	330	4,91	35301	+	Tagatose-6-phosphate kinase	tagatose-6-phosphate kinase (Phosphotagatoki	not_predicted_by_ERGO	Ribokinase|Carbohydrate kinase, PfkB|PfkB	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00431	gntR	435572	434739	277	6,61	30377	-	Transcriptional regulator, RpiR family	gluconate operon transcriptional regulator, RpiR	not_predicted_by_ERGO	Helix-turn-helix protein RpiR|Sugar isomerase (	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+
LC_00432	sgaA	435699	436151	150	5,11	16178	+	PTS system, IIA component	PTS system, IIA component	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00433	null	436152	437465	437	10,26	47098	+	PTS system, IIC component	predicted ORF	not_predicted_by_ERGO	Putative sugar-specific permease, SgaT/UlaA	null	No	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00434	null	437484	437771	95	4,02	10237	+	PTS system, IIB component	PTS system, lactose/cellobiose/galactitol/manni	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose-	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00435	ulaG	437790	438869	359	6,68	41303	+	L-ascorbate-6-phosphate lactonase	L-ascorbate-6-phosphate lactonase ulaG (L-asc	not_predicted_by_ERGO	no annotation	R	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00436	null	438870	439682	270	6,52	29987	+	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily, subfamily IIB, Cof	not_predicted_by_ERGO	Cof protein|HAD-superfamily hydrolase, subfam	R	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00437	glvA	440212	441540	442	5,25	49830	+	Maltose-6'-phosphate glucosidase	maltose-6'-phosphate glucosidase malH (maltos	not_predicted_by_ERGO	Glycoside hydrolase, family 4|Lactate/malate de	G	No	-	IMP	tmhmm:1	LC00437	-	-	-	-	-	-
LC_00438	malP	441666	443549	627	6,96	68271	+	PTS system, IIBC component	PTS system, N-acetylglucosamine/glucose/arbu	not_predicted_by_ERGO	Phosphotransferase system, EIIB|Phosphotran	G	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00439	null	443601	444413	270	8,56	30814	+	Transcriptional regulator, RpiR family	transcriptional regulator	not_predicted_by_ERGO	Helix-turn-helix protein RpiR|Sugar isomerase (	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+
LC_00440	null	444376	444885	169	10,11	18681	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00441	null	444901	445485	194	8,23	21713	+	PTS system, IIB component	predicted ORF	not_predicted_by_ERGO	Phosphotransferase system, EIIB	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00442	null	445564	446052	162	4,26	17352	+	PTS system, IIA component	PTS system, sucrose/trehalose/glucose/glucosi	not_predicted_by_ERGO	Phosphotransferase system, sugar-specific per	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00443	pgm	446129	446809	226	5,03	25960	+	Hydrolase of the HAD superfamily	phosphoglucomutase	not_predicted_by_ERGO	Haloacid dehalogenase-like hydrolase|HAD-sup	R	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00444	licT	447005	447856	283	5	32638	+	Transcriptional antiterminator, BglG family	transcriptional antiterminator (BglG family)	not_predicted_by_ERGO	CAT RNA-binding region|PRD	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-
LC_00445	bglP	448127	449989	620	6,69	65089	+	PTS system, beta-glucoside-specific IIABC co	PTS system, beta-glucoside-specific IIABC con	not_predicted_by_ERGO	Phosphotransferase system, sugar-specific per	G	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_00446	pbg	450116	451600	494	5,07	56926	+	6-phospho-beta-glucosidase	6-phospho-beta-glucosidase. Glycosyl Hydrolas	not_predicted_by_ERGO	Glycoside hydrolase, family 1|Glycoside hydrola	G	No	-	-	tmhmm:0	LC00446	-	-	-	-	-	-
LC_00447	null	451882	453348	488	6,76	55225	+	Transcription antiterminator BglG family protei	predicted ORF	Transcription antiterminator, BglG family	M trans-acting positive regulator|PRD|Phosphot	null	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+
LC_00448	null	453341	453811	156	4,37	16551	+	PTS system, IIA component	predicted ORF	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00449	fba	453813	454754	313	4,75	34127	+	Fructose-bisphosphate aldolase	fructose-bisphosphate aldolase, class II family	Fructose-bisphosphate aldolase (EC 4.1.2.13)	Ketose-bisphosphate aldolase, class-II|Aldolase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00450	null	454783	455256	157	4,43	17082	+	PTS system, fructose-specific IIA component	PTS system, IIA component	PTS SYSTEM, FRUCTOSE-LIKE-1 IIA COM	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00451	fruA-1	455253	455570	105	7,52	11016	+	PTS system, fructose-specific IIB component	PTS system, IIB component	PTS system, fructose-like IIB component (EC	Phosphotransferase system, fructose-specific I	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00452	fruA-2	455585	456670	361	8,65	37803	+	PTS system, fructose-specific IIC component	PTS system, IIC component	PTS system, fructose-like enzyme IIC compor	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_00453	null	456695	457669	324	5,39	35806	+	Conserved protein	pyruvate/2-oxoglutarate dehydrogenase comple	not_predicted_by_ERGO	no annotation	C	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00454	null	457676	458356	226	4,52	26230	+	Conserved protein	sugar ABC transporter, auxiliary component	not_predicted_by_ERGO	Protein of unknown function DUF1498|Cupin, F	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00455	xylB	458453	459919	488	5,43	53825	+	Xylulokinase	D-xylulose kinase	not_predicted_by_ERGO	Carbohydrate kinase, FGGY|Xylulokinase	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00456	glvC	461808	460201	535	9,64	58013	-	PTS system, IIBC component	PTS system, alpha-glucose/maltose/glucoside I	not_predicted_by_ERGO	Phosphotransferase system, EIIB|Phosphotran	G	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00457	celC	462587	461805	260	5,52	28936	-	Conserved protein	phospho-beta-glucosidase	not_predicted_by_ERGO	YdjC-like protein	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00458	glvA	463908	462568	446	4,84	51077	-	Maltose-6'-phosphate glucosidase	glycoside hydrolase, family 4, maltose-6'-phospl	not_predicted_by_ERGO	Glycoside hydrolase, family 4|Lactate/malate de	G	No	-	-	tmhmm:0	LC00458	-	-	-	-	-	+
LC_00459	null	464068	464823	251	6,9	28360	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Helix-turn-helix protein RpiR|Flavodoxin, N-term	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-
LC_00460	pts	465288	465731	147	4,95	16107	+	PTS system, fructose-specfic IIA component	PTS system, mannitol/fructose-specific IIA com	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00461	pts	465801	467348	515	9,76	54255	+	PTS system, fructose-specfic IIBC componen	PTS system, fructose-specfic IIBC component	not_predicted_by_ERGO	Phosphotransferase system, EIIC|Phosphotran	G	No	-	IMP	tmhmm:7	-	-	-	-	-	-	-
LC_00462	patB	467413	468579	388	5,96	43875	+	Maltose regulon modulator MalY	aminotransferase, class II	not_predicted_by_ERGO	1-aminocyclopropane-1-carboxylate synthase|A	E	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00463	null	468581	470290	569	6,25	64400	+	Transcription regulator	predicted ORF	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00464	kpsF	471035	470424	203	5,8	21471	-	Phosphosugar isomerase	phosphosugar isomerase (polysialic acid) involv	not_predicted_by_ERGO	Sugar isomerase (SIS)	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00465	ptsN1	471312	471773	153	6,52	17064	+	PTS system, IIA component	PTS system, mannitol IIA component	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00466	rmpB	471779	472069	96	5,14	10584	+	PTS system, lactose/cellobiose-specific IIB co	PTS system, lactose/cellobiose IIB component	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose-	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00467	ulaA	472094	473353	419	9,46	44652	+	PTS system, IIC component	PTS system, ascorbate-specific IIC component	not_predicted_by_ERGO	Putative sugar-specific permease, SgaT/UlaA	S	No	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00468	dapA3	473392	474291	299	6,17	32642	+	Dihydrodipicolinate synthase	dihydrodipicolinate synthase/N-acetylneuramina	not_predicted_by_ERGO	Dihydrodipicolinate synthetase|Aldolase-type TI	EM	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00469	kdgA	474306	474941	211	5,73	22315	+	2-dehydro-3-deoxyphosphogluconate aldolase	2-dehydro-3-deoxy-6-phosphogluconate aldolas	not_predicted_by_ERGO	KDPG and KHG aldolase|Aldolase-type TIM ba	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00470	null	475003	477072	689	7,24	78682	+	Transcription antiterminator, BglG family / PTS	PTS system, IIA compoenent / nitrogen-regulat	Transcription antiterminator, BglG family / PTS	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00471	hxlR	477407	477090	105	9,75	11711	-	Transcriptional regulator, HxlR family	DNA-binding protein, transcriptional regulator H	not_predicted_by_ERGO	Helix-turn-helix, HxlR type	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-
LC_00472	null	477546	478190	214	7,04	23909	+	p-nitrobenzoate reductase	p-nitrobenzoate reductase	not_predicted_by_ERGO	Nitroreductase	C	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00473	null	478963	478226	245	9,92	27099	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00474	null	479737	480234	165	11,24	19277	+	DNA-directed RNA polymerase specialized sig	DNA-directed RNA polymerase specialized sigr	Hypothetical cytosolic protein	Bacterial regulatory protein, LuxR	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-
LC_00475	null	480351	480503	50	7,54	5754	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-

LC_00476	null	480515	481279	254	9,36	28123	+	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)	lyzozyme M1 (1,4-beta-N-acetylmuramidase), e	Lysozyme (EC 3.2.1.17)		Glycoside hydrolase, family 25|Peptidoglycan-bi	M	Yes	peptidoglucar	LysM	tmhmm:0	LC00476	-	-	-	-	-	-		
LC_00477	null	481504	482007	167	7,24	18571	+	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family		Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00478	null	482012	483073	353	10	38423	+	ABC transporter, antimicrobial peptide transpc	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein		Protein of unknown function DUF214, permase	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	-	
LC_00479	yxeB	483078	483767	229	6,53	24409	+	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein		ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00480	npr	485304	483934	456	4,82	49309	-	NADH peroxidase	FAD-dependent pyridine nucleotide-disulphide (	NADH peroxidase (EC 1.11.1.1)		Pyridine nucleotide-disulphide oxidoreductase, (	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00481	null	486379	485552	275	4,82	29647	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)		Cof protein|HAD-superfamily hydrolase, subfar	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00482	null	486765	486493	90	10,47	10541	-	Conserved protein	DNA damage inducible protein, addiction modul	Hypothetical protein		Addiction module toxin, RelE/StbE	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00483	cytR	487004	488011	335	6,94	37142	+	Transcriptional regulator, LacI family	transcriptional regulator, LacI family, sugar-bind	not_predicted_by_ERGO		Bacterial regulatory protein, LacI|Periplasmic bi	K	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00484	pts	488065	488556	163	7,53	18192	+	PTS system, IIB component	PTS system, sorbose/mannose/fructose/N-acet	not_predicted_by_ERGO		Phosphotransferase system, sorbose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00485	null	488588	489394	268	7,79	28583	+	PTS system, IIC component	PTS system, sorbose/mannose/fructose/N-acet	not_predicted_by_ERGO		Phosphotransferase system, sorbose-specific I	G	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	-	
LC_00486	levG	489387	490208	273	9,94	29958	+	PTS system, IID component	PTS system, mannose/fructose/N-acetylgalactc	not_predicted_by_ERGO		Phosphotransferase system, mannose/fructose	G	No	-	IMP	tmhmm:5	-	-	-	-	-	-	-	+	
LC_00487	xylS	490244	492493	749	6,93	85332	+	Glycoside hydrolase, family 31	alpha-glucosidase/xylosidase, family 31 of glycc	not_predicted_by_ERGO		Glycoside hydrolase, family 31	G	No	-	-	tmhmm:0	LC00487	-	-	-	-	-	-	+	
LC_00488	null	492617	493033	138	4,26	15253	+	PTS system, IIA component	PTS system, mannose/fructoseN-acetylgalactc	not_predicted_by_ERGO		Phosphotransferase system, fructose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00489	malL	493026	494711	561	6,16	64710	+	Trehalose-6-phosphate hydrolase (Alpha,alpha	trehalose-6-phosphate hydrolase (Alpha,alpha-(	not_predicted_by_ERGO		Glycosyl hydrolase, family 13, catalytic region|G	G	No	-	-	tmhmm:0	LC00489	-	-	-	-	-	-	+	
LC_00490	null	495548	494778	256	8,19	28623	-	Nucleotidyltransferase	adenylyl transferase	Streptomycin 3"-adenylyltransferase (EC 2.7.7		no annotation	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00491	null	496842	495952	296	4,27	33575	-	Conserved protein	predicted ORF	not_predicted_by_ERGO		no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00492	metQ	498583	499440	285	10,43	30864	+	ABC transporter, metal ion transporter periplas	metal ion ABC transporter, periplasmic compon	ABC transporter substrate-binding protein		NLPA lipoprotein	P	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00493	null	499651	500667	338	4,8	37116	+	Choloylglycine hydrolase	conjugated bile salt hydrolase related amidase /	Choloylglycine hydrolase (EC 3.5.1.24)		Choloylglycine hydrolase	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00494	null	501811	500846	321	6,18	36081	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00495	null	503776	502082	564	5,56	64458	-	Oxidoreductase; Myosin-crossreactive antigen	oxidoreductase, Myosin-crossreactive antigen o	Myosin-crossreactive antigen		Streptococcal 67 kDa myosin-cross-reactive an	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00496	null	503916	503788	42	9,2	4751	-	Conserved protein	conserved hypotetical protein (extracellular pept	Hypothetical protein		no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	+	
LC_00497	null	504571	504005	188	6,39	21363	-	Transcriptional regulator	transcriptional regulator	Transcriptional regulator, TetR family		Homeodomain-like	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00498	null	505029	504661	122	4,38	12937	-	Dihydroxyacetone kinase, phosphotransfer sul	dihydroxyacetone kinase, phosphotransfer subu	Dihydroxyacetone kinase phosphotransfer pro		Phosphotransferase system, fructose subfamily	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00499	dak2	505759	505178	193	6,81	20662	-	Dihydroxyacetone kinase	dihydroxyacetone kinase, phosphatase domain (	Dihydroxyacetone kinase (EC 2.7.1.29)		Dak phosphatase|Dihydroxyacetone kinase, sut	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00500	dAK	506765	505746	339	4,95	35872	-	Dihydroxyacetone kinase	dihydroxyacetone kinase DAK1 domain protein	Dihydroxyacetone kinase (EC 2.7.1.29)		Dak kinase|Dihydroxyacetone kinase DhaK, sut	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00501	null	507386	506958	142	4,67	15548	-	Redox protein, regulator of disulfide bond form	redox protein, regulator of disulfide bond format	Osmotically inducible protein C		OsmC-like protein|KH, prokaryotic type	O	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00502	null	507916	508605	229	9,5	25979	+	Peptidase S54, rhomboid	conserved hypothetical protein	not_predicted_by_ERGO		Peptidase S54, rhomboid	R	No	-	IMP	tmhmm:5	-	-	-	-	-	-	protease	-	
LC_00503	null	508671	508823	50	9,44	5640	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00504	null	509705	509097	202	4,63	21797	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		no annotation	null	No	-	Sec	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00505	null	509911	509732	59	10,58	6649	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO		no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-	-	
LC_00506	null	510155	511027	290	9,18	34114	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	not_predicted_by_ERGO		Transcriptional activator Rgg/GadR/MutR, C-ter	null	No	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00507	null	512685	511270	471	10,45	52897	-	DNA polymerase III, alpha subunit (Gram-pos	DNA polymerase III, alpha subunit (gram-positi	DNA polymerase III alpha subunit (EC 2.7.7.7		Exonuclease|Polynucleotidyl transferase, Ribon	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00508	null	513094	512909	61	7,92	6782	-	Conserved protein	conserved hypothetical protein	DNA damage inducible protein yafQ		Plasmid stabilization system	S	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00509	dinJ	513394	513122	90	9,63	10006	-	Conserved protein	addiction module antitoxin, RelB/DinJ family	RelB/DinJ family protein		RelB antitoxin	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00510	null	513956	514204	82	10,11	9473	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO		no annotation	null	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-	-	
LC_00511	yceK	514447	514740	97	9,63	11428	+	Transcriptional regulator, ArsR family	transcriptional regulator, ArsR family	Transcriptional regulator, ArsR family		Bacterial regulatory protein, ArsR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00512	yceJ	514822	515985	387	10,2	41397	+	Transporter, major facilitator superfamily MFS	permease, multidrug resistance protein of the m	Multidrug resistance protein B		Major facilitator superfamily|Major facilitator sup	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	-	
LC_00513	tag-2	516139	516714	191	7,74	21884	+	DNA-3-methyladenine glycosylase I	dna-3-methyladenine glycosylase 1 (tagI)	DNA-3-methyladenine glycosylase (EC 3.2.2.2		Methyladenine glycosylase|DNA glycosylase	L	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	+	
LC_00514	tnpB	516857	517453	198	9,86	23274	+	ISSoc2, resolvase	transposase (OrfA), ISSoc2, resolvase, IS trans	not_predicted_by_ERGO		Bacterial regulatory protein, MerR|Resolvase, N	L	No	-	-	tmhmm:0	-	phage	-	-	-	regulator	-	+	
LC_00515	tnpB	517488	518669	393	10,54	46133	+	Transposase, IS605 family protein	transposase, IS605-TNPB	not_predicted_by_ERGO		Transposase (probable), IS891/IS1136/IS1341|	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00516	null	518901	519119	72	4,25	8064	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00517	fba	520129	519248	293	4,79	31535	-	Fructose-bisphosphate aldolase	fructose-bisphosphate aldolase class II transm	Fructose-bisphosphate aldolase (EC 4.1.2.13)		Ketose-bisphosphate aldolase, class-II|Fructos	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00518	cidC	520718	522451	577	4,77	62677	+	Pyruvate oxidase	pyruvate oxidase and acetolactate synthase	Pyruvate dehydrogenase [cytochrome] (EC 1.2		TPP-binding enzymes|Thiamine pyrophosphate EH	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00519	null	522950	522663	95	9,76	10733	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00520	null	524166	523153	337	6,51	38100	-	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin binding	Beta-lactamase family protein		Beta-lactamase|Penicillin-binding protein, trans	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	-	
LC_00521	ykfB	525276	524209	355	4,6	37013	-	L-alanine-DL-glutamate epimerase related enz	L-alanine-DL-glutamate epimerase related enzy	L-Ala-D/L-Glu racemase (EC 5.1.1.-)		Mandelate racemase/muconate lactonizing enz	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00522	null	525315	525476	53	6,22	6100	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00523	null	525460	526194	244	6,12	27648	+	Methyltransferase	S-adenosylmethionine (SAM)-dependent methy	SAM-dependent methyltransferase		Methyltransferase type 11	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00524	yvdE	526299	527051	250	5,76	27712	+	Glutamine amidotransferase	glutamine amidotransferase class I :peptidase (	Glutamine amidotransferase, class I		Peptidase C26	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	+	
LC_00525	null	528013	527138	291	9,38	33156	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		Domain of unknown function DUF1814	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00526	null	528609	528013	198	8,63	22571	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-	
LC_00527	null	528916	530259	447	4,68	49242	+	Glutamine synthetase	L-glutamine synthetase	Glutamine synthetase (EC 6.3.1.2)		Glutamine synthetase, catalytic region|Glutamin	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00528	null	530469	531611	380	5,36	43148	+	Metal-dependent hydrolase of the TIM-barrel f	metal-dependent hydrolase of the TIM-barrel fol	Superfamily II DNA and RNA helicase		Amidohydrolase 2	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00529	null	531767	533002	411	9,39	44142	+	Amino acid transporter	amino acid transporter	Amino acid permease		Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-	-	
LC_00530	rmeB	533537	533112	141	6,23	16073	-	Transcriptional regulator, MerR family	transcriptional regulator, MerR family	Transcriptional regulator, MerR family		Bacterial regulatory protein, MerR|Putative DNA	null	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-	
LC_00531	ycgG	533715	534581	288	5,21	32302	+	Oxidoreductase, aldo/keto reductase family pr	aldo/keto reductase of diketogulonate reductase	Aldose reductase (EC 1.1.1.21)		Aldo/keto reductase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00532	qor	535783	534761	340	7,99	36974	-	Alcohol dehydrogenase	NADPH:quinone reductase related Zn-depende	Quinone oxidoreductase (EC 1.6.5.5)		Alcohol dehydrogenase superfamily, zinc-conta	CR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00533	ydeP	535887	536231	114	5,67	12362	+	Transcriptional regulator, HxlR family	transcriptional regulator, DUF24 family (related	Transcriptional regulator, MarR family		Helix-turn-helix, HxlR type	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+	
LC_00534	null	537057	536305	250	10,32	26516	-	Conserved integral membrane protein	transport protein	Hypothetical membrane spanning protein		Protein of unknown function DUF81	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	-	
LC_00535	null	537283	538422	379	10,11	42973	+	ABC transporter, permease protein	predicted ORF	ABC transporter permease protein		no annotation	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	-	
LC_00536	natA	538548	539282	244	4,82	27096	+	ABC transporter, ATP binding protein	ABC transporter, ATPase component	ABC transporter ATP-binding protein		ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00537	null	539275	540891	538	10,28	61397	+	ABC transporter, ATPase component	conserved hypothetical protein	ABC transporter ATP-binding protein		no annotation	GEPF	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	+	
LC_00538	eriR	541098	541778	226	7,62	25667	+	Two-component response regulator	DNA-binding two component response regulato	Two-component response regulator		Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	-	regulator	-	-	
LC_00539	null	541766	542890	374	6,32	41047	+	Two component sensor transduction histidine	signal transduction histidine kinase	Sensory transduction protein kinase (EC 2.7.3		ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	-	-	
LC_00540	mppX	543082	543981	299	10,15	33174	+	ABC transporter, ATPase component	efflux ABC transporter, ATPase component, Pil	ABC transporter ATP-binding protein		ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+	
LC_00541	null	543994	545121	375	10,66	42007	+	Conserved protein	conserved hypothetical protein	ABC transporter permease protein		no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	+	
LC_00542	null	545081	545710	209	9,99	22748	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO		no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	-	
LC_00543	pepN	545995	548529	844	4,75	94564	+	Aminopeptidase N	lysyl aminopeptidase N. Metallo peptidase. MEF	Aminopeptidase N (EC 3.4.11.15)		Peptidase M1, membrane alanine aminopeptida	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	+	
LC_00544	ylcA	548791	550239	482	9,66	53609	+	Amino acid permease family protein	amino acid transporters	Amino acid permease		Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-	+	

LC_00545	null	550447	550265	60	10,96	6683	-	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00546	xylP	551805	550471	444	9,82	49336	-	Transporter, major facilitator superfamily MFS	Na+/xyloside symporter related transporter	Sugar/proton symporter	Sodium:galactoside symporter	Major facilitator s	G	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+
LC_00547	null	552462	551962	166	8,05	17979	-	Conserved periplasmic/secreted protein	conserved hypothetical protein (periplasmic/sec	Hypothetical membrane associated protein	Protein of unknown function DUF1440	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_00548	metA	552950	553777	275	7,39	32109	+	Homoserine O-succinyltransferase	homoserine o-succinyltransferase	Homoserine O-succinyltransferase (EC 2.3.1.	Homoserine O-succinyltransferase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00549	cysK1	553790	554719	309	5,21	32607	+	Cysteine synthase	cysteine synthase K/M:Cysteine synthase A	Cysteine synthase (EC 2.5.1.47)	Cysteine synthase/cystathionine beta-synthase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00550	null	555166	555939	257	6,13	28558	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00551	null	556427	556227	66	10,33	7600	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00552	metB	557613	556477	378	5,17	40998	-	Cystathionine gamma-synthase	cystathionine beta-lyase/cystathionine gamma-s	Cystathionine beta-lyase (EC 4.4.1.8) / Cystat	Cys/Met metabolism pyridoxal-phosphate-deper	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00553	cnb	558520	557708	270	10,34	29319	-	ABC transporter, amino acid-binding protein	amino acid ABC transporter/signal transduction	Cystine-binding protein	Bacterial extracellular solute-binding protein, far	ET	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_00554	yckJ	559260	558547	237	10,08	26050	-	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease compon	Cystine transport system permease protein	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00555	null	559993	560901	302	4,72	32537	+	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_00556	brnQ	562459	561068	463	10,06	49597	-	Branched-chain amino acid transport protein	branched-chain amino acid permease	Branched-chain amino acid transport system (	Branched-chain amino acid transport system II	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00557	null	563370	564038	222	4,53	22401	+	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	Calcium-binding EF-hand	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00558	null	564103	565125	340	10	37752	+	Cell surface protein	cell surface protein	Hypothetical protein	Protein of unknown function DUF916, cell surfa	null	Yes	-	Cterm	tmhmm:1	-	-	-	-	-	-	+
LC_00559	null	565106	565462	118	6,53	12747	+	Conserved protein	conserved hypothetical protein (spread-like prot	Hypothetical exported protein	Surface protein from Gram-positive cocci, anch	null	Yes	-	LPxTG	tmhmm:2	-	-	-	-	-	-	-
LC_00560	null	565459	567534	691	5,71	73962	+	Conserved extracellular protein	conserved hypothetical protein	Hypothetical exported protein	Concanavalin A-like lectin/glucanase	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00561	null	567630	567749	39	11,1	4076	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	-
LC_00562	null	568366	569082	238	5,03	24849	+	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00563	null	569197	569571	124	10,47	13812	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	Surface protein from Gram-positive cocci, anch	null	Yes	-	LPxTG	tmhmm:2	-	-	-	-	-	-	-
LC_00564	null	569552	570241	229	6,25	23755	+	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	Calcium-binding EF-hand	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	-
LC_00565	null	570225	570404	59	12,34	6862	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00566	null	570367	570495	42	11,06	4686	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00567	null	570511	572550	679	6,52	72873	+	Conserved protein	conserved hypothetical protein	cell surface protein	Concanavalin A-like lectin/glucanase	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_00568	yicL	573608	572658	316	11,79	34869	-	Carboxylate/amino acid/amine transporter	permease of the drug/metabolite transporter (DI	Transporter, drug/metabolite exporter family	Protein of unknown function DUF6, transmemb	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_00569	null	575515	573797	572	10,45	62892	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	+
LC_00570	CcmA5	576299	575499	266	4,74	29017	-	ABC transporter, ATPase component	daunorubicin resistance ABC transporter, ATPa	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00571	null	577099	576551	182	10,84	19458	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00572	null	578155	577331	274	7,7	28992	-	Pyridoxal/pyridoxine/pyridoxamine kinase	pyridoxal/pyridoxine/pyridoxamine kinase	Pyridoxine kinase (EC 2.7.1.35)	PfkB	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00573	metF	579315	578443	290	6,08	31959	-	Methylenetetrahydrofolate reductase	5,10-methylenetetrahydrofolate reductase (FAD	Methylenetetrahydrofolate reductase (EC 1.5.1	Methylenetetrahydrofolate reductase|5,10-meth	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00574	metE	581578	579293	761	6,22	86967	-	5-methyltetrahydropteroyltriglutamate--homocy	5-methyltetrahydropteroyltriglutamate--homocys	5-methyltetrahydropteroyltriglutamate--homocy	Methionine synthase, vitamin-B12 independent|	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00575	null	582472	582930	152	9,89	16999	+	ABC transporter, transmembrane region	ABC transporter homolog W	not_predicted_by_ERGO	ABC transporter, transmembrane region, type 1	null	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00576	null	582931	584190	419	6,81	46331	+	ABC transporter, ATP-binding and permease	ABC transporter, ATPase/permease componen	Multidrug resistance ABC transporter ATP-bin	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_00577	ydbA	584194	585975	593	6,15	65923	+	ABC transporter, ATP-binding and permease	ABC transporter, ATPase/permease componen	Multidrug/protein/lipid ABC transporter family,	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_00578	oxfP	586134	587357	407	9,92	43078	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily:O>	Transporter, MFS superfamily	Major facilitator superfamily|Major facilitator sup	GEPR	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00579	treR	587661	588377	238	8,35	27127	+	Trehalose operon repressor	transcriptional regulator, GntR family	Trehalose operon transcriptional repressor	Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00580	treA	588426	590081	551	6,56	62826	+	Alpha,alpha-phosphotrehalase (GH13)	trehalose-6-phosphate hydrolase (alpha,alpha-p	Trehalose-6-phosphate hydrolase (EC 3.2.1.9	Glycosyl hydrolase, family 13, catalytic region|G	G	Yes	fibronectin	-	tmhmm:0	LC00580	-	-	-	-	-	+
LC_00581	pts	590085	592085	666	7,67	70365	+	PTS system, beta-glucoside-specific IIABC co	PTS system, beta-glucoside/glucose/trehalose/l	PTS system, trehalose-specific IIA componen	Phosphotransferase system, sugar-specific per	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+
LC_00582	null	592340	592837	165	10,57	17534	+	Sodium:dicarboxylate symporter	predicted ORF	not_predicted_by_ERGO	Sodium:dicarboxylate symporter	E	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00583	null	592831	593625	264	6,25	27599	+	Serine/threonine symporter	sodium:dicarboxylate/amino acid:cation (Na+ or	Serine/threonine sodium symporter	Sodium:dicarboxylate symporter	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00584	bcaP	593930	595411	493	8,78	52853	+	Amino acid transporter	cationic amino acid transporter	Amino acid permease	Major intrinsic protein|Amino acid/polyamine tra	P	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_00585	ldh	596524	595688	278	5,12	29873	-	L-lactate dehydrogenase	L-lactate dehydrogenase 1 (L-LDH 1)	L-lactate dehydrogenase (EC 1.1.1.27)	Lactate/malate dehydrogenase|L-lactate/malate	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00586	gdh	596759	598102	447	6,02	47856	+	Glutamate dehydrogenase	glutamate dehydrogenase (NAD(P)+)	NADP-specific glutamate dehydrogenase (EC	Glu/Leu/Phe/Val dehydrogenase|Glu/Leu/Phe/V	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00587	cspA	598317	598517	66	4,38	7203	+	Cold shock protein	cold-shock DNA-binding protein family A	Cold shock protein	Cold-shock protein, DNA-binding|Cold shock pr	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00588	null	598808	599920	370	9,72	41128	+	Transposase	transposase, IS1533	Transposase	Transposase, IS116/IS110/IS902	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00589	null	600838	600410	142	10,33	15645	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00590	null	601481	601041	146	4,5	16302	-	Redox protein, regulator of disulfide bond form	redox protein, regulator of disulfide bond format	Osmotically inducible protein C	OsmC-like protein|KH, prokaryotic type	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00591	lsa	603065	601581	494	8,78	56323	-	ABC transporter, ATPase component	drug resistance ABC transporter with duplicatec	ABC transporter ATP-binding protein uup	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00592	null	603255	603100	51	11,84	5817	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00593	null	603438	603271	55	9,8	6226	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00594	ybE	604137	603514	207	5,05	22661	-	Nucleoside-diphosphate-sugar epimerase	nucleoside-diphosphate-sugar epimerase	NAD-dependent epimerase/dehydratase famil	NAD-dependent epimerase/dehydratase	MG	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00595	ara1	605098	604253	281	4,89	30971	-	Aldo/keto reductase	aldo/keto reductase family enzyme	Aldo/keto reductase family protein	Aldo/keto reductase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00596	ybxG	606689	605298	463	9,65	50645	-	Amino acid permease	amino acid permease-associated region	Amino acid permease	Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00597	null	606935	609139	734	10,8	80673	+	Conserved protein	conserved hypothetical protein	Translation initiation factor 2	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00598	null	611240	609258	660	9,49	73385	-	NhaP-type Na+/H+ and K+/H+ antiporter	NhaP-type Na+/H+ and K+/H+ antiporter	Na+/H+ antiporter nhaP	Sodium/hydrogen exchanger	P	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00599	null	611904	611497	135	10,2	15005	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	Ribosomal protein S2	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00600	null	612365	611913	150	9,7	16673	-	Response regulator of the LytR/AlgR family pr	response regulator of the LytR/AlgR family	Transcriptional regulator	LytTr DNA-binding region	KT	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_00601	cylB	613329	612463	288	10,68	32110	-	ABC transporter, multidrug transporter perme	multidrug ABC transporter, permease compone	ABC transporter permease protein	no annotation	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00602	cylA	614224	613331	297	6,9	32777	-	ABC transporter, ATPase component	multidrug ABC transporter, ATPase component	ABC transporter ATP-binding protein	Aminoacyl-tRNA synthetase, class I|ABC trans	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00603	null	615315	614533	260	10,99	29354	-	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Lipase, active site|Protein of unknown function I	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00604	cah	616028	615387	213	6,51	24090	-	Carbonic anhydrase	carbonic anhydrase precursor	Carbonic anhydrase (EC 4.2.1.1)	Carbonic anhydrase, eukaryotic	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00605	yjfJ	616490	616164	108	5,72	11600	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	Protein of unknown function DUF74	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00606	null	616581	616766	61	6,18	6306	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00607	null	617231	616722	169	4,69	19072	-	Hydrolase, NUDIX family protein	hydrolase, nudix family	NADH pyrophosphatase (EC 3.6.1.22)	NUDIX hydrolase|NUDIX	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00608	null	618378	617467	303	6,98	31655	-	NADPH:quinone reductase related Zn-depend	NADPH:quinone reductase related Zn-depende	Quinone oxidoreductase (EC 1.6.5.5)	Alcohol dehydrogenase superfamily, zinc-conta	CR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00609	amtB	619840	618524	438	6,57	46533	-	Ammonium transporter	ammonium permease AmtB1	Ammonium transporter / Methylammonium tra	Ammonium transporter|Lipase, active site|Rh-lik	P	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_00610	null	621125	620184	313	4,47	35111	-	Dyp-type peroxidase family protein	Dyp-type iron-dependent peroxidase family prot	Dyp-type peroxidase family protein	Dyp-type peroxidase|CRISPR-associated protei	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00611	yqgG	621416	622081	221	9,84	24416	+	Mg2+ transporter-C (MgtC) family protein	Mg2+ transporter-C (MgtC) family protein	Membrane protein, MgtC/SapB family	MgtC/SapB transporter	S	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00612	endA	622908	622087	273	10,44	30470	-	DNA-entry nuclease	DNA-entry nuclease	DNA-entry nuclease (EC 3.1.30.-)	no annotation	V	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00613	null	623263	623574	103	12,37	11435	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-

LC_00614	ykpA	623691	625265	524	4,45	58479	+	ABC transporter, ATPase component	ABC transporter with duplicated ATPase domai	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00615	null	625414	627090	558	8,81	61763	+	Putative protein without homology	mismatch repair ATPase (MutS family)	DNA mismatch repair protein mutS	DNA mismatch repair protein MutS, C-terminal	L	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_00616	ysiD	627087	627668	193	10,2	22042	+	Uracil-DNA glycosylase	uracil DNA glycosylase family protein	Uracil DNA glycosylase superfamily protein	Uracil-DNA glycosylase superfamily	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00617	glpF3	628549	627842	235	7,09	24405	-	Glycerol uptake facilitator	glycerol uptake facilitator related permease (Maj	Glycerol uptake facilitator protein	Major intrinsic protein|Aquaporin	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00618	glpD	630417	628564	617	4,8	67112	-	Alpha-glycerophosphate oxidase	alpha-Glycerophosphate dehydrogenase	Alpha-glycerophosphate oxidase (EC 1.1.3.21	FAD-dependent glycerol-3-phosphate dehydrog	C	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00619	glpK	631999	630482	505	4,79	55651	-	Glycerol kinase	glycerol kinase (ATP:glycerol 3-phosphotransfe	Glycerol kinase (EC 2.7.1.30)	Carbohydrate kinase, FGGY|Glycerol kinase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00620	null	632934	632206	242	6,02	27233	-	Glycosyl transferase, group 2	predicted ORF	Glycosyltransferase (EC 2.4.1.-)	Glycosyl transferase, family 2	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00621	lacT	633376	634254	292	6,43	33958	+	Transcription antiterminator lacT	transcription antiterminator, lacT	Transcription antiterminator lacT	Transcriptional antiterminator bgl|G|CAT RNA-b	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00622	lacE	634304	636016	570	5,5	61953	+	PTS system, lactose-specific IIBC component	PTS system, lactose-specific IIBC component (	PTS system, lactose-specific IIBC component	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-	
LC_00623	lacG	636072	637496	474	5,98	53727	+	6-phospho-beta-galactosidase	6-phospho-beta-galactosidase (Beta-D-phosph	not_predicted_by_ERGO	Glycoside hydrolase, family 1|6-phospho-beta-g	G	No	-	-	tmhmm:0	LC00623	-	-	-	-	-	-	
LC_00624	lacF	637785	638120	111	4,44	12292	+	PTS system, lactose-specific IIA component	PTS system, lactose-specific IIA component (E	PTS system, lactose-specific IIA component (	Phosphotransferase system, lactose/cellobiose	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00625	galK	638454	639620	388	4,7	42396	+	Galactokinase	galactokinase, galK (EC 2.7.1.6)	Galactokinase (EC 2.7.1.6)	Galactokinase|GHMP kinase, ATP-binding regi	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00626	galE	639687	640682	331	6,19	36335	+	UDP-glucose 4-epimerase	UDP-glucose 4-epimerase (Galactowaldenase)	UDP-glucose 4-epimerase (EC 5.1.3.2)	NAD-dependent epimerase/dehydratase|UDP-g	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00627	galT	640679	642136	485	6,42	54397	+	Galactose-1-phosphate uridylyltransferase	galactose-1-phosphate uridylyltransferase, GalT	Galactose-1-phosphate uridylyltransferase (EC	Galactose-1-phosphate uridyl transferase, class	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00628	galR	642178	643173	331	6,81	36430	+	Galactose operon repressor	transcriptional regulator, helix-turn-helix protein	Galactose operon repressor	Bacterial regulatory protein, LacI|Periplasmic bi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00629	galM	643248	644258	336	5,15	36966	+	Aldose 1-epimerase	galactose-1-epimerase / GalM	Aldose 1-epimerase (EC 5.1.3.3)	Aldose 1-epimerase|Glycoside hydrolase-type c	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00630	null	644527	645261	244	10,32	28117	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00631	pts	645634	646128	164	4,28	18510	+	PTS system, galactitol-specific IIA component	PTS system, galactitol-specific IIA component (I	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyru	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00632	null	646143	646451	102	9,01	11355	+	PTS system, galactitol-specific IIB component	PTS system, galactitol/fructose specific IIB com	not_predicted_by_ERGO	Phosphotransferase system, lactose/cellobiose	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00633	gatC	646508	647959	483	6,1	52708	+	PTS system, galactose-specific IIC componer	PTS system, galactitol IIC component	PTS system, galactose-specific IIC componer	Phosphotransferase system, galactitol-specific	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_00634	null	648160	648366	68	10,48	7648	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00635	null	648765	648559	68	11,19	7971	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	Sec	tmhmm:2	-	-	-	-	-	-	-	
LC_00636	dacA	650039	649014	341	6,52	36866	-	Beta-lactamase class C related penicillin bindi	predicted ORF	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, trans	V	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00637	null	650805	650125	226	5,81	24888	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00638	lacC	651764	650826	312	4,83	33719	-	Tagatose-6-phosphate kinase	tagatose-6-phosphate kinase (Phosphotagatoki	Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate kinase, PfkB|Tagatose-6-phosph	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00639	lacD	652895	651894	333	4,75	36467	-	Tagatose 1,6-diphosphate aldolase	tagatose 1,6-diphosphate aldolase 2 (tagatose-1	Tagatose-bisphosphate aldolase (EC 4.1.2.40	Deoxyribose-phosphate aldolase/phospho-2-del	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00640	lacB	653446	652928	172	4,64	18867	-	Galactose-6-phosphate isomerase subunit B	galactose-6-phosphate isomerase LacB subunit	Galactose-6-phosphate isomerase LacB subu	Ribose/galactose isomerase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00641	lacA	653915	653487	142	5,6	15691	-	Galactose-6-phosphate isomerase subunit A	galactose-6-phosphate isomerase LacA subunit	Galactose-6-phosphate isomerase lacA subur	Ribose/galactose isomerase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00642	lacR	654695	653919	258	6,98	28864	-	Lactose phosphotransferase system represso	lactose phosphotransferase system repressor, I	Lactose phosphotransferase system represso	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00643	null	655772	655146	208	6,69	23227	-	Phosphatase	phosphatase	Phosphoglycolate phosphatase (EC 3.1.3.18)	Haloacid dehalogenase-like hydrolase|HAD-sup	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00644	sbcD	655835	656959	374	6,24	42090	+	Exonuclease	ATP-dependent dsDNA exodeoxyribonuclease (	Exonuclease sbcD (EC 3.1.11.-)	Exonuclease SbcD|Metallophosphoesterase	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00645	sbcD	656956	660087	1043	5,64	114737	+	DNA repair ATPase	ATPase involved in DNA repair, nuclease sbcC	Exonuclease sbcC (EC 3.1.11.-)	SMC protein, N-terminal	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00646	null	660899	660396	167	11,67	18510	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00647	hsp1	661113	661589	158	4,68	17831	+	Small heat shock protein	molecular chaperone, small heat shock protein,	Small heat shock protein	Heat shock protein Hsp20|HSP20-like chaperor	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00648	mutY	661887	662984	365	8,65	41050	+	A/G-specific adenine glycosylase	A/G-specific DNA-adenine glycosylase MutY	A/G-specific adenine DNA glycosylase (EC 3.	NUDIX hydrolase|Helix-hairpin-helix motif|HhH-	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00649	null	663076	663867	263	5,08	28371	+	Esterase/lipase	esterase/lipase	Lipase (EC 3.1.1.3)	Alpha/beta hydrolase fold-3	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00650	ywrO	663864	664532	222	5	25014	+	NAD(P)H oxidoreductase	NADPH-quinone oxidoreductase (modulator of	NAD(P)H oxidoreductase YRKL (EC 1.6.99.-)	Flavodoxin-like fold	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00651	null	664529	664708	59	4,32	6948	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00652	null	664982	665506	174	10,55	19258	+	Conserved protein	conserved hypothetical protein	HdeD protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_00653	thiD	666518	665697	273	5,09	29471	-	Phosphomethylpyrimidine kinase	hydroxymethylpyrimidine / phosphomethylpyrimi	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	Phosphomethylpyrimidine kinase type-2|Phospl	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00654	null	667672	666611	353	4,71	39407	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00655	null	668498	667665	277	4,83	31844	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00656	ywnB	668670	669323	217	4,63	23168	+	NADH-flavin reductase	NADH-flavin reductase	Quinate/shikimate dehydrogenase [Pyrroloquin	NmrA-like	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00657	gluA	670148	672535	795	6,11	87197	+	Beta-glucosidase (GH3)	beta-glucosidase-related glycosidases	Beta-glucosidase (EC 3.2.1.21)	Glycoside hydrolase, family 3, N-terminal|Ribos	G	Yes	-	-	tmhmm:0	LC00657	-	-	-	-	-	+	
LC_00658	null	672981	672625	118	10,88	12869	-	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00659	null	673016	673210	64	9,46	7020	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00660	null	673286	674242	318	10,51	34077	+	ABC transporter, substrate-binding protein	ABC transporter, substrate-binding component	ABC transporter substrate-binding protein	ABC transporter substrate binding protein	R	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_00661	abc	674830	675795	321	10,43	33874	+	ABC transporter, substrate-binding protein	ABC transporter, permease component	ABC transporter substrate-binding protein	ABC transporter substrate binding protein	R	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_00662	abc	675824	676795	323	9,26	33998	+	ABC transporter, permease protein	ABC transporter, permease component	ABC transporter permease protein	Bacterial inner-membrane translocator	E	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_00663	agr	676797	677600	267	7,97	29262	+	ABC transporter, ATPase component	ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00664	yhfP	678650	677691	319	9,04	33606	-	Zinc-binding alcohol dehydrogenase	NADPH:quinone reductase related Zn-depende	Alcohol dehydrogenase (EC 1.1.1.1)	Alcohol dehydrogenase superfamily, zinc-conta	CR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00665	pacL3	681459	678793	888	6,34	95164	-	Cation-transporting ATPase	cation-transporting ATPase, E1-E2 family prote	Cation-transporting ATPase (EC 3.6.3.-)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_00666	null	683217	682105	370	9,72	41128	-	Transposase	transposase, IS1533	Transposase	Transposase, IS116/IS110/IS902	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00667	ykcC	684495	683518	325	9,84	36577	-	Glycosyl transferase, group 2	glycosyltransferase family 2	Polyprenyl-phosphate glycosyltransferase (EC	Glycosyl transferase, family 2	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_00668	ykcB	686724	684526	732	10,67	77730	-	4-amino-4-deoxy-L-arabinose transferase relat	4-amino-4-deoxy-L-arabinose transferase relate	Undecaprenyl-phosphosugar--protein glycosyl	Helix-turn-helix, AraC type|Glycosyl transferase	M	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+	
LC_00669	null	687118	686711	135	10,24	15408	-	Conserved membrane protein, GtcA family	conserved membrane protein, GtcA family	GtrA family protein	GtrA-like protein	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00670	null	687368	687571	67	12,22	7243	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00671	null	687617	687841	74	11,95	8176	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00672	llrF	687838	688533	231	4,82	26382	+	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator	Response regulator receiver|Transcriptional reg	K	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_00673	null	688530	689822	430	10,4	48250	+	Two component sensor transduction histidine	signal transduction histidine kinase	Two component system histidine kinase (EC 2	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	+	
LC_00674	null	690345	689965	126	4,76	13803	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00675	ydgI	690627	691286	219	5,35	24804	+	Nitroreductase	NAD(P)H nitroreductase ydgI	NAD(P)H-dependent quinone reductase (EC 1	Nitroreductase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00676	lox	691326	692432	368	6,35	38778	+	L-Lactate dehydrogenase	L-lactate oxidase (1.13.12.)	L-lactate dehydrogenase [cytochrome] (EC 1.1	FMN-dependent alpha-hydroxy acid dehydroger	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00677	null	695572	692705	955	8,8	98242	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Cterm	tmhmm:2	-	-	-	-	-	-	-	
LC_00678	null	696264	697835	523	7,5	60558	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00679	sip	699395	698244	383	10,89	44109	-	Phage-related integrase	site-specific recombinase, prophage lsa1 integr	DNA integration/recombination/inversion prote	Integrase, catalytic core, phage|Integrase, Lamt	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00680	null	700051	699455	198	9,36	22790	-	Transcriptional regulator	transcriptional regulator, Cro/CI family	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00681	null	700158	700367	69	10,53	7614	+	Transcriptional regulator, Cro/CI family protein	transcriptional regulator, Cro/CI family protein	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00682	null	700379	700654	91	6,24	10336	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Putative DNA binding	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	

LC_00683	null	700734	701129	131	3,99	14890	+	Phage-related protein	prophage protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00684	null	701080	701259	59	11,09	6641	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_00685	null	701240	701431	63	10,49	7344	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00686	null	701479	701751	90	4,77	10332	+	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00687	null	701748	701936	62	4,87	6942	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00688	null	701911	702747	278	9,11	30677	+	Phage-related protein, DNA replication	prophage protein, DNA replication	Phage protein	Primase, C-terminal 1|Bifunctional DNA primas	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00689	null	702740	704164	474	7,08	54479	+	Phage-related virulence-associated protein E	prophage protein, helicase/DNA replication / vir	Virulence-associated protein E	Virulence-associated E	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00690	null	704444	704866	140	7,18	16505	+	Phage-related protein	phage protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00691	sb56	704897	705322	141	10,38	16694	+	Phage-related HNH endonuclease	prophage protein, HNH restriction endonucleasi	Phage endonuclease	HNH endonuclease|HNH nuclease	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	+
LC_00692	null	705447	705917	156	8,44	17312	+	Phage-related terminase-small subunit	prophage protein, terminase small subunit, P27	Phage Terminase Small Subunit	Phage terminase, small subunit, putative, P27	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	-
LC_00693	terL	705914	707617	567	5,26	64577	+	Phage-related terminase large subunit	prophage protein, terminase large subunit	Terminase large subunit	Aldo/keto reductase|Phage Terminase	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	+
LC_00694	null	707583	707762	59	11,48	6416	+	Phage-related conserved protein	phage protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	phage	-	-	-	-	-	
LC_00695	null	707767	708951	394	5,11	43457	+	Phage-related portal protein	phage protein, portal protein, HK97 family	Portal protein	Phage portal protein, HK97|Phage portal proteir	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00696	null	708938	710509	523	4,37	57327	+	Phage-related prohead protease	prophage protein, phage prohead protein, peptic	Phage protein	Peptidase U35, phage prohead HK97|Phage m	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	protease	+	
LC_00697	null	710568	710858	96	4,36	10660	+	Phage-related head-to-tail joining	prophage protein, head-to-tail joining, gp	Phage protein	Protein of unknown function, phage	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	+
LC_00698	null	711028	711183	51	10,11	6037	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00699	null	714233	712413	606	6,88	69276	-	Transcriptional regulator	predicted ORF	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00700	null	715848	714841	335	5,8	37237	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_00701	ydaF	716206	715868	112	9,88	12702	-	Transcriptional regulator, PadR family	transcriptional regulator, PadR family protein	Transcriptional regulator, PadR family	Transcriptional regulator PadR-like|Winged heli	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00702	null	716681	716376	101	9,5	11382	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_00703	null	716835	717134	99	5,14	11293	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00704	qor	718192	717167	341	6,74	36488	-	Alcohol dehydrogenase	NADPH:quinone reductase related Zn-depende	Quinone oxidoreductase (EC 1.6.5.5)	Alcohol dehydrogenase superfamily, zinc-conta	CR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00705	null	718403	718765	120	10,05	13206	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00706	null	719318	718839	159	11,24	17840	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_00707	yubA	720477	719311	388	8,22	43117	-	Conserved membrane protein	membrane protein of permease (PerM) family	Hypothetical membrane spanning protein	Protein of unknown function UPF0118	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_00708	null	720923	721117	64	10,71	7344	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:2	-	-	-	-	-	-	-	
LC_00709	null	721315	721103	70	11,29	7628	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00710	lexA	721512	722138	208	4,5	22762	+	LexA repressor	LexA repressor (SOS regulatory protein dinR),	LexA repressor (EC 3.4.21.88)	Peptidase S24, LexA/MucA/RumA/RuvA|Peptic	KT	Yes	-	-	tmhmm:0	-	-	-	-	regulator	protease	+	
LC_00711	null	722732	722259	157	10,79	16854	-	Putative protein without homology	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_00712	mleP1	723690	722743	315	10,06	34984	-	Auxin efflux carrier (AEC) family permease	auxin efflux carrier (AEC) family permease	Malate permease	Auxin efflux carrier	null	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_00713	yaiB	724329	723712	205	8,95	22537	-	Conserved protein	flavoprotein oxygenase DIM6/NTAB family-like p	FAD-dependent oxidoreductase (EC 1.-.-.-)	FMN-binding split barrel, related|FMN-binding s	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00714	null	725587	724628	319	10,11	33568	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+	
LC_00715	fthC	726325	725753	190	5,67	20823	-	5-formyltetrahydrofolate cyclo-ligase	5-formyltetrahydrofolate cyclo-ligase family prot	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3	5-formyltetrahydrofolate cyclo-ligase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00716	yeaO	726683	726333	116	9,69	13574	-	Conserved protein	uroporphyrin-III C-methyltransferase	Hypothetical cytosolic protein	Protein of unknown function DUF488	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00717	null	726774	727709	311	5,16	35291	+	Mg2+ and Co2+ transporter	Mg2+ and Co2+ transporter	Magnesium and cobalt transport protein corA	Mg2+ transporter protein, CorA-like	P	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_00718	mleR	728712	727834	292	10,28	32623	-	Malolactic regulator, LysR family	transcriptional regulator of the malolactic ferme	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR|LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00719	mleS	729257	730924	555	4,47	60457	+	Malic enzyme	NAD-dependent malolactic enzyme MleD	Malolactic enzyme (EC 1.-.-.-)	Malic oxidoreductase|Malic enzyme, N-terminal|	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00720	mleP2	730929	731915	328	9,8	35451	+	Malate permease	malate permease	Malate/lactate antiporter	Auxin efflux carrier	R	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+	
LC_00721	tpx	732470	731973	165	4,66	18497	-	Thiol peroxidase	thiol peroxidase (atypical 2-Cys peroxiredoxin)	Thioredoxin peroxidase (EC 1.11.1.15)	Antioxidant Tpx|Thioredoxin fold|Thioredoxin-lik	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00722	null	732812	733333	173	8,8	19871	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00723	null	734464	733490	324	7,39	37204	-	Transcriptional regulator	transcriptional regulator, MutR family	Transcriptional regulator	Helix-turn-helix type 3|Transcriptional activator f	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00724	null	734582	736171	529	10,4	58219	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase and perme	Multidrug resistance ABC transporter ATP-bir	ABC transporter related|AAA+ ATPase, core|At	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_00725	pepF2	738071	736257	604	4,6	68242	-	Oligoendopeptidase F	oligopeptidase F. Metallo peptidase. MEROPS I	Oligoendopeptidase F (EC 3.4.24.-)	Peptidase M3A and M3B, thimet/oligopeptidase E	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00726	ndk	738409	738855	148	6,52	16235	+	Nucleoside diphosphate kinase	nucleoside diphosphate kinase (NDK) (NDP kin	Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleoside diphosphate kinase|Nucleoside-dipl	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00727	null	739331	739002	109	4,37	12237	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	G	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00728	ctpE	741760	739412	782	8,55	84190	-	Cation-transporting ATPase	cation-transporting ATPase, P-type	Cation-transporting ATPase (EC 3.6.3.-)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+	
LC_00729	pepR1	741927	742850	307	6,34	34706	+	Prolyl aminopeptidase	prolyl aminopeptidase, ABhydrolase 1 family	Proline iminopeptidase (EC 3.4.11.5)	Alpha/beta hydrolase fold-1|Peptidase S33, prol	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00730	null	742903	743250	115	9,11	13245	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00731	ywfD	743315	744307	330	9,86	36113	+	Acetyltransferase	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00732	napA	744332	745486	384	5,58	41174	+	Na+/H+ antiporter	Na+/H+ antiporter NapA	Na+/H+ antiporter napA	Potassium efflux system protein|Sodium/hydrog	P	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-	
LC_00733	null	745646	745443	67	12,29	7610	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00734	gph	745743	746399	218	4,84	24112	+	Hydrolase, haloacid dehalogenase-like family	hydrolase, HAD superfamily / phosphoglycolate	Hydrolase (HAD superfamily)	Haloacid dehalogenase-like hydrolase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00735	null	746971	746513	152	10,39	17380	-	Transcriptional regulator, MarR family	transcriptional regulator, MarR family	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00736	ybcH	747146	748027	293	10,08	32768	+	Alpha/beta hydrolase	hydrolase, alpha/beta superfamily	Alpha/beta hydrolase	Alpha/beta hydrolase fold-1	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00737	nrdI	748513	748043	156	5,24	17241	-	Ribonucleotide reductase, NrdI-protein	ribonucleotide reductase, NrdI family	NrdI protein	Flavodoxin, N-terminal|Ribonucleotide reductas	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00738	dkg	749512	748688	274	6,29	30955	-	Aldo/keto reductase	oxidoreductase, aldo/keto reductase family prot	2,5-diketo-D-gluconic acid reductase (EC 1.1.	Aldo/keto reductase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00739	null	749848	750609	253	9,4	27440	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_00740	null	750615	751460	281	10,19	31548	+	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Protein of unknown function DUF915, hydrolase	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00741	yviA	752117	751470	215	5,7	24007	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane associated protein	Protein of unknown function DUF421	S	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_00742	null	752589	752128	153	10,62	17177	-	Conserved protein	conserved hypothetical protein (LysM motif)	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00743	yxjH	753476	754609	377	5,4	43038	+	Methionine synthase	Methionine synthase II (cobalamin-independent	5-methyltetrahydropteroyltriglutamate--homocy	Methionine synthase, vitamin-B12 independent	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00744	luxS	754744	755217	157	6,23	17256	+	S-ribosylhomocysteine lyase, Autoinducer-2 p	S-ribosylhomocysteine lyase (Autoinducer-2 pro	Autoinducer-2 production protein luxS / Ribos	LuxS protein	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00745	yjbF	755899	755303	198	9,89	22299	-	Snare associated golgi protein	snare associated golgi protein	Hypothetical membrane associated protein	SNARE associated Golgi protein	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_00746	ruvA	755991	756587	198	4,76	21091	+	Holliday junction DNA helicase RuvA	Holliday junction ATP-dependent DNA helicase	Holliday junction DNA helicase ruvA	Bacterial DNA recombination protein RuvA|Heli	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00747	ruvB	756663	757709	348	5,45	38552	+	Holliday junction DNA helicase RuvB	Holliday junction DNA helicase B	Holliday junction DNA helicase ruvB	AAA+ ATPase, core|AAA ATPase, core|Hollida	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00748	queA	757734	758804	356	5,98	40340	+	S-adenosylmethionine:tRNA ribosyltransferas	S-adenosylmethionine:tRNA-ribosyltransferase-	S-adenosylmethionine:tRNA ribosyltransferas	Queuosine biosynthesis protein	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00749	tgt	759294	760436	380	6,68	42647	+	Queuine tRNA-ribosyltransferase	queuine tRNA-ribosyltransferase (tRNA-guanin	Queuine tRNA-ribosyltransferase (EC 2.4.2.2	Queuine/other tRNA-ribosyltransferase|Queuin	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00750	yajC-2	760509	760934	141	4,86	14975	+	Preprotein translocase, YajC subunit	preprotein translocase, YajC subunit	Protein translocase subunit YajC	YajC	U	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00751	adhE	761178	763784	868	6,72	94554	+	Aldehyde-alcohol dehydrogenase	NAD-dependent alcohol-acetaldehyde dehydroc	Alcohol dehydrogenase (EC 1.1.1.1) / Acetald	Iron-containing alcohol dehydrogenase|Aldehyd	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_00752	null	763753	763905	50	9,93	5727	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00753	efaR	763945	764589	214	6,42	23663	+	Iron-dependent transcriptional regulator, FeoA	iron/Mn dependent repressor:FeoA	Iron-dependent repressor	Iron dependent repressor|FeoA|Transcriptional	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00754	zwf	764619	766106	495	5,45	55523	+	Glucose-6-phosphate 1-dehydrogenase	glucose-6-phosphate 1-dehydrogenase (EC 1.1	Glucose-6-phosphate 1-dehydrogenase (EC 1	Glucose-6-phosphate dehydrogenase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00755	dinP	766636	767739	367	10,19	41122	+	DNA polymerase IV	nucleotidyltransferase/DNA polymerase for DN	DNA polymerase IV (EC 2.7.7.7)	UMUC-like DNA-repair protein	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00756	ytol	768339	769652	437	7,22	47219	+	Thioesterase family protein	transcriptional regulator with CBS domains	CBS domain containing protein	Cystathionine-beta-synthase|Thioesterase supe	R	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00757	rpmE2	769659	770615	318	5,01	34477	+	Phosphoesterase, DHH family protein	phosphoesterase, DHH family protein	Phosphoesterase, DHH family protein	Phosphoesterase, RecJ-like|Phosphoesterase,	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00758	srmB	770621	771967	448	10,51	50485	+	ATP-dependent RNA helicase	superfamily II DNA and RNA helicases, ATP-d	ATP-dependent RNA helicase	Helicase, C-terminal|DEAD/DEAH box helicase	LKJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00759	null	771972	772907	311	9,62	34589	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00760	null	773123	773467	114	11,33	12240	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00761	alaS	773606	775738	710	6,09	79632	+	Alanyl-tRNA synthetase	alanyl-tRNA synthetase (Alanine--tRNA ligase)	Alanyl-tRNA synthetase (EC 6.1.1.7)	Alanyl-tRNA synthetase, class IIc|Threonyl/alan	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00762	null	775777	776250	157	10,29	15995	+	Phosphoesterase, DHHA1	predicted ORF	not_predicted_by_ERGO	Phosphoesterase, DHHA1	J	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00763	null	776411	777505	364	4,71	41523	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00764	alaRS	777609	777869	86	5,13	10121	+	Conserved protein	Zn-dependent metalloprotease, insulinase famil	Hypothetical cytosolic protein	Protein of unknown function DUF965, bacterial	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00765	ruvX	777869	778303	144	8,91	16093	+	Holliday junction resolvase	Holliday junction resolvase-like protein	Resolvase	Resolvase, holliday junction-type, YqgF-like|Res	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00766	ybeC	778350	778670	106	3,34	12021	+	Conserved protein	aminotransferase, class V	Hypothetical cytosolic protein	Protein of unknown function DUF1292	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00767	null	778868	779113	81	6,53	9007	+	Stimulator of FtsZ polymerization and compon	stimulator of FtsZ polymerization and componer	no_function_in_ERGO	no annotation	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00768	null	779126	779659	177	9,83	19559	+	Colicin V production protein	membrane ancor connecting MutS2 with cell-di	CvpA family membrane protein	Colicin V production protein	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_00769	mutS	779727	782087	786	7,1	86341	+	DNA mismatch repair protein mutS	DNA mismatch repair MutS2 family ATPase	DNA mismatch repair protein mutS	DNA mismatch repair protein MutS, C-terminal|	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00770	trxA3	782155	782466	103	4,8	11478	+	Thioredoxin	thiol-disulfide isomerase and thioredoxins	Thioredoxin	Thioredoxin|Thioredoxin-related|Thioredoxin fol	OC	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00771	dltX	782834	783016	60	9,47	7258	+	D-Ala-teichoic acid biosynthesis protein	D-Ala-teichoic acid biosynthesis protein	no_function_in_ERGO	no annotation	I	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00772	dltA	783031	784551	506	5,1	55868	+	D-alanine--poly(phosphoribitol) ligase subunit	D-alanine--poly(phosphoribitol) ligase subunit 1	D-alanine-activating enzyme (EC 6.3.2.-)	AMP-dependent synthetase and ligase|Amino a	Q	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00773	dltB	784551	785768	405	9,88	48031	+	D-alanyl transfer protein DltB	transmembrane protein, DltB	Protein dltB	Membrane bound O-acyl transferase, MBOAT	M	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+	
LC_00774	dltC	785838	786083	81	3,9	8920	+	D-alanyl carrier protein DltC	D-alanyl carrier protein DltC	D-alanyl carrier protein	D-alanyl carrier protein|Phosphopantetheine-bin	IQ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00775	dltD	786080	787351	423	10,1	48005	+	Extramembranal protein, DltD protein	D-alanyl transfer protein, extramembranal protei	Protein dltD precursor	DltD, C-terminal|DltD, N-terminal|DltD, central r	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00776	yslB	787969	787487	160	5,17	17705	-	Hydrocarbon binding protein	hydrocarbon binding protein, V4R domain	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00777	murI	788264	789718	484	5,43	52263	+	Glutamate racemase	glutamate racemase with xanthosine/inosine py	Glutamate racemase (EC 5.1.1.3) / Xanthosin	Asp/Glu racemase|Ham1-like protein|Glutamate	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00778	xerD	789715	790239	174	6	18928	+	Phosphoesterase	phosphoesterase family protein	putative phosphoesterase	Protein of unknown function UPF0025|Metallop	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00779	glpF	791063	790332	243	9,52	25360	-	Glycerol uptake facilitator protein	glycerol uptake facilitator related permease (Maj	Aquaporin / Glycerol uptake facilitator protein	Major intrinsic protein|Aquaporin	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_00780	ykuL	791351	791836	161	5,15	18090	+	CBS domain	CBS domain protein YkuL	CBS domain containing protein	Cystathionine-beta-synthase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00781	null	792790	791888	300	9,19	31735	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Integral membrane protein	Protein of unknown function DUF368	S	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_00782	null	793726	792842	294	10,1	32334	-	Small-conductance mechanosensitive channe	small-conductance mechanosensitive channel	Mechanosensitive ion channel	MscS Mechanosensitive ion channel|Like-Sm ri	M	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_00783	null	794458	794886	142	9,11	14892	+	Methyl-accepting chemotaxis-like protein	methyl-accepting chemotaxis-like protein	Hypothetical protein	Protein of unknown function DUF948, bacterial	NT	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00784	null	794901	795401	166	4,13	17876	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_00785	yrxA	795540	796073	177	7,3	19468	+	Transcriptional regulator	transcriptional regulator, biotin repressor family	Transcriptional regulator, biotin repressor fami	3H|Winged helix repressor DNA-binding|Helix-t	R	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00786	pepQ	797330	796227	367	4,59	40371	-	Xaa-Pro dipeptidase	Xaa-Pro dipeptidase (Proline dipeptidase)	Xaa-Pro aminopeptidase (EC 3.4.11.9)	Creatinase|Peptidase M24, catalytic core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00787	ccpA	797685	798686	333	5,14	36315	+	Catabolite control protein A	glucose-resistance amylase regulator (Catabolit	Catabolite control protein A	Bacterial regulatory protein, LacI|Periplasmic bi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00788	pbp1B	801592	798848	914	9,48	99292	-	Membrane carboxypeptidase, penicillin-bindin	membrane carboxypeptidase, penicillin-binding	Multimodular transpeptidase-transglycosylase	Glycosyl transferase, family 51|Penicillin-bindin	M	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+	
LC_00789	yfnB	802217	802900	227	6,52	26381	+	Hydrolase, haloacid dehalogenase-like family	hydrolase, HAD superfamily, 2-haloacid dehaloj	Hydrolase (HAD superfamily)	Haloacid dehalogenase-like hydrolase|HAD-sup	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00790	birA	803663	802917	248	6,9	26324	-	Biotin operon repressor	biotin operon repressor	Biotin operon repressor / Biotin--[acetyl-CoA-c	Biotin protein ligase, C-terminal|Biotin/lipoate A/	H	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00791	pepV	805212	803809	467	4,76	50654	-	Dipeptidase	dipeptidase PepV	Xaa-His dipeptidase (EC 3.4.13.3)	ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|F	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_00792	null	806688	805348	446	6,9	50003	-	Glycerophosphoryl diester phosphodiesterase	cell surface Glycerophosphoryl diester phospho	Glycerophosphoryl diester phosphodiesterase	Glycerophosphoryl diester phosphodiesterase	C	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+	
LC_00793	null	806799	807113	104	6,1	12190	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00794	null	807315	808382	355	10,12	39016	+	Conserved membrane protein	conserved hypothetical protein (multitransmemt	Hypothetical membrane spanning protein	YibE/F-like	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_00795	null	808379	809116	245	6,51	25930	+	Conserved membrane protein	conserved hypothetical protein (multitransmemt	Hypothetical membrane spanning protein	YibE/F-like	null	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_00796	null	809118	809720	200	6,36	22836	+	Phosphoesterase or phosphohydrolase	similar to phosphoesterase or phosphohydrolas	Phosphohydrolase	Phosphoesterase MJ1445	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00797	yunD	809833	811209	458	6,72	51107	+	5'-nucleotidase/2',3'-cyclic phosphodiesterase	5'-nucleotidase/2',3'-cyclic phosphodiesterase n	5'-nucleotidase (EC 3.1.3.5)	Metallophosphoesterase|5'-Nucleotidase, N-terr	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00798	ybiC	811312	811920	202	10,06	23839	+	Transcriptional regulator	transcriptional regulator, YutD	Hypothetical cytosolic protein	Protein of unknown function DUF1027	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_00799	nagD	811929	812705	258	5,96	28515	+	Hydrolase of the HAD superfamily	sugar phosphatase, HAD superfamily, subfamil	Hydrolase (HAD superfamily)	Haloacid dehalogenase-like hydrolase|HAD-sup	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00800	null	812706	813338	210	10,06	24335	+	Integral membrane protein, Rhodopsin-like GF	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Rhodopsin-like GPCR superfamily|Integral men	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_00801	dedA	814052	813399	217	10,03	23889	-	DedA	integral membrane protein, DedA family	DedA family protein	SNARE associated Golgi protein	S	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_00802	ltrC	814641	814138	167	4,5	18621	-	Low temperature requirement C protein	phosphatidylglycerophosphatase A related prot	Low temperature requirement C protein	Phosphatidylglycerophosphatase A	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00803	trxB1	815722	814736	328	6	36000	-	Thioredoxin reductase	thioredoxin-disulfide reductase, NADP-thioredo	Thioredoxin reductase (EC 1.8.1.9)	Pyridine nucleotide-disulphide oxidoreductase, (	O	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_00804	ppiB	815957	816541	194	5,03	21273	+	Peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase (rotamase) -	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8	Peptidyl-prolyl cis-trans isomerase, cyclophilin-t	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00805	yugI	816629	816988	119	8,5	13481	+	General stress protein 13	polyribonucleotide nucleotidyltransferase (gener	S1-type RNA-binding domain	Ribosomal protein S1|RNA binding S1|Nucleic .	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00806	null	818269	818084	61	10,44	6799	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00807	null	818220	818423	67	11,84	7290	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00808	null	818694	818377	105	12,08	11621	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00809	null	818873	818679	64	11,31	7429	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00810	null	819558	819160	132	10,4	14921	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	C-type lectin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00811	null	819746	819534	70	8,5	7801	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00812	null	820548	820153	131	8,72	14815	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00813	null	821762	821463	99	11,9	11432	-	Lipoprotein	lipoprotein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00814	null	821900	822238	112	11,26	12018	+	Conserved protein	metal-dependent RNase, consists of a metallo-l	not_predicted_by_ERGO	KH, prokaryotic type	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00815	null	823959	823648	103	9,17	11379	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00816	null	824872	824723	49	8,51	5352	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00817	null	826432	825893	179	10,07	21174	-	ComX	ComX	RNA polymerase ECF-type sigma factor	RNA polymerase sigma-70 region 2|RNA polym	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00818	ybeC	826946	828529	527	9,9	57778	+	Amino acid permease	amino acid permease-associated region	Amino acid permease	Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	+	
LC_00819	rfaG	828777	829985	402	5,69	45207	+	Glycosyl transferase, group 1	glycosyl transferase, group 1 family protein	1,2-diacylglycerol 3-glucosyltransferase (EC 2	Glycosyl transferase, group 1	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00820	rfaG	829988	831016	342	9,34	39085	+	Glycosyl transferase, group 1	glycosyl transferase CpoA	Glycosyltransferase (EC 2.4.1.-)	Glycosyl transferase, group 1	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_00821	null	831029	832039	336	9,88	37850	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Integral membrane protein	Conserved hypothetical protein 374	S	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_00822	araT1	833376	832204	390	5,74	42652	-	Aminotransferase	aromatic amino acid aminotransferase / acetyldi	Aromatic amino acid aminotransferase (EC 2.(	1-aminocyclopropane-1-carboxylate synthase|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00823	ykuJ	833674	833955	93	3,87	10485	+	Conserved cytosolic protein	YkuJ protein-like protein	Hypothetical cytosolic protein	Protein of unknown function DUF1797	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00824	ispB	834578	836671	697	8,97	77959	+	Sulfatase	sulfatase family protein / phosphoglycerol transf	Sulfatase family protein	Sulfatase|Alkaline phosphatase|Membrane sulp	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_00825	labQ	836883	837323	146	7,18	16331	+	Transcriptional regulator, Fur family	transcriptional regulator, Fur family / Fe2+/Zn2·	Peroxide operon regulator	Ferric-uptake regulator	P	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_00826	null	838244	838447	67	11,84	7290	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00827	null	838718	838401	105	12,08	11621	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00828	null	838897	838703	64	11,31	7429	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00829	null	839582	839184	132	10,4	14921	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	C-type lectin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00830	null	839770	839558	70	8,5	7801	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00831	null	840572	840177	131	8,72	14815	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00832	null	841786	841487	99	11,9	11432	-	Lipoprotein	lipoprotein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00833	null	841924	842262	112	11,26	12018	+	Conserved protein	metal-dependent RNase, consists of a metallo-l	not_predicted_by_ERGO	KH, prokaryotic type	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00834	null	842757	842882	41	8,06	4709	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00835	null	844264	843137	375	10,22	43335	-	Phage-related integrase	phage protein, integrase	not_predicted_by_ERGO	Integrase, catalytic core, phage|Integrase, Lamt	L	No	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00836	null	844635	844372	87	10,35	10253	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00837	null	844990	844733	85	5	9256	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_00838	hsds	846406	845225	393	9,4	44358	-	Type I restriction enzyme, specificity protein	type I restriction modification system DNA spec	not_predicted_by_ERGO	Restriction modification system DNA specificity	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00839	null	846715	846497	72	7,35	8068	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Peptidase S24 and S26, C-terminal region	null	No	-	-	tmhmm:0	-	-	-	-	-	protease	-	
LC_00840	cI	847452	846787	221	4,48	24854	-	Phage-related Cro/CI family transcription regu	Cro/CI family transcription regulator	not_predicted_by_ERGO	Helix-turn-helix type 3|Peptidase S24, S26A an	K	No	-	-	tmhmm:0	-	phage	-	-	regulator	-	+	
LC_00841	cro	847619	847861	80	9,89	9351	+	Phage-related Cro-like protein	transcriptional regulator, xre family	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	phage	-	-	regulator	-	+	
LC_00842	null	847885	848589	234	10,06	26473	+	Phage-related antirepressor	phage protein, antirepressor protein	not_predicted_by_ERGO	Phage antirepressor protein|Phage regulatory p	null	No	-	-	tmhmm:0	-	phage	-	-	regulator	-	-	
LC_00843	null	848590	848850	86	8,22	10011	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00844	null	849148	848843	101	5,47	11567	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00845	null	849223	849579	118	10,19	13790	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00846	null	849579	849707	42	6,51	4603	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_00847	null	849719	849937	72	9,44	8607	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00848	null	849939	850109	56	3,75	6068	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00849	null	850121	850996	291	5,87	32446	+	RecT family protein	prophage protein	RecT protein	RecT protein	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00850	pi	850869	851780	303	9,75	35675	+	Phage-related protein	prophage protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00851	null	851796	852752	318	10,1	35914	+	Phage-related replication protein	Dnad Domain protein	Phage replication protein	DnaD and phage-associated region	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00852	ssb	852765	853250	161	7,37	17696	+	Single-stranded DNA-binding protein	single-stranded DNA-binding protein (SSB) (He	Single-strand DNA binding protein	Single-strand binding protein/Primosomal replic	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00853	ps	853559	853774	71	4,41	7856	+	Phage-related protein with HTH-domain	phage protein, DNA-binding protein	Phage protein	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	phage	-	-	regulator	-	-	
LC_00854	null	853771	853962	63	10,66	7314	+	Phage-related protein DNA-binding protein	phage protein, regulatory protein	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	null	Yes	-	-	tmhmm:0	-	phage	-	-	regulator	-	+	
LC_00855	null	854332	854781	149	10,86	16815	+	Phage-related protein	conserved hypothetical protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00856	null	854828	855082	84	10,47	9537	+	Phage-related protein	phage protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00857	null	855505	855969	154	7,77	16716	+	Phage-related protein	predicted ORF	Phage protein	no annotation	D	Yes	-	Sec	tmhmm:1	-	phage	-	-	-	-	+	
LC_00858	null	856351	856761	136	4,94	15940	+	Conserved protein	conserved hypothetical protein (phage protein)	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00859	null	856758	857198	146	4,95	16574	+	Phage-related protein	phage protein	Phage protein	Protein of unknown function DUF1642	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00860	null	857185	857403	72	4,99	8162	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00861	null	857393	857725	110	4,29	12283	+	Phage-related protein	phage protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00862	null	857722	857961	79	10,1	9327	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00863	null	857958	858350	130	4,09	14829	+	Phage-related protein	conserved hypothetical protein	not_predicted_by_ERGO	Conserved hypothetical protein 1671, phage	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00864	null	859611	859051	186	10,41	21125	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00865	null	859676	860341	221	9,8	25713	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_00866	null	860984	862201	405	6,2	46455	+	Phage-related protein	phage protein	Phage protein	Homeodomain-like|GcrA cell cycle regulator	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00867	null	862188	862718	176	9,88	20386	+	Phage-related HNH endonuclease	prophage protein, HNH homing endonuclease f	HNH endonuclease family protein	HNH endonuclease|Nuclease-associated modu	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00868	null	862821	863144	107	9,82	11380	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00869	null	863162	863326	54	5,48	6072	+	Phage-related protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	phage	-	-	-	-	-	
LC_00870	null	863363	864157	264	9,39	31026	+	Phage-related terminase, small subunit	phage protein, HNH endonuclease family	not_predicted_by_ERGO	HNH endonuclease|HNH nuclease	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00871	null	864358	864813	151	9,22	17061	+	Phage-related terminase, small subunit	terminase subunit	not_predicted_by_ERGO	Phage terminase, small subunit, putative, P27	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00872	null	864835	866547	570	5,08	65143	+	Phage-related terminase, large subunit	phage protein, terminase large subunit	not_predicted_by_ERGO	Phage Terminase	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00873	null	866559	866750	63	9,44	6692	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_00874	null	866756	868009	417	4,81	46384	+	Phage-related portal protein	phage protein, portal protein	not_predicted_by_ERGO	Phage portal protein, HK97|Phage portal proteir	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00875	null	867963	868592	209	5,39	23844	+	Phage-related prohead protein	phage protein, phage prohead protein, peptidas	not_predicted_by_ERGO	Peptidase U35, phage prohead HK97	null	No	-	-	tmhmm:0	-	phage	-	-	-	protease	-	
LC_00876	null	868634	869836	400	4,94	43825	+	Phage-related major head protein	phage protein, major head protein	not_predicted_by_ERGO	Phage major capsid protein, HK97	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00877	null	869854	870093	79	4,33	7781	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	Carbohydrate-binding-like fold	null	No	immunglob/in	-	tmhmm:0	-	-	-	-	-	-	-	
LC_00878	null	870104	870463	119	4,09	13547	+	Phage-related protein	phage protein / DNA packaging protein	not_predicted_by_ERGO	Protein of unknown function, phage	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00879	null	870342	870782	146	10,22	16887	+	Phage-related head-tail joining protein	head-tail joining protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00880	null	870782	871168	128	5,62	13989	+	Phage-related protein	head-tail joining protein, modification system DN	not_predicted_by_ERGO	Phage protein, HK97, gp10	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00881	null	871168	871554	128	4,1	14634	+	Phage-related head-to-tail joining protein	head-tail joining protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00882	null	871588	872205	205	4,32	22046	+	Phage-related major tail protein	phage protein, major tail	not_predicted_by_ERGO	Phage major tail protein phi13	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00883	null	872305	872718	137	6,77	15235	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00884	null	872841	877706	1621	9,96	172697	+	Phage-related protein	phage protein, measure	not_predicted_by_ERGO	Phage tail tape measure protein TP901, core re	NT	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00885	null	877707	879629	640	4,57	70882	+	Phage-related tail component	phage protein, tail	Phage protein / Phage tail protein	Phage tail component, N-terminal|Siphovirus tai	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00886	null	879629	882130	833	4,84	91030	+	Phage-related tail-host interaction protein	tail-host specificity protein	Tail-host specificity protein	Phage minor structural protein, N-terminal	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+	
LC_00887	null	882127	882414	95	4,3	10467	+	Phage-related protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00888	null	882395	882538	47	4,84	5523	+	Phage-related protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-	
LC_00889	null	882568	882861	97	5,09	10878	+	Phage-related protein	phage protein	Phage protein	no annotation	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-	

LC_00890	hol	882851	883264	137	4,56	14414	+	Phage-related holin	holin, LysA	Holin	Holin, phage phi LC3	null	Yes	-	Cterm	tmhmm:2	-	phage	-	-	-	-	-
LC_00891	null	883275	884459	394	9,01	43150	+	Phage-related endolysin	lysin protein	Lysozyme (EC 3.2.1.17)	Glycoside hydrolase, family 25|Peptidoglycan-b	M	Yes	peptidoglucar	LysM	tmhmm:1	LC00891	phage	-	-	-	-	-
LC_00892	null	885831	885178	217	10,39	24486	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00893	metK	886010	887194	394	4,61	43111	+	S-adenosylmethionine synthetase	S-adenosylmethionine synthetase (methionine a	S-adenosylmethionine synthetase (EC 2.5.1.6	S-adenosylmethionine synthetase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00894	mdr	887724	889217	497	9,82	54241	+	Transporter, major facilitator superfamily MFS	drug resistance transporter, EmrB/QacA family	Multidrug resistance protein B	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	+
LC_00895	glnR	889863	889393	156	9,76	17853	-	Transcriptional regulator, MerR family	transcriptional regulator	Transcriptional regulator, MerR family	Bacterial regulatory protein, MerR|Putative DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00896	lmrB-2	890085	891563	492	10,34	52967	+	Transporter, major facilitator superfamily MFS	drug resistance transporter, EmrB/QacA family	Multidrug resistance protein B	Tetracycline resistance protein TetB|Drug resis	GEPF	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_00897	null	891560	892285	241	10,85	26609	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_00898	null	893021	892350	223	11,41	25253	-	Membrane-associated phospholipid phosphata	membrane-associated phospholipid phosphatas	Membrane-associated phospholipid phosphata	Phosphoesterase, PA-phosphatase related|Acid	I	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00899	leuS	893442	895853	803	4,81	91741	+	Leucyl-tRNA synthetase	leucyl-tRNA synthetase (leucine--tRNA ligase) (	Leucyl-tRNA synthetase (EC 6.1.1.4)	Aminoacyl-tRNA synthetase, class I|Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00900	null	896011	896226	71	12,36	8017	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00901	null	896373	897374	333	9,35	37109	+	Polysaccharide transport membrane protein	polysaccharide biosynthesis family protein	Export protein for polysaccharides and teichoi	Polysaccharide biosynthesis protein	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_00902	null	897340	898017	225	10,36	24924	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	R	No	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00903	rsuA2	898022	898732	236	6,1	26152	+	Pseudouridine synthase A	16S rRNA uridine-516 pseudouridylate synthas	Ribosomal small subunit pseudouridine synth	Pseudouridine synthase, Rsu|RNA-binding S4|	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00904	yhcC	898818	899033	71	7,9	8050	+	Zn-ribbon nucleic-acid-binding protein	Zn-ribbon nucleic-acid-binding protein	Zinc finger protein	no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00905	ycfG	899994	899164	276	9,58	28663	-	Sugar kinase	sugar kinase of P-loop ATPase superfamily	Sugar kinase	Carbohydrate kinase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00906	null	900491	899991	166	5,98	18489	-	Phosphohydrolase, MutT/nudix family	MutT/Nudix family hydrolase	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00907	bsaA	900888	901361	157	9,51	17583	+	Glutathione peroxidase	glutathione peroxidase bsaA-like protein	Glutathione peroxidase (EC 1.11.1.9)	Glutathione peroxidase|Thioredoxin fold|Thiored	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00908	malY	901468	902676	402	5,25	44903	+	Aminotransferase	aspartate aminotransferase	Cystathionine beta-lyase (EC 4.4.1.8)	Ferrochelatase|1-aminocyclopropane-1-carboxy	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00909	cpdA	904132	902804	442	9,69	50266	-	Putative protein without homology	phosphohydrolase	Predicted phosphohydrolases, Icc family	Metallophosphoesterase|Phosphoesterase, Imo	R	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00910	gcvR	904348	904614	88	5,75	9573	+	ACT domain-containing protein	ACT domain-containing protein	ACT domain-containing protein	Amino acid-binding ACT	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00911	null	904769	906112	447	4,63	46581	+	Conserved protein	fructose-6-phosphate aldolase / glycerol-3-phos	Hypothetical protein	Protein of unknown function DUF711	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00912	null	906279	907346	355	10,68	41692	+	Competence protein	Competence protein	Putative competence protein/transcription fact	Competence CoiA-like	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00913	null	908222	907587	211	6,42	24661	-	Dithiol-disulfide isomerase	dithiol-disulfide isomerase	Hypothetical cytosolic protein	Thioredoxin-like fold	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00914	null	908885	908292	197	6,24	22421	-	Conserved protein	conserved hypothetical protein	Organic phosphate binding CYTH family prote	Adenylate cyclase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00915	rdpR2	909052	909729	225	5,23	26574	+	GTP pyrophosphokinase	GTP pyrophosphokinase family protein	GTP pyrophosphokinase homolog	RelA/SpoT	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00916	ppnK	909731	910528	265	7,18	29993	+	Inorganic polyphosphate/ATP-NAD kinase	inorganic polyphosphate/ATP-NAD kinase (Poly	ATP-NAD kinase (EC 2.7.1.23)	ATP-NAD/AcoX kinase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00917	rluA4	910528	911430	300	9,88	34051	+	Pseudouridine synthase	ribosomal large subunit pseudouridine synthase	Ribosomal large subunit pseudouridine synthe	Pseudouridine synthase|Pseudouridine synthas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00918	apbE	912632	911574	352	9,93	38500	-	Thiamine biosynthesis lipoprotein	thiamine biosynthesis membrane-associated lip	Iron-sulfur cluster assembly/repair protein Apb	ApbE-like lipoprotein	H	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_00919	cutC	913488	912850	212	4,87	22417	-	Copper homeostasis protein CutC	copper homeostasis protein CutC family protein	Copper homeostasis protein cutC	CutC	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00920	bacA	914326	913508	272	9,66	30173	-	Undecaprenyl-diphosphatase	undecaprenyl-diphosphatase (undecaprenyl pyr	Undecaprenyl-diphosphatase (EC 3.6.1.27) (E	Bacitracin resistance protein BacA	V	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_00921	ykgB	915571	914531	346	4,8	37654	-	3-carboxymuconate cyclase	3-carboxymuconate cyclase	6-phosphogluconolactonase (EC 3.1.1.31)	no annotation	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00922	srlB	915815	916189	124	4,95	13452	+	PTS system, glucitol/sorbitol-specific IIA com	PTS system, glucitol/sorbitol IIA component	PTS system, glucitol/sorbitol-specific IIA com	Phosphotransferase system, glucitol/sorbitol-sp	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00923	rpsN	916508	916239	89	11,28	10215	-	Ribosomal protein S14p/S29e	ribosomal protein S14p/S29e	SSU ribosomal protein S14P	Ribosomal protein S14	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00924	guaC	917612	916623	329	6,91	36521	-	GMP reductase	GMP reductase (Guanosine 5'-monophosphate	GMP reductase (EC 1.7.1.7)	IMP dehydrogenase/GMP reductase|Guanosine	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00925	null	917990	917796	64	10,33	7363	-	Mg2+ transporter protein	conserved hypothetical protein	not_predicted_by_ERGO	Mg2+ transporter protein, CorA-like	P	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00926	null	918742	917987	251	9,39	29299	-	Magnesium transporter, CorA family	predicted ORF	Magnesium and cobalt transport protein corA	no annotation	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00927	rrmA	918808	919650	280	9,77	31093	+	SAM-dependent methyltransferase	SAM-dependent methyltransferase	23S rRNA m(1)G 745 methyltransferase (EC	Methyltransferase type 11	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00928	ylgC	920137	920646	169	6,43	19455	+	RNA methyltransferase, TrmH family, group 2	rRNA_methyl_2: RNA methyltransferase(SpoU	23S rRNA methyltransferase (EC 2.1.1.-)	tRNA/rRNA methyltransferase, SpoU|RNA met	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00929	yqaD	920670	921077	135	4,31	15130	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	Protein of unknown function DUF1149	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00930	null	921306	921100	68	12,31	7596	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00931	ftsK	921603	923903	766	10,04	81865	+	DNA translocase ftsK	DNA segregation ATPase FtsK/SpoIIIE related	Cell division protein ftsK	Cell divisionFtsK/SpoIIIE|AAA+ ATPase, core	D	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00932	null	923912	925174	420	5,01	46531	+	Zn-dependent peptidase	Zn-dependent peptidase	Non-proteolytic protein, peptidase family M16	Peptidase M16, C-terminal	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00933	ymfH	925171	926463	430	4,92	47788	+	Zn-dependent Peptidase, M16 family	Zn-dependent protease, insulinase family	Peptidase, M16 family	ABC transporter related|Peptidase M16, C-term	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00934	fabG	926463	927191	242	6,63	26511	+	3-oxoacyl-acyl carrier protein reductase	oxidoreductase, short-chain dehydrogenase/red	3-oxoacyl-[acyl-carrier protein] reductase (EC	Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00935	null	927278	928213	311	9,15	33290	+	Xre-like DNA-binding protein	Xre-like DNA-binding protein	Transcriptional regulator	Lambda repressor-like, DNA-binding	S	Yes	-	IMP	tmhmm:1	-	-	-	-	regulator	-	+
LC_00936	pgsA	928210	928803	197	10,26	22114	+	CDP-diacylglycerol--glycerol-3-phosphate 3-pl	CDP-diacylglycerol--glycerol-3-phosphate 3-pho	CDP-diacylglycerol--glycerol-3-phosphate 3-pl	CDP-alcohol phosphatidyltransferase|CDP-diac	I	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_00937	cinA	929032	930273	413	8,64	44385	+	Competence-damage inducible protein	nucleotide-utilizing enzyme, CinA	Colligrin	Molybdopterin binding domain|Competence-dan	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00938	recA	930325	931377	350	5,51	37575	+	Protein recA	RecA protein (Recombinase A)	RecA protein	RecA bacterial DNA recombination|AAA+ ATPa	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00939	null	931491	931682	63	10,7	6931	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00940	null	931697	931912	71	11,53	7747	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00941	ymdA	932002	933573	523	5,63	58431	+	2',3'-cyclic-nucleotide 2'-phosphodiesterase	membrane-associated HD superfamily hydrolas	Hydrolase (HAD superfamily)	Metal-dependent phosphohydrolase, HD region	R	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+
LC_00942	yvyE	934315	933662	217	6,93	23995	-	Conserved protein	Xaa-Pro dipeptidase	Hypothetical protein	Protein of unknown function UPF0029, N-termi	S	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00943	comFA	934346	935611	421	10,82	46577	+	ComF operon protein 1	superfamily II DNA/RNA helicase required for C	COMF operon protein 1	Helicase, C-terminal|Type III restriction enzyme	LKJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00944	null	935794	936288	164	10,73	18982	+	ComF operon protein 3	amidophosphoribosyltransferase	COMF operon protein 3	no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00945	yfiA	936413	936970	185	8,76	21090	+	Ribosomal subunit interface protein	Ribosome-associated protein Y (PSrp-1)	Ribosome-associated factor Y	Sigma 54 modulation protein/ribosomal protein	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00946	null	937149	937340	63	10,83	7012	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00947	null	937288	937452	54	11,56	6077	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00948	secA	937554	939917	787	5,2	89469	+	Protein translocase subunit secA	preprotein translocase subunit SecA (ATPase,	Protein translocase subunit secA	SecA protein|Helicase, C-terminal|SecA DEAD-	U	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00949	prfB	940176	941174	332	4,78	37456	+	Peptide chain release factor 2	bacterial peptide chain release factor B-like prot	Bacterial Peptide Chain Release Factor 2 (RF	Class I peptide chain release factor|Peptide cha	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00950	ftsE	941251	941937	228	5,18	25510	+	Cell division ATP-binding protein FtsE	cell division ABC transporter, ATPase compone	Cell division ATP-binding protein ftsE	ABC transporter related|AAA+ ATPase, core|Ce	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00951	null	941927	942286	119	11,72	13451	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00952	null	942259	942813	184	10,12	20374	+	Cell division protein FtsX	cell-division protein	Cell division protein ftsX	Protein of unknown function DUF214, permase	D	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_00953	null	943083	944180	365	10,06	39981	+	Trypsin-like serine protease with PDZ domain	trypsin-like serine protease with PDZ domain	Hypothetical membrane spanning protein	PDZ/DHR/GLGF	O	Yes	-	IMP	tmhmm:8	-	-	-	-	-	protease	+
LC_00954	rrp2	944177	944881	234	5,05	26572	+	Two-component response regulator	DNA-binding response regulator, OmpR family	Alkaline phosphatase synthesis two-componer	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+
LC_00955	hpk2	944874	946541	555	10,4	62400	+	Two component sensor transduction histidine	PAS/PAC sensor signal transduction histidine k	Phosphate regulon sensor protein phoR (EC 2	PAS|ATP-binding region, ATPase-like|Histidine t	T	Yes	-	Cterm	tmhmm:2	-	-	-	HPK	-	-	+
LC_00956	pstS	946631	947497	288	10,37	30812	+	ABC transporter, phosphate-binding protein	phosphate ABC transporter, phosphate-bindin c	Phosphate-binding protein	Bacterial extracellular solute-binding protein, far	P	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_00957	pstC	947645	948568	307	11,08	33000	+	ABC transporter, phosphate transporter perm	phosphate ABC transporter, permease compon	Phosphate transport system permease protein	Binding-protein-dependent transport systems in	P	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_00958	ptsA	948565	949449	294	9,28	31384	+	ABC transporter, phosphate transporter perm	phosphate ABC transporter, permease compon	Phosphate transport system permease protein	Binding-protein-dependent transport systems in	P	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+

LC_00959	pstB2	949520	950338	272	6,06	30858	+	ABC transporter, phosphate transporter ATPa	phosphate ABC transporter, ATPase componer	Phosphate transport ATP-binding protein pstE	ABC transporter related|AAA+ ATPase, core|Pl	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00960	pstA	950348	951112	254	5,14	28306	+	ABC transporter, phosphate transporter ATPa	phosphate ABC transporter, ATPase componer	Phosphate transport ATP-binding protein pstE	ABC transporter related|AAA+ ATPase, core|Pl	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00961	phoU	951123	951800	225	4,96	25803	+	Phosphate transport system regulatory protein	phosphate uptake regulator, PhoU	Phosphate transport system protein phoU	PhoU	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00962	null	952507	953997	496	4,7	54291	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00963	null	954009	954269	86	10,1	9969	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:2	-	-	-	-	-	-	-
LC_00964	null	954272	954607	111	11,68	11911	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Integral membrane protein	Membrane protein of unknown function	S	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00965	hprK	954875	955834	319	5,42	35348	+	HPr kinase/phosphorylase	HPr kinase/phosphorylase (HPrK/P) (HPr(Ser)	HPR(SER) KINASE (EC 2.7.1.-) / PHOSPHA	HPr(Ser) kinase|HPr Serine kinase, C-terminal|	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00966	lgt	955836	956663	275	9,08	31290	+	Prolipoprotein diacylglyceryl transferase	prolipoprotein diacylglyceryl transferase lgt	Prolipoprotein diacylglyceryl transferase (EC 2	Prolipoprotein diacylglyceryl transferase	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_00967	gpsA	956674	957729	351	6,58	37694	+	Glycerol-3-phosphate dehydrogenase	NAD(P)H-dependent glycerol-3-phosphate deh	Glycerol-3-phosphate dehydrogenase [NAD(P	NAD-dependent glycerol-3-phosphate dehydroç	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00968	trxB2	957795	958742	315	5,23	34178	+	Thioredoxin reductase	thioredoxin reductase (NADPH) (general stress	Thioredoxin reductase (EC 1.8.1.9)	Pyridine nucleotide-disulphide oxidoreductase, (	O	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_00969	pgm	958994	960721	575	5,08	63643	+	Phosphoglucomutase	phosphoglucomutase/phosphomannomutase al	Phosphoglucomutase (EC 5.4.2.2) / Phosphoı	Phosphoglucomutase/phosphomannomutase|P	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00970	smrA	960984	961631	215	7,51	24015	+	Two-component response regulator	DNA-binding response regulator, OmpR family	not_predicted_by_ERGO	Response regulator receiver|Transcriptional reg	TK	No	-	-	tmhmm:0	-	-	-	RR	regulator	-	-
LC_00971	null	961624	962634	336	7,85	38015	+	Two component sensor transduction histidine	signal transduction histidine kinase	not_predicted_by_ERGO	ATP-binding region, ATPase-like|Histidine kina	T	No	-	IMP	tmhmm:2	-	-	-	HPK	-	-	-
LC_00972	yxdL	962734	963399	221	6,01	23907	+	ABC transporter, ATPase component	antimicrobial oligopeptide ABC transporter, ATF	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00973	null	963401	964297	298	11,18	32549	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Protein of unknown function DUF214, permase	V	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_00974	null	964304	965770	488	11,29	54483	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Protein of unknown function DUF214, permase	V	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00975	null	966357	967004	215	4,83	24877	+	Hydrolase of the HAD superfamily	metal-dependent phosphohydrolase HD sub do	Hydrolase (HAD superfamily)	no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00976	uvrB	967397	969412	671	5,81	76708	+	Excinuclease ABC, subunit B	UvrABC system protein B (uvrB protein) (Excin	Excinuclease ABC subunit B	Helicase, C-terminal|UvrB/UvrC protein|Excinuc	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00977	uvrA1	969593	972487	964	9,08	106109	+	Excinuclease ABC, subunit A	UvrABC system protein A (uvrA protein) (Excin	Excinuclease ABC subunit A	ABC transporter related|Excinuclease ABC, A s	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00978	null	972689	973228	179	10,44	19801	+	Integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	no annotation	S	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_00979	null	973457	973233	74	12,35	8492	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00980	null	973625	974512	295	6,8	33590	+	Conserved protein	uncharacterised P-loop ATPase protein (UPF0(	ATP-binding protein (contains P-loop)	P-loop ATPase protein	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00981	yvcK	974509	975537	342	5,22	37353	+	Transporter	extracellular lipase/esterase precursor	Hypothetical membrane associated protein	Protein of unknown function UPF0052 and Cof	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00982	yvcL	975542	976489	315	9,84	35677	+	Conserved cytosolic protein	conserved protein YvcL	Hypothetical cytosolic protein	Protein of unknown function DUF199	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00983	ohrR	976780	977235	151	6,68	17382	+	Transcriptional regulator, MarR family	organic hydroperoxide resistance transcriptiona	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR|Winged helix	V	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00984	clpP	977354	977944	196	4,86	21496	+	ATP-dependent Clp protease proteolytic subui	ATP-dependent Clp protease proteolytic subuni	ATP-dependent endopeptidase clp proteolytic	Peptidase S14, ClpP	OU	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_00985	cggR	979140	980177	345	7,89	37446	+	Central glycolytic genes regulator	transcriptional regulator (repressor) of gapA op	Central glycolytic genes regulator	Putative sugar-binding region	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_00986	gapB	980214	981236	340	5,63	36724	+	Glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase, ty	Glyceraldehyde 3-phosphate dehydrogenase (	Glyceraldehyde 3-phosphate dehydrogenase|Gl	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00987	pgk	981419	982609	396	5,73	42214	+	Phosphoglycerate kinase	ADP Complex Of The 3-Phosphoglycerate Kina	Phosphoglycerate kinase (EC 2.7.2.3)	Phosphoglycerate kinase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00988	tpiA	982687	983442	251	4,63	26865	+	Triosephosphate isomerase	Triosephosphate isomerase (TIM) (Triose-phos	Triosephosphate isomerase (EC 5.3.1.1)	Triosephosphate isomerase|Aldolase-type TIM	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00989	eno3	983490	984794	434	4,39	47127	+	Enolase	enolase (2-phosphoglycerate dehydratase) (2-p	Enolase (EC 4.2.1.11)	Enolase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00990	null	984963	985337	124	9,84	14471	+	Conserved protein	conserved hypothetical protein	Macrolide-efflux protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_00991	eriC	985675	987255	526	10,02	57358	+	Chloride channel protein	chloride channel protein, EriC	Chloride channel protein	Chloride channel, voltage gated|TrkA-C|Chlorid	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_00992	null	987435	987725	96	9,5	10448	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_00993	secG	987885	988121	78	5,68	8329	+	Preprotein translocase, SecG subunit	preprotein translocase subunit SecG	Protein translocase subunit secG	Preprotein translocase SecG subunit	U	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_00994	null	988297	988473	58	8,98	6571	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	R	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_00995	null	988479	988691	70	9,95	7329	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_00996	null	988706	989029	107	4,34	11810	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00997	rnr	989031	991400	789	5,96	88724	+	Exoribonuclease R	exoribonuclease R, RNase II family	Exoribonuclease II (EC 3.1.13.1)	Ribonuclease II and R|RNA binding S1|RNase	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00998	smpB	991437	991910	157	10,76	18274	+	SsrA binding protein	SsrA-binding protein-like protein	SsrA-binding protein	SmpB protein	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_00999	null	992458	993570	370	9,72	41128	+	Transposase	transposase, IS1533	Transposase	Transposase, IS116/IS110/IS902	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01000	npIT	993872	995623	583	6,34	66936	+	Neopullulanase (GH13)	maltogenic amylase or neopullulanase	Neopullulanase (EC 3.2.1.135) / Cyclomaltode	Glycoside hydrolase, family 13, N-terminal Ig-lik	G	Yes	-	-	tmhmm:0	LC01000	-	-	-	-	-	+
LC_01001	mapA	995753	998014	753	6,12	85871	+	Maltose phosphorylase (GH65)	maltose phosphorylase	maltose phosphorylase (EC 2.4.1.8)	Glycoside hydrolase, family 65, C-terminal|Glyc	G	Yes	-	-	tmhmm:0	LC01001	-	-	-	-	-	+
LC_01002	pgmA	998007	998678	223	6,15	24190	+	Beta-phosphoglucomutase	beta-phosphoglucomutase and glucose-1-phos	Beta-phosphoglucomutase (EC 5.4.2.6) / Gluc	Haloacid dehalogenase-like hydrolase|HAD-sup	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01003	null	998818	999120	100	9,63	11575	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_01004	null	999181	999483	100	9,58	11337	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_01005	null	999473	999661	62	7,7	7139	+	Transcriptional regulator	transcriptional regulator, xre family	Transcriptional regulator, Cro/CI family	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01006	null	1000954	999626	442	5,74	49568	-	Hydrolase of the metallo-beta-lactamase supe	hydrolase of the metallo-beta-lactamase superf	Metal-dependent hydrolase (EC 3.-.-.-)	Beta-lactamase-like	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01007	malE2	1002463	1001150	437	10,1	48272	-	ABC transporter, sugar transporter periplasmi	sugar ABC transporter, periplasmic component	Sugar-binding protein	Bacterial extracellular solute-binding protein, far	G	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+
LC_01008	malF2	1003294	1002473	273	10,1	30571	-	ABC transporter, sugar transporter permease	sugar ABC transporter, permease component	Sugar transport system permease protein	Binding-protein-dependent transport systems in	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_01009	malG2	1004204	1003311	297	8,92	34151	-	ABC transporter, sugar transporter permease	sugar ABC transporter, permease component	Sugar transport system permease protein	Binding-protein-dependent transport systems in	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_01010	malK2	1005255	1004194	353	6,52	38374	-	ABC transporter, sugar transporter ATPase c	sorbitol/mannitol/maltose ABC transporter, ATP	Sugar transport ATP-binding protein	ABC transporter related|AAA+ ATPase, core|M	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01011	null	1005554	1006126	190	6,52	21098	+	Acetyltransferase, GNAT family protein	N-acetyltransferase, GNAT family	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01012	null	1006775	1006269	168	9,78	18651	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01013	ycsE	1007716	1006823	297	4,66	32299	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)	Cof protein|ATPase, P-type, K/Mg/Cd/Cu/Zn/Na	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01014	ung	1007836	1008525	229	6,85	25273	+	Uracil-DNA glycosylase	uracil-DNA glycosylase (UDG)	Uracil-DNA glycosylase (EC 3.2.2.-)	Uracil-DNA glycosylase|Uracil-DNA glycosylas	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01015	pta	1008701	1009678	325	5,27	35213	+	Phosphate acetyltransferase	phosphate acetyltransferase (phosphotransace	Phosphate acetyltransferase (EC 2.3.1.8)	Phosphate acetyl/butaryl transferase|Phosphate	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01016	yeeE	1009675	1010139	154	4,36	16992	+	ATP/GTP hydrolase	ATP/GTP hydrolase	ATP/GTP hydrolase	Protein of unknown function UPF0079, ATPase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01017	ysdB	1010345	1011241	298	7,19	33137	+	ABC transporter, Na+ efflux transporter ATPa	Na+ efflux ABC transporter, ATPase componer	Sodium export ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01018	null	1011234	1011494	86	10,43	9451	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_01019	null	1011524	1012027	167	10,07	17793	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	CP	No	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01020	null	1012009	1012494	161	10,1	17519	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	CP	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_01021	dnaQ	1013224	1012682	180	8,71	20415	-	DNA polymerase III epsilon subunit	DNA polymerase III, epsilon subunit related 3'-5	DNA polymerase III, epsilon chain (EC 2.7.7.7	DNA polymerase III, epsilon subunit|Exonuclea	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01022	exoA	1013994	1013236	252	6,09	29404	-	Exodeoxyribonuclease III	AP endonuclease, family 1:Exodeoxyribonuclea	Exodeoxyribonuclease III (EC 3.1.11.2)	AP endonuclease, family 1|Exodeoxyribonuclea	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01023	murB	1014484	1015383	299	7,78	32329	+	UDP-N-acetylenolpyruvoylglucosamine reduct	UDP-N-acetylenolpyruvoylglucosamine reducta	UDP-N-acetylenolpyruvoylglucosamine reduct	UDP-N-acetylenolpyruvoylglucosamine reducta	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01024	null	1015420	1017534	704	9,24	78461	+	NhaP-type Na+/H+ and K+/H+ antiporter	NhaP-type Na+/H+ and K+/H+ antiporter	Na+/H+ antiporter nhaP	Sodium/hydrogen exchanger	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_01025	null	1017757	1018296	179	4,53	20219	+	Spermidine/putrescine transport operon transc	double-stranded beta-helix related protein	spermidine/putrescine transport operon transc	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01026	alaS	1018310	1019398	362	4,33	40885	+	ABC transporter, spermidine/putrescine trans	ABC transporter, ATPase component, PotA	Spermidine/putrescine transport ATP-binding	ABC transporter related|AAA+ ATPase, core|M	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01027	potB	1019492	1020316	274	9,68	31020	+	ABC transporter, spermidine/putrescine trans	ABC transporter, permease component, PotB	Spermidine/putrescine transport system perm	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+

LC_01028	potC	1020306	1021139	277	9,36	31142	+	ABC transporter, spermidine/putrescine transp	ABC transporter, permease component, PotC	Spermidine/putrescine transport system perm	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+			
LC_01029	potD	1021123	1022196	357	6,64	40657	+	ABC transporter, spermidine/putrescine-bindir	ABC transporter, spermidine/putrescine-binding	Spermidine/putrescine-binding protein	Bacterial periplasmic spermidine/putrescine-bin	E	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+			
LC_01030	null	1022332	1022177	51	12,19	5635	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01031	null	1022978	1022406	190	9,37	20781	-	Putative protein without homology	predicted ORF	Hypothetical exported protein	no annotation	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+			
LC_01032	null	1023371	1023006	121	9,98	13135	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	phage	-	-	-	-	-			
LC_01033	null	1023693	1023884	63	8,52	6981	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-			
LC_01034	pacL	1026869	1024077	930	7,29	101302	-	Cation-transporting ATPase	cation-transporting ATPase, E1-E2 family prote	Calcium-transporting ATPase (EC 3.6.3.8)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+			
LC_01035	null	1027625	1026945	226	6,9	25355	-	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+			
LC_01036	null	1028798	1027659	379	10,51	42348	-	ABC transporter, multidrug transporter permea	efflux multidrug ABC transporter, permease cor	ABC transporter permease protein	ABC-2|Protein kinase|ABC-2 type transporter	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+			
LC_01037	yhiH	1029522	1028788	244	10,12	26676	-	ABC transporter, ATPase component	multidrug resistance ABC transporter, ATPase	Export ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01038	ossG	1029782	1030639	285	9,65	32121	+	Conserved membrane protein	L-arabinose isomerase	Acyl carrier protein phosphodiesterase (EC 3.:	Protein of unknown function DUF147|Conserve	S	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+			
LC_01039	null	1030636	1031733	365	8,69	38690	+	YbbR family protein	YbbR family protein	Hypothetical membrane associated protein	YbbR-like	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+			
LC_01040	glmM	1031762	1033126	454	4,45	48738	+	Phosphoglucosamine mutase	phosphoglucomutase/phosphomannomutase/Pl	Phosphoglucosamine mutase (EC 5.4.2.10)	Phosphoglucomutase/phosphomannomutase|P	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01041	glmS	1033555	1035366	603	5,37	65771	+	Glucosamine--fructose-6-phosphate aminotra	glucosamine--fructose-6-phosphate aminotrans	Glucosamine--fructose-6-phosphate aminotra	Glutamine amidotransferase, class-II|Sugar iso	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01042	pepF2	1037321	1035516	601	4,75	67303	-	Oligoendopeptidase F	oligoendopeptidase F2	Oligoendopeptidase F (EC 3.4.24.-)	Peptidase M3A and M3B, thimet/oligopeptidase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+			
LC_01043	null	1037395	1037886	163	10,4	18989	+	Conserved integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+			
LC_01044	null	1037957	1038688	243	4,43	27097	+	Integrase	dATP pyrophosphohydrolase	Hypothetical cytosolic protein	Protein of unknown function DUF28|Integrase,	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01045	null	1039008	1039169	53	4,61	5507	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01046	null	1039166	1040119	317	9,51	35127	+	Type II secretory pathway/competence compo	type II secretory pathway/competence compone	ComG operon protein 2	Bacterial type II secretion system protein	NU	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-			
LC_01047	null	1040122	1040442	106	10,43	11516	+	Type II secretory pathway/competence compo	competence protein ComGC	ComG operon protein 4	no annotation	V	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-			
LC_01048	null	1040439	1040861	140	10,29	15989	+	Type II secretory pathway/competence compo	competence protein ComGC	Hypothetical exported protein	Prokaryotic N-terminal methylation site|Prepilin-	NU	Yes	pili	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01049	null	1040831	1041142	103	9,57	11116	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01050	null	1041102	1041569	155	10,79	17556	+	Type II secretory pathway/competence compo	predicted ORF	Hypothetical exported protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01051	null	1041566	1041889	107	10,22	12123	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01052	laaG	1042294	1043307	337	4,83	37077	+	Adenine-specific DNA methylase	type I N-6 adenine-specific DNA restriction-mo	Adenine-specific methyltransferase (EC 2.1.1.	no annotation	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01053	null	1043576	1044031	151	10,01	16475	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-			
LC_01054	ydgF	1044246	1045610	454	9,66	50037	+	Amino acid permease	amino acid permease-associated region	Amino acid permease	amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-			
LC_01055	null	1045642	1046406	254	10,82	29344	+	1-acyl-sn-glycerol-3-phosphate acyltransferas	1-acyl-sn-glycerol-3-phosphate acyltransferase	6-phospho-beta-glucosidase (EC 3.2.1.86)	Phospholipid/glycerol acyltransferase	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01056	arbx	1046403	1047242	279	9,64	32867	+	Lipopolysaccharide biosynthesis glycosyltrans	lipopolysaccharide biosynthesis glycosyltransfe	Lipopolysaccharide 1,2-glucosyltransferase (E	Glycosyl transferase, family 8	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01057	null	1047243	1048199	318	6,51	35883	+	Lipopolysaccharide biosynthesis glycosyltrans	lipopolysaccharide biosynthesis glycosyltransfe	Lipopolysaccharide 1,2-glucosyltransferase (E	Glycosyl transferase, family 8	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01058	arbZ	1048196	1049068	290	9,77	33237	+	Phospho-beta-glycosidase	1-acyl-sn-glycerol-3-phosphate acyltransferase	6-phospho-beta-glucosidase (EC 3.2.1.86)	Phospholipid/glycerol acyltransferase|Cupin, Rr	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01059	galA	1049292	1051586	764	6,82	85632	+	Alpha-galactosidase (GH36)	alpha-galactosidase AgaN	Alpha-galactosidase (EC 3.2.1.22)	Glycoside hydrolase, clan GH-D|Glycoside hydr	G	Yes	-	-	tmhmm:0	LC01059	-	-	-	-	-	+			
LC_01060	null	1053400	1052252	382	10,56	43132	-	Phage-related integrase	predicted ORF	not_predicted_by_ERGO	Integrase, catalytic core, phage|Lambda repres	L	No	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01061	null	1054147	1053494	217	5,95	24063	-	Phage-related transcriptional regulator	transcriptional regulator, Cro/CI family protein	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+			
LC_01062	null	1054276	1054554	92	9,66	10241	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	Putative DNA binding	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01063	null	1054622	1055017	131	3,96	14976	+	Phage-related protein	prophage protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01064	null	1054968	1055147	59	7,36	6477	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01065	null	1055128	1055319	63	10,49	7450	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01066	null	1055367	1055636	89	4,47	9943	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01067	null	1055617	1056447	276	9,48	30415	+	Phage-related protein, DNA replication	prophage protein, DNA replication	Phage protein	Primase, C-terminal 1|Bifunctional DNA primas	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01068	null	1056440	1057864	474	7,41	54500	+	Phage-related virulence-associated protein E	prophage protein, helicase / virulence-associate	not_predicted_by_ERGO	Virulence-associated E	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01069	null	1058139	1058480	113	8,43	13186	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01070	null	1058518	1058937	139	10,38	16490	+	Phage-related HNH endonuclease	prophage protein, HNH endonuclease family	not_predicted_by_ERGO	HNH endonuclease|HNH nuclease	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01071	null	1059062	1059532	156	8,44	17312	+	Phage-related terminase-small subunit	prophage protein, terminase small subunit, P27	Phage Terminase Small Subunit	Phage terminase, small subunit, putative, P27	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01072	terL	1059529	1061232	567	5,27	64581	+	Phage-related terminase large subunit	prophage protein, terminase large subunit	Terminase large subunit	Aldo/keto reductase|Phage Terminase	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+			
LC_01073	null	1061198	1061377	59	11,48	6430	+	Phage-related conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-			
LC_01074	null	1061382	1062566	394	4,97	43403	+	Phage-related portal protein	prophage protein, portal protein, HK97 family	Portal protein	Phage portal protein, HK97|Phage portal proteir	null	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01075	null	1062553	1064079	508	4,36	55581	+	Phage-related prohead protease	prophage protein, prohead protease, peptidase	not_predicted_by_ERGO	Peptidase U35, phage prohead HK97|Phage m	null	No	-	-	tmhmm:0	-	phage	-	-	-	protease	+			
LC_01076	null	1064135	1064425	96	4,23	10674	+	Phage-related head-to-tail joining, DNA packir	prophage protein, head-to-tail joining, DNA pacl	not_predicted_by_ERGO	Protein of unknown function, phage	null	No	-	-	tmhmm:0	-	phage	-	-	-	-	-			
LC_01077	null	1064595	1064750	51	9,73	5977	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01078	null	1065614	1065474	46	7,54	4763	-	Conserved extracellular protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+			
LC_01079	null	1065878	1065630	82	10,5	8287	-	Transglycosylase-associated protein	conserved hypothetical protein (membrane prot	Integral membrane protein	Transglycosylase-associated protein	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-			
LC_01080	mscL2	1066358	1065990	122	10,37	13591	-	Large-conductance mechanosensitive channe	large conductance mechanosensitive channel p	not_predicted_by_ERGO	Large-conductance mechanosensitive channel	M	No	-	IMP	tmhmm:2	-	-	-	-	-	-	+			
LC_01081	null	1067069	1067464	131	9,33	15079	+	Conserved integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-			
LC_01082	rrp7	1067481	1068212	243	4,59	27565	+	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator yclJ	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+			
LC_01083	hpk	1068202	1069749	515	6,98	57739	+	Two component sensor transduction histidine	integral membrane sensor signal transduction h	Two-component sensor kinase yclK (EC 2.7.3	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:3	-	-	-	HPK	-	-	+			
LC_01084	null	1069899	1070432	177	6,8	19291	+	Acetyltransferase	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01085	null	1070700	1070506	64	9,24	7151	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01086	pheB	1071134	1071568	144	6,8	15900	+	Amino acid-binding ACT domain protein	ACT domain protein pheB	Chorismate mutase (EC 5.4.99.5)	Amino acid-binding ACT	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01087	null	1071593	1072096	167	10,21	18623	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	regulator	-	-			
LC_01088	null	1072631	1072287	114	11,59	13947	-	Acetyl-CoA carboxylase, carboxyltransferase (	similar to acetyl-CoA carboxylase, carboxyltrans	Transcriptional regulator	no annotation	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01089	uvrA	1073919	1072612	435	9,73	49125	-	ImpB/MucB/SamB family protein	nucleotidyltransferase/DNA polymerase for DN/	ImpB/MucB/SamB family protein	UMUC-like DNA-repair protein	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01090	null	1074251	1074069	60	8,57	6715	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-			
LC_01091	null	1075548	1074364	394	5,01	43005	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane associated protein	Carbohydrate-binding-like fold|NUDIX	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+			
LC_01092	null	1076334	1075552	260	10,19	27526	-	Lysophospholipase L1 related esterase	lysophospholipase L1 related esterase	Acyl-CoA thioesterase I (EC 3.1.2.-)	Lipolytic enzyme, G-D-S-L|Esterase, SGNH hyd	E	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	-			
LC_01093	null	1076705	1076385	106	9,82	12286	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+			
LC_01094	pcrA	1077000	1079252	750	5,36	84630	+	ATP-dependent DNA helicase PcrA	superfamily I DNA and RNA helicases, ATP-de	ATP-dependent DNA helicase pcrA (EC 3.6.1	UvrD/REP helicase|ATP-dependent DNA helic	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01095	ligA	1079300	1081324	674	6,32	73863	+	NAD-dependent DNA ligase	DNA ligase (polydeoxyribonucleotide synthase (	NAD-dependent DNA ligase (EC 6.5.1.2)	BRCT|NAD-dependent DNA ligase|Helix-hairpi	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01096	camS	1081379	1082488	369	6,54	40180	+	Lipoprotein	lipoprotein precursor	Lipoprotein (pheromone precursor)	CamS sex pheromone cAM373	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			

LC_01097	gatC	1082540	1082836	98	4,42	10807	+	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfer	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	Glu-tRNAGln amidotransferase, C subunit	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01098	gatA	1082840	1084294	484	5,08	51306	+	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfer	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	Amidase|Glutamyl-tRNA(Gln) amidotransferase	J	Yes	adhesion	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01099	gatB	1084296	1085726	476	5,27	53534	+	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	aspartyl/glutamyl-tRNA(Asn-Gln) amidotransfer	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransfe	GatB/Yqey|Glutamyl-tRNA(Gln) amidotransfera	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01100	yecE	1085938	1086972	344	5,76	37466	+	Diacylglycerol kinase	lipid kinase from diacylglycerol kinase catalytic	Diacylglycerol kinase family protein	Diacylglycerol kinase, catalytic region|Conserve	IR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01101	trmA	1086974	1088335	453	9,58	50713	+	tRNA (uracil-5-)-methyltransferase	tRNA (uracil-5-)-methyltransferase related enzy	23S rRNA m(5)U 1939 methyltransferase (EC	23S rRNA methyltransferase/RumA|Deoxyribor	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01102	yttB	1088621	1089820	399	9,12	43791	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein	Tetracycline resistance protein|Major facilitator	GEPR	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+	
LC_01103	null	1089898	1090713	271	5,26	28879	+	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily, Cof family	Hydrolase (HAD superfamily)	Cof protein|HAD-superfamily hydrolase, subfam	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01104	murQ	1091664	1090789	291	6,71	33822	-	Polyphosphate:AMP phosphotransferase	polyphosphate kinase 2-like protein:AMP phosp	Hypothetical protein	Polyphosphate kinase 2	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01105	pepO	1091787	1093685	632	4,98	70895	+	Neutral endopeptidase, endopeptidase O	neutral endopeptidase (endopeptidase O)	Oligoendopeptidase O (EC 3.4.24.-)	Peptidase M13, neprilysin|Peptidase M, neutral	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01106	null	1094268	1093813	151	6,97	16940	-	Acetyltransferase	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01107	degV	1095520	1094648	290	5,77	32376	-	DegV family protein	DegV family protein	DegV family protein	DegV	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01108	hflC	1096644	1095712	310	5,05	33771	-	Spfh domain/band 7 family protein	Band 7 family protein (SPFH domain)	STOMATIN LIKE PROTEIN	Band 7 protein|Stomatin	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+	
LC_01109	null	1096880	1096686	64	5,95	7196	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01110	null	1097225	1097452	75	12,24	8226	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01111	null	1097445	1098170	241	10,75	27632	+	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)	lyzozyme M1 (1,4-beta-N-acetylmuramidase)	Lysozyme (EC 3.2.1.17)	Glycoside hydrolase, family 25|Glycoside hydro	M	Yes	-	IMP	tmhmm:1	LC01111	-	-	-	-	-	+	
LC_01112	null	1098302	1098658	118	9,78	13356	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	Conserved hypothetical protein 1655	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01113	null	1098804	1099058	84	11,46	9063	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01114	null	1099325	1098969	118	6,9	12948	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01115	yrbA	1099651	1100604	317	5,16	34892	+	Oxidoreductase	oxidoreductase, Gfo/Idh/MocA family protein	NAD-dependent oxidoreductase	Oxidoreductase, N-terminal	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01116	rhe2	1100662	1101957	431	10,64	47987	+	ATP-dependent RNA helicase	superfamily II DNA and RNA helicase, C-termir	ATP-dependent RNA helicase	ATP-dependent helicase, DEAD-box|Helicase,	LKJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01117	pts	1101995	1102324	109	7,91	12094	+	PTS system, IIA component	PTS system, cellobiose-specific IIA component	PTS system, cellobiose-specific IIA componer	Phosphotransferase system, lactose/cellobiose	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01118	null	1102334	1102513	59	11,54	6227	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01119	null	1102652	1103074	140	10,62	16083	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01120	null	1103329	1104051	240	11,35	27228	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	Peptidase M, neutral zinc metallopeptidases, zi	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	protease	-	
LC_01121	recQ1	1104174	1105949	591	7,3	66456	+	ATP-dependent DNA helicase RecQ	ATP-dependent DNA helicase RecQ:ATP-requ	ATP-dependent DNA helicase recQ (EC 3.6.1	Helicase, C-terminal|HRDC|ATP-dependent DI	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01122	pepS	1107423	1106188	411	4,75	45484	-	Aminopeptidase S	PepS aminopeptidase. Metallo peptidase. MER	Aminopeptidase S (EC 3.4.11.-)	Peptidase M29, aminopeptidase II|Ribbon-helix	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01123	null	1107698	1108306	202	6,8	23127	+	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	IMP	tmhmm:1	-	-	-	-	regulator	-	+	
LC_01124	null	1108630	1108439	63	9,37	7009	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01125	null	1108965	1110341	458	6,81	52224	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01126	null	1110497	1111501	334	10,68	37402	+	Ribonuclease BN-like family enzyme	ribonuclease BN-like family enzyme	Ribonuclease BN (EC 3.1.-.-)	Ribonuclease BN	S	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_01127	fld	1112036	1111575	153	3,65	16730	-	Flavodoxin	flavodoxin, short chain	Flavodoxin	Flavodoxin/nitric oxide synthase|Flavodoxin	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01128	pepM2	1112890	1113714	274	5,2	29972	+	Methionine aminopeptidase	methionine aminopeptidase, type I	Methionine aminopeptidase (EC 3.4.11.18)	Peptidase M24, catalytic core|Peptidase M24, n	J	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01129	null	1113896	1114942	348	6,73	39545	+	Glycosyl transferase, group 2	glycosyltransferase related enzyme	Glycosyltransferase (EC 2.4.1.-)	Glycosyl transferase, family 2	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01130	null	1115552	1115319	77	9,61	8320	-	Conserved protein	conserved hypothetical protein (small)	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01131	null	1115777	1115568	69	6,67	7624	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01132	mvaK2	1116114	1117187	357	6,92	39197	+	Phosphomevalonate kinase	gram positive phosphomevalonate kinase	Phosphomevalonate kinase (EC 2.7.4.2)	Gram positive phosphomevalonate kinase|GHM I	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01133	galU	1117390	1118310	306	6,53	34025	+	UTP-glucose-1-phosphate uridylyltransferase	UTP-glucose-1-phosphate uridylyltransferase (l	UTP--glucose-1-phosphate uridylyltransferase	UTP--glucose-1-phosphate uridylyltransferase,	M	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+	
LC_01134	null	1118588	1119493	301	5,04	35393	+	Glycosyl transferase, group 8	predicted ORF	not_predicted_by_ERGO	Glycosyl transferase, family 8	M	No	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01135	null	1120643	1119783	286	6,03	33417	-	Glycosyl transferase, group 8	predicted ORF	not_predicted_by_ERGO	Glycosyl transferase, family 8	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01136	null	1120982	1121998	338	5,39	37835	+	Glycosyl transferase, galactofuranosyltransfer	glycosyltransferase	Putative galactofuranosyltransferase (EC 2.4.1	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01137	null	1122190	1122002	62	10,41	7183	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01138	secA2	1122264	1125335	1023	9,07	113755	+	Protein translocase subunit secA	preprotein translocase subunit SecA (ATPase,	not_predicted_by_ERGO	SecA protein|Helicase, C-terminal|SecA DEAD-	U	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01139	bglA1	1126878	1125412	488	5,58	55558	-	6-phospho-beta-glucosidase (GH1)	beta-glucosidase/6-phospho-beta-glucosidase/t	6-phospho-beta-glucosidase (EC 3.2.1.86)	Glycoside hydrolase, family 1|Glycoside hydrola	G	Yes	-	-	tmhmm:0	LC01139	-	-	-	-	-	-	
LC_01140	bglH	1128728	1126893	611	9,72	64780	-	PTS system, beta-glucoside-specific IIABC co	PTS system, beta-glucoside-specific IIABC con	PTS system, beta-glucoside-specific IIABC co	Phosphotransferase system, sugar-specific per	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-	
LC_01141	null	1131821	1129173	882	10,31	97498	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Integral membrane protein	no annotation	null	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_01142	null	1132124	1131933	63	8,79	6802	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01143	null	1132181	1133908	575	9,78	64450	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_01144	null	1134081	1134602	173	4,64	19237	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01145	null	1134559	1134780	73	10,51	8474	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01146	rfaG	1135822	1134893	309	7,64	35091	-	Glycosyl transferase, group 2	teichoic acid/polysaccharide glycosyl transferas	Bactoprenol glucosyl transferase (EC 2.4.1.-)	Glycosyl transferase, family 2	M	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_01147	null	1136533	1135889	214	5,29	23499	-	Conserved protein	conserved hypothetical protein	Hypothetical secreted protein	no annotation	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_01148	null	1136840	1137805	321	6,8	35940	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Integral membrane protein	Protein of unknown function DUF939, bacterial	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_01149	csp3	1138323	1138523	66	4,25	7369	+	Cold shock protein	cold shock protein, CspA family	Cold shock protein	Cold-shock protein, DNA-binding|Cold shock pr	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01150	null	1138744	1138986	80	4,51	9018	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01151	null	1139227	1139709	160	7,66	18314	+	Acetyltransferase, GNAT family protein	N-acetyltransferase, GNAT family	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01152	acmA	1139715	1140350	211	10,17	23870	+	N-acetylmuramidase	N-acetylmuramidase (EC 3.5.1.28)	Peptidoglycan hydrolase (3.2.1.-)	Flagellar protein FlgJ type-1|Mannosyl-glycopro	NU	Yes	-	Sec	tmhmm:1	LC01152	-	-	-	-	-	+	
LC_01153	xpt	1140541	1141119	192	6,37	21417	+	Xanthine phosphoribosyltransferase	purine biosynthesis xanthine phosphoribosyltrar	Xanthine phosphoribosyltransferase (EC 2.4.2	Phosphoribosyltransferase|Xanthine phosphorit	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01154	pucK	1141128	1142456	442	9,66	47281	+	Xanthine permease	uracil-xanthine permease	Xanthine permease	Xanthine/uracil permease|Xanthine/uracil/vitami	F	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_01155	purK2	1142477	1143586	369	4,54	40695	+	Phosphoribosylaminoimidazole carboxylase (N	phosphoribosylaminoimidazole carboxylase II (N	Phosphoribosylaminoimidazole carboxylase NI	ATP-grasp fold, ATP-dependent carboxylate-an	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01156	purB2	1143689	1144984	431	6,29	48687	+	Adenylosuccinate lyase	adenylosuccinate lyase (EC 4.3.2.2)	Adenylosuccinate lyase (EC 4.3.2.2)	Fumarate lyase|Delta crystallin|Adenylosuccinat	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01157	null	1145739	1145170	189	8,21	21636	-	ABC family transporter	ABC transporter	Hypothetical membrane spanning protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01158	null	1146495	1145749	248	10,28	28493	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_01159	ispB	1148838	1146580	752	7,22	84093	-	Sulfatase	phosphoglycerol transferase related protein, alk	Sulfatase family protein	Sulfatase|Alkaline phosphatase|Membrane sulp	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_01160	vanZ	1149379	1149984	201	10,31	23385	+	Glycopeptide antibiotics resistance protein	glycopeptide antibiotics resistance protein	VanZ family protein	VanZ like protein	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_01161	glcU	1150264	1151121	285	9,83	29967	+	Glucose uptake protein	glucose uptake permease glcU	Glucose uptake protein	Sugar transport	GER	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_01162	pgi	1151318	1152658	446	4,73	49365	+	Glucose-6-phosphate isomerase	glucose-6-phosphate isomerase (GPI) / phosph	Glucose-6-phosphate isomerase (EC 5.3.1.9)	Phosphoglucose isomerase (PGI)	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01163	ycnE	1153292	1152996	98	5,47	11219	-	Antibiotic biosynthesis monooxygenase	antibiotic biosynthesis monooxygenase	Hypothetical cytosolic protein	Antibiotic biosynthesis monooxygenase|Dimeric	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01164	laaO	1154438	1153587	283	8,36	31219	-	DNA-entry nuclease	DNA-entry nuclease	DNA-entry nuclease (EC 3.1.30.-)	DNA/RNA non-specific endonuclease	V	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_01165	null	1155181	1154891	96	12,03	10495	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-	

LC_01166	null	1156473	1155310	387	8,3	44315	-	Glycosyl transferase, group 1	glycosyltransferase	Glycosyltransferase (EC 2.4.1.-)	Glycosyl transferase, group 1	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01167	ysjB	1156930	1157847	305	4,94	33346	+	Oxidoreductase	oxidoreductase, Gfo/Idh/MocA family protein	NAD-dependent oxidoreductase	Oxidoreductase, N-terminal	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01168	guaD	1157948	1158415	155	6,66	16748	+	Guanine deaminase	cytosine/adenosine/cytidine/deoxycytidylate dea	Guanine deaminase (EC 3.5.4.3)	CMP/dCMP deaminase, zinc-binding	FJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01169	null	1159305	1159514	69	9,18	8086	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01170	null	1160367	1160561	64	4,52	7752	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01171	null	1161224	1161379	51	4,96	6125	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01172	null	1161582	1161812	76	6,52	9176	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01173	null	1162199	1162384	61	9,93	7076	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01174	null	1162681	1162818	45	9,22	5137	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01175	null	1164092	1162899	397	10,48	44146	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	not_predicted_by_ERGO	Tetracycline resistance protein|Major facilitator	GEPF	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-		
LC_01176	pepD2	1165955	1164525	476	4,74	54256	-	Dipeptidase A	dipeptidase A. Cysteine peptidase. MEROPS fa	Dipeptidase A (EC 3.4.13.-)	Peptidase C69, dipeptidase A	C	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+		
LC_01177	null	1166918	1167094	58	10,06	6884	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01178	null	1167759	1167574	61	10,65	6980	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-		
LC_01179	null	1168087	1167752	111	4,39	12761	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01180	null	1168504	1168878	124	11,36	13910	+	Phosphoglycerate mutase	phosphoglycerate mutase	not_predicted_by_ERGO	Phosphoglycerate/bisphosphoglycerate mutase	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01181	null	1168839	1169261	140	5,6	15583	+	Phosphoglycerate mutase family protein	predicted ORF	Phosphoglycerate mutase family protein	Phosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01182	null	1169667	1170323	218	9,99	25210	+	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	+		
LC_01183	ycfI	1170379	1172109	576	8,57	63765	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, transmembrane reg	Multidrug resistance ABC transporter ATP-bir	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+		
LC_01184	yfiC	1172109	1173992	627	6	69497	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, transmembrane reg	Multidrug/protein/lipid ABC transporter family,	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+		
LC_01185	null	1174874	1174116	252	9,7	28071	-	Flavoprotein	flavoprotein	IRON-SULFUR FLAVOPROTEIN	NADPH-dependent FMN reductase	R	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-		
LC_01186	null	1175117	1175983	288	5,02	32600	+	Ring-cleavage extradiol dioxygenase	ring-cleavage extradiol dioxygenase / glyoxalase	Glyoxalase family protein	Glyoxalase/bleomycin resistance protein/dioxyg	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01187	ampC	1176017	1177021	334	9,85	37601	+	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin bindin	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, trans	V	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+		
LC_01188	murC	1178439	1177087	450	8,4	49423	-	Mur ligase family protein	UDP-N-acetylmuramyl tripeptide synthase, mur	UDP-N-acetylmuramoylalanyl-D-glutamate--2,	Mur ligase, middle region|Domain of unknown fi	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01189	tdk	1178567	1179160	197	6,23	22589	+	Thymidine kinase	thymidine kinase (deoxuuridine kinase)	Thymidine kinase (EC 2.7.1.21)	Thymidine kinase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01190	prf1	1179330	1180409	359	4,69	40964	+	Peptide chain release factor 1	bacterial peptide chain release factor 1 (bRF-1)	Bacterial Peptide Chain Release Factor 1 (RF	Class I peptide chain release factor|Peptide cha	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01191	hemK	1180402	1181232	276	6,35	30848	+	Modification methylase HemK protein	methylase of polypeptide chain release factors,	Peptide release factor-glutamine N5-methyltra	Modification methylase HemK|Methyltransferas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01192	ywlC	1181387	1182355	322	8,05	34729	+	Sua5/YciO/YrdC/YwlC family protein	Sua5/YciO/YrdC/YwlC family protein	Sua5/YciO/YrdC/YwlC family protein	Sua5/YciO/YrdC/YwlC|SUA5|SUA5/yciO/yrdC,	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01193	glyA	1182762	1184003	413	6,2	45134	+	Serine hydroxymethyltransferase	Serine hydroxymethyltransferase (Serine methy	Serine hydroxymethyltransferase (EC 2.1.2.1)	Glycine hydroxymethyltransferase|Pyridoxal phc	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01194	upp	1184044	1184673	209	8,81	22794	+	Uracil phosphoribosyltransferase	uracil phosphoribosyltransferase (ump pyrophor	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Phosphoribosyltransferase|Uracil phosphoribos	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01195	null	1184794	1184958	54	7,8	6140	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-		
LC_01196	atpB	1184972	1185682	236	9,53	26509	+	ATP synthase A chain	F0F1 ATP synthase subunit A	ATP synthase A chain (EC 3.6.3.14)	ATPase, F0 complex, subunit A	C	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+		
LC_01197	atpE	1185705	1185917	70	9,69	7180	+	ATP synthase C chain	F0F1 ATP synthase subunit C	ATP synthase C chain (EC 3.6.3.14)	ATPase, F0 complex, subunit C|ATPase, F0/V(	C	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+		
LC_01198	atpF	1185953	1186441	162	7,68	17676	+	ATP synthase B chain	F0F1 ATP synthas, subunit B	ATP synthase B chain (EC 3.6.3.14)	ATPase, F0 complex, subunit B/B', bacterial an	C	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+		
LC_01199	atpH	1186428	1186973	181	9,51	19422	+	ATP synthase D chain	F0F1 ATP synthase subunit D	ATP synthase delta chain (EC 3.6.3.14)	ATPase, F1 complex, OSCP/delta subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01200	atpA	1186997	1188526	509	4,99	55261	+	ATP synthase A chain	F0F1 ATP synthase subunit A	ATP synthase alpha chain (EC 3.6.3.14)	ATPase, F1/V1/A1 complex, alpha/beta subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01201	atpG	1188538	1189461	307	4,86	33740	+	ATP synthase G chain	F0F1 ATP synthase subunit G	ATP synthase gamma chain (EC 3.6.3.14)	ATPase, F1 complex, gamma subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01202	null	1189511	1189741	76	9,31	8547	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01203	atpD	1189722	1191188	488	4,28	53143	+	ATP synthase B chain	F0F1 ATP synthase subunit B	ATP synthase beta chain (EC 3.6.3.14)	ATPase, F1/V1/A1 complex, alpha/beta subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01204	uncC	1191203	1191634	143	5,93	15742	+	ATP synthase E chain	FOF1 ATP synthase subunit E	ATP synthase epsilon chain (EC 3.6.3.14)	ATPase, F1 complex, delta/epsilon subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01205	null	1191911	1192183	90	12,66	9886	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01206	null	1192353	1192589	78	10,24	8788	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane associated protein	Conserved hypothetical protein, integral membr	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-		
LC_01207	mbl	1192654	1193643	329	5,1	34930	+	Rod shape-determining protein MreB	actin-like ATPase for cell morphogenesis / rod s	Rod shape-determining protein mreB	Heat shock protein Hsp70|Cell shape determini	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01208	null	1193656	1193826	56	10,63	6516	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-		
LC_01209	null	1193835	1194140	101	10,3	11551	+	Conserved protein	alpha-hemolysin homolog	Hypothetical cytosolic protein	Protein of unknown function DUF37	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01210	null	1194133	1194354	73	6,8	8112	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01211	ftsW	1194476	1195681	401	7,04	44475	+	Rod shape-determining protein RodA	bacterial cell division membrane protein / rod sh	Rod shape-determining protein rodA	Cell cycle protein	D	Yes	-	LPxTG	tmhmm:8	-	-	-	-	-	-	+		
LC_01212	gcsH2	1195693	1195992	99	4,18	10793	+	Glycine cleavage system H protein	aminomethyltransferase, family of glycine cleav	Glycine cleavage system H protein	Glycine cleavage H-protein|2-oxo acid dehydrog	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01213	dapE	1197246	1196122	374	5	40373	-	Succinyl diaminopimelate desuccinylase	acetylornithine deacetylase/Succinyl-diaminopin	Succinyl-diaminopimelate desuccinylase (EC :	ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01214	plpC	1197748	1198575	275	10,72	30268	+	ABC transporter, substrate-binding protein, NI	metal ion ABC transporter, periplasmic compon	ABC transporter substrate-binding protein	NLPA lipoprotein	P	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+		
LC_01215	plpB	1199425	1200255	276	10,56	30665	+	ABC transporter, substrate-binding protein, NI	metal ion ABC transporter, periplasmic compon	ABC transporter substrate-binding protein	Ribosomal L23 protein|NLPA lipoprotein	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+		
LC_01216	metN	1200292	1201326	344	6,73	37678	+	ABC transporter, ATPase component	methionine ABC transporter, ATPase compone	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01217	ydcC	1201331	1202020	229	6,8	24402	+	ABC transporter, permease protein	ABC transporter, permease component	ABC transporter permease protein	Proteinase inhibitor I4, serpin|Binding-protein-d	P	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+		
LC_01218	ysfB	1202201	1202968	255	4,84	28179	+	ABC transporter, Fe-S cluster assembly trans	Fe-S cluster assembly ABC transporter, ATPas	ATP-dependent transporter sufC	ABC transporter related|AAA+ ATPase, core|Fe-S	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01219	null	1202961	1203992	343	6,12	36738	+	ABC transporter, Fe-S cluster assembly trans	Fe-S cluster assembly ABC transporter, permea	SufD protein	SufBD	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01220	csd1	1203961	1205181	406	5,8	43834	+	Cysteine desulfurase	cysteine sulfinate desulfinase/cysteine desulfur	Cysteine desulfurase (EC 2.8.1.7) / Selenocys	Aminotransferase, class V|Cysteine desulphura	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01221	iscU	1205168	1205614	148	4,76	16067	+	Fe-S assembly protein SufA, SUF sytem	SUF system FeS assembly protein, NifU family	IscU protein	Nitrogen-fixing NifU-like, N-terminal|SUF syster	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01222	sufB	1205607	1207043	478	4,67	53519	+	Fe-S assembly protein SufB, SUF system	Fe-S cluster assembly, ABC transporter, SufB	ABC transporter-associated protein sufB	SufBD|FeS assembly protein SufB	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01223	null	1207285	1207467	60	10,39	7042	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01224	null	1207802	1208182	126	10,7	14504	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	Protein of unknown function DUF1694	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01225	null	1208243	1209211	322	7,78	37105	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01226	null	1209875	1210762	295	8,97	33945	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator, Xre family	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	+		
LC_01227	usp	1211454	1210954	166	6,8	18173	-	Universal stress protein family	universal stress protein UspA related nucleotide	Universal stress protein family	Universal stress protein (Usp)|UspA|Rossmann	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01228	null	1211793	1211515	92	11,75	10341	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+		
LC_01229	null	1212075	1212287	70	12,11	7776	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_01230	cshA3	1213832	1212537	431	9,7	47140	-	ATPase, AAA family	recombination factor protein RarA	ATPase, AAA family	AAA+ ATPase, core|AAA ATPase, core	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01231	null	1214173	1216134	653	6,15	71838	+	Glutathione biosynthesis bifunctional protein	glutathione biosynthesis bifunctional protein	UDP-N-acetylmuramoylalanyl-D-glutamate--2,	ATP-grasp fold	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01232	yueI	1216738	1216316	140	7,61	15688	-	Conserved protein	conserved hypothetical protein (YueI-like protein	Hypothetical cytosolic protein	Protein of unknown function DUF1694	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01233	null	1216903	1217511	202	10,31	22892	+	Conserved protein	DUF1054 domain-containing protein	Hypothetical cytosolic protein	Protein of unknown function DUF1054	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_01234	sdhB-2	1217677	1218342	221	6,23	23947	+	L-serine dehydratase, iron-sulfur-dependent, b	L-serine ammonia-lyase/dehydratase, iron-sulfu	L-serine dehydratase beta subunit (EC 4.3.1.1	Response regulator receiver|Amino acid-binding	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		

LC_01235	sdhA-2	1218390	1219259	289	5,37	30007	+	L-serine dehydratase, iron-sulfur-dependent, a	L-serine ammonia-lyase/dehydratase, iron-sulfu	L-serine dehydratase alpha subunit (EC 4.3.1.	L-serine dehydratase, alpha subunit|Serine deh	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01236	null	1219353	1220045	230	6,9	25315	+	Phosphoglycerate mutase family protein	phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate/bisphosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01237	msrA1	1220229	1221065	278	8,59	31309	+	Peptide methionine sulfoxide reductase	peptide methionine sulfoxide reductase msrA 2	Peptide methionine sulfoxide reductase msrA	Methionine sulfoxide reductase A	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01238	null	1221123	1222022	299	11,14	32198	+	Short-chain alcohol dehydrogenase	oxidoreductase, short chain dehydrogenase/red	Short chain dehydrogenase (EC 1.-.-.-)	Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01239	null	1222249	1222980	243	9,07	27416	+	Nicotinamide mononucleotide transporter	nicotinamide mononucleotide transporter PnuC	Nicotinamide mononucleotide transporter	Nicotinamide mononucleotide transporter PnuC	H	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_01240	dgk	1223056	1223784	242	4,85	27155	+	Deoxynucleoside kinase	deoxyguanosine kinase (DGUO kinase) (DGK)	Deoxyadenosine kinase (EC 2.7.1.76) / Deoxy	Deoxynucleoside kinase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01241	hisK	1224046	1224858	270	4,81	30935	+	Histidinol phosphatase related hydrolase of the	histidinol phosphatase related hydrolase of the I	Histidinol-phosphatase (EC 3.1.3.15)	PHP, C-terminal	ER	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01242	oppA	1226554	1224914	546	9,96	60464	-	ABC transporter, oligopeptide-binding protein	oligopeptide ABC transporter, oligopeptide-bind	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_01243	null	1227590	1226685	301	7,22	34232	-	Two component sensor transduction histidine	signal transduction histidine kinase	Sensory Transduction Histidine Kinase (EC 2.	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	Nterm	tmhmm:1	-	-	-	HPK	-	-	-	
LC_01244	phoB	1228280	1227606	224	6,15	25447	-	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_01245	glrA	1228426	1229355	309	6,52	34175	+	ABC transporter, ATPase component	bacitracin ABC transporter, ATPase componen	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01246	null	1229352	1230122	256	9,67	28142	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_01247	hypR	1231096	1230212	294	9,83	32542	-	Transcriptional regulator, LysR family	transcriptional regulator, LysR family	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR|LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01248	yphH	1231210	1231626	138	6,22	15456	+	Cupin 2 barrel domain protein	cupin 2 conserved barrel domain protein	Hypothetical cytosolic protein	Cupin, RmlC-type|Cupin 2, conserved barrel|Rr	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01249	yphJ	1231630	1231947	105	9,13	11598	+	Carboxymuconolactone decarboxylase	gamma-carboxymuconolactone decarboxylase s	4-carboxymuconolactone decarboxylase (EC 4	Carboxymuconolactone decarboxylase	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01250	null	1232486	1232980	164	10,93	18505	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01251	null	1233198	1234061	287	5,35	32046	+	Acetyltransferase	acetyltransferase	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01252	null	1234075	1234548	157	7,62	17924	+	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01253	null	1234704	1235561	285	6,42	30212	+	DegV family protein	DegV family protein	DegV family protein	DegV	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01254	null	1236297	1235716	193	8,76	22630	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01255	rrp6	1237276	1236668	202	4,66	21902	-	Two-component response regulator, LuxR fam	DNA-binding response regulator, CitB family (R	Two-component response regulator	Bacterial regulatory protein, LuxR|Response reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-		
LC_01256	hpk	1238385	1237279	368	9,5	42241	-	Two component sensor transduction histidine	signal transduction histidine kinase	Sensory transduction histidine kinase (EC 2.7.3	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:5	-	-	-	HPK	-	-	+	
LC_01257	null	1239139	1238375	254	10,39	28245	-	ABC transporter, multidrug transporter perme	multidrug ABC transporter, permease compone	ABC transporter permease protein	ABC-2 type transporter	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_01258	yvfR	1240025	1239141	294	6,61	32504	-	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01259	null	1240280	1241776	498	5,84	55310	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01260	null	1241791	1243329	512	5,15	58032	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01261	null	1243379	1244026	215	5,54	24098	+	Acetyltransferase, GNAT family protein	predicted ORF	not_predicted_by_ERGO	GCN5-related N-acetyltransferase	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01262	tex	1244272	1246449	725	6,41	80428	+	RNA binding S1 domain protein	transcriptional accessory protein, RNA binding :	Transcription accessory protein (S1 RNA bind	RNA binding S1|Resolvase, RNase H-like fold|I	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01263	radC	1246690	1247439	249	6,08	26693	+	Glutamine amidotransferase	glutamine amidotransferase class-I:Peptidase C	Glutamine amidotransferase, class I	Peptidase C26	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01264	null	1247432	1248055	207	8,99	22064	+	Amino acid/polyamine transporter I	predicted ORF	not_predicted_by_ERGO	Amino acid/polyamine transporter I	E	No	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_01265	null	1248036	1248734	232	10,49	24481	+	Amino acid permease	predicted ORF	Amino acid permease	Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_01266	dcm	1249049	1250296	415	9,73	47956	+	Cytosine-specific methyltransferase	DNA-cytosine methyltransferase	not_predicted_by_ERGO	C-5 cytosine-specific DNA methylase	L	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01267	null	1252285	1250324	653	7,13	73895	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01268	null	1255790	1252278	1170	6,34	131810	-	Helicase domain protein	DNA helicase	not_predicted_by_ERGO	Helicase, C-terminal	R	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01269	null	1258222	1255805	805	6,33	92394	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01270	rpsD	1259243	1258632	203	10,23	23333	-	SSU/30S ribosomal protein S4P	30S ribosomal protein S4P (BS4)	SSU ribosomal protein S4P	Ribosomal protein S4|RNA-binding S4|Riboson	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01271	ytsP	1259901	1259419	160	4,16	17132	-	GAF domain protein	GAF domain-containing proteins	GAF domain-containing proteins	GAF	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01272	null	1260076	1261779	567	5,02	64782	+	Septation ring formation regulator, EzrA	septation ring formation regulator EzrA	Septation ring formation regulator	Septation ring formation regulator, EzrA	L	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01273	nifS	1262224	1263381	385	7,5	42033	+	Aminotransferase class V	cysteine desulfurase, aminotransferase class V	Cysteine desulfurase (EC 2.8.1.7) / Selenocys	Aminotransferase, class V|Pyridoxal phosphate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01274	thiI	1263511	1264728	405	6,97	45216	+	Thiamine biosynthesis protein thiI	thiamine biosynthesis ATP pyrophosphatase TI	Thiamine biosynthesis protein thiI	Thiamine biosynthesis protein|THUMP	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01275	null	1265030	1264854	58	11,57	6731	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_01276	null	1265052	1265714	220	9,93	24197	+	Redox-sensing transcriptional repressor Rex	redox-sensing transcriptional repressor rex2	AT-rich DNA-binding protein	CoA-binding|Rex DNA-binding, C-terminal|Win	R	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01277	valS	1266404	1269046	880	6,29	100722	+	Valyl-tRNA synthetase	valyl-tRNA synthetase (valine--tRNA ligase) (Va	Valyl-tRNA synthetase (EC 6.1.1.9)	Aminoacyl-tRNA synthetase, class I|Aminoacyl-	J	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	+	
LC_01278	folC1	1269326	1270612	428	7,02	46590	+	Folylpolyglutamate synthase	folylpolyglutamate synthase (folylpoly-gamma-gl	Folylpolyglutamate synthase (EC 6.3.2.17) / D	Folylpolyglutamate synthetase|Cytoplasmic pep	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01279	null	1270609	1271253	214	4,98	22715	+	Sugar phosphatase of HAD family	sugar phosphatase, HAD superfamily	Beta-phosphoglucomutase (EC 5.4.2.6)	Haloacid dehydrogenase/epoxide hydrolase|Hal	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01280	radC	1271357	1272025	222	6,64	24408	+	DNA repair protein radC	DNA repair protein radC homolog (25 kDa prote	DNA repair protein radC	DNA repair protein RadC	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01281	mreB	1272164	1273165	333	4,5	34931	+	Rod shape-determining protein MreB	actin-like ATPase for cell morphogenesis / rod s	Rod shape-determining protein mreB	Heat shock protein Hsp70|Cell shape determini	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01282	mreC	1273253	1274113	286	10,07	30673	+	Rod shape-determining protein MreC	Rod shape-determining protein MreC, subtype	Rod shape-determining protein mreC	Rod shape-determining protein MreC, subtype|M	M	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_01283	null	1274115	1274645	176	7,17	19637	+	Rod shape-determining protein MreD	rod shape-determining protein MreD	Rod shape-determining protein mreD	Rod shape-determining protein MreD	M	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_01284	minC	1274660	1275316	218	5,26	23541	+	Cell division inhibitor	Septum formation inhibitor	Cell division inhibitor MinC	Septum formation inhibitor MinC, C-terminal	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01285	minD	1275317	1276114	265	5,02	28881	+	Septum site-determining protein MinD	Septum site-determining protein minD (Cell divi	Cell division inhibitor MinD	Cobyrinic acid a,c-diamide synthase|Septum sit	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01286	glnP2	1276705	1277361	218	9,99	23859	+	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease compon	Histidine transport system permease protein h	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_01287	glnQ4	1277373	1278011	212	7,68	22726	+	ABC transporter, amino acid transporter ATPa	polar amino acid ABC transporter, ATPase com	Histidine transport ATP-binding protein hisP	ABC transporter related|AAA+ ATPase, core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01288	glnH2	1278008	1278820	270	9,94	30478	+	ABC transporter, amino acid-binding protein	amino acid ABC transporter/signal transduction	Histidine-binding protein	Bacterial extracellular solute-binding protein, far	ET	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+	
LC_01289	null	1279006	1279221	71	10,74	7832	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01290	null	1279284	1279478	64	11,43	7057	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01291	cls1	1279670	1281103	477	10,16	53220	+	Cardiolipin synthetase	Phosphatidylserine/phosphatidylglycerophosph	Cardiolipin synthetase (EC 2.7.8.-)	Phospholipase D/Transphosphatidylase	I	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_01292	null	1281304	1281185	39	11,5	4375	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-	
LC_01293	null	1281796	1282128	110	8,48	12994	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_01294	mraZ	1282304	1282735	143	5,03	16233	+	Cell division protein MraZ	Cell division protein mraZ	Cell division protein mraZ	WD-40 repeat|MraZ	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01295	null	1282738	1283382	214	9,97	23909	+	S-adenosyl-methyltransferase MraW	S-adenosyl-methyltransferase MraW	S-adenosyl-methyltransferase mraW (EC 2.1.	Bacterial methyltransferase	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01296	null	1283333	1283680	115	10,61	12844	+	Methyltransferase	predicted ORF	not_predicted_by_ERGO	Bacterial methyltransferase	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01297	ftsL	1283694	1284059	121	9,42	13394	+	Cell division protein FtsL	cell division protein FtsL	Cell division protein ftsL	Septum formation initiator|Cell division protein, I	D	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01298	pbp2B1	1284056	1286200	714	10,19	76828	+	Cell division protein FtsI	cell division protein FtsI/low-affinity penicillin-bir	Division specific D,D-transpeptidase / Cell divi	Penicillin-binding protein, transpeptidase|Penici	M	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	protease	+	
LC_01299	mraY	1286215	1287180	321	7,4	36107	+	Phospho-N-acetylmuramoyl-pentapeptide-tran	phospho-N-acetylmuramoyl-pentapeptide-transf	Phospho-N-acetylmuramoyl-pentapeptide-tran	Glycosyl transferase, family 4|Phospho-N-acety	M	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+	
LC_01300	murD	1287209	1288588	459	6,94	50388	+	UDP-N-acetylmuramoylalanine--D-glutamate li	UDP-N-acetylmuramoylalanine-D-glutamate ligz	UDP-N-acetylmuramoylalanine--D-glutamate li	Cytoplasmic peptidoglycan synthetases, C-term	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01301	murG	1288589	1289680	363	10,38	38466	+	UDP-N-acetylglucosamine--N-acetylmuramyl-(	UDP-N-acetylglucosamine-N-acetylmuramyl-(pe	UDP-N-acetylglucosamine--N-acetylmuramyl-	Glycosyl transferase, family 28|N-acetylglucosa	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01302	null	1289686	1290540	284	10,55	32032	+	Cell division septal protein, FtsQ	cell division septal protein	Cell-division initiation protein DivIB	Cell division protein FtsQ|Polypeptide-transport	D	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01303	ftsA	1290653	1291990	445	4,98	47989	+	Cell division protein, FtsA	similar to cell division protein FtsA	Cell division protein ftsA	Cell division protein FtsA|Heat shock protein 70	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_01304	ftsZ	1292015	1293280	421	4,52	44634	+	Cell division protein, FtsZ	cell division protein FtsZ	Cell division protein ftsZ	Cell division protein FtsZ|Tubulin/FtsZ, GTPase	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01305	null	1293298	1293753	151	4,34	16764	+	Cell division protein, sepF	cell division protein	Hypothetical cytosolic protein	Protein of unknown function DUF552	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01306	ylmG	1293766	1294053	95	10,04	11114	+	Cell division membrane protein, YlmG	Cell division membrane protein	Integral membrane protein	Homeobox|Protein of unknown function YGGT	S	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+			
LC_01307	ylmH	1294059	1294838	259	6,29	29181	+	RNA-binding S4 domain protein	cell division RNA-binding protein, S4-like domai	RNA binding protein	RNA-binding S4	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01308	divIVA	1295009	1295797	262	4,26	28834	+	Cell-division initiation protein, DivIVA	cell division initiation protein (septum placement	Cell division initiation protein DivIVA	DivIVA	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01309	ileS	1296040	1298826	928	5,57	104982	+	Isoleucyl-tRNA synthetase	Isoleucyl-tRNA synthetase (Isoleucine--tRNA lig	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	Aminoacyl-tRNA synthetase, class I|Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01310	cspC	1298839	1299063	74	4,51	8124	+	Cold shock protein	major cold shock protein CspA	Cold shock protein	Cold-shock protein, DNA-binding|Cold shock pr	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01311	pstF	1300190	1299285	301	10,02	31970	-	ABC transporter, phosphate-binding protein	phosphate ABC transporter, phosphate-binding	Phosphate-binding protein	Bacterial extracellular solute-binding protein, far	P	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+			
LC_01312	ydiC	1300366	1302708	780	10,29	84447	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily / n	Efflux pump antibiotic resistance protein	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:21	-	-	-	-	-	-	-			
LC_01313	ynhC	1304033	1302837	398	5	44459	-	Tellurite resistance protein	tellurite resistance protein TelA	Tellurite resistance protein	Toxic anion resistance	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01314	null	1304692	1304030	220	6,81	24852	-	5-bromo-4-chloroindolyl phosphate hydrolysis	5-bromo-4-chloroindolyl phosphate hydrolysis p	XpaC protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+			
LC_01315	nudF	1304901	1305449	182	5,02	20315	+	NUDIX hydrolase	Phosphohydrolase (MutT/nudix family protein)	ADP-ribose pyrophosphatase (EC 3.6.1.13)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01316	null	1305436	1305696	86	11,01	10095	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+			
LC_01317	pfs	1305773	1306483	236	5	24996	+	5'-methylthioadenosine/S-adenosylhomocystei	MTA/SAH nucleosidase (5'-methylthioadenosin	5'-methylthioadenosine nucleosidase (EC 3.2.2.	Nucleoside phosphorylase|MTA/SAH nucleosid	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01318	csd2	1306495	1307658	387	6,51	41980	+	Cysteine desulfurase	cysteine sulfinate desulfinase/cysteine desulfur	Cysteine desulfurase (EC 2.8.1.7) / Selenocys	Aminotransferase, class V|Pyridoxal phosphate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01319	null	1307952	1308293	113	9,95	12662	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	Domain of unknown function DUF1831	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01320	uvrA2	1308510	1310783	757	8,68	83554	+	Excinuclease ABC, subunit A	excinuclease ABC transporter, ATPase A subui	Excinuclease ABC subunit A	ABC transporter related	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01321	trmU	1310914	1312032	372	4,75	41161	+	tRNA-specific 2-thiouridylase mnmA	tRNA(5-methylaminomethyl-2-thiouridylate) met	tRNA (5-methylaminomethyl-2-thiouridylate)-m	tRNA (5-methylaminomethyl-2-thiouridylate)-me	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01322	null	1312123	1312431	102	11,04	10871	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01323	gpm4	1312490	1313152	220	8,82	24286	+	Phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01324	null	1313198	1313869	223	5,08	24048	+	TPR repeats containing protein	TPR repeats containing protein	Tetratricopeptide repeat family protein	Tetratricopeptide-like helical|Tetratricopeptide re	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01325	recD	1313856	1316321	821	5,46	90091	+	Helicase, RecD/TraA family protein	ATP-dependent exoDNAse (exonuclease V), al	Exodeoxyribonuclease V alpha chain (EC 3.1.1.	Helicase RecD/TraA	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01326	null	1316327	1317544	405	5,01	47472	+	Acetyltransferase	acetyltransferase (Gnat Family)	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase|Predicted ac	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01327	null	1318624	1317674	316	9,1	35040	-	Diacylglycerol kinase family protein	diacylglycerol kinase family protein	Hypothetical protein	Diacylglycerol kinase, catalytic region|Conserve	IR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01328	ykqC	1320558	1318876	560	6,6	61592	-	Metallo-beta-lactamase superfamily protein	mRNA degradation ribonuclease J1/J2, RNA m	Zn-dependent hydrolase (EC 3.-.-.-)	Beta-lactamase-like|Conserved hypothetical pro	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01329	null	1320775	1320563	70	4,7	8208	-	Conserved domain protein	RNA binding protein, RRM domain	Putative transcriptional regulator	Protein of unknown function DUF1447	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+			
LC_01330	null	1321270	1321722	150	6,81	16981	+	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+			
LC_01331	null	1321745	1322044	99	10,47	11418	+	Putative protein without homology	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01332	def	1322640	1322086	184	5,79	20620	-	Peptide deformylase	Peptide deformylase (PDF) (Polypeptide deform	Peptide deformylase (EC 3.5.1.88)	Formylmethionine deformylase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01333	null	1323153	1323794	213	10,39	22518	+	ATPase, P-type (Transporting), HAD superfar	predicted ORF	Calcium-transporting ATPase (EC 3.6.3.8)	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-t	P	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+			
LC_01334	pdhA	1324232	1325344	370	5,15	40724	+	Pyruvate dehydrogenase E1 component alpha	pyruvate/acetoin dehydrogenase complex E1 cc	Pyruvate dehydrogenase E1 component alpha	Dehydrogenase, E1 component	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01335	pdhB	1325347	1326324	325	5,09	35272	+	Pyruvate dehydrogenase E1 component beta	pyruvate/acetoin dehydrogenase complex E1 cc	Pyruvate dehydrogenase E1 component beta s	Transketolase, central region|Transketolase, C-	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01336	pdhC	1326342	1327982	546	4,48	57416	+	Pyruvate dehydrogenase complex E2 compon	puruvate dehydrogenase complex, E2 compone	Dihydrolipoamide acetyltransferase componen	Biotin/lipoyl attachment|Catalytic domain of com	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01337	pdhD	1327985	1329388	467	5,69	49085	+	Pyruvate dehydrogenase complex, E3 compor	Pyruvate dehydrogenase complex, E3 compone	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	Mercuric reductase|Pyridine nucleotide-disulphi	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01338	null	1329632	1330522	296	4,52	31404	+	Malate/lactate dehydrogenase	Malate/lactate dehydrogenase	L-lactate dehydrogenase (EC 1.1.1.27)	Lactate/malate dehydrogenase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01339	yktA	1330512	1330793	93	8,79	10724	+	Conserved cytosolic protein	conserved hypothetical protein (UPF0223 protei	Hypothetical cytosolic protein	Protein of unknown function UPF0223	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01340	suhB	1330796	1331590	264	5,88	28353	+	Inositol monophosphatase family protein	Archaeal fructose-1,6-bisphosphatase related e	Myo-inositol-1(or 4)-monophosphatase (EC 3.	Inositol monophosphatase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01341	typA	1331843	1333687	614	4,87	67999	+	GTP-binding protein TypA	GTP-binding protein TypA (stress response GT	GTP-binding protein TypA/BipA	Translation elongation factor EFG/EF2, C-termi	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01342	ftsW	1333933	1335102	389	9,78	43618	+	Cell division protein FtsW	Integral bacterial membrane cell division protein	Cell division protein ftsW	Cell cycle protein	D	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+			
LC_01343	pycA	1335095	1338532	1145	6,64	125042	+	Pyruvate carboxylase	pyruvate carboxylase (EC: 6.4.1.1)	Pyruvate carboxylase (EC 6.4.1.1)	Biotin/lipoyl attachment|Pyruvate carboxyltransfe	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01344	null	1338550	1338897	115	10,63	13672	+	Conserved protein	conserved hypothetical protein (YlbG-like protei	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01345	ywdG	1338884	1339450	188	7,18	20692	+	Methyltransferase	N6-adenine-specific DNA methyltransferase	Methyltransferase (EC 2.1.1.-)	N-6 Adenine-specific DNA methylase|Conserve	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01346	coaD	1339443	1339946	167	6,53	18226	+	Phosphopantetheine adenylyltransferase	phosphopantetheine adenylyltransferase (Pante	Phosphopantetheine adenylyltransferase (EC	Coenzyme A biosynthesis protein|Cytidylyltrans	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01347	lon	1339951	1341012	353	10,5	38160	+	PDZ domain protein	Lon-like protease with PDZ domain	ATP-dependent endopeptidase Lon (EC 3.4.2	no annotation	T	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	protease	+			
LC_01348	comEA	1341110	1341775	221	9,26	23296	+	DNA uptake protein related DNA-binding prote	DNA uptake protein related DNA-binding protei	COME operon protein 1	Helix-hairpin-helix motif|Competence protein Cc	L	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-			
LC_01349	null	1341772	1343976	734	9,88	81879	+	Hydrolase (Metallo-beta-lactamase superfamil	hydrolase, metallo-beta-lactamase superfamily	COME operon protein 3	Beta-lactamase-like|ComEC/Rec2-related prote	R	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+			
LC_01350	holA	1343963	1345024	353	9,64	39422	+	DNA polymerase III, delta subunit	DNA-directed DNA polymerase III, delta subuni	DNA polymerase III, delta subunit (EC 2.7.7.7	DNA polymerase III, delta subunit|DNA polymer	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01351	rpsT	1345391	1345137	84	11,42	9358	-	SSU/30S ribosomal protein S20P	SSU ribosomal protein S20P (30S ribosomal pr	SSU ribosomal protein S20P	Ribosomal protein S20	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01352	rpsO	1345640	1345909	89	10,4	10313	+	SSU/30S ribosomal protein S15P	SSU ribosomal protein S15P	SSU ribosomal protein S15P	Ribosomal protein S15|Ribosomal protein S15,	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01353	null	1346027	1346716	229	6,97	24980	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+			
LC_01354	yqgA	1347016	1348698	560	6,81	62249	+	Metallo-beta-lactamase superfamily protein	hydrolase, metallo-beta-lactamase superfamily (	Zn-dependent hydrolase (EC 3.-.-.-)	Beta-lactamase-like|RNA-metabolising metallo-l	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01355	null	1348779	1349684	301	4,72	33624	+	Conserved protein (TPR repeats)	BS_ysoA related protein with TPR repeats	Tetratricopeptide repeat family protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01356	tuf	1349905	1351095	396	4,56	43560	+	Elongation factor Tu (EF-TU)	translation elongation factor (EF-1A/EF-Tu)	Protein Translation Elongation Factor Tu (EF-	Protein synthesis factor, GTP-binding|Translati	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01357	null	1351284	1351111	57	12,06	6093	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01358	null	1351363	1351232	43	8,52	4576	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01359	null	1352503	1351637	288	6,5	32368	-	Putative protein without homology	hydrogenase-4 component C	Hypothetical cytosolic protein	Pectin lyase fold/virulence factor	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01360	null	1353297	1352572	241	7,63	26900	-	Silent information regulator protein Sir2	NAD-dependent protein deacetylase, Silent info	SIR2 family protein	Silent information regulator protein Sir2	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01361	pcaC	1353677	1353303	124	4,86	13680	-	Carboxymuconolactone decarboxylase	Gamma-carboxymuconolactone decarboxylase-	4-carboxymuconolactone decarboxylase (EC 4	Carboxymuconolactone decarboxylase	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-			
LC_01362	merR	1354123	1353740	127	10,61	15053	-	Transcriptional regulator, MerR family	transcriptional regulator, MerR family	Transcriptional regulator, MerR family	Bacterial regulatory protein, MerR|Putative DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-			
LC_01363	yknV	1354273	1356009	578	9,45	64336	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase and perme	Multidrug/protein/lipid ABC transporter family,	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+			
LC_01364	tig	1356181	1357521	446	4,31	49782	+	Trigger factor	Trigger factor (TF) (Vegetative protein 2) (VEG	Trigger factor, ppiase (EC 5.2.1.8)	Peptidyl-prolyl cis-trans isomerase, FKBP-type|	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01365	clpX	1357684	1358934	416	4,62	45684	+	ATP-dependent Clp protease, ATP-binding su	ATP-dependent Clp protease, ATP-binding sub	ATP-dependent endopeptidase clp ATP-bindi	AAA+ ATPase, core|ClpX, ATPase regulatory s	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+			
LC_01366	ysxL	1359121	1359720	199	9,95	22281	+	GTP-binding protein engB	GTP-binding protein (EngB family)	GTP-binding protein YihA	GTP-binding protein, HSR1-related|Small GTP	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01367	null	1359720	1360010	96	5,68	10826	+	MazG nucleotide pyrophosphohydrolase	nucleoside pyrophosphatase	Phage protein	NTP pyrophosphohydrolase MazG, putative cat	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01368	null	1360300	1360139	53	10,33	6001	-	Putative protein without homology	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01369	glnPH2	1360540	1361997	485	10,06	52785	+	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease compon	Arginine-binding protein / Arginine transport sy	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+			
LC_01370	glnQ3	1361987	1362733	248	4,71	27338	+	ABC transporter, amino acid transporter ATPa	amino acid ABC transporter, ATPase componer	Arginine transport ATP-binding protein artP	ABC transporter related|AAA+ ATPase, core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01371	uvrC	1362938	1364746	602	10,11	68825	+	Excinuclease ABC subunit C, UvrABC system	UvrABC system protein C (uvrC protein) (Excin	Excinuclease ABC subunit C	Excinuclease ABC, C subunit, N-terminal|Excin	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+			
LC_01372	fruA	1366959	1364986	657	6,7	70028	-	PTS system, fructose-specific IIABC compon	PTS system, mannitol/fructose-specific IIABC (	PTS system, fructose-specific IIABC compon	Carbohydrate kinase, PfkB|Phosphotransferase	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+			

LC_01373	fruK	1367883	1366969	304	5,53	32371	-	1-phosphofructokinase	1-phosphofructokinase (fructose-1-phosphate k	1-phosphofructokinase (EC 2.7.1.56)	Carbohydrate kinase, PfkB	PfkB	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01374	fruR	1368629	1367880	249	6,09	27026	-	Fructose repressor	lactose transport regulator, DeoR	Fructose repressor	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01375	cgtA	1368879	1370165	428	5,13	46387	+	GTP-binding protein	GTPase ObgE	GTP-binding protein CgtA (probably involved i	GTP-binding protein, HSR1-related|GTP1/OBG	R	Yes	invasin	-	tmhmm:0	-	-	-	-	-	-	+
LC_01376	yvhB	1370221	1372200	659	9,86	74861	+	Acyltransferase	acyltransferase family protein	Acyltransferase family	Acyltransferase 3|Esterase, SGNH hydrolase-ty	I	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+
LC_01377	rnz	1372415	1373374	319	9,86	34998	+	Ribonuclease Z	metal-dependent hydrolase of the beta-lactamas	Ribonuclease Z (EC 3.1.26.11)	Beta-lactamase-like|Ribonuclease Z	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01378	dltE	1373552	1374337	261	10,06	27831	+	Oxidoreductase, short-chain dehydrogenase/r	oxidoreductase, short-chain dehydrogenase/red	Short chain dehydrogenase (EC 1.-.-.-)	Short-chain dehydrogenase/reductase SDR|Gl	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01379	null	1374351	1374677	108	10,79	11779	+	Conserved integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01380	clpB	1374791	1377397	868	5,29	96339	+	ATP-dependent chaperone ClpB	ATP-dependent chaperone ClpB	ClpB protein	Chaperonin clpA/B|AAA+ ATPase, core|AAA A	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01381	rpmF	1377578	1377769	63	11,24	7081	+	LSU/50S ribosomal protein L32P	50S ribosomal protein L32-2	LSU ribosomal protein L32P	Ribosomal L32p protein	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01382	null	1377938	1378492	184	9,54	20418	+	Conserved protein (TPR repeats)	BS_ykrK family protein	Hypothetical cytosolic protein	Domain of unknown function DUF1836	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01383	null	1378489	1379643	384	5,83	41941	+	2',3'-cyclic-nucleotide 2'-phosphodiesterase	2',3'-cyclic-nucleotide 2'-phosphodiesterase	2',3'-cyclic-nucleotide 2'-phosphodiesterase (E	Metallophosphoesterase|5'-Nucleotidase, N-terr	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01384	null	1379705	1380040	111	9,23	12759	+	5'-Nucleotidase and apyrase|5'-Nucleotidase	predicted ORF	not_predicted_by_ERGO	5'-Nucleotidase and apyrase|5'-Nucleotidase, C	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01385	null	1380111	1380989	292	10,99	30897	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+
LC_01386	null	1381297	1381103	64	9,1	7051	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_01387	null	1381393	1383303	636	6,77	70187	+	DNA polymerase III, alpha subunit	predicted ORF	DNA polymerase III alpha subunit (EC 2.7.7.7	Polymerase and histidinol phosphatase, N-term	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01388	dnaE	1383321	1384622	433	10,19	48402	+	DNA polymerase III alpha subunit	DNA polymerase III alpha subunit	not_predicted_by_ERGO	Nucleic acid binding, OB-fold, tRNA/helicase-ty	L	No	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_01389	pfk	1384799	1385758	319	5,96	34197	+	6-phosphofructokinase	6-phosphofructokinase (Phosphofructokinase) (	6-phosphofructokinase (EC 2.7.1.11)	Phosphofructokinase|ATP-dependent phosphof	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01390	pyk	1385818	1387584	588	5,07	62849	+	Pyruvate kinase	pyruvate kinase (PK) (Vegetative protein 17) (VI	Pyruvate kinase (EC 2.7.1.40)	Pyruvate kinase|PEP-utilising enzyme, mobile r	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01391	ytwI	1387812	1388273	153	10,17	15936	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF441	S	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_01392	infC	1388307	1389191	294	6,64	32474	+	S1 RNA binding domain	RNA-binding protein, S1-like domain	S1 RNA binding domain	no annotation	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01393	XerD	1389193	1390074	293	10,19	33203	+	Tyrosine recombinase xerD	tyrosine recombinase XerD subunit	Integrase/recombinase (XerD/RipX family)	Integrase, catalytic core, phage|Integrase, N-ter	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+
LC_01394	ribT	1390266	1390652	128	6,3	14572	+	RibT protein, riboflavin biosynthesis acetyltran	RibTD gene product, riboflavin biosynthesis ace	RibT protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01395	scpA	1390627	1391352	241	4,29	26795	+	Segregation and condensation protein A	segregation and condensation protein A ScpA	Segregation and condensation protein ScpA	Prokaryotic chromosome segregation and condi	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01396	scpB	1391349	1391969	206	4,22	22788	+	Segregation and condensation protein B	chromosome segregation and condensation pro	Segregation and condensation protein ScpB	Prokaryotic chromosome segregation and condi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01397	rluB	1391953	1392699	248	9,94	27429	+	Ribosomal large subunit pseudouridine syntha	Ribosomal large subunit pseudouridine synthas	Ribosomal large subunit pseudouridine syntha	Pseudouridine synthase, Rsu|RNA-binding S4|	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01398	null	1392995	1393573	192	10,75	20774	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Riboflavin transporter	no annotation	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01399	fer	1394001	1393744	85	7,38	9605	-	Ferredoxin	ferredoxin (4Fe-4S)	Ferredoxin	4Fe-4S ferredoxin, iron-sulfur binding	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01400	null	1394081	1395070	329	10,06	37285	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01401	recQ1	1395057	1396466	469	7,4	52034	+	ATP-dependent DNA helicase RecQ	ATP-dependent DNA helicase, RecQ family	ATP-dependent DNA helicase recQ (EC 3.6.1	Helicase, C-terminal|ATP-dependent helicase, I	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01402	null	1396526	1397167	213	10,05	22724	+	Putative protein without homology	predicted ORF	LysM domain protein	Peptidoglycan-binding LysM	M	Yes	peptidoglucar	LysM	tmhmm:1	-	-	-	-	-	-	+
LC_01403	cmk	1397233	1397901	222	6,81	24571	+	Cytidylate kinase	cytidylate kinase (CK) / Cytidine monophosphat	Cytidylate kinase (EC 2.7.4.14)	Cytidylate kinase|Adenylate/cytidine kinase, N-t	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01404	rpsA	1397986	1399296	436	4,9	47171	+	SSU/30S ribosomal protein S1P	30S ribosomal protein S1-like protein	SSU ribosomal protein S1P	Ribosomal protein S1|RNA binding S1|Nucleic	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01405	serA	1399443	1400750	435	4,97	48520	+	GTP-binding protein EngA	GTP-binding protein, EngA family	GTP-binding protein	GTP-binding protein, HSR1-related|Small GTP	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01406	hbsU	1400984	1401259	91	10,65	9512	+	DNA-binding protein HU	bacterial nucleoid, histone-like DNA-binding pro	DNA-binding protein HU	Histone-like bacterial DNA-binding protein|IHF-l	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01407	null	1401442	1402707	421	3,96	46690	+	TPR repeats containing protein	TPR repeats (Tetratricopeptide repeat) containi	Tetratricopeptide repeat family protein	Tetratricopeptide TPR_1|Tetratricopeptide-like	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01408	yudJ	1403604	1402726	292	8,4	32150	-	Conservedmembrane protein	conserved hypothetical protein (YitT-like protein	Hypothetical membrane spanning protein	Protein of unknown function DUF161	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01409	papL	1403705	1404901	398	7,06	43993	+	tRNA nucleotidyltransferase, CCA-adding enz	CCA-adding enzyme (tRNA nucleotidyltransferz	tRNA nucleotidyltransferase (EC 2.7.7.25)	Polynucleotide adenylyltransferase region|Poly-/	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01410	null	1405027	1405482	151	5,23	17532	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01411	yfmR	1405631	1407544	637	5,99	71444	+	ABC transporter, ATPase component	ABC transporter, ATPase component, uup	ABC transporter ATP-binding protein uup	ABC transporter related|AAA+ ATPase, core	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01412	null	1407561	1407734	57	9,97	6668	+	Thymidylate synthase	predicted ORF	not_predicted_by_ERGO	Thymidylate synthase, C-terminal	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01413	thyA	1407742	1408512	256	5,78	29707	+	Thymidylate synthase	thymidylate Synthase	Thymidylate synthase (EC 2.1.1.45)	Thymidylate synthase, C-terminal	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01414	dfrA	1408629	1409120	163	6,14	18439	+	Dihydrofolate reductase	dihydrofolate Reductase (NADPH)	Dihydrofolate reductase (EC 1.5.1.3)	Dihydrofolate reductase region|Dihydrofolate re	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01415	null	1409897	1409250	215	9,96	23785	-	Hemolysin III related protein	predicted ORF	Conserved membrane protein (hemolysin III h	Hly-III related proteins|HylIII	R	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_01416	DegV	1410139	1410981	280	5,14	30222	+	DegV family protein	DegV family protein	DegV family protein	DegV	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01417	null	1411244	1412089	281	10,12	30729	+	Lipase/acylhydrolase	Lysophospholipase L1 related esterase / lipase/	Lipase/Acylhydrolase with GDSL-like motif	Lipolytic enzyme, G-D-S-L|Esterase, SGNH hy	E	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_01418	null	1412094	1412735	213	10,64	23689	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_01419	msrA	1412761	1413279	172	4,74	19473	+	Peptide methionine sulfoxide reductase	Peptide methionine sulfoxide reductase (msrA)	Peptide methionine sulfoxide reductase msrA	Methionine sulfoxide reductase A	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01420	null	1413282	1413524	80	4,46	9526	+	Conserved domain protein	D-alanyl-D-alanine carboxypeptidase	Hypothetical cytosolic protein	Protein of unknown function DUF1250	C	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01421	ctpA	1413493	1414935	480	10,35	50783	+	Carboxyl-terminal protease	periplasmic carboxyl-terminal protease	Carboxy-terminal processing protease precurs	PDZ/DHR/GLGF|Peptidoglycan-binding domair	M	Yes	peptidoglucar	Sec	tmhmm:1	-	-	-	-	-	protease	+
LC_01422	null	1415301	1418756	1151	8,88	132379	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01423	null	1418731	1420074	447	9,32	51970	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01424	null	1420080	1420874	264	10,18	30674	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	LPxTG	tmhmm:0	-	-	-	-	-	-	-
LC_01425	null	1421086	1421796	236	9,74	26752	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01426	ylqL	1421814	1422671	285	10,1	31949	+	GTP-binding protein	ribosomal biogenesis GTPase	GTP-binding protein	GTP-binding protein, HSR1-related|GTP-bindin	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01427	rnhB	1422655	1423413	252	7,95	27907	+	Ribonuclease HII	Ribonuclease HII (RNase HII)	Ribonuclease HII (EC 3.1.26.4)	Ribonuclease HII/HIII|Polynucleotidyl transferas	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01428	dprA	1423461	1424276	271	9,71	29281	+	DNA processing SMF protein	DNA processing Smf protein / Rossmann fold r	DNA processing protein	SMF protein	LU	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01429	topA	1424521	1426605	694	9,94	78113	+	DNA topoisomerase I	DNA topoisomerase 1 (DNA topoisomerase I) (	DNA topoisomerase I (EC 5.99.1.2)	DNA topoisomerase, type IA|DNA topoisomeras	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01430	gid	1426772	1428094	440	7,23	47904	+	Glucose inhibited division protein A	tRNA (uracil-5-)-methyltransferase Gid	Glucose inhibited division protein A	Glucose-inhibited division protein A|Gid protein	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01431	xerC2	1428291	1429190	299	9,37	34785	+	Tyrosine recombinase xerD	tyrosine recombinase XerC subunit	Integrase/recombinase (XerC/CodV family)	Integrase, catalytic core, phage|Integrase, N-ter	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+
LC_01432	hslV	1429309	1429833	174	4,82	18790	+	ATP-dependent endopeptidase hsl proteolytic	ATP-dependent protease, HslVU (ClpYQ) pepti	ATP-dependent endopeptidase hsl proteolytic	20S proteasome, A and B subunits	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01433	hslU	1430175	1431584	469	4,91	52191	+	ATP-dependent endopeptidase hsl ATP-bindi	ATP-dependent protease, ATP-binding subunit	ATP-dependent endopeptidase hsl ATP-bindi	AAA+ ATPase, core|Heat shock protein HslU|A	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01434	lacX	1431624	1432502	292	6,35	32624	+	Galactose mutarotase related enzyme	Galactose mutarotase related enzyme	Aldose 1-epimerase family protein	Aldose 1-epimerase|Glycoside hydrolase-type c	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01435	yneS	1433219	1432596	207	9,41	22636	-	Conserved membrane protein	conserved hypothetical protein (UPF0078 mem	Hypothetical membrane spanning protein	Protein of unknown function DUF205	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01436	parE	1433471	1435483	670	8,81	74546	+	DNA topoisomerase IV, B subunit	dna topoisomerase iv subunit b protein	Topoisomerase IV subunit B (EC 5.99.1.-)	DNA topoisomerase, type IIA, subunit B|DNA to	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01437	parC	1435490	1437931	813	6,65	90764	+	DNA topoisomerase IV, A subunit	DNA topoisomerase IV subunit A	Topoisomerase IV subunit A (EC 5.99.1.-)	DNA topoisomerase, type IIA, subunit A or C-te	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01438	pflB	1438176	1440437	753	5,06	85189	+	Formate acetyltransferase	formate C-acetyltransferase (Pyruvate formate-l	Formate acetyltransferase (EC 2.3.1.54)	Formate C-acetyltransferase glycine radical|Pyr	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01439	pflA2	1440623	1441426	267	5,04	30297	+	Pyruvate formate-lyase activating enzyme	formate C-acetyltransferase activating enzyme (	Pyruvate formate-lyase activating enzyme (EC	Radical-activating enzyme|Radical SAM|Pyruva	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01440	lysR	1441548	1442516	322	6,9	37031	+	Transcriptional regulator, LysR family	transcriptional regulator, LysR family	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR|LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01441	ppa	1442546	1443478	310	4,53	33522	+	Manganese-dependent inorganic pyrophospha	manganese-dependent inorganic pyrophosphat	Inorganic pyrophosphatase (EC 3.6.1.1)	Phosphoesterase, RecJ-like|DHHA2	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+

LC_01442	xerD	1444306	1445418	370	9,69	42731	+	Tyrosine recombinase xerC	tyrosine recombinase XerC subunit	DNA integration/recombination/inversion prote	Integrase, catalytic core, phage|Integrase, N-ter	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	+
LC_01443	null	1447579	1445594	661	10,59	74203	-	ABC transporter, permease component	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein	Haem peroxidase, plant/fungal/bacterial	V	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	+
LC_01444	ysaC	1448346	1447576	256	5,75	28323	-	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+
LC_01445	null	1449399	1448440	319	7,66	36097	-	Two component sensor transduction histidine	integral membrane sensor signal transduction h	Two component system histidine kinase (EC 2	ATP-binding region, ATPase-like|Histidine kina	null	Yes	-	Nterm/Cter	tmhmm:2	-	-	-	HPK	-	-	+
LC_01446	mbrC	1450087	1449392	231	4,97	26061	-	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+
LC_01447	null	1450185	1451399	404	9,88	44087	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily MF	Macrolide-efflux protein	Major facilitator superfamily|Major facilitator sup	GEPF	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_01448	msi198	1451874	1451479	131	9,75	14620	-	Acetyltransferase	acetyltransferase, GNAT family protein	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01449	null	1452276	1451878	132	5,09	15014	-	Acetyltransferase	acetyltransferase, GNAT family protein	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01450	null	1453052	1452417	211	6,02	23092	-	Nitroreductase	Nitroreductase	NAD(P)H-dependent quinone reductase (EC :	Nitroreductase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01451	hpaG	1453970	1453161	269	5,81	28857	-	Fumarylacetoacetate hydrolase family protein	bifunctional 2-hydroxyhepta-2,4-diene-1,7-dioat	Fumarylacetoacetate hydrolase family protein	Fumarylacetoacetate (FAA) hydrolase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01452	hisC	1455148	1454015	377	8,96	42157	-	Histidinol-phosphate aminotransferase	histidinol-phosphate/aromatic aminotransferase	Histidinol-phosphate aminotransferase (EC 2.6	Aminotransferase, class I and II|Histidinol-phos	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01453	hisE	1455553	1455221	110	5,93	12340	-	Phosphoribosyl-ATP pyrophosphatase	Phosphoribosyl-ATP pyrophosphatase (PRA-PI	Phosphoribosyl-ATP pyrophosphatase (EC 3.6	Phosphoribosyl-ATP pyrophosphohydrolase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01454	hisI	1455882	1455550	110	7,44	12235	-	Phosphoribosyl-AMP cyclohydrolase	phosphoribosyl-AMP cyclohydrolase/phosphorib	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4	Phosphoribosyl-AMP cyclohydrolase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01455	hisF	1456637	1455879	252	9,51	26754	-	Imidazole glycerol phosphate synthase subuni	HisF, imidazoleglycerol phosphate synthase, cy	Imidazole glycerol phosphate synthase, cyclas	Histidine biosynthesis, HisF|Histidine biosynthe	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01456	hisA	1457355	1456606	249	8	26557	-	1-(5-phosphoribosyl)-5-[(5- phosphoribosylam	1-(5-phosphoribosyl)-5-((5-phosphoribosylamin	1-(5-phosphoribosyl)-5-[(5-phosphoribosylami	Histidine biosynthesis|Ribulose-phosphate bind	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01457	hisH	1457959	1457333	208	6,79	22264	-	Imidazole glycerol phosphate synthase, glutan	Imidazole glycerol phosphate synthase subunit	Imidazole glycerol phosphate synthase, glutan	Glutamine amidotransferase class-I|Imidazole g	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01458	hisB	1458543	1457956	195	5,86	21052	-	Imidazoleglycerol-phosphate dehydratase	Imidazoleglycerol-phosphate dehydratase (IGPI	Imidazoleglycerol-phosphate dehydratase (EC	Imidazole glycerol-phosphate dehydratase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01459	null	1458881	1458648	77	11,48	8095	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	-
LC_01460	hisD	1460242	1458962	426	6,17	44723	-	Histidinol dehydrogenase	Histidinol dehydrogenase (HDH)	Histidinol dehydrogenase (EC 1.1.1.23)	Histidinol dehydrogenase|Histidinol dehydrogen	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01461	hisG	1460873	1460244	209	8,68	23247	-	ATP phosphoribosyltransferase	ATP phosphoribosyltransferase catalytic subun	ATP phosphoribosyltransferase (EC 2.4.2.17)	Histidine biosynthesis HisG: ATP phosphoribos	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01462	null	1462018	1460870	382	5,63	42838	-	ATP phosphoribosyltransferase regulatory sut	ATP phosphoribosyltransferase regulatory subu	ATP phosphoribosyltransferase regulatory sut	tRNA synthetase, class II (G, H, P and S)|Histi	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01463	hisC	1463631	1462534	365	8,19	40773	-	Histidinol-phosphate aminotransferase	histidinol-phosphate aminotransferase (imidazol	Histidinol-phosphate aminotransferase (EC 2.6	Aminotransferase, class I and II|Histidinol-phos	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01464	nudF	1464416	1463856	186	6,15	20599	-	Phosphohydrolase, MutT/nudix family	MutT/nudix family protein	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01465	degV	1465331	1464465	288	5,38	31974	-	DegV family protein	DegV family protein	DegV family protein	DegV	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01466	null	1466409	1465495	304	9,72	32563	-	Putative protein without homology	predicted ORF	Hypothetical exported protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01467	fbpS	1466804	1468507	567	9,7	64360	+	Fibronectin-binding protein	Fibronectin-binding protein / Fibrinogen-binding	Fibronectin-binding protein / Fibrinogen-bindin	Protein of unknown function DUF814|Fibronect	K	Yes	fibronectin	-	tmhmm:0	-	-	-	-	-	-	+
LC_01468	null	1468521	1468832	103	5,1	11562	+	Pyrophosphatase	pyrophosphatase	Hypothetical cytosolic protein	NTP pyrophosphohydrolase MazG, putative cat	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01469	null	1470094	1468952	380	9	39205	-	Membrane protein, toxin regulator-like protein	membrane protein, toxin regulator	Hypothetical membrane spanning protein	Sodium:dicarboxylate symporter	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_01470	pyrE	1470978	1470340	212	8,82	22382	-	Orotate phosphoribosyltransferase	orotate phosphoribosyltransferase (OPRT) (OP	Orotate phosphoribosyltransferase (EC 2.4.2.1	Regulator of chromosome condensation, RCC1	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01471	pyrF	1471690	1470971	239	9,8	25496	-	Orotidine 5'-phosphate decarboxylase	orotidine 5'-phosphate decarboxylase (OMP de	Orotidine 5'-phosphate decarboxylase (EC 4.1	Orotidine 5'-phosphate decarboxylase, core|Rib	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01472	pyrDB	1472559	1471687	290	6,24	29880	-	Dihydroorotate dehydrogenase	dihydroorotate dehydrogenase B, catalytic subu	Dihydroorotate dehydrogenase (EC 1.3.3.1)	Dihydroorotate dehydrogenase, core|Dihydroorc	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01473	pyrAb1	1475793	1472611	1060	4,88	116219	-	Carbamoyl-phosphate synthase, large subunit	Carbamoyl-phosphate synthase, large subunit,	Carbamoyl-phosphate synthase large chain (E	Carbamoyl-phosphate synthase L chain, ATP-b	EF	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01474	pyrAA	1476878	1475796	360	5,55	39433	-	Carbamoyl-phosphate synthase, small subunit	carbamoyl phosphate synthase small subunit	Carbamoyl-phosphate synthase small chain (E	Glutamine amidotransferase class-I|Carbamoyl-	EF	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01475	pyrC	1478149	1476875	424	6,66	45093	-	Dihydroorotase	Dihydroorotase (DHOase)	Dihydroorotase (EC 3.5.2.3)	Aminoacyl-tRNA synthetase, class I|Dihydrooro	F	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01476	pyrB	1479094	1478153	313	5,35	35045	-	Aspartate carbamoyltransferase	aspartate carbamoyltransferase, catalytic chain	Aspartate carbamoyltransferase (EC 2.1.3.2)	Aspartate carbamoyltransferase, eukaryotic|Asp	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01477	pyrP	1480388	1479081	435	9	46333	-	Uracil permease	Xanthine/uracil permease family	Uracil permease	Xanthine/uracil permease|Xanthine/uracil/vitami	F	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_01478	pyrR1	1480940	1480392	182	6,25	20471	-	Pyrimidine operon regulatory protein, bifunctio	pyrimidine operon attenuation protein/uracil pho	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Phosphoribosyltransferase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01479	rluA2	1482095	1481175	306	9,96	33586	-	Ribosomal large subunit pseudouridine syntha	ribosomal large subunit pseudouridine synthase	Ribosomal large subunit pseudouridine syntha	RNA-binding S4|Pseudouridine synthase|Pseu	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01480	lspA	1482559	1482092	155	8,47	17834	-	Lipoprotein signal peptidase	lipoprotein signal peptidase (prolipoprotein signa	Lipoprotein signal peptidase (EC 3.4.23.36)	Peptidase A8, signal peptidase II	MU	Yes	-	IMP	tmhmm:4	-	-	-	-	-	protease	-
LC_01481	fhs-1	1484615	1482942	557	6,96	58955	-	Formate-tetrahydrofolate ligase	Formate--tetrahydrofolate ligase (Formyltetrahyc	formyl-tetrahydrofolate synthetase	Formate-tetrahydrofolate ligase, FTHFS	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01482	null	1485032	1484628	134	11,06	15068	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01483	esbB	1485057	1485455	132	7,25	14237	+	Ribonuclease HI	ribonuclease HI / Cell-wall enzyme EBSB	Ribonuclease HI (EC 3.1.26.4) / Cell wall enzy	Ribonuclease H|Polynucleotidyl transferase, Rit	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01484	null	1486174	1485572	200	4,91	22760	-	Nitroreductase family protein	nitroreductase-like oxidoreductase	Nitroreductase family protein	Nitroreductase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01485	cls2	1486464	1487933	489	9,54	55650	+	Cardiolipin synthetase	cardiolipin synthetase 2 (Cardiolipin synthase 2	Cardiolipin synthetase (EC 2.7.8.-)	Phospholipase D/Transphosphatidylase	I	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01486	null	1487935	1488087	50	12,36	5623	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01487	null	1488586	1488260	108	4,58	12442	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01488	null	1488842	1488663	59	11,61	6189	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01489	null	1490403	1488952	483	10,06	54708	-	Transcriptional regulator	conserved hypothetical protein	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01490	nrdH	1490764	1490994	76	7,41	8851	+	Glutaredoxin	Glutaredoxin related protein	Glutaredoxin	Glutaredoxin|Glutaredoxin-like protein NrdH|Thi	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01491	nrdE	1491062	1493233	723	6,43	82192	+	Ribonucleoside-diphosphate reductase, alpha	ribonucleoside-diphosphate reductase class Ib	Ribonucleoside-diphosphate reductase alpha	Ribonucleotide reductase large subunit, C-term	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01492	nrdF	1493285	1494265	326	4,23	37746	+	Ribonucleoside-diphosphate reductase, beta s	ribonucleoside-diphosphate reductase class Ib	Ribonucleoside-diphosphate reductase beta c	Ribonucleotide reductase|Ferritin/ribonucleotide	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01493	null	1495314	1494424	296	6,05	32909	-	Transcriptional regulator, LysR family	transcription regulator, FHU operon	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR|LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01494	pepO	1497434	1495530	634	5,33	71709	-	Endopeptidase O	neutral endopeptidase (Endopeptidase O)	Oligoendopeptidase O (EC 3.4.24.-)	Peptidase M13, neprilysin|Peptidase M, neutral	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01495	lplA1	1497801	1498814	337	5,29	38401	+	Lipoate-protein ligase A	Lipoate-protein ligase A-like protein	Lipoate-protein ligase A (EC 6.3.2.-)	Biotin/lipoate A/B protein ligase|Lipoyltransferas	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01496	null	1499117	1498890	75	9,66	8502	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01497	serA3	1500268	1499333	311	6,63	33845	-	D-3-phosphoglycerate dehydrogenase	D-3-phosphoglycerate dehydrogenase	D-3-phosphoglycerate dehydrogenase (EC 1.1	D-isomer specific 2-hydroxyacid dehydrogenas	HE	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01498	ypsC	1501419	1500280	379	9,03	42320	-	Methyltransferase	N6-adenine-specific DNA methyltransferase	Methyltransferase (EC 2.1.1.-)	Putative RNA methylase|N-6 Adenine-specific D	L	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	+
LC_01499	yraB	1502662	1502264	132	4,72	15128	-	Cell division initiation protein, gpsB	Cell division initiation protein DivIVA	Cell division initiation protein DivIVA	DivIVA	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01500	ypsA	1503293	1502718	191	4,39	21818	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	Protein of unknown function DUF1273	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01501	recU	1503360	1503986	208	10,08	24069	+	Holliday junction resolvase recU	Holliday junction endonuclease/resolvase recU	Recombination protein recU	Recombination protein U	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01502	mrcA	1503979	1506288	769	9,49	83494	+	Penicillin-binding protein 1A	membrane carboxypeptidase, penicillin-binding	Multimodular transpeptidase-transglycosylase	Glycosyl transferase, family 51|Penicillin-bindin	M	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+
LC_01503	comEB	1506871	1506407	154	7,13	17123	-	CMP/dCMP deaminase, zinc-binding protein	CMP/dCMP deaminase, zinc-binding protein	CMP/dCMP deaminase family protein	CMP/dCMP deaminase, zinc-binding|Cytidine d	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01504	nth	1507518	1506868	216	10	23380	-	Endonuclease III	endonuclease III (DNA repair)	Endonuclease III (EC 4.2.99.18)	Helix-hairpin-helix motif|HhH-GPD|Endonuclea	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01505	dnaD	1508193	1507573	206	6,4	23694	-	DNA replication protein DnaD	DNA replication protein DnaD (Primosomal prot	DNA replication protein dnaD	Endoplasmic reticulum targeting sequence|Dna	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01506	asnC	1509546	1508248	432	4,96	49935	-	Asparaginyl-tRNA synthetase	Aspartyl/asparaginyl-tRNA synthetases	Asparaginyl-tRNA synthetase (EC 6.1.1.22)	Aspartyl-tRNA synthetase, class IIb|tRNA synth	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01507	aspB	1510745	1509570	391	6,43	42552	-	Aspartate aminotransferase	aspartate/tyrosine/aromatic aminotransferase (ta	Aspartate aminotransferase (EC 2.6.1.1)	1-aminocyclopropane-1-carboxylate synthase|A	E	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_01508	null	1511289	1510798	163	10,97	18573	-	Conserved extracellular protein	conserved hypothetical protein (extracellular prc	Hypothetical exported protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_01509	null	1511676	1511485	63	10,87	6997	-	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01510	dinG	1514492	1511691	933	9,3	104491	-	DNA polymerase III, Rad3-related DNA helica	Rad3-related DNA helicase	ATP-dependent helicase, DinG family	DNA polymerase III, epsilon subunit|Exonuclea	KL	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+

LC_01511	rexA	1518246	1514536	1236	5,18	137656	-	ATP-dependent nuclease, subunit A	ATP-dependent exoDNAse (exonuclease V) be	ATP-dependent nuclease subunit A	UvrD/REP helicase|Helicase superfamily 1, Uvr	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01512	rexB	1521782	1518243	1179	6,62	132269	-	ATP-dependent nuclease, subunit B	ATP-dependent DNA helicase/exodeoxyribonuc	ATP-dependent nuclease subunit B	Death	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01513	mvaK1	1522324	1523259	311	8,43	32808	+	Mevalonate kinase	mevalonate kinase	Mevalonate kinase (EC 2.7.1.36)	GHMP kinase|Mevalonate kinase|Mevalonate ar	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01514	mvaD	1523267	1524271	334	7,26	36098	+	Diphosphomevalonate decarboxylase	diphosphomevalonate/mevalonate pyrophospha	Diphosphomevalonate decarboxylase (EC 4.1.	Diphosphomevalonate decarboxylase|GHMP kir	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01515	fni	1524237	1525271	344	6,22	37779	+	Isopentenyl-diphosphate delta-isomerase	type II isopentenyl-diphosphate delta-isomerase	Isopentenyl-diphosphate delta-isomerase (EC	Isopentenyl-diphosphate delta-isomerase, FMN	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01516	Sun2	1526709	1525378	443	8,3	49007	-	tRNA and rRNA cytosine-C5-methylases	tRNA and rRNA cytosine-C5-methylases, NOL	23S rRNA m(5)C methyltransferase (EC 2.1.1	Glycoside hydrolase, family 5|Bacterial Fmu (Su	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01517	null	1527652	1526696	318	10,15	35214	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	no annotation	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+						
LC_01518	null	1527855	1527649	68	12,6	7445	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01519	null	1528598	1527855	247	9,8	28350	-	SAM-dependent methyltransferase	SAM-dependent methyltransferase	Hypothetical membrane spanning protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01520	yitW	1529064	1528714	116	4,09	12866	-	Metal-sulfur cluster biosynthetic enzyme	metal-sulfur cluster biosynthetic enzyme	Hypothetical cytosolic protein	Protein of unknown function DUF59	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01521	xylH	1529286	1529098	62	6,07	6770	-	4-oxalocrotonate tautomerase	4-oxalocrotonate tautomerase 4-OT	4-oxalocrotonate tautomerase (EC 5.3.2.-)	4-oxalocrotonate tautomerase|Tautomerase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01522	null	1531350	1529845	501	10,17	55917	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter related|ABC transporter, transı	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-						
LC_01523	null	1533046	1531334	570	9,17	63568	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core|AI	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-						
LC_01524	null	1534216	1533422	264	4,89	28925	-	NIF3-related protein	NIF3-related protein	NIF3-related protein	NGG1p interacting factor 3, NIF3	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01525	ykiC	1534913	1534203	236	5,99	25938	-	SAM-dependent methyltransferase	SAM-dependent methyltransferase	Hypothetical cytosolic protein	Protein of unknown function DUF633	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01526	sigA	1536352	1535102	416	9,65	46950	-	RNA polymerase sigma factor	RNA polymerase sigma factor RpoD-like	RNA polymerase sigma factor rpoD	RNA polymerase, Sigma-70 factor|RNA polyme	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01527	dnaG	1538135	1536366	589	5,77	65619	-	DNA primase	DNA primase (bacterial type)	DNA primase (EC 2.7.7.-)	Zinc finger, CHC2-type|Toprim subdomain|TOF	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01528	glyS	1540390	1538321	689	5,17	76158	-	Glycyl-tRNA synthetase, beta subunit	glycyl-tRNA synthetase beta subunit (Glycine--t	Glycyl-tRNA synthetase beta chain (EC 6.1.1.	Glycyl-tRNA synthetase, beta subunit|Heterodir	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01529	glyQ	1541288	1540392	298	4,97	34162	-	Glycyl-tRNA synthetase, alpha subunit	glycyl-tRNA synthetase alpha subunit (Glycine-	Glycyl-tRNA synthetase alpha chain (EC 6.1.1	Glycyl-tRNA synthetase, alpha subunit|Heterodi	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01530	RimL	1542195	1541668	175	6,53	20354	-	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family	Ribosomal-protein-alanine acetyltransferase (E	GCN5-related N-acetyltransferase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01531	null	1542920	1542291	209	10,03	23543	-	Conserved protein	predicted ORF	ABC transporter, permease	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+						
LC_01532	null	1543623	1542901	240	9,28	26428	-	ABC transporter, ATPase component	ABC transporter	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01533	null	1544587	1544276	103	10,07	11776	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01534	recO	1545552	1544737	271	9,2	31068	-	DNA repair protein recO	DNA repair protein recO (Recombination protei	DNA repair protein recO	Recombination protein O, RecO	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01535	era	1546454	1545552	300	6,65	33956	-	GTP-binding protein era	Small GTP-binding protein domain:GTP-bindin	GTP-binding protein era	GTP-binding protein, HSR1-related|KH, type 2|	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01536	cdd	1546840	1546451	129	5,03	13411	-	Cytidine deaminase	Cytidine deaminase, homotetrameric	Cytidine deaminase (EC 3.5.4.5)	CMP/dCMP deaminase, zinc-binding|Cytidine c	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01537	null	1547242	1546844	132	9,66	14791	-	Diacylglycerol kinase	diacylglycerol kinase	Diacylglycerol kinase (EC 2.7.1.107)	Prokaryotic diacylglycerol kinase	M	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+						
LC_01538	null	1547684	1547226	152	4,42	17398	-	Metalloprotease	metal-dependent hydrolase	Hypothetical metal-binding protein	Protein of unknown function UPF0054	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+						
LC_01539	phoH	1548674	1547688	328	6,53	35970	-	PhoH family protein	starvation induced PhoH family protein, predicte	PhoH protein	PhoH-like protein	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01540	null	1549693	1549250	147	8,97	16104	-	GatB/YqeY domain protein	conserved hypothetical protein / GatB/YqeY-dor	GatB/Yqey domain protein	GatB/Yqey	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01541	rpsU	1549888	1549712	58	11,38	6964	-	SSU/30S ribosomal protein S21P	ribosomal protein S21 (30S ribosomal protein S	SSU ribosomal protein S21P	Ribosomal protein S21	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01542	yqfL	1550161	1550991	276	4,95	31041	+	Phosphotransferase	phosphotransferase	Hypothetical protein	Protein of unknown function DUF299	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01543	nfo	1551875	1550988	295	6,57	32477	-	Endonuclease 4	endonuclease IV (Endodeoxyribonuclease IV)	Endonuclease IV (EC 3.1.21.2)	AP endonuclease, family 2|Xylose isomerase-lik	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01544	yudL	1552943	1552023	306	10,05	34346	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF161	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+						
LC_01545	msrA	1553694	1553248	148	6,27	16517	-	Peptide methionine sulfoxide reductase	methionine sulfoxide reductase B	Peptide methionine sulfoxide reductase msrB	Methionine sulfoxide reductase B|Mss4-like	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01546	aspS	1555585	1553780	601	4,9	67709	-	Aspartyl-tRNA synthetase	probable aspartyl-trna synthetase (aspartate--tr	Aspartyl-tRNA synthetase (EC 6.1.1.12)	Aspartyl-tRNA synthetase, class IIb|GAD|tRNA	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01547	hisS	1556870	1555587	427	5,24	47710	-	Histidyl-tRNA synthetase	Histidyl-tRNA synthetase (Histidine--tRNA ligas	Histidyl-tRNA synthetase (EC 6.1.1.21)	tRNA synthetase, class II (G, H, P and S)|Antic	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01548	null	1558938	1557430	502	10,79	55143	-	ABC transporter, permease component	ABC transporter, permease component	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-						
LC_01549	mppX	1559810	1558935	291	8,77	31537	-	ABC transporter, ATPase component	ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01550	null	1560010	1560456	148	5,16	16913	+	Diadenosine tetraphosphate (Ap4A) hydrolase	Diadenosine tetraphosphate (Ap4A) hydrolase r	HIT family hydrolase	Histidine triad (HIT) protein	FGR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01551	ami	1560544	1561866	440	9,27	47318	+	N-acetylmuramoyl-L-alanine amidase	N-acetylmuramoyl-L-alanine amidase precursor	N-acetylmuramoyl-L-alanine amidase (EC 3.5.	Cell wall hydrolase/autolysin|Bacterial SH3-like	M	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+						
LC_01552	null	1562594	1561968	208	6,8	23127	-	P-Ser-HPr phosphatase	P-Ser-HPr phosphatase	Phosphoglycolate phosphatase (EC 3.1.3.18)	Haloacid dehalogenase-like hydrolase|HAD-sup	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01553	dtd	1563040	1562594	148	4,67	15565	-	D-tyrosyl-tRNA(Tyr) deacylase	D-tyrosyl-tRNA(Tyr) deacylase	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	D-tyrosyl-tRNA(Tyr) deacylase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01554	relA	1565392	1563167	741	7,84	84548	-	GTP pyrophosphokinase	Guanosine polyphosphate pyrophosphohydrolas	GTP pyrophosphokinase (EC 2.7.6.5) / Guano	Metal-dependent phosphohydrolase, HD region	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01555	null	1566269	1565946	107	11,56	12811	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	T	Yes	-	IMP	tmhmm:4	-	-	-	-	-	protease	-						
LC_01556	nadD	1567035	1566307	242	6,63	26173	-	RNA methyltransferase	nicotinic acid mononucleotide adenyltransferase	Hypothetical cytosolic protein	Protein of unknown function DUF558, methyltra	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01557	prmA	1568018	1567074	314	4,86	33761	-	Ribosomal protein L11 methyltransferase	ribosomal protein L11 methyltransferase (L11 N	Ribosomal protein L11 methyltransferase (EC	Ribosomal protein L11 methyltransferase|Ribos	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01558	null	1568593	1568099	164	3,52	18400	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01559	mpg	1569195	1568590	201	9,8	22226	-	3-methyladenine DNA glycosylase	3-methyladenine DNA glycosylase	DNA-3-methyladenine glycosylase II (EC 3.2.2	Methylpurine-DNA glycosylase (MPG)|Formyl tr	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01560	null	1569301	1569549	82	4,22	9258	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01561	null	1570004	1569618	128	10,09	14218	-	Conserved membrane protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+						
LC_01562	null	1570469	1570290	59	11,24	7120	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01563	null	1570855	1570469	128	10,38	14060	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-						
LC_01564	null	1571863	1571273	196	9,57	22559	-	NADPH-quinone reductase (Modulator of drug	NADPH-quinone reductase (modulator of drug	NAD(P)H dehydrogenase [quinone] (EC 1.6.5	Flavodoxin-like fold	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01565	null	1572423	1571866	185	6,53	21418	-	Transcriptional regulator, TetR family	transcriptional regulator	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-						
LC_01566	null	1572848	1573852	334	5,56	37452	+	Oxidoreductase	oxidoreductase, Gfo/Idh/MocA family protein, N	NAD-dependent oxidoreductase	Oxidoreductase, N-terminal	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01567	yohH	1575571	1573955	538	5,2	62159	-	Glycosyl transferase, group 1	lipopolysaccharide biosynthesis protein, glycos	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Protein of unknov	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01568	yohJ	1577124	1575568	518	5,46	58405	-	Glycosyl transferase, group 1	lipopolysaccharide biosynthesis protein, alpha-g	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Protein of unknov	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01569	null	1578441	1577176	421	4,4	45394	-	Putative protein without homology	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01570	null	1580334	1578616	572	5,19	61553	-	Cell surface protein	predicted ORF	Cell surface protein	Bacterial Ig-like|SCP-like extracellular	null	Yes	immunglob	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01571	null	1580710	1580471	79	5,01	8903	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	immunglob	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01572	null	1583457	1580716	913	6,4	93072	-	Conserved membrane protein	conserved hypothetical protein	Cell surface protein	Bacterial Ig-like	null	Yes	immunglob	IMP	tmhmm:7	-	-	-	-	-	-	-						
LC_01573	null	1593969	1583797	3390	4,98	322780	-	Putative protein without homology	predicted ORF	Cell surface anchor protein	Surface protein from Gram-positive cocci, anch	null	Yes	-	LPxTG	tmhmm:1	-	-	-	-	-	-	+						
LC_01574	null	1595738	1594728	336	6,44	38694	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-						
LC_01575	null	1596707	1595913	264	9,3	30724	-	N-formylglutamate amidohydrolase	N-formylglutamate amidohydrolase	N-formylglutamate deformylase (EC 3.5.1.68)	N-formylglutamate amidohydrolase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01576	folE	1597193	1596876	105	4,13	11817	-	GTP cyclohydrolase I	GTP cyclohydrolase I	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01577	ydbF	1597709	1597209	166	7,32	18262	-	Transcriptional regulator	transcriptional regulator, YbaK	Transcriptional regulator	Conserved hypothetical protein 11|YbaK/prolyl-t	S	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-						
LC_01578	apt	1598315	1597788	175	5,8	18867	-	Adenine phosphoribosyltransferase	adenine phosphoribosyltransferase (APRT)	Adenine phosphoribosyltransferase (EC 2.4.2.	Phosphoribosyltransferase|Purine/pyrimidine ph	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						
LC_01579	recJ	1600606	1598312	764	5,89	82778	-	Single-stranded-DNA-specific exonuclease R	single-stranded-DNA-specific exonuclease Rec	Single-stranded-DNA-specific exonuclease re	Phosphoesterase, RecJ-like|Phosphoesterase,	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+						

LC_01580	null	1600921	1601292	123	4,89	14267	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01581	null	1601500	1601976	158	4,29	17634	+	Conserved protein	cytoplasmic protein	Hypothetical protein	Protein of unknown function DUF984	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01582	null	1601982	1602200	72	10,35	8165	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_01583	lepA	1604229	1602391	612	4,84	68165	-	GTP-binding protein LepA	small GTP-binding protein domain:GTP-binding	GTP-binding protein lepA	Initiation factor 2	Translation elongation factor E	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01584	dnaJ	1605663	1604503	386	7,12	41467	-	Chaperone protein dnaJ	molecular chaperone protein DnaJ with C-termi	Chaperone protein dnaJ	DnaJ central region	Heat shock protein DnaJ, N	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01585	dnaK	1607635	1605776	619	4,57	67221	-	Chaperone protein dnaK	class I, chaperone protein dnaK (Heat shock pr	Chaperone protein dnaK	Heat shock protein Hsp70	Chaperone DnaK	He	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01586	grpE	1608258	1607665	197	5,18	21836	-	GrpE protein (HSP-70 Cofactor HSP20)	molecular chaperone heat shock protein GrpE (	GrpE protein	GrpE nucleotide exchange factor	GrpE nucleoti	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01587	hrcA	1609374	1608328	348	5,87	38499	-	Heat-inducible transcription repressor hrcA	heat-inducible transcription repressor hrcA	Heat-inducible transcription repressor hrcA	Bacterial regulatory protein, DeoR N-terminal	N	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01588	hemN	1610677	1609532	381	5,93	44001	-	Oxygen-independent coproporphyrinogen III o	coproporphyrinogen III oxidase, anaerobic	Oxygen-independent coproporphyrinogen-III o	Putative oxygen-independent coproporphyrinog	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01589	ribC2	1611626	1610679	315	9,84	34959	-	Riboflavin biosynthesis protein RibF	macrolide-efflux protein mreA/riboflavin biosynt	Riboflavin kinase (EC 2.7.1.26) / FMN adenyl	Riboflavin kinase / FAD synthetase	Rossmann-	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01590	truB	1612539	1611634	301	9,9	33156	-	tRNA pseudouridine synthase B	tRNA pseudouridine synthase B (Psi55 synthas	tRNA pseudouridine synthase B (EC 4.2.1.70	tRNA pseudouridine synthase B, N-terminal-2	t	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01591	terC	1613394	1612615	259	9,27	28683	-	Tellurium resistance protein	integral membrane protein, tellurium resistance	Tellurite resistance protein terC	Integral membrane protein TerC	P	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_01592	rbfA	1613903	1613544	119	9	13569	-	Ribosome-binding factor A	ribosome-binding factor A	Ribosome-binding factor A	Ribosome-binding factor A	KH, prokaryotic type	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01593	null	1614105	1613872	77	10,35	8328	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01594	null	1614494	1614273	73	11,7	7986	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:0	-	-	-	-	-	-	-
LC_01595	infB	1617234	1614445	929	10,23	102123	-	Translation initiation factor IF-2	Translation initiation factor IF-2	Bacterial Protein Translation Initiation Factor 2	Initiation factor 2	Protein synthesis factor, GTP-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01596	ylxQ	1617554	1617255	99	10,66	10760	-	Ribosomal protein L7A	Ribosomal protein HS6-type (S12/L30/L7a)	LSU ribosomal protein L7AE	Ribosomal protein L7Ae/L30e/S12e/Gadd45	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01597	nusA	1617850	1617557	97	10,48	10877	-	Nucleic-acid-binding protein implicated in tran	nucleic-acid-binding protein implicated in transc	Hypothetical cytosolic protein	Protein of unknown function DUF448	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01598	nusA	1619076	1617862	404	4,2	44760	-	Transcription elongation factor NusA	transcription elongation factor NusA	N utilization substance protein A	RNA binding S1	KH	KH, type 1	KH, prokaryotic	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01599	ylxS	1619572	1619093	159	4,76	17987	-	Conserved hypotehtical protein	conserved hypothetical protein (UPF0090)	Hypothetical cytosolic protein	Protein of unknown function DUF150	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01600	polC	1624160	1619826	1444	5,15	161535	-	DNA polymerase III alpha subunit	DNA polymerase III, epsilon subunit:DNA polyn	DNA polymerase III alpha subunit (EC 2.7.7.7	Polymerase and histidinol phosphatase, N-term	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01601	proS	1626012	1624282	576	5,19	64233	-	Prolyl-tRNA synthetase	prolyl-tRNA synthetase (proline--tRNA ligase)(F	Prolyl-tRNA synthetase (EC 6.1.1.15)	tRNA synthetase, class II (G, H, P and S)	Proly	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01602	eep	1627277	1626036	413	8,37	45282	-	Membrane-associated zinc metalloprotease	Zn-dependent metalloproease 1, membrane-ass	Membrane endopeptidase, M50 family	PDZ/DHR/GLGF	Multicopper oxidase, copper-t	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	protease	+
LC_01603	cdsA	1628082	1627294	262	9,51	28683	-	Phosphatidate cytidylyltransferase	phosphatidate cytidylyltransferase (CDP-diglyc	Phosphatidate cytidylyltransferase (EC 2.7.7.4	Phosphatidate cytidylyltransferase	I	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+
LC_01604	uppS	1628870	1628118	250	8,77	27915	-	Undecaprenyl pyrophosphate synthetase	Undecaprenyl pyrophosphate synthetase (UPP	Undecaprenyl pyrophosphate synthetase (EC	Di-trans-poly-cis-decaprenylcistransferase	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01605	null	1629228	1629052	58	8,78	6596	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_01606	frr	1629802	1629245	185	5,2	20593	-	Ribosome-recycling factor	Ribosome recycling factor (Ribosome-releasing	Ribosome Recycling Factor (RRF)	Ribosome recycling factor	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01607	smbA	1630521	1629802	239	6,29	25964	-	Uridylate kinase	uridylate kinase (Uridine monophosphate kinase	Uridylate kinase (EC 2.7.4.-)	Aspartate/glutamate/uridylate kinase	Uridylate k	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01608	tsf	1631771	1630890	293	4,72	31577	-	Protein Translation Elongation Factor Ts (EF-	Protein Translation Elongation Factor Ts (EF-T	Protein Translation Elongation Factor Ts (EF-	Ubiquitin-associated/Translation elongation fact	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01609	rpsB	1632644	1631856	262	4,99	29642	-	SSU/30S ribosomal protein S2P	SSU 30S ribosomal protein S2P (BS1) (Vegeta	SSU ribosomal protein S2P	Ribosomal protein S2	Ribosomal protein S2, ba	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01610	yazA	1633065	1632784	93	10,21	10715	-	GIY-YIG domain endonuclease	URI-like endonuclease	Hypothetical protein with endo/excinuclease d	Excinuclease ABC, C subunit, N-terminal	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01611	yabB	1633780	1633055	241	9,76	26401	-	Methyltransferase	O-methyltransferase-like protein	Methyltransferase (EC 2.1.1.-)	Methyltransferase small	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01612	plsC	1634002	1634652	216	10,13	24268	+	1-acyl-sn-glycerol-3-phosphate acyltransferas	1-acyl-sn-glycerol-3-phosphate acyltransferase	1-acyl-sn-glycerol-3-phosphate acyltransferas	Phospholipid/glycerol acyltransferase	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01613	yfnA	1634710	1636104	464	9,72	49699	+	Amino acid permease	IMP dehydrogenase/GMP reductase:Amino aci	Amino acid permease	Major intrinsic protein	Amino acid/polyamine tra	E	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	+
LC_01614	yejC	1636129	1636911	260	6,37	30041	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function DUF1003	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01615	mdlB	1638777	1636975	600	7,1	67790	-	ABC transporter, multidrug/protein/lipid transp	multidrug ABC transporter, ATPase/permease (	Multidrug/protein/lipid ABC transporter family,	ABC transporter, transmembrane region	ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01616	ynaD	1640524	1638767	585	7,33	65344	-	ABC transporter, ATPase component	multidrug ABC transporter, ATPase/permease (	Multidrug resistance ABC transporter ATP-bin	ABC transporter, transmembrane region	ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01617	null	1640936	1640715	73	10,97	8210	-	Putative protein without homology	conserved hypothetical protein	Hypothetical cytosolic protein	Protein of unknown function UPF0154	S	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_01618	ynzC	1641242	1640997	81	10,02	9740	-	Conserved cytosolic protein	conserved protein YnzC/ylaC	Hypothetical cytosolic protein	Protein of unknown function DUF896, bacterial	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01619	null	1641561	1641385	58	5,43	6764	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01620	rplS	1642237	1641890	115	11,65	13351	-	LSU/50S ribosomal protein L19P	ribosomal protein L19 (50S ribosomal protein L	LSU ribosomal protein L19P	Ribosomal protein L19	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01621	trmD	1643227	1642442	261	5,38	29809	-	tRNA (guanine-N(1)-)-methyltransferase	tRNA-(guanine-N1)-methyltransferase	tRNA (Guanine-N(1)-)-methyltransferase (EC	tRNA (guanine-N1-)-methyltransferase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01622	rimM	1643735	1643217	172	5,66	19192	-	16S rRNA processing protein rimM	16S rRNA processing protein RimM	16S rRNA processing protein rimM	RimM protein	PRC-barrel	PRC-barrel-like	16S r	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01623	ylqC	1644015	1643803	70	9,63	7680	-	RNA-binding protein, KH domain	RNA-binding protein, KH domain	RNA binding protein	no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01624	rpsP	1644344	1644069	91	10,87	10521	-	SSU/30S ribosomal protein S16P	SSU ribosomal protein S16P	SSU ribosomal protein S16P	Ribosomal protein S16	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01625	ffh	1645876	1644440	478	10,23	52965	-	Signal recognition particle protein	signal recognition particle subunit FFH/SRP54 (	SIGNAL RECOGNITION PARTICLE, SUBUI	GTP-binding signal recognition particle SRP54, T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01626	null	1646230	1645889	113	4,58	13186	-	Conserved protein	helix-turn-helix protein, YlxM/p13 family	Signal recognition particle associated protein	Putative helix-turn-helix protein, YlxM/p13-like\M	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01627	null	1646385	1646552	55	8,83	6125	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01628	null	1646636	1646827	63	4,22	6920	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01629	null	1646894	1647208	104	8,45	12033	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_01630	ftsY	1648275	1647280	331	4,62	36199	-	cell division protein, signal recognition particle	cell division protein, signal recognition particle ((	Cell division protein ftsY	GTP-binding signal recognition particle SRP54, U	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01631	smc	1651829	1648275	1184	6,66	130058	-	Chromosome partition protein smc	chromosome segregation SMC protein homolg	Chromosome partition protein smc	SMC protein, N-terminal	ABC transporter relate	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01632	rnc	1652544	1651849	231	5,88	25959	-	Ribonuclease III	dsRNA-specific ribonuclease 3 (Ribonuclease I	Ribonuclease III (EC 3.1.26.3)	Ribonuclease III	Double-stranded RNA binding		null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01633	oppA	1654439	1652646	597	9,91	66490	-	ABC transporter, oligopeptide-binding protein	oligopeptide ABC transporter, periplasmic comp	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	C	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_01634	oppC	1655540	1654629	303	8,75	33133	-	ABC transporter, oligopeptide transporter pern	dipeptide/oligopeptide/nickel ABC transporter, p	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	EP	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01635	oppB	1656519	1655557	320	10,03	35583	-	ABC transporter, oligopeptide transporter pern	dipeptide/oligopeptide/nickel ABC transporter, p	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	C	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_01636	oppF	1657472	1656519	317	8,39	36372	-	ABC transporter, oligopeptide transporter ATP	oligopeptide ABC transporter, ATPase compon	Oligopeptide transport ATP-binding protein op	Glycoside hydrolase, chitinase active site\ABC t	EP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01637	oppD	1658497	1657475	340	4,79	37931	-	ABC transporter, oligopeptide transporter ATP	dipeptide/oligopeptide/nickel ABC transporter, A	Oligopeptide transport ATP-binding protein op	ABC transporter related\AAA+ ATPase, core\OI	EP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01638	null	1658590	1658754	54	10,4	6155	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01639	acpP	1659029	1658787	80	3,8	9055	-	Acyl carrier protein	Acyl carrier protein (ACP) (Cytosolic-activating	Acyl carrier protein	Acyl carrier protein (ACP)	Phosphopantetheine-	IQ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01640	plsX	1660108	1659083	341	7,42	36063	-	Fatty acid/phospholipid synthesis protein plsX	Fatty acid/phospholipid synthesis protein plsX	Fatty acid/phospholipid synthesis protein plsX	Fatty acid synthesis plsX protein\Phospholipid t	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01641	recG	1662171	1660132	679	9,26	75011	-	ATP-dependent DNA helicase RecG	ATP-dependent DNA helicase recG, transcripti	ATP-dependent DNA helicase recG (EC 3.6.1	Helicase, C-terminal\ATP-dependent DNA helic	LK	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01642	prfC	1663960	1662284	558	4,66	59429	-	Dihydroxyacetone kinase(DAK2) related enzyr	dihydroxyacetone kinase related enzyme, DAK2	Dihydroxyacetone kinase family protein	Dak phosphatase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01643	asp	1664383	1664021	120	9,42	13031	-	Alkaline shock protein, general stress protein (	similar to alkaline-shock protein homolog yloU /	General stress protein, Gls24 family	Protein of unknown function DUF322	S	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_01644	rpmB	1664794	1664609	61	12,74	6949	-	LSU/50S ribosomal protein L28P	ribosomal protein L28 (50S ribosomal protein L	LSU ribosomal protein L28P	Ribosomal protein L28	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01645	thiN	1665617	1664949	222	5,26	24608	-	Thiamine pyrophosphokinase	thiamine pyrophosphokinase	Thiamin pyrophosphokinase (EC 2.7.6.2)	Thiamine pyrophosphokinase	Thiamin pyrophos	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01646	rpe	1666264	1665614	216	4,72	22745	-	Ribulose-phosphate 3-epimerase	D-ribulose-5-phosphate 3-epimerase (EC 5.1.3.	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Ribulose-phosphate 3-epimerase\Ribulose-pho	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01647	engC	1667197	1666292	301	6,95	33086	-	GTPase	ribosome-associated GTPase engC protein 1 Y	GTPase (EC 3.6.1.-)	GTPase EngC\EngC GTPase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01648	pkn1	1669194	1667194	666	7,19	72617	-	Serine/threonine protein kinase	serine/threonine protein kinase with beta-lactam	Serine/threonine protein kinase (EC 2.7.11.1)	Protein kinase\Tyrosine protein kinase\Serine/th	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+

LC_01649	pppL	1669934	1669191	247	4,56	27335	-	Serine/threonine protein phosphatase	serine/threonine protein phosphatase family pro	Protein phosphatase 2C (EC 3.1.3.16)	Protein phosphatase 2C-related	Protein phosph	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01650	sunL	1671284	1669944	446	9,18	48836	-	tRNA and rRNA cytosine-C5-methyltransferas	tRNA and rRNA cytosine-C5-methylases (sun (	16S rRNA m(5)C 967 methyltransferase (EC :	Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01651	fmt	1672227	1671271	318	9,19	34256	-	Methionyl-tRNA formyltransferase	methionyl-tRNA formyltransferase FMT	Methionyl-tRNA formyltransferase (EC 2.1.2.9	Formyl transferase, N-terminal	Formyl transfera	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01652	priA	1674703	1672286	805	8,78	90039	-	Primosomal protein N'	Primosomal protein N' (replication factor Y) - su	Primosomal protein N'	Helicase, C-terminal	Primosomal protein n	DEA	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01653	dfp	1675907	1674708	399	9,89	42432	-	Phosphopantothenoylcysteine decarboxylase/	Phosphopantothenate-cysteine ligase / Phosph	Phosphopantothenoylcysteine decarboxylase (	Flavoprotein	Bifunctional phosphopantothenoylc	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01654	rpoZ	1676339	1676097	80	5,74	8912	-	DNA-directed RNA polymerase subunit omeg	DNA-directed RNA polymerase, subunit K/ome	DNA-directed RNA polymerase omega chain (	RNA polymerase, omega subunit	RNA polymer	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01655	gmk	1677024	1676398	208	6,96	23795	-	Guanylate kinase	guanylate kinase (GMP kinase)	Guanylate kinase (EC 2.7.4.8)	Guanylate kinase	Guanylate kinase/L-type calci	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01656	null	1677774	1677091	227	10,91	24396	-	Esterase of the alpha-beta hydrolase superfan	esterase of the alpha-beta hydrolase superfamil	Patatin-like phospholipase	Patatin	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01657	null	1677902	1678204	100	10,03	11694	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01658	recN	1680052	1678349	567	4,92	62752	-	DNA repair protein RecN	DNA repair ATPase recN (Recombination prote	DNA repair protein recN	SMC protein, N-terminal	DNA repair protein Re	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01659	argR	1680509	1680057	150	6,54	16879	-	Arginine repressor	arginine repressor, ArgR	Arginine repressor, argR	Arginine repressor	Winged helix repressor DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01660	tlyA	1681443	1680613	276	9,82	30271	-	Ribosomal RNA methyltransferase, hemolysin	rRNA methylase, hemolysin A homolog	Cell adhesion protein (contact hemolysin TlyA	Ribosomal RNA methyltransferase RrmJ/FtsJ	F	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01661	crtE	1682291	1681440	283	4,42	29759	-	Geranyltranstransferase	polyprenyl synthetase / geranylgeranyl pyrophos	Dimethylallyltransferase (EC 2.5.1.1) / Gerany	Polyprenyl synthetase	Terpenoid synthase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01662	xseB	1682515	1682288	75	4,13	8334	-	Exodeoxyribonuclease VII small subunit	Exodeoxyribonuclease 7 small subunit (Exodeo	Exodeoxyribonuclease VII small subunit (EC 3	Exonuclease VII, small subunit	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01663	xseA	1683857	1682508	449	9,94	50114	-	Exodeoxyribonuclease VII large subunit	Exodeoxyribonuclease 7 large subunit (Exodeo	Exodeoxyribonuclease VII large subunit (EC 3	Exonuclease VII, large subunit	Nucleic acid bin	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01664	folD	1684701	1683850	283	6,37	29916	-	Methylenetetrahydrofolate dehydrogenase/met	bifunctional enzyme: methylenetetrahydrofolate	Methylenetetrahydrofolate dehydrogenase (NA	Tetrahydrofolate dehydrogenase/cyclohydrolase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01665	nusB	1685232	1684825	135	4,96	14786	-	N utilization substance protein B homolog	transcription antitermination protein NusB, utiliz	N utilization substance protein B	NusB/RsmB/TIM44	NusB antitermination factor	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01666	asp3	1685698	1685234	154	3,76	16700	-	Alkaline shock protein, Gls24 family	alkaline shock protein, general stress protein, G	General stress protein, Gls24 family	Protein of unknown function DUF322	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01667	null	1686040	1685717	107	4,42	11862	-	Translation elongation factor P	translation elongation factor P (EF-P)	Protein Translation Elongation Factor P (EF-P	Translation elongation factor P/YeiP, central	Nu	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01668	null	1686278	1686015	87	5,85	9950	-	Elongation factor P	elongation factor P	not_predicted_by_ERGO	Translation elongation factor P/YeiP, central	Tra	J	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01669	pepQ-1	1687618	1686551	355	5,09	38792	-	Xaa-Pro dipeptidase	proline dipeptidase, Xaa-Pro dipeptidase	Xaa-Pro dipeptidase (EC 3.4.13.9)	Creatinase	Peptidase M24, catalytic core	Peptic	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01670	rpmA	1687984	1687694	96	11,25	10382	-	LSU/50S ribosomal protein L27P	LSU 50S ribosomal protein L27P (BL30) (BL24	LSU ribosomal protein L27P	Ribosomal protein L27	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01671	null	1688353	1688003	116	4,84	12585	-	Ribosomal protein	ribosomal protein	hypothetical ribosome-associated protein	Protein of unknown function DUF464	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01672	rplU	1688676	1688365	103	10,01	11307	-	LSU/50S ribosomal protein L21P	LSU ribosomal protein L21P	LSU ribosomal protein L21P	Ribosomal protein L21	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01673	null	1689166	1688927	79	7,34	8787	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_01674	null	1689615	1689493	40	10,57	4628	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01675	null	1689902	1690180	92	10,06	10601	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_01676	null	1690140	1690346	68	10,83	7500	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01677	null	1690526	1691122	198	10,12	22159	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01678	null	1693121	1691487	544	8,93	60555	-	ABC transporter, ATPase and permease com	drug efflux ABC transporter, ATPase/permease	ABC transporter ATP-binding protein	ABC transporter related	AAA+ ATPase, core	AA	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_01679	pepX	1695578	1693185	797	6,61	87996	-	Xaa-Pro dipeptidyl-peptidase	Xaa-Pro dipeptidyl-peptidase (X-Pro dipeptidyl-(	Xaa-Pro dipeptidyl-peptidase (EC 3.4.14.11)	Peptidase S15	Aminoacyl-tRNA synthetase, cla	C	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_01680	glnA	1697344	1696004	446	5,73	50430	-	Glutamine synthetase	glutamate--ammonia ligase (glutamine synthetas	Glutamine synthetase (EC 6.3.1.2)	Glutamine synthetase type I	Glutamine synthetas	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01681	glnR	1697725	1697363	120	9,01	13762	-	Transcriptional regulator, MerR family	transcriptional regulator, MerR/GlnR	Transcriptional regulator, MerR family	Bacterial regulatory protein, MerR	Putative DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01682	speF	1698036	1699160	374	5,81	40438	+	Ornithine decarboxylase, inducible	ornithine decarboxylase	Ornithine decarboxylase (EC 4.1.1.17)	Orn/Lys/Arg decarboxylase, major region	CheY-	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01683	null	1699228	1700130	300	8,92	32951	+	Arginine/lysine/ornithine decarboxylases	predicted ORF	not_predicted_by_ERGO	Orn/Lys/Arg decarboxylase, major region	Orn/L	E	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01684	Alu-2	1701506	1700244	420	4,57	44952	-	Aluminum resistance protein	cystathionine beta-lyase family protein involved i	Aluminum resistance protein	Aluminium resistance	Pyridoxal phosphate-dep	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01685	miaA	1702449	1701490	319	8,42	35749	-	tRNA delta(2)-isopentenylpyrophosphate trans	tRNA delta(2)-isopentenylpyrophosphate transfe	tRNA delta(2)-isopentenylpyrophosphate trans	tRNA isopentenyltransferase	Isopentenyl transf	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01686	null	1702518	1702697	59	11,16	6730	+	Conserved extracellular protein	exported protein	hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_01687	yqhL	1703179	1702778	133	10,39	15726	-	Rhodanese-like domain protein	rhodanese related sulfurtransferase-like protein	Rhodanese-related sulfurtransferases	Rhodanese-like	P	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01688	glk	1704163	1703201	320	4,48	33561	-	Glucokinase	glucokinase (Glucose kinase), ROK family	Glucokinase (EC 2.7.1.2)	ROK	Glucokinase ROK	KG	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01689	null	1704410	1704156	84	6,63	10039	-	Conserved cytosolic protein	yqqQ-related protein	Hypothetical cytosolic protein	Protein of unknown function DUF910, bacterial	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01690	null	1705096	1704407	229	10,54	24821	-	Membrane-associated serine protease	membrane-associated serine protease	Integral membrane protein (Rhomboid family)	Peptidase S54, rhomboid	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	protease	-	
LC_01691	pbp2B2	1707406	1705280	708	9,56	77432	-	Cell division protein/penicillin-binding protein 2	Cell division protein FtsI/penicillin-binding protei	Penicillin-binding protein	Penicillin-binding protein, transpeptidase	Amino	M	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	protease	+	
LC_01692	null	1707553	1710177	874	9,97	97762	+	Conserved membrane protein	conserved hypothetical protein (integral membr	Integral membrane protein	no annotation	null	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-	
LC_01693	yneR	1710562	1710263	99	4,54	11418	-	HesB/YadR/YfhF-family protein	HesB/YadR/YfhF/YneR-family protein	HesB/YadR/YfhF family protein	HesB/YadR/YfhF	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01694	RR	1711208	1710543	221	4,79	24616	-	Two-component response regulator	DNA-binding response regulator, CitB family (R	Two-component response regulator yvqC	Bacterial regulatory protein, LuxR	Response reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_01695	hk	1712265	1711201	354	10,37	39691	-	Two component sensor transduction histidine	ATP-binding region, ATPase-like:two-componer	Two-component sensor protein yvqE (EC 2.7.:	ATP-binding region, ATPase-like	Histidine kina	T	Yes	-	Cterm	tmhmm:2	-	-	-	HPK(bile)	-	-	+	
LC_01696	null	1712966	1712262	234	9,96	26308	-	Conserved membrane protein	conserved hypothetical protein	Transporter yvqF	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_01697	greA	1713713	1713243	156	4,52	17155	-	Transcription elongation factor greA	Transcription elongation factor GreA (Transcrip	Transcription elongation factor greA	Transcription elongation factor, GreA/GreB regi	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01698	udk	1714316	1713780	178	7,32	20915	-	Uridine kinase	uridine kinase (Uridine monophosphokinase) (C	Uridine kinase (EC 2.7.1.48)	Uridine kinase	Phosphoribulokinase/uridine kina	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01699	yrrL	1715792	1714641	383	10,11	42138	-	Aminodeoxychorismate lyase	aminodeoxychorismate lyase family	Aminodeoxychorismate lyase family protein	Aminodeoxychorismate lyase	R	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01700	pheT	1718427	1716016	803	5,01	88022	-	Phenylalanyl-tRNA synthetase, beta subunit	phenylalanyl-tRNA synthetase beta subunit	Phenylalanyl-tRNA synthetase beta chain (EC	t-RNA-binding region	Bacterial phenylalanyl-tRI	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01701	pheS	1719475	1718429	348	5,27	39311	-	Phenylalanyl-tRNA synthetase, alpha subunit	phenylalanyl-tRNA synthetase alpha chain (phe	Phenylalanyl-tRNA synthetase alpha chain (E	Aminoacyl-tRNA synthetase, class I	Phenylalan	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01702	yodB	1720302	1719916	128	6,1	14350	-	Transcriptional regulator, HxlR family	transcriptional regulator, HxlR family	Transcriptional regulator, MarR family	Helix-turn-helix, HxlR type	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01703	null	1721104	1720694	136	10,08	16052	-	Hydrolase of the HAD superfamily	conserved hypothetical protein (HD-domain pro	Hydrolase (HAD superfamily)	Metal-dependent phosphohydrolase, HD region	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01704	spoU	1721949	1721188	253	9,13	27549	-	rRNA methyltransferase	rRNA methylases	23S rRNA methyltransferase (EC 2.1.1.-)	tRNA/rRNA methyltransferase, SpoU	RNA 2-O	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01705	null	1722098	1721895	67	12,62	7794	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01706	null	1722268	1722549	93	10,28	10091	+	Acylphosphatase	acylphosphatase	Acylphosphatase (EC 3.6.1.7)	Acylphosphatase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01707	oxaA1	1722608	1723600	330	10,08	36542	+	Preprotein translocase subunit YidC	preprotein translocase subunit YidC	60 kDa inner membrane protein YIDC	60 kDa inner membrane insertion protein	U	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_01708	hpk5	1725401	1723818	527	6,64	58762	-	Two component sensor transduction histidine	integral membrane sensor signal transduction h	Two component system histidine kinase (EC 2	ATP-binding region, ATPase-like	Histidine kina	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	+	
LC_01709	rrp5	1726087	1725401	228	5,09	26319	-	Two-component response regulator	DNA-binding response regulator, OmpR family	Response regulator CsrR	Response regulator receiver	Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR(bile)	regulator	-	+	
LC_01710	gndA	1727824	1726436	462	5,14	51011	-	6-phosphogluconate dehydrogenase, decarbo	6-phosphogluconate dehydrogenase, decarbox	6-phosphogluconate dehydrogenase (EC 1.1.1.:	6-phosphogluconate dehydrogenase, decarboxy	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01711	null	1728641	1728093	182	3,85	20504	-	Metal-binding, possibly nucleic acid-binding pr	metal-binding, possibly nucleic acid-binding pro	Hypothetical cytosolic protein	Protein of unknown function DUF177	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01712	null	1729837	1728701	378	9,97	41796	-	Nucleotidyltransferase	nucleotidyltransferase	Hypothetical cytosolic protein	Protein of unknown function DUF795	R	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	+	
LC_01713	yccK	1730619	1729882	245	4,18	28265	-	Methyltransferase	SAM-dependent methyltransferases	Methyltransferase (EC 2.1.1.-)	Methyltransferase type 12	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01714	yqeL	1730975	1730616	119	4,25	13554	-	Iojap-related protein	Iojap-related protein precursor	iojap protein family	Iojap-related protein	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01715	yqeK	1731578	1730979	199	6,4	22678	-	Hydrolase of the HAD superfamily	NAD metabolism hydrolase of HD superfamily	Hydrolase (HAD superfamily)	Metal-dependent phosphohydrolase, HD region	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01716	nadD	1732125	1731571	184	6,63	20905	-	Nicotinate-nucleotide adenylyltransferase	nicotinate-nucleotide adenylyltransferase (Dear	Nicotinate-nucleotide adenylyltransferase (EC	Cytidyltyltransferase	Cytidyltransferase-related	F	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01717	yccF	1732541	1732230	103	10,01	11229	-	RNA-binding protein	RNA-binding protein, KH domain	RNA binding protein (CRS1/YhbY family)	CRS1/YhbY	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_01718	yqeH	1733751	1732627	374	7,99	41343	-	GTP-binding protein	GTP-binding protein, HSR1-related	GTP-binding protein	GTP-binding protein, HSR1-related	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01719	yqeG	1734268	1733735	177	10,47	19781	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)	Haloacid dehalogenase-like hydrolase|HAD-sup	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01720	null	1734778	1735677	299	5,35	33416	+	Glyoxalase family protein	glyoxalase / lactoylglutathione lyase related lyas	Glyoxalase family protein	Glyoxalase/bleomycin resistance protein/dioxyg	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01721	yaiA	1735670	1736638	322	4,98	36431	+	Glyoxalase/bleomycin resistance protein/dioxy	glyoxalase / lactoylglutathione lyase related lyas	Glyoxalase family protein	Glyoxalase/bleomycin resistance protein/dioxyg	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01722	yahD	1736654	1737295	213	5,07	24176	+	Phospholipase/Carboxylesterase	similar to phospholipase/carboxylesterase famil	Carboxylesterase (EC 3.1.1.1)	Phospholipase/Carboxylesterase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01723	null	1737301	1738269	322	6,93	34841	+	NADPH:quinone reductase related Zn-depend	NADPH:quinone reductase related Zn-depende	Quinone oxidoreductase (EC 1.6.5.5)	Alcohol dehydrogenase superfamily, zinc-conta	CR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01724	fas6	1738345	1738908	187	5,72	20037	+	Lysine decarboxylase protein	lysine decarboxylase / Rossmann fold nucleotid	Lysine decarboxylase family	Conserved hypothetical protein 730	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01725	rplT	1739352	1738996	118	12,01	13464	-	LSU/50S ribosomal protein L20P	LSU ribosomal protein L20P	LSU ribosomal protein L20P	Ribosomal protein L20, bacterial and organelle l	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01726	rpmI	1739587	1739387	66	12,83	7778	-	LSU/50S ribosomal protein L35P	ribosomal protein L35 (50S ribosomal protein L	LSU ribosomal protein L35P	Ribosomal protein L35	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01727	infC	1740133	1739669	154	10,84	17292	-	Translation initiation factor IF-3	translation bacterial initiation factor IF-3 infC	Bacterial Protein Translation Initiation Factor 3	Initiation factor 3	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01728	sp5k	1743224	1740666	852	4,66	93327	-	Stage V sporulation protein K	stage V sporulation protein K	not_predicted_by_ERGO	CbxX/CfqX|AAA+ ATPase, core|AAA ATPase,	O	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01729	null	1743854	1743297	185	10,85	20526	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_01730	null	1744838	1744101	245	9,77	27774	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01731	null	1745047	1744907	46	12,33	5071	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01732	null	1745937	1745242	231	4,51	25715	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01733	null	1746319	1745930	129	10,27	14830	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_01734	thrS	1748460	1746487	657	5,13	74840	-	Threonyl-tRNA synthetase	threonyl-tRNA synthetase / Ser-tRNA(Thr) hydr	Threonyl-tRNA synthetase (EC 6.1.1.3)	tRNA synthetase, class II (G, H, P and S)|Thre	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01735	dnaI	1749932	1748997	311	5,54	34533	-	Primosomal protein DnaI	Primosomal protein DnaI (Helicase loader)	Primosomal protein dnaI	Primosomal DnaI, N-terminal	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01736	null	1751278	1749932	448	9,69	50745	-	Replication initiation/membrane attachment pr	chromosome replication initiation / membrane a	Replication initiation and membrane attachmer	Replication initiation and membrane attachment	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01737	nrdR	1751821	1751354	155	9,28	18035	-	Transcriptional repressor nrdR	transcriptional regulator, consists of a Zn-ribbor	Putative regulatory protein	Ribonucleotide reductase regulator NrdR-like|A	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01738	coaE	1752478	1751876	200	8,94	21166	-	Dephospho-CoA kinase	dephospho-CoA kinase (dephosphocoenzyme /	Dephospho-CoA kinase (EC 2.7.1.24)	Dephospho-CoA kinase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01739	mutM	1753323	1752475	282	9,65	31503	-	Formamidopyrimidine-DNA glycosylase	formamidopyrimidine-DNA glycosylase/DNA-(a	Formamidopyrimidine-DNA glycosylase (EC 3	Formamidopyrimidine-DNA glycolase|Formamic	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01740	null	1753908	1753333	191	9,19	21793	-	DNA-directed DNA polymerase	DNA polymerase I	not_predicted_by_ERGO	DNA-directed DNA polymerase|DNA polymeras	L	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01741	polA	1755977	1753905	690	6,04	77577	-	DNA polymerase I	DNA polymerase I	DNA polymerase I (EC 2.7.7.7)	DNA-directed DNA polymerase|5'-3' exonuclea	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01742	null	1757254	1756544	236	9,78	25593	-	Integral membrane protein, interacts with FtsH	integral membrane protein, interacts with FtsH	Integral membrane protein	Protein of unknown function UPF0005	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_01743	yqbJ	1759151	1758096	351	10,1	38462	-	Cell surface protein	conserved hypothetical protein (cell-surface/sec	Hypothetical protein	Protein of unknown function DUF916, cell surfa	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-	
LC_01744	null	1759504	1759166	112	10,42	12384	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_01745	null	1760326	1759538	262	7,65	27766	-	Cell surface protein	predicted ORF	Hypothetical secreted protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	-	
LC_01746	null	1763864	1760358	1168	8,98	129503	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_01747	null	1765758	1764301	485	9,49	55420	-	Transcriptional regulator	predicted ORF	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_01748	murC1	1767457	1766147	436	6,65	48827	-	UDP-N-acetylmuramate--L-alanine ligase	UDP-N-acetylmuramate--L-alanine ligase (UDP	UDP-N-acetylmuramate--alanine ligase (EC 6	Cytoplasmic peptidoglycan synthetase, N-termi	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01749	null	1767654	1767457	65	7,77	7332	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	D	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01750	null	1769873	1767654	739	8,64	79056	-	Cell division protein, DNA segregation ATPase	cell division protein ftsK	Cell division protein ftsK	Cell divisionFtsK/SpoIIIE|AAA+ ATPase, core	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01751	null	1770179	1770430	83	8,21	9428	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_01752	pheT	1771512	1770541	323	4,51	35057	-	tRNA binding domain protein	tRNA binding domain protein	tRNA binding domain protein	t-RNA-binding region|Thioredoxin-related|Thior	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01753	null	1771795	1772133	112	11,94	12749	+	Conserved secreted protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-	
LC_01754	trmB	1772847	1772203	214	8,42	24775	-	tRNA (guanine-N(7)-)-methyltransferase	S-adenosylmethionine-dependent tRNA (guanir	tRNA (m(7)G46) methyltransferase (EC 2.1.1.	Putative methyltransferase|Conserved hypothet	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01755	ytmP	1773752	1772979	257	7,14	29353	-	Aminoglycoside phosphotransferase family pr	aminoglycoside phosphotransferase family prot	Phosphotransferase enzyme family	Aminoglycoside phosphotransferase|Protein kin	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01756	null	1774070	1773855	71	10,73	7506	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01757	null	1774813	1774241	190	10,12	22155	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Bacterial ABC transporter EcsB	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_01758	null	1775454	1774894	186	10,24	21403	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Bacterial ABC transporter EcsB	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_01759	ecsA	1776131	1775451	226	5,66	25092	-	ABC transporter, ATPase component	multidrug ABC transporter, ATPase component	ABC-type transporter ATP-binding protein ecs	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01760	hit	1776281	1776709	142	6,88	15921	+	HIT family protein	diadenosine tetraphosphate (Ap4A) hydrolase n	Adenosine 5'-monophosphoramidase	Histidine triad (HIT) protein	FGR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01761	null	1776712	1777071	119	6,53	12830	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	NT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01762	prtM	1777219	1778121	300	10,27	33547	+	Peptidylprolyl cis-trans isomerase PrsA1	parvulin-like peptidyl-prolyl isomerase / export p	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8	Peptidyl-prolyl cis-trans isomerase, PpiC-type	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_01763	cbf	1779564	1778596	322	6,68	36420	-	CMP-binding factor	hydrolase, HD-superfamily / Cmp-binding-facto	CMP-binding factor	Metal-dependent phosphohydrolase, HD region	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01764	null	1779611	1779775	54	11,01	6240	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01765	null	1780225	1779878	115	4,37	13303	-	Conserved protein	conserved hypothetical protein (UPF0342-prote	Hypothetical cytosolic protein	Protein of unknown function DUF964	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01766	pbp2A	1782289	1780247	680	9,59	74791	-	Membrane carboxypeptidase, penicillin-binding	membrane carboxypeptidase, penicillin-binding	Multimodular transpeptidase-transglycosylase	Glycosyl transferase, family 51|Penicillin-bindin	M	Yes	-	Sec	tmhmm:1	-	-	-	-	-	protease	+	
LC_01767	rluA1	1782401	1783237	278	9,52	31283	+	Ribosomal large subunit 23S pseudouridine s	ribosomal large subunit pseudouridine synthase	Ribosomal large subunit pseudouridine syntha	Pseudouridine synthase|Pseudouridine synthas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01768	argR1	1783820	1783365	151	5,81	16878	-	Arginine repressor	arginine repressor argR (AHRC)	Arginine repressor, argR	Arginine repressor|Winged helix repressor DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01769	argS	1785718	1784036	560	5,97	62438	-	Arginyl-tRNA synthetase	arginyl-tRNA synthetase (arginine-tRNA ligase)	Arginyl-tRNA synthetase (EC 6.1.1.19)	Legume lectin, beta domain|Arginyl-tRNA synth	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01770	null	1786174	1786560	128	6,34	14358	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01771	null	1786573	1786755	60	12,22	6545	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_01772	URA1	1786921	1787862	313	4,84	34083	+	Dihydroorotate dehydrogenase	dihydroorotate dehydrogenase 1A	Dihydroorotate dehydrogenase (EC 1.3.3.1)	Dihydroorotate dehydrogenase, core|Dihydroorc	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01773	glpQ4	1787859	1789676	605	8,55	68231	+	Glycerophosphodiester phosphodiesterase	membrane domain of membrane-anchored glyc	Hypothetical protein / Glycerophosphodiester p	Glycerophosphoryl diester phosphodiesterase	C	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_01774	mecA	1790443	1789760	227	4,17	25546	-	Adapter protein mecA	adaptor protein	Negative regulator of genetic competence mec	Negative regulator of genetic competence	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01775	spxA	1791123	1790725	132	8,72	15320	-	Arsenate reductase family protein	arsenate reductase related protein, glutaredoxin	Arsenate reductase family protein	Conserved hypothetical protein, ArsC related|Ar	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01776	yhfI	1792111	1791374	245	6,22	26645	-	Metal-dependent hydrolase	metal-dependent hydrolase of the beta-lactamas	Metal-dependent hydrolase (EC 3.-.-.-)	Beta-lactamase-like	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01777	null	1792180	1792683	167	6,63	18972	+	Monooxygenase	monooxygenase	Monooxygenase (EC 1.14.13.-)	Dimeric alpha-beta barrel	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01778	null	1794932	1792857	691	10,75	77328	-	ABC transporter, antimicrobial peptide transpo	antimicrobial peptide ABC transport system, pe	ABC transporter permease protein	Protein of unknown function DUF214, permase	V	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+	
LC_01779	yxdL	1795686	1794916	256	7,33	28370	-	ABC transporter, ATPase component	efflux antimicrobial peptide ABC transporter, AT	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01780	rrp1	1796153	1796827	224	5,37	26018	+	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator ytsA	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_01781	hpk1	1796837	1797940	367	6,9	41556	+	Two component sensor transduction histidine	integral membrane sensor signal transduction h	Sensory transduction protein kinase (EC 2.7.3	ATP-binding region, ATPase-like|Histidine kina	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	+	
LC_01782	nrdG	1798669	1798091	192	7,05	22062	-	Anaerobic ribonucleoside-triphosphate reducta	anaerobic ribonucleoside-triphosphate reductas	Anaerobic ribonucleoside-triphosphate reducta	Radical SAM|Ribonucleoside-triphosphate redu	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01783	atkB	1801118	1798890	742	6,2	79709	-	Copper-translocating P-type ATPase	ATPase E1-E2 type:Copper-translocating P-typ	Copper-silver efflux ATPase (EC 3.6.3.-)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_01784	copR	1801548	1801102	148	7,97	16207	-	Transcriptional regulator	negative transcriptional regulator, CopY	CopAB ATPases metal-fist type repressor	Penicillinase repressor|Winged helix repressor	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01785	purD	1803006	1801765	413	5,86	44387	-	Phosphoribosylamine--glycine ligase	phosphoribosylamine-glycine ligase (GARS) (gl	Phosphoribosylamine--glycine ligase (EC 6.3.4	Phosphoribosylglycinamide synthetase|Rudimer	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01786	purH	1804694	1803171	507	5,32	54620	-	Bifunctional purine biosynthesis protein purH	bifunctional protein: phosphoribosylaminoimida	Phosphoribosylaminoimidazolecarboxamide fo	AICARFT/IMPCHase bienzyme|MGS-like|AICA	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_01787	purN	1805264	1804695	189	6,63	20279	-	Phosphoribosylglycinamide formyltransferase	folate-dependent phosphoribosylglycinamide for	Phosphoribosylglycinamide formyltransferase	Phosphoribosylglycinamide formyltransferase, ε	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01788	null	1805881	1805261	206	6,6	22083	-	Phosphoribosylformylglycinamidine cyclo-ligas	predicted ORF	Phosphoribosylformylglycinamidine cyclo-ligas	AIR synthase related protein	AIR synthase relat	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01789	null	1806272	1805859	137	4,35	14279	-	Putative protein without homology	phosphoribosylaminoimidazole synthetase	not_predicted_by_ERGO	AIR synthase related protein	F	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01790	purF	1807723	1806269	484	6,3	52311	-	Amidophosphoribosyltransferase	amidophosphoribosyltransferase precursor (glu	Amidophosphoribosyltransferase (EC 2.4.2.14	Glutamine amidotransferase, class-II	Phosphor	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01791	purL	1809915	1807699	738	4,47	79115	-	Phosphoribosylformylglycinamidine synthase I	phosphoribosylformylglycinamidine synthase 2 (	Phosphoribosylformylglycinamidine synthase (	AIR synthase related protein	Phosphoribosylfor	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01792	purL	1810588	1809902	228	4,58	24369	-	Phosphoribosylformylglycinamidine synthase I	phosphoribosylformylglycinamidine (FGAM) syr	Phosphoribosylformylglycinamidine synthase (	Phosphoribosylformylglycinamidine synthase I(	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01793	purS	1810845	1810585	86	4,64	9997	-	Phosphoribosylformylglycinamidine synthase,	phosphoribosylformylglycinamidine (FGAM) syr	Phosphoribosylformylglycinamidine synthase,	Phosphoribosylformylglycinamidine synthetase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01794	purC	1811563	1810838	241	6,26	27099	-	Phosphoribosylaminoimidazole-succinocarbox	Phosphoribosylaminoimidazole-succinocarboxa	Phosphoribosylamidoimidazole-succinocarbox	SAICAR synthetase	ATP-grasp fold, subdomai	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01795	purK1	1812675	1811560	371	6,15	40569	-	Phosphoribosylaminoimidazole carboxylase, A	phosphoribosylaminoimidazole carboxylase ATF	Phosphoribosylaminoimidazole carboxylase N(	ATP-grasp fold, ATP-dependent carboxylate-an	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01796	purE	1813156	1812668	162	6,08	16782	-	Phosphoribosylaminoimidazole carboxylase, c	phosphoribosylaminoimidazole carboxylase/mut	Phosphoribosylaminoimidazole carboxylase ca	1-(5-Phosphoribosyl)-5-amino-4-imidazole-carb	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01797	null	1814000	1813395	201	10,37	21280	-	Proton-coupled thiamine transporter	proton-coupled thiamine transporter (YuaJ)	Thiamine transporter	Thiamine transporter YuaJ	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	-				
LC_01798	null	1814399	1814178	73	13,03	8632	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01799	iolT	1816075	1814660	471	11,65	50873	-	Transporter, major facilitator superfamily MFS	sugar transporter, D-xylose proton-symporter, I	Sugar transporter	Sugar transporter	General substrate transporter	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	-				
LC_01800	null	1816587	1816312	91	10,93	9774	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01801	ptsI	1817822	1816680	380	4,9	41774	-	Phosphoenolpyruvate-protein phosphotransfer	phosphoenolpyruvate-protein phosphotransfera	Phosphoenolpyruvate-protein phosphotransfer	PEP-utilizing enzyme	Phosphoenolpyruvate-pro	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01802	null	1818405	1817869	178	4,35	19811	-	Phosphoenolpyruvate--protein phosphotransfe	phosphoenolpyruvate-protein phosphotransfera	not_predicted_by_ERGO	PEP-utilising enzyme, mobile region	phosphotra	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01803	ptsH	1818671	1818405	88	4,57	9254	-	Phosphocarrier protein HPr	PTS phosphocarrier protein Hpr (histidine conta	Phosphocarrier protein HPr	Phosphotransferase system, phosphocarrier HI	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01804	null	1819007	1818816	63	5	7420	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01805	clpE	1819227	1821455	742	5,92	81776	+	ATP-dependent clp protease ATP-binding sut	ATP-dependent Clp protease ATP-binding subu	ATP-dependent endopeptidase clp ATP-bindi	Chaperonin clpA/B|UvrB/UvrC protein|AAA+ A1	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	+				
LC_01806	null	1821802	1822095	97	9,19	11059	+	Conserved cytosolic protein	conserved hypothetical protein	Hypothetical cytosolic protein	Domain of unknown function DUF1827	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01807	prfC	1823836	1822262	524	6,53	59424	-	Peptide chain release factor 3	bacterial peptide chain release factor 3 (bRF-3)	Bacterial Peptide Chain Release Factor 3 (RF	Protein synthesis factor, GTP-binding	Translati	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01808	hlyX	1825250	1823904	448	4,43	49191	-	CBS domain protein	hemolysins related protein with CBS domains	Magnesium and cobalt efflux protein corC	Cystathionine-beta-synthase	Protein of unknow	R	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	+				
LC_01809	yueF	1826502	1825324	392	9	43789	-	Conserved membrane protein	permease / UPF0118 membrane protein yueF	Hypothetical membrane spanning protein	Protein of unknown function UPF0118	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	-				
LC_01810	ysiC	1826579	1827013	144	6,39	16135	+	Acetyltransferase, GNAT family	acetyltransferase (GNAT) family protein	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01811	null	1827639	1827121	172	5,19	19396	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01812	groEL	1828199	1827663	178	7,32	21085	-	chaperonin GroEL	chaperonin GroEL	Hypothetical cytosolic protein	Protein of unknown function DUF402	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01813	null	1829474	1828677	265	6,98	30535	-	Regulatory protein recX	regulatory protein, RecX family	Regulatory protein recX	Regulatory protein RecX	R	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+				
LC_01814	null	1829546	1831066	506	6,52	58781	+	Transcriptional regulator	conserved hypothetical protein	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+				
LC_01815	null	1831453	1831073	126	9,8	14439	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	+				
LC_01816	trmA	1831531	1832898	455	9,97	50628	+	RNA methyltransferase	tRNA (uracil-5-)-methyltransferase, TrmA famil	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1	23S rRNA methyltransferase/RumA	Deoxyribor	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01817	null	1833009	1833488	159	5,6	17325	+	Nucleoside 2-deoxyribosyltransferase	nucleoside 2-deoxyribosyltransferase	Nucleoside deoxyribosyltransferase (EC 2.4.2	Nucleoside 2-deoxyribosyltransferase	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01818	poxL	1835304	1833550	584	4,8	64016	-	Pyruvate oxidase	pyruvate oxidase or other thiamine pyrophospha	Pyruvate oxidase (EC 1.2.3.3)	TPP-binding enzymes	Thiamine pyrophosphate	EH	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01819	null	1835707	1835405	100	10,75	11367	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01820	mvaS	1837089	1835917	390	5,4	42903	-	Hydroxymethylglutaryl-CoA synthase	3-hydroxy-3-methylglutaryl-CoA synthase (EC 4	Hydroxymethylglutaryl-CoA synthase (EC 2.3.	Hydroxymethylglutaryl-coenzyme A synthase|H	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01821	mvaA	1838353	1837109	414	8,82	43008	-	Hydroxymethylglutaryl-CoA reductase	hydroxymethylglutaryl-CoA reductase, degradat	3-hydroxy-3-methylglutaryl-coenzyme A reduct	Hydroxymethylglutaryl-coenzyme A reductase|H	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01822	atoB1	1839547	1838366	393	5,63	40643	-	Acetyl-CoA acetyltransferase	acetyl-CoA acetyltransferases	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Thiolase	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01823	null	1840141	1840440	99	10,36	11235	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01824	pepQ	1841267	1840437	276	9,57	31628	-	Sugar phosphate isomerase/epimerase	sugar phosphate isomerase/epimerase / Xylose	Hypothetical cytosolic protein	Xylose isomerase-like TIM barrel	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01825	null	1841864	1841301	187	10,09	21678	-	5-methylcytosine-specific restriction enzyme M	Mrr endonuclease	5-methylcytosine-specific restriction enzyme M	Restriction endonuclease	V	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	+				
LC_01826	null	1842318	1843151	277	6,68	30703	+	Aldose 1-epimerase	Aldose 1-epimerase	Aldose 1-epimerase (EC 5.1.3.3)	aldose 1-epimerase|Glycoside hydrolase-type c	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01827	dapE	1844390	1843248	380	4,74	40525	-	Succinyl diaminopimelate desuccinylase	acetylornithine deacetylase / Succinyl-diaminopi	Succinyl-diaminopimelate desuccinylase (EC :	ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01828	null	1845127	1844522	201	11,81	21264	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Integral membrane protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	+				
LC_01829	null	1845299	1845481	60	7,12	6193	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01830	null	1845828	1846292	154	6,23	17240	+	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01831	ydcK	1846741	1846289	150	10,96	17436	-	Metallopeptidase, SprT family	Zn-dependent metalloprotease	Metallopeptidase, SprT family (EC 3.4.24.-)	Protein of unknown function DUF335, SprT|Prc	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	+				
LC_01832	null	1847741	1846989	250	10,47	26938	-	ABC transporter, ATPase component	ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01833	abc	1848633	1847734	299	9,55	31234	-	ABC transporter, permease protein	ribose/xylose/arabinose/galactoside ABC transp	ABC transporter permease protein	Bacterial inner-membrane translocator	E	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	-				
LC_01834	abc	1849625	1848630	331	10,38	34953	-	ABC transporter, substrate-binding protein	ABC transporter, substrate-binding lipoprotein ;	ABC transporter substrate-binding protein	ABC transporter substrate binding protein	R	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	-	+				
LC_01835	null	1850447	1850010	145	5,23	16380	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+				
LC_01836	null	1850882	1850508	124	10,63	13884	-	Calcium-translocating P-type ATPase, PMCA-	cation transport ATPase	not_predicted_by_ERGO	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-t	P	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-	+				
LC_01837	pacL2	1853172	1850896	758	4,62	81032	-	Cation-transporting ATPase	cation-transporting ATPase, E1-E2 family prote	Calcium-transporting ATPase (EC 3.6.3.8)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	+				
LC_01838	null	1853630	1853346	94	11,4	10481	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01839	null	1854847	1853687	386	9,94	42794	-	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin binding	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, transj	V	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	protease	+				
LC_01840	nadE	1855786	1854959	275	6,06	30203	-	NH(3)-dependent NAD(+) synthetase	NAD synthetase, ammonia dependent	NH(3)-dependent NAD(+) synthetase (EC 6.3	NAD+ synthase|Rossmann-like alpha/beta/alph	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01841	null	1856982	1855786	398	10,26	44218	-	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin binding	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, transj	V	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	protease	+				
LC_01842	nadC1	1858462	1856996	488	4,97	54998	-	Nicotinate phosphoribosyltransferase	nicotinate phosphoribosyltransferase related pro	Nicotinate phosphoribosyltransferase (EC 2.4.	Nicotinate phosphoribosyltransferase related|Ni	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01843	def	1859632	1858931	233	9,79	26340	-	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	+				
LC_01844	nagA	1860803	1859658	381	4,92	42327	-	N-acetylglucosamine-6-phosphate deacetylase	N-acetylglucosamine-6-phosphate deacetylase	N-acetylglucosamine-6-phosphate deacetylase	N-acetylglucosamine-6-phosphate deacetylase|	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01845	proC	1861698	1860901	265	5,6	27173	-	Pyrroline-5-carboxylate reductase	delta 1-pyrroline-5-carboxylate reductase	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	Delta 1-pyrroline-5-carboxylate reductase|NADF	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01846	yuxL	1863686	1861701	661	5,61	74502	-	Dipeptidyl aminopeptidase/acylaminoacyl-pept	dipeptidyl aminopeptidase / acylaminoacyl-pepti	Acylamino-acid-releasing enzyme (EC 3.4.19.	Peptidase S9, prolyl oligopeptidase active site r	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	protease	+				
LC_01847	null	1870715	1863942	2257	5,09	235392	-	Conserved extracellular matrix binding protein	predicted ORF	Extracellular matrix binding protein	Aminoacyl-tRNA synthetase, class I|Surface pr	null	Yes	fibronectin	LPxTG	tmhmm:2	-	-	-	-	-	-	-	+				
LC_01848	null	1870991	1872481	496	7,55	57941	+	Transcriptional antiterminator	transcriptional antiterminator	Transcriptional regulator	M trans-acting positive regulator|Helix-turn-helix	null	Yes	-	-	tmhmm:0	-	-	-	-	-	regulator	-	-				
LC_01849	null	1873612	1872779	277	6,51	31228	-	Phosphohydrolase	phosphohydrolase	Phosphoesterase	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	+				
LC_01850	dtpT	1875126	1873660	488	9,93	53951	-	Transporter, major facilitator superfamily MFS	dipeptide/tripeptide permease (Peptide:H+ symp	Di-/tripeptide transporter	TGF-beta receptor, type I/II extracellular region|	E	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	-	+				
LC_01851	abc	1877733	1875415	772	9,78	84289	-	ABC transporter, ATPase component	macrolide efflux antimicrobial peptide ABC trans	ABC transporter ATP-binding protein / ABC tr	Cytochrome c oxidase, subunit II|ABC transport	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	+				
LC_01852	null	1878314	1877940	124	7,82	14493	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01853	null	1878786	1878364	140	5,18	15751	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	-				
LC_01854	null	1879363	1880793	476	10,07	52802	+	Melibiose permease II	Na+/melibiose symporter and related transporte	Melibiose carrier protein	Sodium:galactoside symporter	G	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-	+				
LC_01855	null	1881011	1882147	378	7,97	44179	+	Alpha-L-fucosidase (GH29)	alpha-L-fucosidase	Alpha-L-fucosidase (EC 3.2.1.51)	Glycoside hydrolase, family 29 (alpha-L-fucosid	G	Yes	-	-	tmhmm:0	LC01856	-	-	-	-	-	-	+				

LC_01856	null	1882632	1882315	105	8,26	12097	-	Glutaredoxin related protein	glutaredoxin related protein	Arsenate reductase family protein	Thioredoxin-like fold	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01857	pck	1884522	1882870	550	5,95	60216	-	Phosphoenolpyruvate carboxykinase (ATP)	phosphoenolpyruvate carboxykinase (ATP)	Phosphoenolpyruvate carboxykinase [ATP] (E	no annotation	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01858	null	1884898	1884728	56	10,07	6223	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01859	feoB	1886287	1884953	444	9,02	48270	-	Ferrous iron transport protein B	ferrous iron transport and uptake protein B	Ferrous iron transport protein B	Ferrous iron transport protein B, N-terminal|Fer	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_01860	null	1887056	1886271	261	5,97	29211	-	Ferrous iron transport protein B	ferrous iron transport protein B / GTP-binding	not_predicted_by_ERGO	GTP-binding protein, HSR1-related|GTP1/OBG	P	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01861	feoA	1887540	1887049	163	9,66	17411	-	Ferrous iron transport protein A	Fe2+ transport system protein A	Ferrous iron transport protein A	FeoA|Transcriptional repressor, C-terminal	P	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01862	null	1888508	1887750	252	10,07	27855	-	Acyltransferase	acyltransferase	Acyltransferase family	Esterase, SGNH hydrolase-type	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_01863	null	1888758	1889261	167	6,94	18227	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01864	ywnB	1889977	1890615	212	6,08	23368	+	NADH-flavin reductase	NADH-flavin reductase / saccharopine dehydro	Quinate/shikimate dehydrogenase [Pyrroloquin	NADP oxidoreductase, coenzyme F420-depenc	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01865	null	1890652	1891140	162	9,33	18214	+	Internalin-I	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01866	null	1891731	1891207	174	10,43	18933	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_01867	null	1892103	1891978	41	8,06	4709	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01868	null	1892935	1892597	112	11,26	12018	-	Conserved protein	metal-dependent RNase, consists of a metallo-l	not_predicted_by_ERGO	KH, prokaryotic type	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01869	null	1893073	1893372	99	11,9	11432	+	Lipoprotein	lipoprotein	not_predicted_by_ERGO	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01870	null	1894287	1894682	131	8,72	14815	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01871	null	1895089	1895301	70	8,5	7801	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01872	null	1895523	1895888	121	10,58	13519	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	C-type lectin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01873	null	1896175	1896369	64	11,31	7429	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01874	null	1896354	1896671	105	12,08	11649	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01875	null	1896828	1896625	67	11,84	7290	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01876	null	1896779	1896964	61	10,44	6799	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01877	serS	1898924	1897641	427	6,05	48673	-	Seryl-tRNA synthetase	seryl-tRNA synthetase (Seryl-tRNA(Ser/Sec) s	Seryl-tRNA synthetase (EC 6.1.1.11)	tRNA synthetase, class II (G, H, P and S)|Seryl	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01878	null	1900944	1899367	525	6,27	60226	-	Transcriptional regulator	conserved hypothetical protein	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01879	null	1901323	1902849	508	6,38	59863	+	Transcriptional regulator	conserved hypothetical protein	Transcriptional regulator	M trans-acting positive regulator	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_01880	lysP	1904441	1902978	487	10,14	52562	-	Lysine-specific permease	amino acid transporter, lysine-specific permeas	Lysine-specific permease	Amino acid/polyamine transporter I|Amino acid	E	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_01881	null	1904484	1904801	105	10,16	11529	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_01882	null	1904867	1905019	50	5,62	5595	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01883	aldB	1905808	1905098	236	5,44	25730	-	Alpha-acetolactate decarboxylase	acetolactate decarboxylase (Alpha-acetolactate	Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Alpha-acetolactate decarboxylase	Q	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01884	null	1906022	1905915	35	12,51	3795	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01885	als	1907836	1906160	558	4,74	60403	-	Acetolactate synthase	acetolactate synthase (large subunit) IlvB1_1	Acetolactate synthase (EC 2.2.1.6)	TPP-binding enzymes|Thiamine pyrophosphate EH		Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01886	null	1908710	1908159	183	6,12	20913	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01887	null	1909350	1908817	177	7,99	20326	-	Ribosomal-protein-S5-alanine acetyltransferas	acetyltransferase, including N-acetylase of ribos	Ribosomal-protein-S5-alanine acetyltransferas	GCN5-related N-acetyltransferase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01888	null	1909751	1909560	63	10,88	6888	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01889	null	1910391	1911422	343	10,17	37581	+	Cell surface protein	cell surface protein	Hypothetical protein	Protein of unknown function DUF916, cell surfa	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-	
LC_01890	null	1911749	1911597	50	11,83	5620	-	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01891	null	1911714	1912289	191	4,06	21042	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01892	rpmG3	1912352	1912501	49	11,42	5862	+	LSU/50S ribosomal protein L33P	LSU ribosomal protein L33P	LSU ribosomal protein L33P	Ribosomal protein L33	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01893	rluD	1913576	1912707	289	9,71	32290	-	Ribosomal large subunit pseudouridine syntha	ribosomal large subunit pseudouridine synthase	Ribosomal large subunit pseudouridine syntha	Pseudouridine synthase|Pseudouridine synthas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01894	null	1913712	1914521	269	4,73	29940	+	Esterase/lipase	Esterase/lipase	Lipase (EC 3.1.1.3)	no annotation	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01895	null	1915237	1914626	203	9,58	21023	-	Putative protein without homology	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	-	
LC_01896	null	1915458	1915856	132	7,82	14979	+	Phage-related infection protein	conserved hypothetical protein (possible phage	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01897	null	1916472	1916161	103	6,53	11852	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01898	citG	1918070	1917210	286	8,05	31149	-	Triphosphoribosyl-dephospho-CoA synthase	triphosphoribosyl-dephospho-CoA synthase Cit	2'-(5"-triphosphoribosyl)-3-dephospho-CoA sy	Triphosphoribosyl-dephospho-CoA protein	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01899	citR	1918758	1918063	231	7,19	27084	-	Transcriptional regulator, GntR family	citrate catabolism transcriptional regulator, GntF	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|GntR, C	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01900	oadA	1920339	1918936	467	5,23	51754	-	Oxaloacetate decarboxylase, alpha chain	pyruvate carboxylase/oxaloacetate decarboxylas	Na+ transporting oxaloacetate decarboxylase a	Serine/threonine dehydratase, pyridoxal-phosph	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01901	citX	1920880	1920332	182	7,51	20159	-	Apo-citrate lyase phosphoribosyl-dephospho-C	apo-citrate lyase phosphoribosyl-dephospho-Cc	Apo-citrate lyase phosphoribosyl-dephospho-C	Apo-citrate lyase phosphoribosyl-dephospho-Cc	HI	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01902	citF	1922405	1920873	510	6,09	54570	-	Citrate lyase, alpha subunit, Citrate CoA-trans	citrate lyase alpha subunit, acetyl-ACP:citrate A	Citrate lyase alpha chain (EC 4.1.3.6) / Citrate	Citrate lyase, alpha subunit	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01903	citE	1923283	1922405	292	4,64	31347	-	Citrate lyase beta subunit, Citryl-CoA lyase su	citrate lyase beta subunit	Citrate lyase beta chain (EC 4.1.3.6) / Citryl-C	HpcH/HpaI aldolase|Malate synthase-like|Citrat	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01904	citD	1923576	1923271	101	4,77	10854	-	Citrate lyase acyl carrier protein	Citrate lyase acyl carrier protein (Citrate lyase g	Citrate lyase acyl carrier protein	Citrate lyase acyl carrier protein CitD	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01905	citC	1924570	1923566	334	5,22	36985	-	Citrate lyase ligase	acetate: SH-citrate (pro-3S)-lyase ligase (citrate	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	GCN5-related N-acetyltransferase|Cytidyltransf	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01906	oadB	1925906	1924782	374	8,94	39730	-	Oxaloacetate decarboxylase, beta chain	Na+-transporting methylmalonyl-CoA/oxaloacet	Na+ transporting oxaloacetate decarboxylase l	Na+-transporting methylmalonyl-CoA/oxaloacet	P	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-	
LC_01907	oadG	1926328	1925921	135	4,2	13455	-	Biotin carboxyl carrier protein of oxaloacetate c	acetyl-CoA carboxylase biotin carboxyl carrier p	Biotin carboxyl carrier protein of oxaloacetate c	Biotin/lipoyl attachment|Biotin-binding site|Singl	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01908	null	1926657	1926334	107	8,97	11576	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_01909	citM	1928401	1927052	449	9,61	48622	-	ABC transporter, citrate transporter	Mg2+/citrate transporter	Mg2+/citrate complex secondary transporter	ABC transporter related|Divalent ion symporter|	C	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	-	
LC_01910	null	1928940	1928683	85	4,87	10079	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01911	kptA	1929577	1929023	184	10,67	20950	-	RNA 2'-phosphotransferase	RNA:NAD 2'-phosphotransferase	tRNA 2'phosphotransferase (EC 2.7.-.-)	Phosphotransferase KptA/Tpt1	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01912	yveC	1929630	1930136	168	9,83	18330	+	Acetyltransferase, GNAT family protein	acetyltransferase (GNAT) family protein	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01913	null	1930758	1930141	205	5,22	22029	-	NADP oxidoreductase coenzyme F420-depen	dinucleotide-binding enzymes, NADP oxidoredu	Oxidoreductase (EC 1.1.1.-)	NADP oxidoreductase, coenzyme F420-depenc	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01914	null	1930990	1931328	112	5,12	12560	+	Transcriptional regulator, PadR family	transcriptional regulator, PadR family protein	Transcriptional regulator, PadR family	Transcriptional regulator PadR-like|Winged heli	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_01915	null	1931291	1931509	72	10,72	7813	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_01916	null	1931460	1932305	281	9,95	32465	+	Conserved transmembrane protein	conserved hypothetical protein (transmembrane	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_01917	nfrA	1932414	1933169	251	6,8	27857	+	Oxygen-insensitive NADPH nitroreductase	subunit of oxygen-insensitive NADPH nitroredu	Chromate reductase (EC 1.-.-.-) / NADPH-dep	Nitroreductase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01918	yjjC	1933475	1934392	305	6,35	33904	+	ABC transporter, ATPase component	tetronasin multidrug ABC transporter, ATPase c	Tetronasin resistance ATP-binding protein	ABC transporter related|AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_01919	null	1934379	1935995	538	10,39	58247	+	Exporter of polyketide antibiotics	exporter of polyketide antibiotics	Tetronasin resistance transmembrane protein	no annotation	M	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_01920	null	1935992	1936624	210	8,75	23956	+	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01921	null	1938175	1936772	467	9,78	50648	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-	
LC_01922	null	1938522	1939259	245	10,54	25626	+	Conserved permease	permease	Transport protein	Protein of unknown function DUF81	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_01923	null	1939363	1940403	346	5,44	38718	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator, Cro/CI family	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_01924	null	1941364	1940507	285	10,72	31386	-	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Protein of unknown function DUF915, hydrolase	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+	

LC_01925	gntR	1941531	1941908	125	4,77	14424	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH	Winged	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01926	null	1941898	1942614	238	6,42	26678	+	ABC transporter, ATPase component	ABC transporter, ATPase component, ABC1AT	ABC transporter ATP-binding protein	ABC transporter related	AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01927	null	1942607	1943320	237	9,73	26895	+	ABC transporter, permease component	ABC transporter, permease component	ABC transporter ATP-binding and permease p	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_01928	null	1943450	1944826	458	10,03	50397	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_01929	abc	1944860	1945549	229	5,42	25399	+	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	not_predicted_by_ERGO	ABC transporter related	AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01930	oppF	1946830	1945940	296	7,02	32870	-	ABC transporter, oligopeptide transporter ATP	oligopeptide ABC transporter, ATPase compon	Oligopeptide transport ATP-binding protein op	ABC transporter related	AAA+ ATPase, core	Ol	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01931	oppD	1947915	1946851	354	6,9	38918	-	ABC transporter, oligopeptide transporter ATP	dipeptide/oligopeptide/nickel ABC transporter, A	Oligopeptide transport ATP-binding protein op	ABC transporter related	AAA+ ATPase, core	Ol	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01932	null	1948296	1947988	102	10,44	11094	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_01933	oppC	1949354	1948398	318	6	34770	-	ABC transporter, oligopeptide transported perr	dipeptide/oligopeptide/nickel ABC transporter, p	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	C	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_01934	oppB	1950319	1949369	316	8,66	34696	-	ABC transporter, oligopeptide transported perr	dipeptide/oligopeptide/nickel ABC transporter, p	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	C	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_01935	null	1952093	1950423	556	10,25	61180	-	ABC transporter, oligopeptide transporter peri	oligopeptide ABC transporter, periplasmic comp	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_01936	null	1952292	1952501	69	8,81	7876	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01937	null	1953325	1953062	87	12,51	9358	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_01938	null	1955043	1953391	550	10,24	60549	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter related	AAA+ ATPase, core	At	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_01939	null	1956484	1955045	479	10,01	52012	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter, transmembrane region	ABC tr	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_01940	null	1957492	1957094	132	5,11	14280	-	Conserved protein	Fe-S biosynthesis protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01941	null	1958411	1957569	280	8,61	31688	-	Aminoglycoside phosphotransferase	conserved hypothetical protein	Phosphotransferase family protein	Aminoglycoside phosphotransferase	Protein kin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01942	null	1958613	1959359	248	9,21	26496	+	Zn-dependent endopeptidase, M10 family	Zn-dependent protease	Endopeptidase, M10 family (EC 3.4.24.-)	Peptidase M10A and M12B, matrixin and adam	O	Yes	-	Sec	tmhmm:1	-	-	-	-	-	protease	+
LC_01943	null	1959557	1959760	67	9,91	7920	+	Transcription regulator	transcriptional regulator, DNA-binding protein	not_predicted_by_ERGO	Helix-turn-helix type 3	Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01944	null	1959747	1960271	174	10	19480	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_01945	null	1964106	1960504	1200	6,82	128255	-	Conserved protein	conserved hypothetical protein	Surface antigen	Peptidoglycan-binding LysM	null	Yes	peptidoglucar	LysM	tmhmm:0	-	-	-	-	-	-	+
LC_01946	lciIC	1964764	1965090	108	5,78	12333	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator	Helix-turn-helix type 3	Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01947	mrr	1966232	1965330	300	5,56	33671	-	Restriction endonuclease	similar to C-terminus restriction endonuclease h	not_predicted_by_ERGO	Restriction endonuclease	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01948	null	1967041	1966334	235	4,64	27047	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	Plasmid pRiA4b ORF-3-like	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01949	null	1967349	1967558	69	5,44	7879	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01950	null	1967864	1967553	103	9,13	11824	-	Transcription regulator	DNA-binding protein, xre family	not_predicted_by_ERGO	RNA polymerase, Sigma-70 factor	Helix-turn-he	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_01951	null	1969089	1969478	129	5,5	14371	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01952	null	1969667	1969512	51	7,51	6063	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_01953	null	1971269	1969698	523	7,97	51424	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Peptidoglycan-binding LysM	null	No	peptidoglucar	LysM	tmhmm:0	-	-	-	-	-	-	+
LC_01954	null	1972342	1971497	281	11,05	32396	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01955	null	1973994	1972756	412	5,15	48034	-	Abi-alpha protein	Abi-alpha protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01956	null	1974931	1974848	27	10,99	3195	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01957	null	1976104	1975025	359	10,22	41004	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:7	-	-	-	-	-	-	+
LC_01958	abi	1977575	1976664	303	6,69	34042	-	Abortive phage resistance protein	abortive phage resistance protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01959	guaA	1979368	1977815	517	5,06	57799	-	GMP synthase	bifunctional GMP synthase/glutamine amidotrar	GMP synthase [glutamine-hydrolyzing] (EC 6.	Glutamine amidotransferase class-I	Carbamoyl-	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01960	coaA	1980476	1979550	308	6,43	35918	-	Pantothenate kinase	pantothenate kinase, Rts protein	Pantothenate kinase (EC 2.7.1.33)	Bacterial pantothenate kinase	Phosphoribulokin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01961	null	1980792	1981142	116	4,58	13229	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_01962	null	1981192	1981479	95	12,43	11272	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_01963	pepD3	1982937	1981528	469	4,76	52409	-	Dipeptidase A	dipeptidase A. Cysteine peptidase. MEROPS fa	Dipeptidase A (EC 3.4.13.-)	Peptidase C69, dipeptidase A	C	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01964	null	1983592	1983440	50	9,25	5421	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01965	ykhA	1984415	1983921	164	9,61	17942	-	Acyl-CoA hydrolase	cytosolic long-chain acyl-CoA thioester hydrolas	Acyl-CoA hydrolase (EC 3.1.2.20)	Thioesterase superfamily	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01966	rep	1986693	1984402	763	8,36	87725	-	DNA helicase	superfamily I DNA and RNA helicase-like protei	ATP-dependent DNA helicase rep (EC 3.6.1.-	UvrD/REP helicase	Helicase superfamily 1, Uvr	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01967	null	1986946	1986728	72	12,08	8134	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01968	null	1987116	1986961	51	8,79	5255	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01969	null	1987322	1987125	65	11,76	7108	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_01970	napA2	1987394	1989223	609	7,13	66811	+	Na(+)/H(+) antiporter	Kef-type K+ transport system, membrane comp	Na+/H+ antiporter napA	TrkA-C	Sodium/hydrogen exchanger	P	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_01971	pepR	1989380	1990285	301	5,64	34152	+	Prolyl aminopeptidase	prolinase, serine peptidase, MEROPS family S	Proline iminopeptidase (EC 3.4.11.5)	Alpha/beta hydrolase fold-1	Peptidase S33, prol	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_01972	yjhE	1990364	1990825	153	9,45	17103	+	Conserved protein	conserved protein	hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01973	mntH3	1992220	1990856	454	9,71	49481	-	Mn2+/Fe2+ transporter, NRAMP family	Mn2+/Fe2+ transporter NRAMP family protein	Manganese transport protein mntH	Natural resistance-associated macrophage prot	P	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	-
LC_01974	hemH	1993175	1992204	323	9,65	36409	-	Ferrochelatase	protoheme ferro-lyase (ferrochelatase)	Ferrochelatase (EC 4.99.1.1)	Ferrochelatase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01975	gpm2	1993470	1994135	221	6,97	25041	+	Phosphoglycerate mutase	phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate/bisphosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01976	araD	1995161	1994268	297	5,82	33658	-	Rhamnulose-1-phosphate aldolase	L-Rhamnulose-1-Phosphate Aldolase From	Rhamnulose-1-phosphate aldolase (EC 4.1.2.	Class II aldolase/adducin, N-terminal	Rhamnulc	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01977	null	1997403	1995595	602	10,6	66848	-	ABC transporter, permease protein	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein	Protein of unknown function DUF214, permase	V	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_01978	null	1997754	1997416	112	4,67	12317	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	ABC transporter related	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01979	null	1998173	1997706	155	10,46	16827	-	ABC transporter, ATPase component	predicted ORF	ABC transporter ATP-binding protein	ABC transporter related	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01980	null	1998473	2000143	556	9,23	62069	+	Amino acid transporter	Amino acid transporter	Amino acid permease	Amino acid/polyamine transporter I	Amino acid	E	Yes	-	IMP	tmhmm:15	-	-	-	-	-	-	+
LC_01981	null	2000469	2000996	175	10,1	18769	+	Lipid kinase from diacylglycerol kinase family p	predicted ORF	Diacylglycerol kinase family protein	Diacylglycerol kinase, catalytic region	IR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01982	null	2000993	2001352	119	9,03	13127	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	IR	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_01983	hflX	2001630	2002925	431	5,39	48212	+	GTP-binding protein, HflX subfamily	GTP-binding protein, HflX subfamily	GTP-binding protein hflX	GTP-binding protein, HSR1-related	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01984	null	2004123	2003158	321	9,57	35604	-	Xylanase/chitin deacetylase	xylanase/chitin deacetylase	Peptidoglycan N-acetylglucosamine deacetyla	Polysaccharide deacetylase	G	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	-
LC_01985	null	2006594	2004264	776	9,53	89870	-	Teichoic acid/polysaccharide phosphoglycerol	teichoic acid/polysaccharide phosphoglycerol tr	not_predicted_by_ERGO	Sulfatase	M	No	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_01986	null	2007927	2006878	349	9,81	39233	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_01987	null	2008641	2008003	212	5,6	22469	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	D	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01988	null	2009395	2008703	230	10,09	24695	-	Lipopolysaccharide biosynthesis	predicted ORF	not_predicted_by_ERGO	Lipopolysaccharide biosynthesis	null	No	-	Cterm	tmhmm:2	-	-	-	-	-	-	+
LC_01989	null	2010921	2009482	479	9,64	54064	-	Polysaccharide biosynthesis protein	predicted ORF	not_predicted_by_ERGO	Polysaccharide biosynthesis protein	null	No	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_01990	null	2012072	2010936	378	9,07	43360	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01991	null	2013090	2012125	321	9,41	36985	-	Glycosyl transferase, group 2	predicted ORF	not_predicted_by_ERGO	Glycosyl transferase, family 2	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01992	slp	2015132	2013351	593	10,33	66224	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	ABC transporter related	C	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_01993	null	2017402	2015327	691	9,38	74499	-	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)	conserved hypothetical protein	Lysozyme (EC 3.2.1.17)	Glycoside hydrolase, family 25	Glycoside hydro	null	Yes	-	GW	tmhmm:1	LC01993	-	-	-	-	-	+

LC_01994	null	2017767	2017528	79	9,99	9619	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_01995	null	2019016	2017904	370	9,99	41854	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:9	-	-	-	-	-	-	+
LC_01996	null	2019290	2020330	346	9,67	39314	+	Acyltransferase 3	predicted ORF	not_predicted_by_ERGO	Acyltransferase 3	null	No	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_01997	ykcG	2021434	2020442	330	9,03	37262	-	Glycosyl transferase, group 2	glycosyltransferase related enzyme	not_predicted_by_ERGO	Glycosyl transferase, family 2	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_01998	mnaA	2022648	2021506	380	6,41	42920	-	UDP-N-acetylglucosamine 2-epimerase	UDP-N-acetylglucosamine 2-epimerase (UDP-(	UDP-N-acetylglucosamine 2-epimerase (EC 5	UDP-N-acetylglucosamine 2-epimerase	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_01999	null	2023709	2022855	284	9,93	29992	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_02000	epsC	2025356	2023956	466	9,78	54235	-	UDP-galactosephosphotransferase	lipopolysaccharide synthesis sugar transferase	Undecaprenyl-phosphate galactosephosphotra	Bacterial sugar transferase	M	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_02001	epsB	2026214	2025474	246	9,49	28886	-	Glycosyltransferase	glycosyltransferase	not_predicted_by_ERGO	Glycosyltransferase sugar-binding region conta	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02002	epsA	2026992	2026237	251	6,86	28912	-	Glycosyl transferase, group 2	teichuronic acid biosynthesis glycosyl transfera	not_predicted_by_ERGO	Glycosyl transferase, family 2	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02003	galE3	2028010	2027075	311	5,38	34620	-	NAD-dependent epimerase/dehydratase	NAD-dependent nucleoside-diphosphate-sugar	NAD dependent epimerase/dehydratase famil	NAD-dependent epimerase/dehydratase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02004	glnP	2029110	2028448	220	9,88	24707	-	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease compon	Glutamine transport system permease protein	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02005	glnM	2029770	2029126	214	9,7	23601	-	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease compon	Glutamine transport system permease protein	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+
LC_02006	glnH1	2030596	2029772	274	10,45	29718	-	ABC transporter, amino acid-binding periplas	amino acid ABC transporter/signal transduction	Glutamine-binding protein	Ionotropic glutamate receptor	Bacterial extracell	ET	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_02007	glnQ	2031527	2030790	245	6,04	27397	-	ABC transporter, amino acid tranporter ATPas	polar amino acid ABC transporter, ATPase com	Glutamine transport ATP-binding protein glnQ	ABC transporter related|AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02008	null	2032794	2031835	319	7,79	35338	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_02009	null	2033258	2032815	147	4,25	14895	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02010	fur	2033967	2033515	150	8,15	17582	-	Fe2+/Zn2+ uptake transcriptional regulation pr	Fe2+/Zn2+ uptake regulation proteins / transcri	Ferric uptake regulation protein	Ferric-uptake regulator	P	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02011	null	2034076	2034189	37	12,11	4219	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02012	gmk1	2034993	2034391	200	9,19	22811	-	Guanylate kinase	guanylate kinase (Gmk)	Guanylate kinase (EC 2.7.4.8)	Guanylate kinase|Guanylate kinase/L-type calci	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02013	null	2035510	2035103	135	4,77	15231	-	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family protein	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02014	null	2036297	2035806	163	8,39	16142	-	NLP/P60	predicted ORF	not_predicted_by_ERGO	NLP/P60	M	No	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_02015	null	2037006	2036332	224	10,1	23689	-	Surface antigen	predicted ORF	not_predicted_by_ERGO	no annotation	NT	No	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_02016	null	2037126	2037302	58	10,55	6602	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02017	tyrS	2038579	2037308	423	5,89	47727	-	Tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase (tyrosine--tRNA ligase)	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	Aminoacyl-tRNA synthetase, class I|Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02018	null	2039314	2038985	109	4,03	12078	-	Cation diffusion facilitator family transporter	conserved hypothetical protein	Cobalt-zinc-cadmium resistance protein czcD	Cation efflux protein	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02019	null	2039922	2039371	183	10,24	19994	-	Cation diffusion facilitator family transporter	cation efflux family protein	Cobalt-zinc-cadmium resistance protein czcD	Cation efflux protein	P	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02020	null	2040432	2040097	111	9,51	12189	-	Transcriptional regulator, ArsR family	transcriptional regulator, ArsR family	Transcriptional regulator, ArsR family	Bacterial regulatory protein, ArsR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02021	apbE	2040583	2041512	309	4,65	33130	+	Thiamine biosynthesis lipoprotein	thiamine biosynthesis membrane-associated lip	Iron-sulfur cluster assembly/repair protein ApbE	ApbE-like lipoprotein	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02022	amy1	2043404	2041626	592	4,95	66641	-	Amylopullulanase (GH13)	amylopullulanase (EC 3.2.1.41)	Maltogenic alpha-amylase (EC 3.2.1.133)	Glycosyl hydrolase, family 13, catalytic region|G	G	Yes	-	-	tmhmm:0	LC02022	-	-	-	-	-	-
LC_02023	glgP	2045837	2043426	803	6,45	90559	-	Glycogen/starch/alpha-glucan phosphorylases	glycogen/starch/alpha-glucan phosphorylases	Glycogen phosphorylase (EC 2.4.1.1)	Glycosyl transferase, family 35|Glycogen/starch	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02024	glgA	2047430	2045985	481	6,3	54053	-	Glycogen synthase	bacterial glycogen synthase	Glycogen synthase (EC 2.4.1.21)	Glycosyl transferase, group 1|Glycogen/starch :	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02025	glgD	2048592	2047423	389	5,11	42998	-	Glucose-1-phosphate adenylyltransferase reg	ADP-glucose pyrophosphorylase	Glucose-1-phosphate adenylyltransferase regi	Trimeric LpxA-like|Glucose-1-phosphate adenyl	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02026	glgC	2049731	2048589	380	6,11	41885	-	Glucose-1-phosphate adenylyltransferase cat	glucose-1-phosphate adenylyltransferase (ADP	Glucose-1-phosphate adenylyltransferase cat	Nucleotidyl transferase|ADP-glucose pyrophosp	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02027	glgB	2051824	2049761	687	7,37	79173	-	1,4-alpha-glucan branching enzyme (GH13)	1,4-alpha-glucan-branching enzyme (Glycogen-	1,4-alpha-glucan branching enzyme (EC 2.4.1	Glycoside hydrolase, family 13, N-terminal|Glyc	G	Yes	-	-	tmhmm:0	LC02027	-	-	-	-	-	-
LC_02028	ilvE	2052186	2053217	343	5,49	37540	+	Branched-chain amino acid aminotransferase	branched-chain amino acid aminotransferase IlvE	Branched-chain amino acid aminotransferase	Aminotransferase, class IV|Branched-chain am	EH	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02029	null	2054271	2053369	300	9,91	30535	-	Conserved protein	predicted ORF	Hypothetical exported protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02030	null	2055476	2054646	276	6,36	30270	-	Conserved integral membrane protein	YitT family protein	Hypothetical membrane spanning protein	Protein of unknown function DUF161	S	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02031	fbp	2057512	2055629	627	6,59	72080	-	Fructose-1,6-bisphosphatase	fructose-1,6-bisphosphatase (YYDE B.subtilis o	Fructose-1,6-bisphosphatase (EC 3.1.3.11)	Carbamoyl-phosphate synthase L chain, ATP-b	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02032	nrp	2058216	2057815	133	10,39	15046	-	Arsenate reductase family protein	arsenate reductase related protein, glutaredoxin	Arsenate reductase family protein	Conserved hypothetical protein, ArsC related|Ar	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02033	clpL	2061007	2058857	716	5,44	78430	-	ATP-dependent Clp protease, ATP-binding su	ATP-dependent Clp protease, ATP-binding sub	ATP-dependent endopeptidase clp ATP-bindi	Chaperonin clpA/B|UvrB/UvrC protein|AAA+ A1	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02034	wzb	2062165	2061488	225	6,18	25336	-	Capsular polysaccharide biosynthesis protein	capsular polysaccharide biosynthesis protein C	Phosphotyrosine-protein phosphatase (capsul	PHP, C-terminal	M	Yes	-	-	tmhmm:0	-	-	Wzb	-	-	-	+
LC_02035	wzr	2062322	2063215	297	9,47	32740	+	Cell envelope-related transcriptional attenuator	cell envelope-related transcriptional attenuator /	Transcriptional activator CpsA	Cell envelope-related transcriptional attenuator	K	Yes	-	Nterm	tmhmm:1	-	-	Wzr	-	regulator	-	+
LC_02036	welE	2064702	2064034	222	10,03	25341	-	Undecaprenyl-phosphate beta-glucosephosph	capsularpolysaccharide synthesis, undecapren	Undecaprenyl-phosphate beta-glucosephosph	Bacterial sugar transferase	M	Yes	-	IMP	tmhmm:1	-	-	WelE	-	-	-	+
LC_02037	rmlD	2066371	2065529	280	5,98	32028	-	dTDP-4-dehydrorhamnose reductase	dTDP-4-keto-L-rhamnose reductase RmlD / Po	dTDP-4-dehydrorhamnose reductase (EC 1.1	dTDP-4-dehydrorhamnose reductase	M	Yes	-	-	tmhmm:0	-	-	RmlD	-	-	-	+
LC_02038	rmlB	2067457	2066432	341	6,45	38487	-	dTDP-glucose 4,6-dehydratase	dTDP-glucose 4,6-dehydratase Cps19aN RmlB	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	NAD-dependent epimerase/dehydratase|Short-(	M	Yes	-	-	tmhmm:0	-	-	RmlB	-	-	-	+
LC_02039	rmlC	2068032	2067460	190	5,56	21589	-	dTDP-4-dehydrorhamnose 3,5-epimerase	dTDP-4-dehydrorhamnose 3,5-epimerase relate	dTDP-4-dehydrorhamnose 3,5-epimerase (EC	dTDP-4-dehydrorhamnose 3,5-epimerase relate	M	Yes	-	-	tmhmm:0	-	-	RmlC	-	-	-	+
LC_02040	rmlA	2068918	2068046	290	4,96	32428	-	Glucose-1-phosphate thymidylyltransferase	glucose-1-phosphate thymidylyltransferase RmlA	Glucose-1-phosphate thymidylyltransferase (E	Nucleotidyl transferase|Glucose-1-phosphate th	M	Yes	-	-	tmhmm:0	-	-	RmlA	-	-	-	+
LC_02041	wzm	2070096	2069107	329	9,54	38303	-	Exopolysaccharide protein Wzm	capsular exopolysaccharide biosynthesis protein	not_predicted_by_ERGO	no annotation	M	No	-	-	tmhmm:0	-	-	Wzm	-	-	-	+
LC_02042	welJ	2071174	2070098	358	7,65	40302	-	Exopolysaccharide related glycosyl transferase	glycosyltransferase (WelJ)	not_predicted_by_ERGO	Glycosyl transferase, group 1	M	No	-	-	tmhmm:0	-	-	WelJ	-	-	-	+
LC_02043	wzy	2072281	2071190	363	9,73	40896	-	Exopolysaccharide protein Wzy	capsular exopolysaccharide biosynthesis protein	not_predicted_by_ERGO	no annotation	M	No	-	IMP	tmhmm:8	-	-	Wzy	-	-	-	+
LC_02044	welI	2073300	2072281	339	9,7	38641	-	alpha-L-Rha alpha-1,3-L-rhamnosyltransferas	glycosyltransferase (WelI)	alpha-L-Rha alpha-1,3-L-rhamnosyltransferas	Glycosyl transferase, family 2	M	Yes	-	-	tmhmm:0	-	-	WelI	-	-	-	+
LC_02045	welH	2074099	2073281	272	9,01	30882	-	Exopolysaccharide protein glycosyl transferase	glycosyltransferase (WelH)	not_predicted_by_ERGO	Glycosyl transferase, family 2	M	No	-	-	tmhmm:0	-	-	WelH	-	-	-	-
LC_02046	welG	2075168	2074089	359	9,67	41125	-	Exopolysaccharide protein glycosyl transferase	glycosyltransferase (WelG)	not_predicted_by_ERGO	Glycosyl transferase, group 1	M	No	-	-	tmhmm:0	-	-	WelG	-	-	-	+
LC_02047	welF	2075966	2075184	260	9,54	30125	-	Exopolysaccharide protein glycosyl transferase	glycosyltransferase (WelF)	not_predicted_by_ERGO	Glycosyl transferase, family 2	R	No	-	-	tmhmm:0	-	-	WelF	-	-	-	+
LC_02048	wzx	2077354	2075963	463	10	51297	-	Exopolysaccharide protein Wzx	capsular exopolysaccharide biosynthesis protein	not_predicted_by_ERGO	Polysaccharide biosynthesis protein	R	No	-	IMP	tmhmm:14	-	-	Wzx	-	-	-	-
LC_02049	wze	2078484	2077732	250	8,89	27422	-	Tyrosine-protein kinase (capsular polysacchar	capsular exopolysaccharide biosynthesis protein	Tyrosine-protein kinase (capsular polysacchar	no annotation	D	Yes	-	-	tmhmm:0	-	-	Wze	-	-	-	+
LC_02050	wzd	2079417	2078503	304	10,22	33999	-	Chain length regulator (capsular polysacchari	capsular exopolysaccharide biosynthesis protein	Chain length regulator (capsular polysacchari	Lipopolysaccharide biosynthesis|Sugar transpo	M	Yes	-	IMP	tmhmm:2	-	-	Wzd	-	-	-	+
LC_02051	oatA	2080215	2080940	241	9,77	26532	+	Acyltransferase	acyltransferase family protein	Acyltransferase family	Esterase, SGNH hydrolase-type|Esterase, SGN	null	Yes	-	Sec	tmhmm:1	-	-	oatA	-	-	-	+
LC_02052	yiaC	2081789	2081289	166	10,52	18170	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF988	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02053	yiaB	2082619	2081906	237	4,95	24536	-	Short-chain dehydrogenase/reductase SDR	3-ketoacyl-(acyl-carrier-protein) reductase / deh	Short chain dehydrogenase (EC 1.-.-.-)	Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_02054	yiaA	2082840	2082616	74	3,93	8337	-	Methionyl-tRNA synthetase	methionyl-tRNA synthetase	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02055	bcnIC	2083432	2083121	103	7,7	11651	-	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02056	gpm5	2084318	2083680	212	4,9	23417	-	Phosphoglycerate mutase	phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02057	oppF	2085546	2084563	327	6,09	36500	-	ABC transporter, oligopeptide transporter ATP	oligopeptide ABC transporter, ATPase compon	Oligopeptide transport ATP-binding protein op	ABC transporter related|AAA+ ATPase, core|Ol	EP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02058	oppD	2086600	2085548	350	6,01	38209	-	ABC transporter, oligopeptide transporter ATP	dipeptide/oligopeptide/nickel ABC transport syst	Oligopeptide transport ATP-binding protein op	ABC transporter related|AAA+ ATPase, core|Ol	EP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02059	oppC	2087610	2086612	332	10,28	36480	-	ABC transporter, oligopeptide transporter perm	dipeptide/oligopeptide/nickel ABC transport syst	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	EP	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_02060	oppB	2088533	2087610	307	9,72	33523	-	ABC transporter, oligopeptide transporter perm	dipeptide/oligopeptide/nickel ABC transport syst	Oligopeptide transport system permease prote	Binding-protein-dependent transport systems in	EP	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_02061	oppA	2090316	2088715	533	9,95	58638	-	ABC transporter, oligopeptide-binding protein	oligopeptide ABC transporter, oligopeptide-bind	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_02062	null	2092196	2090733	487	10,59	52340	-	Transporter, major facilitator superfamily MFS	predicted ORF	Multidrug resistance protein B	Tetracycline resistance protein TetB|Major facili	GEPF	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-

LC_02063	efp	2092950	2092387	187	4,92	20498	-	Protein elongation factor P	protein translation elongation factor P (EF-P)	Protein Translation Elongation Factor P (EF-P	Translation elongation factor P/YeiP, central|Tra	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02064	yrjD	2094135	2093428	235	5,1	25925	-	Conerved protein	conserved hypothetical protein (YkgG family prc	Hypothetical protein	Protein of unknown function DUF162	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02065	yrjC	2095612	2094128	494	7,08	55440	-	Iron-sulfur cluster binding protein	Iron-sulfur cluster binding protein YvfW	iron-sulfur cluster-binding protein	4Fe-4S ferredoxin, iron-sulfur binding|Protein of	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02066	yrjB	2096391	2095609	260	6,1	29305	-	Cysteine-rich domain protein	Fe-S oxidoreductase	Cysteine-rich domain of 2-hydroxy-acid oxidas	Cysteine-rich region, CCG	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02067	null	2096605	2096423	60	9,14	6589	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02068	null	2096820	2097365	181	5,01	20010	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02069	pts	2097882	2097541	113	4,42	11861	-	PTS system, cellobiose-specific IIA componer	PTS system, cellobiose-specific IIA component	PTS system, cellobiose-specific IIA componer	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02070	ybhE	2099006	2097906	366	6,63	40983	-	Conserved outer surface protein	conserved hypothetical protein (outer surface pr	outer surface protein	Peptidyl-prolyl cis-trans isomerase, cyclophilin-t	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02071	null	2099498	2099088	136	10,89	15541	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02072	null	2099740	2099576	54	8,79	5964	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	Sec	tmhmm:2	-	-	-	-	-	-	-
LC_02073	pts	2101173	2099737	478	9,68	52481	-	PTS system, cellobiose-specific IIC componer	PTS system, cellobiose-specific IIC component	PTS system, cellobiose-specific IIC componer	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_02074	melA	2101774	2103996	740	6,09	82350	+	Alpha-galactosidase (GH36)	alpha-galactosidase 2, melibiase	Alpha-galactosidase (EC 3.2.1.22)	Glycoside hydrolase, clan GH-D|Glycoside hydr	G	Yes	-	-	tmhmm:0	LC02074	-	-	-	-	-	+
LC_02075	yaaA	2104054	2104797	247	9,3	27996	+	Conserved protein (Yya-protein)	cytoplasmic protein YaaA	Hypothetical cytosolic protein	Protein of unknown function DUF328	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02076	null	2104953	2105696	247	9,15	28403	+	Transcriptional regulator, LuxR family	DNA-binding response regulator, CitB family (R	Transcriptional regulator	Bacterial regulatory protein, LuxR|Winged helix	TK	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02077	null	2106177	2105773	134	6,68	15260	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02078	null	2108347	2106248	699	9,07	78440	-	ATP-dependent exoDNAse (Exonuclease V),	predicted ORF	Exodeoxyribonuclease V alpha chain (EC 3.1.	no annotation	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02079	null	2108990	2108388	200	7,29	22719	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02080	null	2109652	2110269	205	4,37	20587	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	Peptidase aspartic, active site	C	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_02081	null	2111560	2110748	270	5,3	28704	-	Sugar kinase, ribokinase family protein	sugar kinase, ribokinase family	Fructokinase family protein	PfkB	G	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_02082	null	2114832	2112151	893	6,34	93200	-	N-acetylmuramoyl-L-alanine amidase	conserved hypothetical protein (secreted by hon	not_predicted_by_ERGO	Surface protein from Gram-positive cocci, anch	null	No	iG/intimin	LPxTG	tmhmm:2	-	-	-	-	-	-	-
LC_02083	null	2115701	2115147	184	8,6	20785	-	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_02084	hyuA	2117358	2115802	518	5,09	54893	-	Hydantoinase/oxoprolinase	hydantoinase/oxoprolinase family protein	Hydantoinase/oxoprolinase family	Hydantoinase/oxoprolinase|Hydantoinaseoxopro	EQ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02085	null	2118517	2117429	362	4,91	39255	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	ATP-dependent DNA ligase|Alcohol dehydroge	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02086	null	2119893	2118634	419	9,79	43959	-	Cytosine permease	cytosine/purines/uracil/thiamine/allantoin perme	Cytosine permease	Permease for cytosine/purines, uracil, thiamine,	F	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_02087	null	2121133	2120327	268	9,41	32059	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02088	null	2121280	2122455	391	10,16	45032	+	Type I restriction-modification system specific	type I restriction-modification endonuclease S s	not_predicted_by_ERGO	Restriction modification system DNA specificity	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02089	int	2122543	2123469	308	9,81	35430	+	Phage-related integrase	bacteriophage integrase	DNA integration/recombination/inversion prote	Integrase, catalytic core, phage|DNA breaking-r	L	Yes	-	-	tmhmm:0	-	phage	-	-	-	-	-
LC_02090	null	2124725	2123517	402	10,57	45585	-	Putative protein without homology	restriction modification system DNA specificity	not_predicted_by_ERGO	Restriction modification system DNA specificity	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02091	hsdM	2126367	2124718	549	4,59	61757	-	Type I restriction-modification system, M subu	type I restriction-modification system M subunit	not_predicted_by_ERGO	N-6 Adenine-specific DNA methylase|N6 adeni	V	No	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_02092	hsdR	2129472	2126383	1029	6,53	117910	-	Type I site-specific restriction-modification sys	restriction enzyme, endonuclease subunit / type	not_predicted_by_ERGO	Type I restriction modification system site-speci	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02093	null	2129829	2131013	394	9,86	44850	+	Transcriptional regulator	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Transcriptional regulator AbrB|SpoVT/AbrB-like	K	Yes	-	IMP	tmhmm:10	-	-	-	-	regulator	-	+
LC_02094	null	2131869	2131378	163	9,91	18146	-	Putative protein without homology	phage protein, infection protein	not_predicted_by_ERGO	no annotation	S	No	-	IMP	tmhmm:4	-	phage	-	-	-	-	-
LC_02095	null	2134109	2132088	673	9,4	72734	-	Phage-related infection protein	phage protein, infection protein / membrane pro	Phage infection protein	no annotation	S	Yes	-	IMP	tmhmm:1	-	phage	-	-	-	-	+
LC_02096	Span	2135135	2134344	263	4,84	27490	-	PTS system, sucrose-specific IIABC	PTS system, beta-glucoside/sucrose-specific II	PTS system, sucrose-specific IIABC componen	Phosphotransferase system, sugar-specific per	G	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	+
LC_02097	scrA	2136309	2135122	395	8,86	41799	-	PTS system, sucrose-specific IIBC componer	PTS system, sucrose-specific EIIABC compon	not_predicted_by_ERGO	Phosphotransferase system, EIIB|Phosphotran	G	No	-	IMP	tmhmm:7	-	-	-	-	-	-	+
LC_02098	agl4	2137975	2136311	554	5,21	62288	-	Oligo-1,6-glucosidase (GH13)	oligo-1,6-glucosidase (alpha-glucosidase, Gsj)(	Oligo-1,6-glucosidase (EC 3.2.1.10)	Glycosyl hydrolase, family 13, catalytic region|G	G	Yes	fibronectin	-	tmhmm:0	LC02098	-	-	-	-	-	-
LC_02099	null	2138424	2138032	130	4,32	13699	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_02100	null	2139034	2138429	201	9,33	21717	-	Transcriptional regulator, LacI family	predicted ORF	Transcriptional regulator, LacI family	Bacterial regulatory protein, LacI|Periplasmic bi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_02101	scrB	2140804	2139326	492	5,42	55022	-	Sucrose-6-phosphate hydrolase (GH32)	sucrose-6-phosphate hydrolase (Sucrase) (Inve	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Glycoside hydrolase, family 32|Sucrose-6-phos	G	Yes	-	-	tmhmm:0	LC02101	-	-	-	-	-	+
LC_02102	null	2142143	2141274	289	10,3	32348	-	NmrA family protein	nucleoside-diphosphate-sugar epimerases	Hypothetical protein	NmrA-like	MG	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02103	cfa	2143413	2142232	393	6,24	45517	-	Cyclopropane-fatty-acyl-phospholipid synthase	cyclopropane-fatty-acyl-phospholipid synthase-r	Cyclopropane-fatty-acyl-phospholipid synthase	Peptidase S8 and S53, subtilisin, kexin, sedolis	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02104	null	2143892	2143512	126	6,59	13643	-	Acetyl-CoA carboxylase alpha subunit	predicted ORF	not_predicted_by_ERGO	Acetyl-CoA carboxylase, alpha subunit|Acetyl-c	I	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02105	null	2144284	2143961	107	9,96	11959	-	Acetyl-CoA carboxylase alpha subunit	predicted ORF	not_predicted_by_ERGO	Acetyl-CoA carboxylase, alpha subunit|Acetyl-c	I	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02106	null	2144283	2144588	101	10,46	11351	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02107	accD	2145383	2144568	271	6,86	29476	-	Acetyl-CoA carboxylase carboxyl transferase,	AccD, acetyl-CoA carboxylase carboxyl transfer	Acetyl-coenzyme A carboxylase carboxyl trans	Carboxyl transferase|Acetyl-CoA carboxylase ca	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02108	accC	2146747	2145365	460	5,09	49780	-	Acetyl-CoA carboxylase, biotin carboxylase	biotin carboxylase / acetyl-coenzyme A carboxyl	Biotin carboxylase (EC 6.3.4.14)	Carbamoyl-phosphate synthase L chain, ATP-b	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02109	fabZ2	2147225	2146785	146	8,47	15947	-	(3R)-hydroxymyristoyl-[acyl-carrier-protein] del	beta-hydroxyacyl-(acyl-carrier-protein) dehydrat	(3R)-hydroxyacyl-[acyl carrier protein] dehydra	Beta-hydroxyacyl-(acyl-carrier-protein) dehydrat	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02110	accB	2147721	2147275	148	4,52	15757	-	Acetyl-CoA carboxylase, biotin carboxyl carrie	acetyl-CoA carboxylase biotin carboxyl carrier p	Biotin carboxyl carrier protein of acetyl-CoA ca	Biotin/lipoyl attachment|Acetyl-CoA biotin carbo	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02111	fabF	2148947	2147727	406	5	42277	-	3-oxoacyl-[acyl-carrier-protein] synthase II	3-oxoacyl-acyl carrier protein synthase II (EC 2.	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2	Beta-ketoacyl synthase|Beta-ketoacyl synthase,	IQ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02112	fabG	2149698	2148970	242	6,27	25342	-	3-oxoacyl-(Acyl-carrier-protein) reductase	i-oxoacyl-acyl carrier protein reductase (EC 1.1.	3-oxoacyl-[acyl-carrier protein] reductase (EC	Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02113	null	2150618	2149695	307	4,58	32361	-	(Acyl-carrier-protein) S-malonyltransferase	acyl-carrier-protein S-malonyltransferase	Malonyl-CoA-[acyl-carrier-protein] transacylas	Acyl transferase region|Acyl transferase	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02114	fabK	2151628	2150648	326	5,43	34065	-	Enoyl-(Acyl-carrier-protein) reductase II	enoyl-(acyl-carrier-protein) reductase II / dioxyg	Enoyl-[acyl-carrier protein] reductase (NADH)	2-nitropropane dioxygenase, NPD|Aldolase-type	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02115	acpP	2151890	2151651	79	3,6	8963	-	Acyl carrier protein	strongly similar to acyl carrier protein AcpP	Acyl carrier protein	Acyl carrier protein (ACP)|Phosphopantetheine-	IQ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02116	fabH2	2152917	2151958	319	4,71	34849	-	3-oxoacyl-[acyl-carrier-protein] synthase III	3-oxoacyl-acyl-carrier-protein synthase III / Beta	3-oxoacyl-[acyl-carrier-protein] synthase III (EC	Beta-ketoacyl-acyl carrier protein synthase III (F	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02117	marR	2153382	2152933	149	10,24	17326	-	Transcriptional regulator, MarR family	transcriptional regulator, MarR family	Transcriptional regulator, MarR family	Ribosomal protein S16|Bacterial regulatory prot	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02118	fabA	2153889	2153452	145	5,15	15631	-	(3R)-hydroxymyristoyl-[acyl-carrier-protein] del	beta-hydroxyacyl-(acyl-carrier-protein) dehydrat	(3R)-hydroxyacyl-[acyl carrier protein] dehydra	Beta-hydroxyacyl-(acyl-carrier-protein) dehydrat	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02119	null	2155553	2154570	327	7,06	36490	-	Alpha/beta superfamily hydrolase	alpha/beta superfamily hydrolase	Lipase (EC 3.1.1.3)	Alpha/beta hydrolase fold-1	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02120	bdh	2156796	2155600	398	5,11	43301	-	Iron-containing alcohol dehydrogenase	iron-containing alcohol dehydrogenase YugJ	NADH-dependent butanol dehydrogenase A (I	Iron-containing alcohol dehydrogenase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02121	null	2157487	2157122	121	6,97	13545	-	Rhodanese-related sulfurtransferases	rhodanese-related sulfurtransferase	Rhodanese-related sulfurtransferases	Rhodanese-like	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02122	null	2158016	2157474	180	8,98	20499	-	Transcriptional regulator, MarR family	transcription regulator	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02123	null	2159317	2158460	285	9,13	32031	-	Conserved protein	membrane associated GGDEF domain (possibl	not_predicted_by_ERGO	Tetracyclin repressor-like, C-terminal	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02124	null	2160353	2159298	351	10,7	38654	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02125	null	2161317	2160442	291	7,84	32014	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02126	ydaM	2162626	2161373	417	9,36	47299	-	Glycosyl transferase, group 2	glycosyl transferase, group 2 family protein	not_predicted_by_ERGO	Glycosyl transferase, family 2	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02127	null	2164233	2162674	519	10,58	57650	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02128	null	2165720	2164230	496	10,29	55367	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_02129	null	2166661	2165717	314	9,56	34939	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	Six-hairpin glycosidase-like	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02130	null	2166868	2166695	57	11,31	6271	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Lipobox	tmhmm:0	-	-	-	-	-	-	-
LC_02131	null	2167674	2167075	199	5,87	23028	-	Diguanylate cyclase	conserved hypothetical protein	not_predicted_by_ERGO	GGDEF	T	No	-	-	tmhmm:0	-	-	-	-	-	-	-

LC_02132	null	2168269	2167655	204	9,36	22537	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02133	nox1	2169648	2168275	457	6,34	50384	-	NADH oxidase	NADH oxidase (NOXase)	not_predicted_by_ERGO	Pyridine nucleotide-disulphide oxidoreductase,	R	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02134	null	2170378	2169692	228	6,53	26098	-	C-di-GMP-specific phosphodiesterase	C-di-GMP-specific phosphodiesterase	not_predicted_by_ERGO	EAL	T	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02135	null	2170948	2170757	63	11,84	7048	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02136	null	2171577	2171308	89	10,73	10013	-	Transcriptional regulator, MarR family	predicted ORF	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02137	null	2172502	2171747	251	4,32	26788	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02138	null	2172954	2172607	115	6,8	12834	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02139	null	2173609	2172923	228	9,24	24521	-	Esterase	predicted ORF	Acetyl esterase (EC 3.1.1.-)	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-	
LC_02140	null	2174849	2173770	359	9,89	38382	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Acid phosphatase/vanadium-dependent haloper	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02141	null	2175328	2175170	52	7,96	5990	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02142	null	2175755	2175321	144	5,01	16134	-	Transcriptional regulator, MarR family	transcriptional regulator, MarR family	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02143	null	2176003	2175842	53	9,53	5666	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02144	null	2176508	2176041	155	4,76	17493	-	Phosphohydrolase, MutT/nudix family	ADP-ribose Phosphohydrolase (MutT/nudix fan	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02145	gpmA	2177435	2176746	229	5,19	25955	-	2,3-bisphosphoglycerate-dependent phosphog	phosphoglycerate mutase 1 family protein	Phosphoglycerate mutase (EC 5.4.2.1)	Phosphoglycerate/bisphosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02146	null	2177705	2177911	68	10,17	7677	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02147	null	2178015	2179061	348	7,49	36805	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02148	null	2180322	2179225	365	9,89	40419	-	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin bindi	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, trans	V	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+	
LC_02149	null	2181388	2180312	358	8,7	40236	-	Permease	permease	Hypothetical membrane spanning protein	Protein of unknown function UPF0118	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02150	srtA	2182180	2181479	233	10,51	25788	-	Sortase A	sortase (surface protein transpeptidase)	Hypothetical protein ylcC	Peptidase C60, sortase A and B	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+	
LC_02151	gtcA2	2182479	2182889	136	10,18	15932	+	Cell wall teichoic acid glycosylation protein gtc	cell wall teichoic acid glycosylation protein, gtcA	Cell wall teichoic acid glycosylation protein gtc	GtrA-like protein	M	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02152	poxF	2184744	2182981	587	5,33	63466	-	Pyruvate oxidase	pyruvate oxidase or other thiamine pyrophospha	Pyruvate oxidase (EC 1.2.3.3)	TPP-binding enzymes|Thiamine pyrophosphate	EH	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02153	gbuC	2185829	2184927	300	10,16	32828	-	ABC transporter, glycine/betaine/carnitine sub	glycine/betaine/carnitine ABC transporter, subs	Glycine betaine-binding protein	Substrate-binding region of ABC-type glycine be	E	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_02154	gbuB	2186692	2185841	283	9,85	30968	-	ABC transporter, binding-protein-dependent tr	glycine betaine/L-proline ABC transporter, perm	Glycine betaine transport system permease pr	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02155	gbuA	2187908	2186685	407	5,03	44741	-	ABC transporter, glycine betaine/L-proline trar	glycine betaine/L-proline ABC transporter, ATP-	Glycine betaine transport ATP-binding protein	Cystathionine-beta-synthase|ABC transporter re	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02156	sfsA	2188992	2188261	243	9,32	27238	-	Sugar fermentation stimulation protein	sugar fermentation stimulation protein, DNA-bin	Sugar fermentation stimulation protein	Sugar fermentation stimulation protein	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02157	null	2189106	2189309	67	12,32	7764	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02158	usp1	2189787	2189326	153	5	16741	-	Universal stress protein, UspA family	universal stress protein UspA related nucleotid	Universal stress protein family	UspA|Rossmann-like alpha/beta/alpha sandwich	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02159	yxbA	2191094	2189766	442	8,49	51093	-	ATP-grasp enzyme	ATP-grasp enzyme	RepB family protein	ATP-grasp fold	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02160	thrB	2192254	2191376	292	4,89	31254	-	Homoserine kinase	homoserine kinase ThrB	Homoserine kinase (EC 2.7.1.39)	Homoserine kinase|GHMP kinase, ATP-binding	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02161	thrC	2193734	2192220	504	7,1	55110	-	Threonine synthase	L-threonine synthase	Threonine synthase (EC 4.2.3.1)	Serine/threonine dehydratase, pyridoxal-phosph	E	Yes	-	LPxTG	tmhmm:0	-	-	-	-	-	-	+	
LC_02162	thrA	2193842	2195041	399	5,66	44303	+	Homoserine dehydrogenase	homoserine dehydrogenase	Homoserine dehydrogenase (EC 1.1.1.3)	Homoserine dehydrogenase, catalytic|Homoseri	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02163	apk	2195038	2196384	448	6,33	49695	+	Aspartokinase	aspartate kinase	Aspartokinase (EC 2.7.2.4)	Aspartate/glutamate/uridylate kinase|Aspartate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02164	Flot1	2198042	2196510	510	4,87	55350	-	Membrane protease subunit, stomatin/prohibit	membrane protease subunit, stomatin/prohibitin	Flotillin	Band 7 protein|Flotillin	S	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02165	null	2198439	2198026	137	6,08	15069	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02166	pfoSR	2199711	2198668	347	9,59	35584	-	Conserved membrane spanning protein	PTS system, fructose-specific IIBC component	Hypothetical membrane spanning protein	no annotation	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02167	ldhA	2200717	2199725	330	4,83	35314	-	D-2-hydroxyacid dehydrogenase	D-Lactate dehydrogenase related 2-hydroxyacid	D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	D-isomer specific 2-hydroxyacid dehydrogenase	CHR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02168	araT	2201929	2200766	387	6,61	42189	-	Aspartate/tyrosine/aromatic aminotransferase	aspartate/tyrosine/aromatic aminotransferase cl	Aromatic amino acid aminotransferase (EC 2.6	1-aminocyclopropane-1-carboxylate synthase|A	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02169	yfhL	2202384	2203091	235	4,5	24835	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	Protein of unknown function DUF124	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02170	null	2203112	2203900	262	7,53	28978	+	Alpha/beta superfamily hydrolase	predicted ORF	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hy	Alpha/beta hydrolase fold-1|Phosphatidylinositol	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02171	null	2204550	2203960	196	7,9	22581	-	Transcriptional regulator, TetR family	transcriptional regulator, TetR family	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomain	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02172	null	2204803	2206284	493	10	52841	+	Phage-related infection protein	predicted ORF	Phage infection protein	no annotation	S	Yes	-	IMP	tmhmm:6	-	phage	-	-	-	-	+	
LC_02173	null	2206541	2207479	312	7,32	33558	+	Cation efflux family protein	predicted ORF	Cobalt-zinc-cadmium resistance protein czcD	Cation efflux protein	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02174	asnH	2209500	2207596	634	6,41	73299	-	Asparagine synthase	asparagine synthase (glutamine-hydrolyzing)	Asparagine synthetase [glutamine-hydrolyzing	Glutamine amidotransferase, class-II|Asparagin	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02175	null	2209889	2209626	87	12,39	9922	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02176	null	2211494	2210520	324	10,26	36642	-	Metallophosphoesterase	predicted ORF	Metallo-phosphoesterase (EC 3.1.-.-)	Metallophosphoesterase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02177	menA	2212536	2211622	304	9,37	33925	-	1,4-dihydroxy-2-naphthoate octaprenyltransfer	1,4-dihydroxy-2-naphthoate octaprenyltransfera	1,4-dihydroxy-2-naphthoate polyprenyltransfer	UbiA prenyltransferase	H	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02178	sds	2212612	2213580	322	7,19	35512	+	Octaprenyl-diphosphate synthase	octaprenyl-diphosphate synthase	Farnesyl pyrophosphate synthetase (EC 2.5.1	Polyprenyl synthetase|Terpenoid synthase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02179	ack2	2213802	2215007	401	7,43	44068	+	Acetate kinase	acetate kinase	Acetate kinase (EC 2.7.2.1)	Acetate and butyrate kinase|Acetate kinase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02180	ysdB	2215285	2216172	295	7,8	32905	+	ABC transporter, ATPase component	Na+ efflux ABC transporter, ATPase componer	Sodium export ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02181	null	2216175	2217446	423	10,46	45576	+	ABC transporter, Na+ efflux pump transporter	Na+ efflux ABC transporter, permease compon	Sodium export permease protein	no annotation	CP	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_02182	gntR	2217465	2217860	131	4,92	14315	+	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|Winged	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02183	CcmA	2217850	2218716	288	5,27	31616	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02184	null	2218709	2219353	214	9,76	23939	+	Conserved protein	conserved hypothetical protein	ABC transporter ATP-binding protein	Beta tubulin, autoregulation binding site	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02185	gdh	2220205	2219420	261	5,89	27724	-	Glucose 1-dehydrogenase	Glucose 1-dehydrogenase 4 (GLCDH-IV)	Glucose 1-dehydrogenase (EC 1.1.1.47)	Short-chain dehydrogenase/reductase SDR|Glu	IQR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02186	pbg9	2222114	2220666	482	5,31	55152	-	6-phospho-beta-glucosidase (GH1)	beta-glucosidase/6-phospho-beta-glucosidase/t	6-phospho-beta-glucosidase (EC 3.2.1.86)	Glycoside hydrolase, family 1|Glycoside hydrola	G	Yes	-	-	tmhmm:0	LC02186	-	-	-	-	-	-	
LC_02187	pts	2223968	2222133	611	6,72	64118	-	PTS system, beta-glucoside-specific IIABC co	PTS system, beta-glucoside/trehalose-specific	PTS system, beta-glucoside-specific IIABC co	Phosphotransferase system, sugar-specific per	G	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02188	bglG4	2225163	2224291	290	7,14	33123	-	Beta-glucoside operon antiterminator	beta-glucoside operon antiterminator	Transcription antiterminator, BglG family	CAT RNA-binding region|PRD	G	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02189	null	2225946	2225296	216	5,52	23979	-	ABC transporter, ATPase component	predicted ORF	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02190	null	2226918	2225947	323	10,24	34947	-	ABC transporter, multidrug transporter ATPas	predicted ORF	ABC transporter ATP-binding protein	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02191	null	2228605	2226911	564	9,43	62356	-	ABC transporter, cytochrome bd biosynthesis	cytochrome bd biosynthesis ABC transporter, A	ABC transporter ATP-binding protein	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02192	ynhH	2229251	2228817	144	10,36	16178	-	Conserved protein	conserved hypothetical protein (secreted protei	Hypothetical protein	Protein of unknown function DUF1312	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	-	
LC_02193	null	2230529	2229429	366	9,97	38049	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_02194	cydD	2232509	2230791	572	6,81	64368	-	ABC transporter, ATPase component	Cytochrome bd biosynthesis ABC transporter, A	Transport ATP-binding protein cydC	ABC transporter related|AAA+ ATPase, core|Al	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02195	cydC	2234241	2232499	580	6,9	64274	-	ABC transporter, ATPase component	cytochrome bd biosynthesis ABC transporter, A	Transport ATP-binding protein cydD	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02196	cydB	2235251	2234238	337	8,43	37261	-	Cytochrome D ubiquinol oxidase, subunit II	cytochrome bd-type ubiquinol oxidase subunit 2	Cytochrome d ubiquinol oxidase subunit II (EC	Cytochrome bd ubiquinol oxidase, subunit II	C	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02197	cydA	2236672	2235248	474	9,42	53441	-	Cytochrome D ubiquinol oxidase, subunit I	Cytochrome bd-type ubiquinol oxidase, subunit I	Cytochrome d ubiquinol oxidase subunit I (EC	Cytochrome bd ubiquinol oxidase, subunit I	C	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	+	
LC_02198	pdp	2238208	2236904	434	6,71	45989	-	Pyrimidine-nucleoside phosphorylase	pyrimidine-nucleoside phosphorylase (PYNP)	Pyrimidine-nucleoside phosphorylase (EC 2.4.	Pyrimidine-nucleoside phosphorylase|Glycosyl t	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02199	add	2238307	2239326	339	6,04	37111	+	Adenosine deaminase	adenosine deaminase (adenosine aminohydrola	Adenosine deaminase (EC 3.5.4.4)	Adenosine/AMP deaminase|Adenosine deaminas	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02200	null	2239541	2239777	78	6,22	8891	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	

LC_02201	null	2240269	2239781	162	5,44	17946	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02202	null	2240396	2240566	56	11,03	6573	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02203	null	2241674	2240757	305	10,33	33519	-	Permease of the drug/metabolite transporter (I	permease of the drug/metabolite transporter (DI	Transporter, drug/metabolite exporter family	Protein of unknown function DUF6, transmemb	GER	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_02204	tag1	2242318	2241704	204	7,94	23317	-	DNA-3-methyladenine glycosylase I	dna-3-methyladenine glycosylase 1 (tag1) (dna-3	DNA-3-methyladenine glycosylase (EC 3.2.2.2	IQ calmodulin-binding region	Methyladenine gly	L	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02205	null	2242571	2242753	60	11,66	6561	+	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02206	usp5	2243205	2242759	148	4,75	16236	-	Universal stress protein family	Universal stress protein UspA related nucleotid	Universal stress protein family	Universal stress protein (Usp)	UspA	Rossmann	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02207	null	2243510	2243899	129	5,91	14042	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional repressor	Helix-turn-helix type 3	Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02208	ptp3	2244405	2245193	262	5,04	29298	+	Protein tyrosine/serine phosphatase	protein tyrosine phosphatase	Protein tyrosine phosphatase (EC 3.1.3.48)	no annotation	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02209	ygaP	2245473	2246624	383	9,08	42618	+	Iron-sulfur cluster-binding protein	similar to iron-sulfur cluster-binding protein	iron-sulfur cluster-binding protein	4Fe-4S ferredoxin, iron-sulfur binding	4Fe-4S c	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02210	null	2246664	2247029	121	4,86	13852	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02211	null	2247719	2247177	180	10,92	18968	-	Biotin synthase	conserved hypothetical protein	BioY protein	BioY protein	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02212	null	2248189	2248824	211	7,55	23472	+	SAM-dependent methyltransferase	SAM-dependent methyltransferase	Ubiquinone/menaquinone biosynthesis methyl	no annotation	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02213	null	2249935	2248937	332	7,73	34270	-	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_02214	guaA	2250835	2250215	206	5,04	22503	-	GMP synthase-Glutamine amidotransferase d	GMP synthase - Glutamine amidotransferase d	GMP synthase [glutamine-hydrolyzing] (EC 6.	Glutamine amidotransferase class-I	Glutamine	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02215	null	2251603	2250854	249	8,42	27729	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	Conserved hypothetical protein CHP02452	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02216	null	2251909	2253297	462	4,88	51910	+	Magnesium and cobalt efflux protein, hemolysi	ion Mg(2+)/Co(2+) transport protein corC, hemc	Magnesium and cobalt efflux protein corC	Cystathionine-beta-synthase	Protein of unknow	R	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02217	null	2254325	2253528	265	8,93	28847	-	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Protein of unknown function DUF915, hydrolas	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_02218	null	2255313	2254312	333	9,87	37877	-	Acyltransferase 3	predicted ORF	O-acetyl transferase (EC 2.3.1.-)	Acyltransferase 3	G	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_02219	ImrB-2	2255476	2256933	485	10,12	52238	+	Transporter, major facilitator superfamily MFS	drug resistance transporter, EmrB/QacA family	Multidrug resistance protein B	Tetracycline resistance protein TetB	Drug resis	V	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-
LC_02220	null	2256930	2257424	164	10,1	18199	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_02221	maf	2258070	2257522	182	6,81	19844	-	Septum formation protein Maf	Nucleotide-binding protein implicated in inhibitic	Septum formation protein Maf	Maf-like protein	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02222	mutL	2260019	2258067	650	5,48	71748	-	DNA mismatch repair protein mutL	DNA mismatch repair protein, MutL family	DNA mismatch repair protein mutL	DNA mismatch repair protein	ATP-binding regic	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02223	mutS	2262597	2260024	857	5,62	94991	-	DNA mismatch repair protein mutS	DNA mismatch repair ATPase MutS1	DNA mismatch repair protein mutS	DNA mismatch repair protein MutS, C-terminal	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02224	ydaO	2264874	2263045	609	9,91	66811	-	Amino acid transporter	Amino acid permease-associated region	Amino acid permease	no annotation	E	Yes	-	IMP	tmhmm:11	-	-	-	-	-	-	+
LC_02225	null	2264918	2265073	51	11,66	6139	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02226	null	2265414	2265070	114	7,95	13441	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02227	null	2265473	2265649	58	10,12	6794	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02228	groEL	2267367	2265733	544	4,67	57393	-	60 kDa chaperonin GROEL	60 kDa chaperonin (Protein Cpn60) (groEL prot	60 kDa chaperonin GROEL	Chaperonin Cpn60	Chaperonin Cpn60/TCP-1	C	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02229	groES	2267684	2267403	93	4,65	10040	-	10 kDa chaperonin GROES	Co-chaperonin GroES (HSP10)	10 kDa chaperonin GROES	Chaperonin Cpn10	GroES-like	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02230	null	2267837	2268481	214	9,41	23148	+	Metal-dependent membrane protease	metal-dependent membrane protease	CAAX amino terminal protease family	Abortive infection protein	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	protease	-
LC_02231	epsIIA	2268560	2269618	352	10	39114	+	Transcriptional regulator, LytR family	transcriptional regulator, LytR family	Transcriptional regulator, LytR family	Cell envelope-related transcriptional attenuator	K	Yes	-	Sec	tmhmm:1	-	-	-	-	regulator	-	+
LC_02232	null	2269837	2269625	70	8,05	7800	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02233	nrtD	2271734	2270847	295	7,26	33063	-	ABC transporter, ATPase component	ABC transporter, ATPase component	Acetoin transport ATP-binding protein	ABC transporter related	AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02234	ytrA	2272096	2271731	121	6,81	13333	-	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Acetoin transport repressor	Bacterial regulatory protein GntR, HTH	Winged	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02235	rex	2272860	2272207	217	9,1	24185	-	Redox-sensing transcriptional repressor Rex	redox-sensing transcriptional regulator (repress	AT-rich DNA-binding protein / Redox-sensitive	CoA-binding	Rex DNA-binding, C-terminal	Win	R	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02236	uup	2273079	2275031	650	5,05	72555	+	ABC transporter, ATPase component	ABC transporter with duplicated ATPase domai	ABC transporter ATP-binding protein	ABC transporter related	AAA+ ATPase, core	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02237	celA	2275483	2275157	108	8,48	11613	-	PTS system, cellobiose-specific IIB componer	PTS system, cellobiose-specific IIB component	PTS system, cellobiose-specific IIB componer	Bacterial extracellular solute-binding protein, far	G	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+
LC_02238	gcp	2276603	2275581	340	6,01	36147	-	O-sialoglycoprotein endopeptidase	O-sialoglycoprotein endopeptidase (Glycoprotec	O-sialoglycoprotein endopeptidase (EC 3.4.24	Peptidase M22, glycoprotease	Peptidase M22, (	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_02239	rimI1	2277172	2276639	177	9,44	20973	-	Ribosomal-protein-alanine acetyltransferase	ribosomal-protein-alanine N-acetyltransferase Y	Ribosomal-protein-S18-alanine acetyltransfera	GCN5-related N-acetyltransferase	Ribosomal-p	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02240	gpp	2277878	2277156	240	6,9	26193	-	Glycoprotein endopeptidase	metal-dependent protease, molecular chaperon	Non-proteolytic protein, peptidase family M22	Peptidase M22, glycoprotease	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_02241	null	2278759	2278061	232	10,88	26096	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02242	null	2279716	2279198	172	11,15	19096	-	Conserved hypothetical membrane spanning p	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02243	asnA1	2280313	2281287	324	5,82	34952	+	L-asparaginase	L-asparaginase/archaeal Glu-tRNAGln amidotra	L-asparaginase (EC 3.5.1.1)	Asparaginase/glutaminase	EJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02244	fat	2282119	2281376	247	5,18	28787	-	Acyl-ACP thioesterase	acyl-ACP thioesterase	Acyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.	Acyl-ACP thioesterase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02245	yeaE	2283040	2282183	285	7,98	30790	-	Tetrapyrrole methylase family protein	uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin	Tetrapyrrole (Corrin/Porphyrin) methylase fam	Tetrapyrrole methylase	Protein of unknown func	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02246	null	2283380	2283042	112	4,52	13011	-	Initiation-control protein	Regulator of replication initiation timing, Initiatior	Initiation-control protein	S15/NS1, RNA-binding	Protein of unknown fun	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02247	holB	2284362	2283385	325	6,52	35771	-	DNA polymerase III, delta subunit	DNA-directed DNA polymerase III, delta prime s	DNA polymerase III, delta' subunit (EC 2.7.7.7	DNA polymerase III, delta prime subunit	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02248	yaaQ	2284691	2284362	109	4,71	11873	-	Conserved hypothetical membrane spanning p	aminotransferase, class IV	Hypothetical cytosolic protein	Protein of unknown function DUF970	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02249	tmk	2285293	2284748	181	5,93	20043	-	Thymidylate kinase	thymidylate kinase (dTMP kinase)	Thymidylate kinase (EC 2.7.4.9)	Thymidylate kinase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02250	null	2285396	2285277	39	8,49	4130	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02251	null	2285908	2285645	87	9,97	10253	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02252	recR	2286507	2285908	199	5,66	21963	-	Recombination protein recR	DNA recombination protein recR	Recombination protein recR	RecR protein	Toprim subdomain	TOPRIM	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02253	null	2286943	2286635	102	4,67	11609	-	Conserved protein	conserved hypothetical protein (UPF0133-prote	Hypothetical cytosolic protein	Conserved hypothetical protein 103	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02254	dnaX	2288657	2286960	565	6,69	62417	-	DNA polymerase III gamma and tau subunits	DNA polymerase III, subunits gamma and tau	DNA polymerase III subunit gamma/tau (EC 2	Chaperonin clpA/B	AAA+ ATPase, core	AAA A	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02255	cdd3	2289411	2288905	168	6,75	18141	-	CMP/dCMP deaminase, zinc-binding	CMP/dCMP deaminase, zinc-binding	tRNA-specific adenosine deaminase (EC 3.5.4	CMP/dCMP deaminase, zinc-binding	FJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02256	null	2289928	2289602	108	9,87	11824	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_02257	rsmc	2290581	2289985	198	7,26	21306	-	16S rRNA m(2)G 1207 methyltransferase	16S RNA G1207 methylase RsmC	16S rRNA m(2)G 1207 methyltransferase (EC	Methyltransferase small	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02258	null	2291323	2290727	198	10,02	22608	-	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	Protein of unknown function DUF471	Protein of	S	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02259	null	2293337	2291355	660	9,83	74640	-	Lysyl-tRNA synthetase (Class II)	conserved hypothetical protein	Lysylcardiolipin synthase (EC 2.3.2.-) / Lysyltr	Conserved hypothetical protein 374|Protein of u	S	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	+
LC_02260	null	2293685	2293840	51	8,79	5391	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02261	null	2294321	2294737	138	11	16695	+	Transposase, IS891 family protein	conserved hypothetical protein	not_predicted_by_ERGO	Transposase (probable), IS891/IS1136/IS1341	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02262	null	2294750	2295502	250	10,06	28899	+	Transposase, IS605 family protein	transposase for insertion sequence element	not_predicted_by_ERGO	Transposase (probable), IS891/IS1136/IS1341	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02263	null	2295680	2296093	137	4,21	14936	+	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_02264	ccpB	2296207	2297142	311	9,55	34460	+	Transcriptional regulator, LacI family	sugar-binding transcriptional regulator, LacI fan	Catabolite control protein B	Bacterial regulatory protein, LacI|Periplasmic bi	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02265	prtP	2303232	2297311	1973	5,06	206599	-	Endopeptidase lactocepin (prtP)	subtilisin-like serine peptidase. MEROPS famil	Endopeptidase lactocepin (EC 3.4.21.96)	Peptidase S8 and S53, subtilisin, kexin, sedolis	O	Yes	fibronectin	LPxTG	tmhmm:2	-	-	-	-	-	protease	+
LC_02266	prtM	2303517	2304419	300	10,41	33066	+	Endopeptidase maturation protein prtM	Protein maturation protease precursor prtM (pep	Endopeptidase maturation protein prtM / Pepti	Peptidyl-prolyl cis-trans isomerase, PpiC-type	O	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	protease	+
LC_02267	rplL	2304990	2304622	122	4,24	12589	-	LSU/50S ribosomal protein L7/L12P	50S ribosomal protein L7/L12 (BL9) (Vegetative	LSU ribosomal protein L12P (L7/L12)	Ribosomal protein L7/L12|Ribosomal protein L7	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02268	rplJ	2305537	2305031	168	4,76	18248	-	LSU/50S ribosomal protein L10P	LSU ribosomal protein L10P (50S ribosomal pro	LSU ribosomal protein L10P	Ribosomal protein L10|Eubacterial ribosomal pr	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02269	pmrB	2305859	2307091	410	10,24	44080	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance efflux pump	Tetracycline resistance protein|Major facilitator :	GEPF	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-

LC_02270	null	2308006	2307194	270	6,3	30153	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02271	null	2308538	2308008	176	6,35	20221	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02272	ycel	2308803	2310026	407	10,39	43967	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily MF	Transporter, MFS superfamily	Sugar transporter superfamily|Major facilitator s	GEPF	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	
LC_02273	null	2313646	2310377	1089	4,81	97253	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Surface protein from Gram-positive cocci, anch	null	No	-	LPxTG	tmhmm:1	-	-	-	-	-	-	-	
LC_02274	null	2316961	2313767	1064	4,34	105973	-	Fibrinogen-binding protein	predicted ORF	not_predicted_by_ERGO	DNA topoisomerase, type IIA, subunit B or N-te	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_02275	null	2318658	2317162	498	7,37	57047	-	Glycosyl transferase, group 1	glycosyltransferase	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Protein of unknov	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02276	yohH	2320208	2318655	517	6,39	59258	-	Glycosyl transferase, group 1	glycosyltransferase	Poly(Glycerol-phosphate) alpha-glucosyltransf	Glycosyl transferase, group 1|Protein of unknov	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02277	gabD	2322131	2320758	457	4,77	48868	-	NAD-dependent aldehyde dehydrogenases	NAD-dependent aldehyde dehydrogenases	Succinate-semialdehyde dehydrogenase [NAD	Aldehyde dehydrogenase|NAD-dependent aldel	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02278	null	2322843	2322298	181	6,52	20452	-	Acetyltransferase	acetyltransferase	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02279	rplA	2323633	2322944	229	9,91	24530	-	LSU/50S ribosomal protein L1P	50S ribosomal protein L1 (BL1)	LSU ribosomal protein L1P	Ribosomal protein L1|Ribosomal protein L1, bac	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02280	rplK	2324155	2323730	141	9,61	14880	-	LSU/50S ribosomal protein L11P	LSU 50S ribosomal protein L11P (BL11)	LSU ribosomal protein L11P	Ribosomal protein L11|Ribosomal protein L11, l	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02281	mgtA	2326944	2324314	876	5,91	96363	-	Magnesium-translocating P-type ATPase	ATPase, E1-E2 type:Magnesium-translocating	Mg(2+) transport ATPase, P-type (EC 3.6.3.2)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_02282	nylA	2327685	2329136	483	6,73	51189	+	Amidase	amidase family enzyme	Amidase family protein	Amidase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02283	yvqK	2329829	2329293	178	7,85	19504	-	ATP:cob(I)alamin adenosyltransferase	ATP:cob(I)alamin adenosyltransferase, monofu	Cobalamin adenosyltransferase family protein	Adenosylcobalamin biosynthesis, ATP:cob(I)ala	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02284	null	2330387	2329845	180	10,22	19563	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Integral membrane protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02285	null	2330776	2330384	130	11,14	14257	-	Conserved protein	conserved hypothetical protein	Hypothetical exported protein	no annotation	null	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_02286	null	2333045	2330799	748	6,55	82497	-	Adenosylcobalamin-dependent ribonucleoside	adenosylcobalamin-dependent ribonucleoside-tı	Anaerobic ribonucleoside-triphosphate reducta	Ribonucleoside-triphosphate reductase, adenos	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02287	null	2333786	2333343	147	4,41	16197	-	Nucleoside deoxyribosyltransferase	nucleoside 2-deoxyribosyltransferase	nucleoside deoxyribosyltransferase (EC 2.4.2.	Nucleoside 2-deoxyribosyltransferase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02288	null	2334806	2333961	281	10,12	31345	-	Alpha/beta hydrolase superfamily protein	alpha/beta hydrolase superfamily protein	Alpha/beta hydrolase	Lipase, active site|Protein of unknown function I	R	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02289	nusG	2335370	2334816	184	4,85	20783	-	Transcription antitermination protein nusG	transcription antitermination protein NusG:KOV	Transcription antitermination protein nusG	Bacterial transcription antitermination protein N	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02290	secE	2335642	2335472	56	9,87	6515	-	Preprotein translocase, SecE subunit	Preprotein translocase subunit SecE	Protein translocase subunit secE	Protein secE/sec61-gamma protein|SecE subu	U	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02291	rpmG2	2335811	2335662	49	10,49	5651	-	LSU/50S ribosomal protein L33P	50S ribosomal protein L33 type 2, RpmG2	LSU ribosomal protein L33P	Ribosomal protein L33	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02292	null	2337068	2336109	319	10,5	35926	-	1,4-Dihydroxy-2-naphtoate prenyltransferase	1,4-dihydroxy-2-naphthoate octaprenyltransfera	1,4-dihydroxy-2-naphthoate polyprenyltransfer	UbiA prenyltransferase	H	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_02293	ubiA	2338003	2337065	312	7,66	34529	-	1,4-Dihydroxy-2-naphtoate prenyltransferase	1,4-dihydroxy-2-naphthoate octaprenyltransfera	1,4-dihydroxy-2-naphthoate polyprenyltransfer	UbiA prenyltransferase	H	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02294	null	2338214	2337972	80	11,77	8506	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02295	apbE	2339390	2338326	354	10,09	38571	-	Thiamine biosynthesis lipoprotein	thiamine biosynthesis membrane-associated lip	Iron-sulfur cluster assembly/repair protein ApbE	ApbE-like lipoprotein	H	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_02296	tnpB	2340747	2339566	393	10,45	46191	-	Transposase, IS605 family protein	transposase, IS605-TNPB	Transposase	Transposase (probable), IS891/IS1136/IS1341|	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02297	null	2341445	2341200	81	12,24	8935	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02298	cad	2342608	2341700	302	10,03	32688	-	Lipoprotein (pheromone precursor)	sex pheromone cAD1 precursor lipoprotein	Lipoprotein (pheromone precursor)	FMN-binding	T	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_02299	ndh2	2342896	2344794	632	9,45	70801	+	NADH dehydrogenase	NADH dehydrogenase, FAD-containing subunit	NADH dehydrogenase (EC 1.6.99.3)	Pyridine nucleotide-disulphide oxidoreductase, (	C	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+	
LC_02300	ynhH	2344967	2345410	147	10,14	16496	+	Conserved protein	conserved hypothetical protein (secreted protei	Hypothetical protein	Protein of unknown function DUF1312	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_02301	null	2345407	2345994	195	10,54	21368	+	Heptaprenyl diphosphate synthase component	Heptaprenyl diphosphate synthase component I	Heptaprenyl diphosphate synthase component	Heptaprenyl diphosphate synthase component	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02302	hepB	2345969	2346946	325	7,59	36192	+	Geranylgeranyl pyrophosphate synthase	polyprenyl / Geranylgeranyl pyrophosphate synt	Farnesyl pyrophosphate synthetase (EC 2.5.1	Polyprenyl synthetase|Terpenoid synthase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02303	null	2347391	2347888	165	10,04	17543	+	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02304	null	2348039	2348830	263	5,72	29642	+	Metallophosphoesterase	metallophosphoesterase	Bis(5'-nucleosyl)-tetraphosphatase (symmetric	Metallophosphoesterase|Phosphoesterase MJ0	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02305	null	2349278	2349084	64	9,38	7495	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02306	null	2349832	2349272	186	8,19	20654	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_02307	null	2350076	2350960	294	7,05	34518	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator, MutR family	Transcriptional activator Rgg/GadR/MutR, C-ter	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02308	null	2351354	2351169	61	10,11	6954	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02309	stpC	2352383	2351508	291	6,68	32736	-	ABC transporter, ATPase component	multidrug ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02310	null	2353624	2352377	415	10,14	47122	-	Conserved protein	predicted ORF	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02311	null	2354126	2353605	173	9,96	18989	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02312	null	2354719	2354132	195	9,58	21451	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02313	null	2355048	2355371	107	10,62	11968	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02314	null	2356480	2355914	188	7,74	20897	-	Luciferase-like monooxygenase	oxidoreductase	Luciferase-like monooxygenase (EC 1.14.-.-)	Bacterial luciferase-like	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02315	null	2356969	2356502	155	4,23	16959	-	Coenzyme F420-dependent N5,N10-methylen	coenzyme F420-dependent N5,N10-methylene	not_predicted_by_ERGO	Bacterial luciferase-like	C	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02316	yacP	2357737	2357198	179	6,52	21038	-	PIN domain containing protein (Yacp-like prote	RNA-binding protein containing a PIN domain /	Hypothetical cytosolic protein	Protein of unknown function DUF901	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02317	spoU	2358520	2357738	260	8,05	27905	-	RNA methyltransferase, TrmH family, group 3	RNA methyltransferase, TrmH family, group 3	23S rRNA Gm2251 methyltransferase (EC 2.:	tRNA/rRNA methyltransferase, SpoU|RNA met	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02318	ytbE	2358920	2358492	142	8,94	15641	-	Ribonuclease III	Ribonuclease III family protein	Hypothetical protein	Ribonuclease III|Uncharacterised conserved pro	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02319	cysS	2360323	2358917	468	5,15	53090	-	Cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase (Cysteine-tRNA liga	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	Cysteinyl-tRNA synthetase, class Ia|Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02320	loxD	2361854	2360460	464	5,08	49569	-	(S)-2-hydroxy-acid oxidase chain D (EC 1.1.3.	FAD/FMN-containing dehydrogenases / similar	(S)-2-hydroxy-acid oxidase chain D (EC 1.1.3.	FAD linked oxidase, C-terminal|FAD linked oxid	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02321	null	2362549	2361977	190	9,67	21089	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02322	null	2362932	2362822	36	12,27	4022	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02323	gltX	2364672	2363179	497	6,09	56937	-	Glutamyl-tRNA synthetase	glutamyl-tRNA synthetase / glutamate--tRNA(G	Glutamyl-tRNA synthetase (EC 6.1.1.17)	Glutamyl-tRNA synthetase, class Ic|Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02324	null	2366053	2365223	276	10,54	30717	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function UCP033101	null	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	-	
LC_02325	null	2367083	2366067	338	10,8	37138	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02326	gntR	2367466	2367080	128	9,01	13901	-	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|Winged	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02327	null	2369227	2367599	542	9,64	60919	-	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase and perme	Transporter	Formate/nitrite transporter|ABC transporter rela	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02328	inlJ	2371043	2369727	438	9,59	46577	-	Internalin J	internalin J	Hypothetical membrane associated protein	Surface protein from Gram-positive cocci, anch	null	Yes	mucus	LPxTG	tmhmm:2	-	-	-	-	-	-	-	
LC_02329	null	2372086	2371328	252	9,79	28719	-	ABC transporter, permease protein	multi-copper enzyme maturation ABC transporte	not_predicted_by_ERGO	no annotation	R	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02330	null	2373005	2372088	305	8,05	33698	-	ABC transporter, ATPase component	bacitracin multidrug ABC transporter, ATPase c	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02331	null	2373135	2374031	298	7,32	34971	+	Transcriptional regulator, xre family	predicted ORF	Transcriptional regulator, MutR family	Helix-turn-helix type 3|Transcriptional activator f	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02332	yacL	2375238	2374123	371	9,7	41600	-	PIN/TRAM domain protein, Pili retraction prote	PilT protein / integral membrane protein, PIN ar	Pili retraction protein pilT	PilT protein, N-terminal|Nucleotide binding prote	R	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02333	radA	2376623	2375259	454	8,44	49158	-	DNA repair protein RadA	ATP-dependent serine protease / DNA repair p	DNA repair protein RadA	RecA bacterial DNA recombination|Peptidase S	O	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_02334	dut	2377182	2376643	179	9,64	20521	-	Deoxyuridine 5'-triphosphate nucleotidohydrola	Deoxyuridine 5'-triphosphate nucleotidohydrolas	Deoxyuridine 5'-triphosphate nucleotidohydrola	DeoxyUTP pyrophosphatase	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02335	null	2377630	2377322	102	11,75	11270	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02336	null	2377827	2378117	96	4,65	10813	+	Acetyltransferase	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02337	pepC1	2378289	2379608	439	4,66	49661	+	Aminopeptidase C	aminopeptidase C. Cysteine peptidase. MEROF	Aminopeptidase C (EC 3.4.22.40)	Peptidase, cysteine peptidase active site|Peptid	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_02338	pepC2	2379753	2381099	448	4,96	50713	+	Aminopeptidase C	aminopeptidase C. Cysteine peptidase. MEROF	Aminopeptidase C (EC 3.4.22.40)	Peptidase, cysteine peptidase active site|Peptid	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	

LC_02339	null	2381316	2382416	366	9,86	40472	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_02340	null	2382416	2383609	397	9,92	44463	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02341	null	2383623	2384498	291	7,8	32995	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase component	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02342	null	2384650	2386704	684	8,64	76907	+	Potassium transport system protein	potassium transport system protein (kup1)	Kup system potassium uptake protein	K+ potassium transporter	P	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_02343	ppdK	2389554	2386924	876	5,42	95262	-	Pyruvate phosphate dikinase	strongly similar to phosphoenolpyruvate synthas	Pyruvate,phosphate dikinase (EC 2.7.9.1)	PEP-utilizing enzyme|Pyruvate phosphate dikin	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02344	yqzB	2390411	2389854	185	8,87	20077	-	CBS domain protein	CBS domain containing protein	CBS domain containing protein	Cystathionine-beta-synthase|Helix-turn-helix, ty	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02345	gpmA	2391284	2390613	223	10,41	24704	-	2,3-bisphosphoglycerate-dependent phosphoç	2,3-bisphosphoglycerate-dependent phosphogl	Phosphoglycerate mutase (EC 5.4.2.1)	Phosphoglycerate/bisphosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02346	null	2391442	2392560	372	9,53	41960	+	Bacterial low temperature requirement A	conserved hypothetical protein (membrane prot	Low temperature requirement protein A	Protein secE/sec61-gamma protein|Bacterial lo	null	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_02347	null	2392579	2392863	94	6,53	11053	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02348	loxL	2394224	2393109	371	4,74	39346	-	L-Lactate oxidase	L-lactate dehydrogenase (FMN-dependent) rela	L-lactate oxidase (EC 1.13.12.4)	FMN-dependent alpha-hydroxy acid dehydroger	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02349	ej97d	2394596	2394387	69	9,03	7489	-	CsbD-like superfamily protein	CsbD-like superfamily protein	Hypothetical protein	CsbD-like	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02350	deoB	2395914	2394724	396	6,07	44050	-	Phosphopentomutase	Phosphopentomutase (Phosphodeoxyribomutas	not_predicted_by_ERGO	Alkaline phosphatase|Metalloenzyme|Phosphop	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02351	null	2397140	2395911	409	10,14	44180	-	Transporter, major facilitator superfamily MFS	transporter of the major facilitator superfamily (M	not_predicted_by_ERGO	Sugar transporter superfamily|Major facilitator s	GEPR	No	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_02352	null	2397920	2397168	250	5,96	27645	-	Uridine phosphorylase	uridine phosphorylase (UrdPase) (UPase)	not_predicted_by_ERGO	Nucleoside phosphorylase	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02353	null	2399121	2397904	405	10,44	43652	-	Transporter, major facilitator superfamily MFS	transporter of the major facilitator superfamily (M	not_predicted_by_ERGO	Major facilitator superfamily|Major facilitator sup	null	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_02354	null	2399250	2400428	392	8,87	44930	+	Sugar diacid utilization regulator	sugar diacid utilization regulator	not_predicted_by_ERGO	Homeodomain-like	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02355	null	2400885	2400628	85	10,1	9341	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02356	null	2401281	2401075	68	9,54	8001	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02357	null	2401735	2401481	84	7,25	9750	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02358	ProP11	2402305	2403537	410	9,93	45225	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Macrolide-efflux protein	Major facilitator superfamily|Major facilitator sup	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02359	proA	2404862	2403606	418	5,56	44609	-	Gamma-glutamyl phosphate reductase	gamma-glutamyl phosphate reductase (GPR) ((	Gamma-glutamyl phosphate reductase (EC 1.	Gamma-glutamyl phosphate reductase GPR|Al	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02360	proB	2405779	2404943	278	7,86	29967	-	Glutamate 5-kinase	glutamate 5-kinase, ProB-related	Glutamate 5-kinase (EC 2.7.2.11)	Aspartate/glutamate/uridylate kinase|Glutamate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02361	null	2406365	2406228	45	11,11	5193	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02362	null	2407525	2406983	180	11,99	20081	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	Nterm	tmhmm:0	-	-	-	-	-	-	-
LC_02363	null	2409715	2408546	389	10,6	42617	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Protein of unknown function DUF214, permase	null	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02364	salX	2410394	2409726	222	5,76	24587	-	ABC transporter, ATPase component	ABC transporter, ATPase component	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02365	null	2411116	2410391	241	10,15	26466	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_02366	srtC	2412536	2411712	274	11	30768	-	SortaseC	sortase (surface protein transpeptidase)	Sortase	Peptidase C60, sortase A and B	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	protease	-
LC_02367	spaD	2414096	2412543	517	6,73	56235	-	Pilus specific protein, major backbone protein	conserved hypothetical protein	Fimbrial subunit type 2 precursor	Surface protein from Gram-positive cocci, anch	null	Yes	collagen	LPxTG	tmhmm:2	-	-	-	-	-	-	+
LC_02368	spaE	2415442	2414087	451	7,83	50780	-	Pilus specific protein, minor backbone protein	conserved hypothetical protein	Hypothetical exported protein	no annotation	OU	Yes	collagen	LPxTG	tmhmm:2	-	-	-	-	-	protease	-
LC_02369	spaF	2418395	2415444	983	5,22	108431	-	Pilus specific protein, ancillary protein involvec	conserved hypothetical protein (outer membran	Fibronectin-binding protein precursor	Surface protein from Gram-positive cocci, anch	null	Yes	collagen	LPxTG	tmhmm:1	-	-	-	-	-	-	+
LC_02370	null	2419227	2418670	185	4,59	20140	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02371	null	2420604	2419396	402	9,89	45354	-	Conserved protein	unnamed protein product	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02372	null	2420797	2421852	351	9,75	39748	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02373	null	2422146	2422793	215	9,23	24301	+	Transcriptional regulator, xre family	transcriptional regulator, xre family, DNA-bindin	Transcriptional regulator	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	IMP	tmhmm:4	-	-	-	-	regulator	-	-
LC_02374	null	2422924	2423256	110	8,88	12125	+	Transcriptional regulator, PadR family	transcriptional regulator, PadR family	Transcriptional regulator, PadR family	Transcriptional regulator PadR-like|Winged heli	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02375	null	2423253	2424038	261	7,66	28726	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02376	null	2424082	2424858	258	8,75	28592	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02377	null	2425176	2424886	96	9,78	11063	-	Prebacteriocin	Prebacteriocin	Bacteriocin	Protein of unknown function DUF1862	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02378	tas	2425409	2426386	325	5,64	36448	+	Oxidoreductase, aldo/keto reductase family	oxidoreductase protein	Oxidoreductase (EC 1.1.1.-)	Aldo/keto reductase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02379	null	2426591	2426412	59	9,43	6476	-	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02380	null	2428041	2426686	451	8,26	49525	-	Conserved protein	conserved hypothetical protein (integral membr	Threonine/Serine Exporter	Protein of unknown function DUF1212	S	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+
LC_02381	null	2428574	2428221	117	6,63	14356	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02382	null	2429507	2428692	271	9,47	29980	-	ABC transporter, bacteriocin transporter perm	predicted ORF	Bacteriocin export accessory protein	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02383	null	2430070	2429537	177	10,37	20267	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Ribosomal protein L29|Single hybrid motif	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02384	plnG	2432275	2430083	730	7,12	81574	-	Bacteriocin processing peptidase / Bacteriocir	bacteriocin ABC transporter, ATPase and perm	Bacteriocin processing peptidase (EC 3.4.22.-	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	protease	-
LC_02385	null	2433258	2434148	296	9,72	33331	+	Two component sensor transduction histidine	predicted ORF	Sensory transduction protein kinase (EC 2.7.3	ATP-binding region, ATPase-like	null	Yes	-	IMP	tmhmm:2	-	-	-	HPK(bacterioc	-	-	-
LC_02386	null	2434141	2434917	258	7,06	29291	+	Two-component response regulator, bacterioc	Response regulator of the LytR/AlgR family	Response regulator pltR	Response regulator receiver|LytTr DNA-binding	null	Yes	-	-	tmhmm:0	-	-	-	RR(bacteriocin	regulator	-	-
LC_02387	null	2435297	2435037	86	7,69	10020	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_02388	sakXIM	2437064	2436765	99	9,6	11502	-	Bacteriocin immunity protein (homologous to p	immunity protein (homologous to piscicolin, Sak	Bacteriocin immunity protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02389	null	2437401	2437243	52	4,76	5420	-	Protein with bacteriocin-type signal sequence,	conserved hypothetical protein	Hypothetical membrane associated protein	Bacteriocin-type signal sequence	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02390	null	2438055	2437870	61	5,67	6316	-	Protein with bacteriocin-type signal sequence,	conserved hypothetical protein	no_function_in_ERGO	Bacteriocin-type signal sequence	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02391	null	2438300	2438115	61	9,22	6637	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02392	null	2438871	2438686	61	9,1	6833	-	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_02393	null	2439727	2438921	268	10,55	29964	-	Immunity protein PlnI, membrane-bound prote	immunity protein PlnI, membrane-bound protea	CAAX amino terminal protease family	Abortive infection protein	R	Yes	-	IMP	tmhmm:8	-	-	-	-	-	protease	+
LC_02394	null	2439987	2439805	60	12,3	7077	-	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02395	null	2440488	2440048	146	6,53	15734	-	Transcriptional regulator, Rrf2 family	predicted ORF	Rrf2 family protein	Transcriptional regulator, Rrf2	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02396	null	2441970	2440543	475	9,86	50022	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Major facilitator superfamily|Major facilitator sup	GEPR	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-
LC_02397	null	2442475	2442143	110	6,52	12373	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02398	null	2443107	2442766	113	7,82	12366	-	Prebacteriocin	Prebacteriocin	bacteriocin	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02399	aRA12	2444231	2443278	317	5,34	35484	-	Oxidoreductase, aldo/keto reductase family	oxidoreductase, aldo/keto reductase family prot	Oxidoreductase (EC 1.1.1.-)	Peptidase S8 and S53, subtilisin, kexin, sedolis	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02400	null	2444448	2444203	81	12,12	8823	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	Sec	tmhmm:0	-	-	-	-	-	-	-
LC_02401	ypiA	2444691	2445425	244	6,25	26261	+	Short-chain dehydrogenase/reductase SDR	oxidoreductase, short-chain dehydrogenase/red	Short chain dehydrogenase (EC 1.-.-.-)	Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+
LC_02402	yqiG	2445455	2446600	381	5,46	41818	+	NADH-dependent flavin oxidoreductase	NADH:flavin oxidoreductase yqiG, Old Yellow E	Probable NADH-dependent flavin oxidoreducta	NADH:flavin oxidoreductase/NADH oxidase, N-	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02403	null	2446942	2446625	105	9,53	12027	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_02404	fum	2448371	2446992	459	6,58	48866	-	Fumarate hydratase, class II	fumarate hydratase class II (fumarase c) protei	Fumarate hydratase (EC 4.2.1.2)	Fumarate lyase|L-Aspartase-like	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02405	null	2449290	2448547	247	10	27523	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02406	null	2449368	2449559	63	11,01	6906	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02407	null	2449574	2449846	90	11,39	10073	+	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-

LC_02408	null	2449982	2449824	52	8,49	6054	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	-
LC_02409	mntH2	2451552	2449945	535	7,36	57912	-	Mn2+/Fe2+ transporter, NRAMP family	Mn2+ and Fe2+ transporter, NRAMP family	Manganese transport protein mntH	Natural resistance-associated macrophage prot	P	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+
LC_02410	pacL1	2451952	2454669	905	5,77	98004	+	Cation-transporting P-type ATPase	ATPase, P-type (cation transporting), HAD sup	Calcium-transporting ATPase (EC 3.6.3.8)	H+ transporting ATPase, proton pump|ATPase	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_02411	null	2454958	2455323	121	4,56	13880	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02412	null	2457008	2455638	456	10,78	48242	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Multidrug resistance protein B	Major facilitator superfamily|Major facilitator sup	GEPF	Yes	-	IMP	tmhmm:13	-	-	-	-	-	-	-
LC_02413	sufI	2458571	2457042	509	6,05	57170	-	Multicopper oxidase	multicopper oxidase, type 3	Multicopper oxidase family protein	Multicopper oxidase, copper-binding site|Cupre	Q	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02414	null	2458676	2458870	64	7,18	7162	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_02415	null	2458986	2459273	95	9,04	10656	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	+
LC_02416	null	2459246	2459626	126	4,93	13627	+	Cation efflux protein	predicted ORF	Cation transporters	Cation efflux protein	P	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_02417	czcR	2459746	2460078	110	10,26	12285	+	Transcriptional regulator, ArsR family	transcriptional regulator, ArsR family	Transcriptional regulator, ArsR family	Bacterial regulatory protein, ArsR|Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02418	mtsC	2461111	2460170	313	9,81	35017	-	ABC transporter, manganese-binding lipoprote	manganese ABC transporter, manganese-bindi	Manganese-binding protein	Periplasmic solute binding protein|Adhesion lipc	P	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+
LC_02419	mtsB	2462001	2461108	297	7,82	31598	-	ABC transporter, iron transporter membrane p	Mn2+/Zn2+ ABC transporter, permease compo	Manganese transport system membrane prote	ABC-3	P	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-
LC_02420	null	2462276	2461998	92	4,22	10278	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	ABC transporter related	P	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02421	null	2462740	2462273	155	10,82	16911	-	ABC transporter	ABC transporter	not_predicted_by_ERGO	ABC transporter related	P	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02422	rpsN	2463347	2463078	89	11,56	10192	-	SSU/30S ribosomal protein S14P	SSU ribosomal protein S14P	SSU ribosomal protein S14P	TatD-related deoxyribonuclease|Ribosomal prot	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02423	psaA	2463749	2464666	305	9,61	33340	+	ABC transporter, metal ion transporter periplas	metal ion ABC transporter, periplasmic compon	Manganese-binding protein	Periplasmic solute binding protein	P	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+
LC_02424	null	2464945	2465586	213	7,15	23716	+	NAD-dependent epimerase/dehydratase	Saccharopine dehydrogenase related protein	Putative NAD-dependent dehydrogenase	NAD-dependent epimerase/dehydratase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02425	null	2466223	2465714	169	10,03	18642	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_02426	psaA	2466564	2467466	300	9,79	33495	+	ABC transporter, metal ion transporter periplas	metal ion ABC transporter, periplasmic compon	Manganese-binding protein	Periplasmic solute binding protein|Adhesion lipc	P	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+
LC_02427	null	2467661	2467810	49	7,81	5842	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02428	null	2468640	2468452	62	11,23	6344	-	Putative protein without homology	conserved hypothetical protein	Hypothetical protein	Surface protein from Gram-positive cocci, anch	null	No	-	LPxTG	tmhmm:1	-	-	-	-	-	-	-
LC_02429	null	2468669	2469046	125	3,18	13189	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02430	null	2469687	2469337	116	11,79	12350	-	Protein crcB homolog	predicted ORF	CrcB family protein	Protein kinase|Camphor resistance CrcB protei	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02431	null	2470091	2469681	136	9,02	14797	-	Protein crcB homolog	Integral membrane protein for chromosome con	CrcB family protein	Camphor resistance CrcB protein	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02432	melB1	2472108	2470594	504	9,57	56342	-	Transporter, major facilitator superfamily MFS	oligogalacturonide transporter	Oligogalacturonide transporter	Major facilitator superfamily MFS_1	G	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-
LC_02433	null	2472746	2475469	907	5,56	102450	+	Alpha-L-rhamnosidase	conserved hypothetical protein	Alpha-L-rhamnosidase (EC 3.2.1.40)	Bacterial alpha-L-rhamnosidase|Six-hairpin glyc	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02434	null	2475665	2475528	45	11,09	4658	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02435	null	2476650	2475676	324	9,76	34842	-	ABC transporter, nitrate/sulfonate/bicarbonate	nitrate/sulfonate/bicarbonate ABC transporter, p	Alkanesulfonates-binding protein	Bacterial extracellular solute-binding protein, far	Q	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+
LC_02436	4cl1	2478172	2476640	510	6,61	56300	-	Acyl-CoA synthetase family protein	long-chain acyl-CoA synthetase (AMP-forming),	Acyl-CoA synthetase family protein	AMP-dependent synthetase and ligase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02437	null	2479364	2478123	413	10,26	46718	-	Acyltransferase	acyltransferase	Acyltransferase family protein	no annotation	null	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-
LC_02438	ssuB	2480062	2479361	233	9,73	25281	-	ABC transporter, aliphatic sulfonates transpor	nitrate/sulfonate/bicarbonate ABC transporter, A	Alkanesulfonates transport ATP-binding prote	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02439	ssuC	2480873	2480055	272	9,79	29648	-	ABC transporter, permease protein	nitrate/sulfonate/bicarbonate ABC transporter, p	Alkanesulfonates transport system permease	Binding-protein-dependent transport systems in	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_02440	null	2481782	2481114	222	6,03	24731	-	Conserved protein	predicted ORF	Hypothetical protein	B3/4	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02441	null	2483360	2482248	370	9,72	41128	-	Transposase	transposase, IS1533	Transposase	Transposase, IS116/IS110/IS902	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02442	null	2483559	2483702	47	12,14	5252	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02443	null	2483748	2483954	68	12,16	7709	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02444	chpA	2484572	2484225	115	8,44	13150	-	Transcriptional modulator of MazE/toxin, MazF	transcriptional regulator, PemK family	not_predicted_by_ERGO	PemK-like protein|Plasmid maintenance toxin/C	T	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-
LC_02445	null	2484787	2484572	71	5,82	7986	-	Growth regulator	Growth regulator	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02446	null	2486719	2484884	611	8,65	67870	-	ABC transporter, ATPase component/permea	predicted ORF	ABC transporter ATP-binding protein / ABC tr	ABC transporter related|AAA+ ATPase, core|Al	V	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+
LC_02447	null	2488496	2486706	596	8,91	66248	-	ABC transporter, multidrug transporter ATPas	predicted ORF	ABC transporter ATP-binding protein / ABC tr	ABC transporter related|AAA+ ATPase, core|Al	V	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-
LC_02448	null	2488702	2488535	55	4,19	6326	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-
LC_02449	null	2489904	2488720	394	9,85	43258	-	Transporter, major facilitator superfamily MFS	predicted ORF	Macrolide-efflux protein	Major facilitator superfamily MFS_1	GEPF	Yes	-	IMP	tmhmm:9	-	-	-	-	-	-	-
LC_02450	rpsI	2490696	2490304	130	11,22	14274	-	SSU/30S ribosomal protein S9P	30S ribosomal protein S9P	SSU ribosomal protein S9P	Ribosomal protein S9|Ribosomal protein S5 dor	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02451	rplM	2491156	2490710	148	10,1	16604	-	LSU/50S ribosomal protein L13P	ribosomal protein L13 (50S ribosomal protein L1	LSU ribosomal protein L13P	Ribosomal protein L13|Ribosomal protein L13, I	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02452	null	2492054	2491404	216	9,55	24328	-	Transcriptional regulator, TetR family	transcriptional regulator	Transcriptional regulator, TetR family	Bacterial regulatory protein, TetR|Homeodomair	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02453	yxeA	2492135	2493193	352	10,73	38308	+	ABC transporter, permease protein	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein	Protein of unknown function DUF214, permase	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-
LC_02454	ygfA	2493195	2493905	236	9,9	26091	+	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02455	null	2494090	2494311	73	4,22	8557	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02456	mta	2494654	2495415	253	9,98	29290	+	Transcriptional regulator, MerR family	transcriptional regulator, MerR family	Transcriptional activator tipA	Bacterial regulatory protein, MerR|Putative DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+
LC_02457	truA	2496378	2495635	247	9,59	27852	-	tRNA pseudouridine synthase A	tRNA pseudouridine synthase A (tRNA-uridine	tRNA pseudouridine synthase A (EC 4.2.1.70)	tRNA pseudouridine synthase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02458	cbiQ	2497191	2496394	265	10,47	30301	-	Cobalt transport protein	cobalt ABC transporter, permease component, (	Cobalt transport protein cbiQ	Cobalt transport protein	P	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+
LC_02459	cbiO	2498050	2497184	288	5,52	31177	-	ABC transporter, cobalt import transporter ATI	cobalt ABC transporter, ATPase component, Cl	Cobalt transport ATP-binding protein cbiO	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02460	ybxA	2498862	2498026	278	4,77	30474	-	ABC transporter, cobalt import transporter ATI	cobalt ABC transporter, ATPase component, Cl	Cobalt transport ATP-binding protein cbiO	ABC transporter related|AAA+ ATPase, core	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02461	null	2499664	2498999	221	10,32	24941	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-
LC_02462	rplQ	2500579	2500199	126	10,72	14162	-	LSU/50S ribosomal protein L17P	50S ribosomal protein L17 (BL15) (BL21)	LSU ribosomal protein L17P	Ribosomal protein L17	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02463	rpoA	2501539	2500601	312	4,75	34745	-	DNA-directed RNA polymerase, subunit alpha	DNA-directed RNA polymerase subunit alpha (I	DNA-directed RNA polymerase alpha chain (E	RNA polymerase, RBP11-like|RNA polymerase	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02464	rpsK	2502003	2501614	129	12,16	13772	-	SSU/30S ribosomal protein S11P	SSU 30S ribosomal protein S11P (BS11)	SSU ribosomal protein S11P	Ribosomal protein S11	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02465	rpsM	2502389	2502024	121	11,16	13557	-	SSU/30S ribosomal protein S13P	SSU 30S ribosomal protein S13P (BS14)	SSU ribosomal protein S13P	Ribosomal protein S13|Ribosomal protein S13-l	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02466	rpmJ	2502538	2502422	38	11,74	4449	-	LSU/50S ribosomal protein L36P	50S ribosomal protein L36	LSU ribosomal protein L36P	Ribosomal protein L36	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02467	infA	2502784	2502566	72	9,58	8148	-	Translation initiation factor IF-1	bacterial translation initiation factor 1 (bIF-1 2)	Bacterial Protein Translation Initiation Factor 1	RNA binding S1|Translation initiation factor IF-1	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02468	adk	2503584	2502928	218	6,52	23711	-	Adenylate kinase	adenylate kinase (ATP-AMP transphosphorylas	Adenylate kinase (EC 2.7.4.3) / Nucleoside-di	Adenylate kinase|Adenylate kinase, subfamily|A	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02469	secY	2505054	2503732	440	10,34	48090	-	Preprotein translocase secY subunit	protein translocase subunit secY/sec61 alpha	Protein translocase subunit secY	SecY protein	U	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+
LC_02470	rplO	2505494	2505054	146	11,24	15494	-	LSU/50S ribosomal protein L15P	LSU ribosomal protein L15P	LSU ribosomal protein L15P	Peptidase S8 and S53, subtilisin, kexin, sedolis	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02471	rpmD	2505712	2505527	61	11,35	6792	-	LSU/50S ribosomal protein L30P	50S ribosomal protein L30 -related protein	LSU ribosomal protein L30P	Ribosomal protein L30|Ribosomal protein L30, I	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02472	rpsE	2506227	2505724	167	7,81	17519	-	SSU/30S ribosomal protein S5P	SSU ribosomal protein S5P	SSU ribosomal protein S5P	Ribosomal protein S5|Ribosomal protein S5, C-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02473	rplR	2506609	2506250	119	10,7	13015	-	LSU/50S ribosomal protein L18P	LSU 50S ribosomal protein L18P	LSU ribosomal protein L18P	Ribosomal protein L18|Ribosomal protein L18P,	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02474	rplF	2507177	2506647	176	10,24	19317	-	LSU/50S ribosomal protein L6P	50S ribosomal protein L6P (BL10)	LSU ribosomal protein L6P	Ribosomal protein L6|Ribosomal protein L6, sig	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02475	rpsH	2507606	2507208	132	10,14	14774	-	SSU/30S ribosomal protein S8P	SSU 30S ribosomal protein S8P (BS8)	SSU ribosomal protein S8P	Ribosomal protein S8	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02476	rplE	2508375	2507833	180	8,81	20211	-	LSU/50S ribosomal protein L5P	50S ribosomal protein L5 (BL6)	LSU ribosomal protein L5P	Ribosomal protein L5|Mitochondrial ribosomal p	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+

LC_02477	rplX	2508711	2508400	103	10,79	11246	-	LSU/50S ribosomal protein L24P	LSU ribosomal protein L24P (50S ribosomal pr	LSU ribosomal protein L24P	Ribosomal protein L24	KOW	Ribosomal protein	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02478	rplN	2509109	2508741	122	10,75	13035	-	LSU/50S ribosomal protein L14P	LSU ribosomal protein L14P (50S ribosomal pr	LSU ribosomal protein L14P	Ribosomal protein L14b/L23e	Ribosomal proteir	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02479	rpsQ	2509404	2509141	87	10,58	10116	-	SSU/30S ribosomal protein S17P	SSU 30S ribosomal protein S17P (BS16)	SSU ribosomal protein S17P	Ribosomal protein S17	Nucleic acid-binding, OI	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02480	rpmC	2509631	2509425	68	10,73	8008	-	LSU/50S ribosomal protein L29P	ribosomal protein L29 (50S ribosomal protein L	LSU ribosomal protein L29P	Ribosomal protein L29	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02481	rplP	2510043	2509609	144	11,41	16009	-	LSU/50S ribosomal protein L16P	LSU ribosomal protein L16P (50S ribosomal pr	LSU ribosomal protein L16P	Ribosomal protein L16	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02482	rpsC	2510709	2510047	220	10,65	24949	-	SSU/30S ribosomal protein S3P	SSU 30S ribosomal protein S3P (BS2) (BS3/B	SSU ribosomal protein S3P	Ribosomal protein S3, C-terminal	KH, type 2	KH	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02483	rplV	2511076	2510723	117	10,62	12730	-	LSU/50S ribosomal protein L22P	ribosomal protein L22 (50S ribosomal protein L	LSU ribosomal protein L22P	Ribosomal protein L22/L17	Ribosomal protein L	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02484	rpsS	2511375	2511094	93	10,83	10577	-	SSU/30S ribosomal protein S19P	SSU 30S ribosomal protein S19P (BS19) (BS1	SSU ribosomal protein S19P	Ribosomal protein S19/S15	Ribosomal protein S	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02485	rplB	2512251	2511415	278	11	30397	-	LSU/50S ribosomal protein L2P	50S ribosomal protein L2 (BL2)	LSU ribosomal protein L2P	Ribosomal protein L2	Ribosomal protein L2, ba	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02486	rplW	2512582	2512280	100	10,61	11533	-	LSU/50S ribosomal protein L23P	LSU ribosomal protein L23P (50S ribosomal pr	LSU ribosomal protein L23P	Nucleotide-binding, alpha-beta plait	Ribosomal I	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02487	rplD	2513205	2512582	207	10,59	22397	-	LSU/50S ribosomal protein L4P	50S ribosomal protein L4 (BL4)	LSU ribosomal protein L1E (= L4P)	Ribosomal protein L4/L1e	Ribosomal protein L4	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02488	rplC	2513860	2513228	210	10,47	22627	-	LSU/50S ribosomal protein L3P	LSU ribosomal protein L3P (50S ribosomal prot	LSU ribosomal protein L3P	Ribosomal protein L3	Translation elongation an	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02489	rpsJ	2514194	2513886	102	10,51	11722	-	SSU/30S ribosomal protein S10P	30S ribosomal protein S10 (BS13)	SSU ribosomal protein S10P	Ribosomal protein S10	Ribosomal protein S10,	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02490	null	2514525	2514962	145	6,51	16662	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Phosphate-starvation-inducible E	S	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02491	ahpC	2515697	2515134	187	4,56	20490	-	Alkyl hydroperoxide reductase, subunit C	Alkyl hydroperoxide reductase subunit C (Alkyl I	Peroxiredoxin (EC 1.11.1.15)	Alkyl hydroperoxide reductase/ Thiol specific an	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02492	null	2516958	2515927	343	8,08	39804	-	Transcriptional regulator	transcriptional regulator	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02493	null	2517197	2517379	60	12,51	6634	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02494	EF-G	2519492	2517390	700	4,5	76936	-	Protein Translation Elongation Factor G (EF-G	Protein Translation Elongation Factor G (EF-G)	Protein Translation Elongation Factor G (EF-G	Translation elongation factor EFG/EF2, C-termi	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02495	rpsG	2520052	2519582	156	10,49	17924	-	SSU/30S ribosomal protein S7P	30S ribosomal protein S7 (BS7)	SSU ribosomal protein S7P	Ribosomal protein S7	Ribosomal protein S7, ba	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02496	rpsL	2520647	2520231	138	11,96	15162	-	SSU/30S ribosomal protein S12P	ribosomal protein S12 (30S ribosomal protein S	SSU ribosomal protein S12P	Ribosomal protein S12, bacterial and chloroplas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02497	null	2531459	2521035	3474	5,58	382118	-	Conserved protein	conserved hypothetical protein (outer membran	not_predicted_by_ERGO	Cna B-type	Bacterial adhesion	Carboxypeptidas	null	No	collagen	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02498	null	2531968	2531429	179	11,19	20235	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Carbohydrate-binding-like fold	null	No	collagen	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02499	null	2532349	2532852	167	7	18017	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02500	rpoC	2536692	2533030	1220	6,46	136553	-	DNA-directed RNA polymerase, beta chain	DNA-directed RNA polymerase subunit beta'/1(	DNA-directed RNA polymerase beta' chain (E	RNA polymerase, alpha subunit	RNA polymera	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02501	rpoB	2540307	2536705	1200	4,97	133894	-	DNA-directed RNA polymerase, beta chain	DNA-directed RNA polymerase subunit beta (R	DNA-directed RNA polymerase beta chain (E(	RNA polymerase Rpb2, domain 6	RNA polymer	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02502	null	2540686	2540525	53	6,78	6388	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02503	clpC	2543256	2540749	835	6,54	91642	-	ATP-dependent Clp protease ATP-binding sul	ATP-binding subunit of Clp protease and DnaK	Negative regulator of genetic competence clpC	Chaperonin clpA/B	UvrB/UvrC protein	AAA+ AT	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02504	ctsR	2543763	2543296	155	9,48	18110	-	Transcriptional regulator, CtsR family	transcriptional regulator CtsR	Transcriptional regulator ctsR	Firmicute transcriptional repressor of class III st	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02505	null	2545603	2545265	112	11,26	12018	-	Conserved protein	metal-dependent RNase, consists of a metallo-l	not_predicted_by_ERGO	KH, prokaryotic type	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02506	null	2545741	2546040	99	11,9	11432	+	Lipoprotein	lipoprotein	not_predicted_by_ERGO	no annotation	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02507	null	2546955	2547350	131	8,72	14815	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02508	null	2547757	2547969	70	8,5	7801	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02509	null	2548191	2548556	121	10,58	13519	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	C-type lectin	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02510	null	2548843	2549037	64	11,31	7429	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02511	null	2549022	2549339	105	12,08	11621	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02512	null	2549496	2549293	67	11,84	7290	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02513	null	2549447	2549632	61	10,44	6799	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02514	lysS	2551836	2550340	498	5,09	56593	-	Lysyl-tRNA synthetase	Lysyl-tRNA synthetase (class II)	Lysyl-tRNA synthetase (EC 6.1.1.6)	Lysyl-tRNA synthetase, class-2	tRNA synthetas	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02515	yacF	2552988	2551987	333	8,26	36752	-	tRNA-dihydrouridine synthase 1	tRNA-dihydrouridine synthase 1	tRNA-dihydrouridine synthase	Dihydrouridine synthase, DuS	Dihydrouridine sy	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02516	hslO	2553935	2553051	294	5,62	31422	-	33 kDa chaperonin	chaperonin (Heat Shock Protein 33 Homolog) (I	33 kDa chaperonin	Hsp33 protein	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02517	null	2553968	2554129	53	7,25	5560	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02518	ftsH	2556404	2554254	716	5,13	78224	-	Cell division protein FtsH	FtsH-2 peptidase. Metallo peptidase. MEROPS	Cell division protein ftsH (EC 3.4.24.-)	Peptidase M41	AAA+ ATPase, core	AAA ATPa	O	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	protease	+	
LC_02519	hpt	2557014	2556466	182	4,6	20476	-	Hypoxanthine phosphoribosyltransferase	hypoxanthine phosphoribosyltransferase (hypox	Hypoxanthine-guanine phosphoribosyltransfer	Phosphoribosyltransferase	Purine/pyrimidine ph	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02520	null	2558318	2557011	435	11,23	48913	-	tRNA(Ile)-lysidine synthetase, MesJ	tRNA(Ile)-lysidine synthetase, MesJ	tRNA(Ile)-lysidine synthetase TilS	PP-loop	Cell cycle control PP-loop ATPase Mes	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02521	yabR	2558918	2558439	159	10,43	17267	-	RNA binding S1 domain protein	RNA binding protein (S1 domain)	S1-type RNA-binding domain	RNA binding S1	Nucleic acid-binding, OB-fold	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02522	null	2559603	2559202	133	11	14976	-	Septum formation initiator	Septum formation initiator	Cell division protein DIVIC	Septum formation initiator	D	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02523	yabO	2559959	2559696	87	10,28	9780	-	Heat shock protein 15	Ribosome-associated heat shock protein 15 imj	Heat shock protein 15	RNA-binding S4	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02524	null	2561540	2559966	524	10,56	57119	-	Polysaccharide transport membrane protein	Polysaccharide transport membrane protein	Export protein for polysaccharides and teichoi	Polysaccharide biosynthesis protein	R	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-	
LC_02525	mfd	2565145	2561618	1175	5,71	131754	-	Transcription-repair coupling factor	Transcription-repair coupling factor (superfamil	Transcription-repair coupling factor	Helicase, C-terminal	Transcription factor CarD	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02526	pth	2565778	2565221	185	9,66	20823	-	Peptidyl-tRNA hydrolase	stage V sporulation protein C (peptidyl-tRNA hy	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	Peptidyl-tRNA hydrolase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02527	L-LDH	2566239	2567219	326	5,09	35531	+	L-lactate dehydrogenase	L(+)-lactate dehydrogenase (L-LDH)	L-lactate dehydrogenase (EC 1.1.1.27)	Lactate/malate dehydrogenase	L-lactate/malate	G	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02528	null	2567627	2568997	456	8,91	50176	+	ErfK/YbiS/YcfS/YnhG family protein	ErfK/YbiS/YcfS/YnhG	ErfK/YbiS/YcfS/YnhG family protein	ErfK/YbiS/YcfS/YnhG	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02529	null	2569662	2569126	178	7,09	20691	-	Transcriptional regulator, PadR family	transcriptionaf regulator, PadR family	Transcriptional repressor PadR	Transcriptional regulator PadR-like	Winged heli	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02530	null	2569809	2571260	483	9,62	51800	+	Phage-related protein	phage protein, infection protein	Phage infection protein	no annotation	S	Yes	-	IMP	tmhmm:6	-	-	phage	-	-	-	-	
LC_02531	null	2571342	2571920	192	9,78	22326	+	NADPH-quinone reductase (Modulator of drug	NADPH-quinone reductase (modulator of drug ;	NAD(P)H dehydrogenase [quinone] (EC 1.6.5	Flavodoxin-like fold	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02532	dsg	2572089	2572754	221	6,79	24931	+	CBS domain containing protein	hemolysin-like protein (CBS domain protein)	CBS domain containing protein	Cystathionine-beta-synthase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02533	yciB	2573051	2573749	232	9,69	26237	+	ErfK/YbiS/YcfS/YnhG family protein	cell surface protein, ErfK family	ErfK/YbiS/YcfS/YnhG family protein	ErfK/YbiS/YcfS/YnhG	S	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02534	gltB	2575265	2573829	478	8,41	52076	-	Glutamate synthase, small subunit	glutamate synthase (NADH) subunit beta	Glutamate synthase [NADPH] small chain (EC	Pyridine nucleotide-disulphide oxidoreductase, (	ER	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02535	gltA	2579796	2575330	1488	6,29	163542	-	Glutamate synthase, large subunit	glutamate synthase (NADH) large subunit	Glutamate synthase [NADPH] large chain (EC	Glutamine amidotransferase, class-II	Glutamate	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02536	ccl	2580619	2580092	175	10,88	19222	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF988	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02537	null	2580652	2580909	85	8,65	9392	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02538	null	2580924	2581136	70	12,32	7766	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02539	MazF	2581516	2581133	127	10,98	13757	-	Transcriptional regulator, PemK family	toxin-antitoxin addiction module toxin componer	MazF protein	PemK-like protein	Plasmid maintenance toxin/C	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02540	null	2581784	2581536	82	4,48	8936	-	Conserved protein	conserved hypothetical protein	MazE protein	Ribbon-helix-helix	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02541	alr	2583035	2581896	379	6,83	41281	-	Alanine racemase	alanine racemase region	Alanine racemase (EC 5.1.1.1)	Alanine racemase region	Alanine racemase, N-t	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02542	acpS	2583396	2583022	124	6,81	13663	-	Holo-[acyl-carrier-protein] synthase	phosphopantetheinyl transferase (holo-ACP syr	Holo-[acyl-carrier protein] synthase (EC 2.7.8.	Holo-acyl carrier protein synthase	Phosphopant	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02543	srmB	2585073	2583565	502	9,72	56458	-	ATP-dependent RNA helicase	ATP-dependent RNA helicase, DEAD/DEAH bi	ATP-dependent RNA helicase	ATP-dependent helicase, DEAD-box	Helicase,	LKJ	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02544	murF	2586735	2585347	462	5,61	50439	-	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D	D-Ala-D-Ala adding enzyme, UDP-N-acetylmur	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D	Cytoplasmic peptidoglycan synthetase, N-termi	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02545	null	2587646	2586882	254	8,45	30165	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_02546	null	2587848	2588489	213	5,18	24246	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02547	null	2589179	2588505	224	8,92	25226	-	Conserved integral membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02548	null	2589435	2589863	142	4,04	15839	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02549	rpmE	2590550	2590299	83	9,93	9612	-	LSU/50S ribosomal protein L31P	LSU 50S ribosomal protein L31P type B-2	LSU ribosomal protein L31P	Ribosomal protein L31	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02550	murA	2591906	2590647	419	5,27	44856	-	UDP-N-acetylglucosamine 1-carboxyvinyltrans	UDP-N-acetylglucosamine 1-carboxyvinyltransf	UDP-N-acetylglucosamine 1-carboxyvinyltrans	3-phosphoshikimate 1-carboxyvinyltransferase|I	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02551	null	2592217	2591984	77	8,32	8581	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02552	null	2592460	2592272	62	10,47	6681	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02553	null	2592735	2592580	51	4,66	5431	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02554	pyrG	2594451	2592847	534	6,62	59927	-	CTP synthase	CTP synthase (UTP--ammonia ligase)	CTP synthase (EC 6.3.4.2)	Glutamine amidotransferase class-I|CTP synth	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02555	ndh1	2594882	2596069	395	7,37	42600	+	Pyridine nucleotide-disulphide oxidoreductase	NADH dehydrogenase, FAD-containing subunit	NADH dehydrogenase (EC 1.6.99.3)	Pyridine nucleotide-disulphide oxidoreductase,	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02556	null	2596514	2596170	114	4,34	13311	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02557	null	2596910	2596554	118	8,47	13358	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02558	null	2598036	2597161	291	10,06	33674	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF1211	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02559	null	2598935	2598264	223	3,51	25071	-	DNA-directed RNA polymerase, delta subunit	DNA-directed RNA polymerase subunit delta	DNA-directed RNA polymerase delta chain (E	DNA-directed RNA polymerase delta subunit	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02560	null	2599180	2598995	61	4,97	7052	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Calycin-like|Domain of unknown function DUF1	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02561	null	2599433	2599170	87	3,96	9663	-	Conserved protein	predicted ORF	hypothetical protein	Calycin-like|Domain of unknown function DUF1	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02562	null	2599846	2600694	282	7,38	30954	+	Lipoate-protein ligase A	Lipoate-protein ligase A	Lipoate-protein ligase A (EC 6.3.2.-)	Biotin/lipoate A/B protein ligase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02563	ykiG	2600684	2602036	450	5,53	51757	+	HD superfamily phosphohydrolases	HD superfamily phosphohydrolases	dGTP triphosphohydrolase	Short-chain dehydrogenase/reductase SDR|Me	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02564	null	2602501	2602253	82	6,97	8892	-	MutT/nudix family protein	predicted ORF	7,8-dihydro-8-oxoguanine-triphosphatase (EC	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02565	null	2602573	2603631	352	10,38	39085	+	Conserved domain protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF218	S	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02566	mscL	2603693	2604073	126	10,41	13813	+	Large-conductance mechanosensitive channe	MscL, large conductance mechanosensitive ch	Large-conductance mechanosensitive channe	Large-conductance mechanosensitive channel	M	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_02567	null	2604659	2604225	144	9,91	16505	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02568	null	2605077	2604748	109	6,8	12238	-	Conserved protein	ProFAR isomerase-like	Hypothetical cytosolic protein	ProFAR isomerase-like	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02569	prs	2606148	2605174	324	7,3	35415	-	Ribose-phosphate pyrophosphokinase	ribose-phosphate pyrophosphokinase 1 (RPPK	Ribose-phosphate pyrophosphokinase (EC 2.7	Phosphoribosyltransferase|Phosphoribosyl pyrc	FE	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02570	null	2606488	2606246	80	6,23	8920	-	UDP-N-acetylglucosamine pyrophosphorylase	N-acetylglucosamine-1-phosphate uridyltransfe	not_predicted_by_ERGO	Bacterial transferase hexapeptide repeat|Trimer	M	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02571	gcaD	2607635	2606529	368	5,53	40189	-	UDP-N-acetylglucosamine pyrophosphorylase	transferase hexapeptide repeat:Nucleotidyl tran	Glucosamine-1-phosphate acetyltransferase (I	Bacterial transferase hexapeptide repeat|Nuclec	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02572	null	2609174	2607969	401	9,91	45841	-	Glycopeptide antibiotics resistance protein	glycopeptide antibiotics resistance protein	VanZ family protein / RDD family protein	VanZ like protein|RDD	S	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_02573	purR	2610019	2609171	282	9,89	31215	-	Pur operon repressor	purine operon repressor, PurR	Pur operon repressor	Phosphoribosyltransferase|ATP-dependent DN	F	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02574	ybbL	2610241	2610891	216	5,07	23928	+	ABC transporter, ATPase component	ABC transporter, ATPase component, YbbL	ABC transporter ATP-binding protein	Orn/DAP/Arg decarboxylase 2|ABC transporter	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02575	ybbM	2610888	2611649	253	10,67	27123	+	ABC transporter, permease protein	ABC transporter, metal resistance protein, YbbM	ABC transporter permease protein	Conserved hypothetical protein 245	R	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02576	czcD	2612620	2611742	292	4,71	31246	-	Cation diffusion facilitator family transporter	cation diffusion facilitator family transporter, Co	Cobalt-zinc-cadmium resistance protein czcD	Cation efflux protein|Phosphopantetheine attacl	P	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02577	ispE	2613554	2612676	292	9,07	31902	-	4-diphosphocytidyl-2-C-methyl-D-erythritol kin	4-diphosphocytidyl-2-C-methyl-D-erythritol kinas	4-diphosphocytidyl-2-C-methyl-D-erythritol kin	Ribosomal protein L29|4-diphosphocytidyl-2C-n	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02578	veg	2614055	2613804	83	10,1	9320	-	VEG protein homologue	VEG protein homologue	VEG protein	Protein of unknown function DUF1021	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02579	ksgA	2615497	2614613	294	6,69	31805	-	Dimethyladenosine transferase	dimethyladenosine transferase (rRNA methylati	Dimethyladenosine transferase (EC 2.1.1.-)	Peptidase M14, carboxypeptidase A|Ribosomal	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02580	rnmV	2616059	2615490	189	9,78	20620	-	Primase-related protein, ribonuclease M5	ribonuclease M5 (toprim domain)	Ribonuclease M5 (EC 3.1.26.8)	Primase-related protein|Toprim subdomain|TOF	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02581	tatD	2616835	2616056	259	6,51	29339	-	Mg-dependent Dnase, TatD family	Mg-dependent Dnase, TatD family hydrolase	DNase, TatD family (EC 3.1.-.-)	TatD-related deoxyribonuclease|Mg-dependent	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02582	gatA	2617333	2616842	163	7,52	18233	-	PTS system, galactitol-specific IIA component	PTS system, galacitol-specific IIA component (I	PTS system, galactitol-specific IIA component	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02583	lacD	2617548	2618546	332	4,9	36325	+	Tagatose 1,6-diphosphate aldolase	tagatose 1,6-diphosphate aldolase (tagatose-bis	Tagatose-bisphosphate aldolase (EC 4.1.2.40	Deoxyribose-phosphate aldolase/phospho-2-del	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02584	null	2618769	2618569	66	10,86	6918	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02585	aldE	2618838	2619719	293	4,9	32565	+	Galactose mutarotase enzyme, lacX protein	galactose mutarotase related enzyme	Aldose 1-epimerase family protein	Aldose 1-epimerase|Glycoside hydrolase-type c	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02586	null	2619855	2620559	234	7,97	26327	+	Two-component response regulator, LytR/AlgF	response regulator RmnR, LytR/AlgR family	Two-component response regulator	Response regulator receiver|LytTr DNA-binding	KT	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_02587	null	2620546	2621457	303	7,29	34764	+	Two component sensor transduction histidine	signal transduction protein with a C-terminal HA	Two-component sensor kinase virS (EC 2.7.3.	ATP-binding region, ATPase-like	T	Yes	-	IMP	tmhmm:2	-	-	-	HPK	-	-	+	
LC_02588	null	2621511	2623337	608	9,21	67022	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase and permea	ABC transporter ATP-binding protein / ABC tr	ABC transporter related|AAA+ ATPase, core|Al	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02589	null	2623324	2625237	637	9,39	71825	+	ABC transporter, multidrug transporter ATPas	multidrug ABC transporter, ATPase and permea	ABC transporter ATP-binding protein / ABC tr	Bacterial type II secretion system protein E|ABC	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02590	null	2625401	2625613	70	6,24	8106	+	Transcriptional regulator	transcriptional regulator, PbsX family	Transcriptional regulator, Cro/CI family	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02591	null	2625664	2626110	148	10,59	16636	+	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02592	metS	2628151	2626169	660	5,92	74833	-	methionyl-tRNA synthetase / protein secretion	methionyl-tRNA synthetase / protein secretion c	Methionyl-tRNA synthetase (EC 6.1.1.10) / Pr	Aminoacyl-tRNA synthetase, class I|Methionyl-t	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02593	null	2628365	2628186	59	11,58	6658	-	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02594	null	2628522	2628415	35	12,06	3851	-	Putative protein without homology	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02595	pepI	2629545	2628670	291	4,81	33110	-	Proline iminopeptidase	proline iminopeptidase, PIP / prolyl aminopeptid	Proline iminopeptidase (EC 3.4.11.5)	Alpha/beta hydrolase fold-1|Peptidase S33, prol	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_02596	null	2629629	2629829	66	11,72	7779	+	Putative protein without homology	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02597	yunF	2630669	2629857	270	7,82	29954	-	Uracil-xanthine permease, YunF like protein	uracil-xanthine permease	Hypothetical cytosolic protein	Protein of unknown function DUF72	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02598	null	2631141	2630662	159	5,21	17850	-	ADP-ribose pyrophosphatase	ADP-ribose pyrophosphatase	7,8-dihydro-8-oxoguanine-triphosphatase (EC	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02599	hicD2	2632204	2631299	301	5,17	32474	-	L-2-hydroxyisocaproate dehydrogenase	L-2-hydroxyisocaproate / malate dehydrogenase	L-2-hydroxyisocaproate dehydrogenase (EC 1	Lactate/malate dehydrogenase|L-lactate/malate	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02600	yiiE	2632825	2632229	198	8,03	22619	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF1211	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02601	npdA	2633552	2632860	230	4,98	25040	-	NAD-dependent protein deacetylase, SIR2 far	NAD-dependent deacetylase (Regulatory protei	SIR2 family protein	Silent information regulator protein Sir2	K	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02602	null	2633771	2633917	48	10,01	5658	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02603	null	2634840	2633914	308	4,71	34910	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	Peptidase M, neutral zinc metallopeptidases, zi	null	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_02604	laaT	2634972	2635481	169	6,29	18316	+	Phospholipid-binding protein	phospholipid-binding protein	Phosphatidylethanolamine-binding protein	YbhB and YbcL|PEBP	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02605	null	2635858	2635583	91	9,53	9219	-	Conserved protein	conserved hypothetical protein	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02606	null	2636894	2635911	327	10,19	34714	-	Conserved secreted protein	conserved hypothetical protein (secreted protei	Hypothetical exported protein	Protein of unknown function DUF1002	null	Yes	-	Sec	tmhmm:0	-	-	-	-	-	-	+	
LC_02607	ppx2	2637928	2636987	313	9,82	35158	-	Exopolyphosphatase	exopolyphosphatase	Exopolyphosphatase (EC 3.6.1.11)	Ppx/GppA phosphatase	FP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02608	null	2639274	2637925	449	6,56	51428	-	Polyphosphate kinase	predicted ORF	Polyphosphate kinase (EC 2.7.4.1)	Polyphosphate kinase	P	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02609	ppk	2640086	2639430	218	6,82	25277	-	Polyphosphate kinase	polyphosphate kinase	not_predicted_by_ERGO	Polyphosphate kinase	P	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02610	ppx3	2641612	2640083	509	5,51	57331	-	Exopolyphosphatase	exopolyphosphatase 3	Exopolyphosphatase (EC 3.6.1.11)	no annotation	FP	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02611	aRA12	2641973	2642905	310	6,31	34720	+	Aldo/keto reductase	oxidoreductase, aldo/keto reductase family prot	Oxidoreductase (EC 1.1.1.-)	Peptidase S8 and S53, subtilisin, kexin, sedolis	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02612	null	2643000	2643824	274	5,48	29871	+	SAM-dependent methyltransferase	SAM-dependent methyltransferase	Methyltransferase (EC 2.1.1.-)	Methyltransferase type 11	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02613	bar	2643843	2644337	164	6,27	18350	+	Phosphinothricin N-acetyltransferase	phosphinothricin acetyltransferase, sortase rela	Phosphinothricin N-acetyltransferase (EC 2.3.	GCN5-related N-acetyltransferase	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02614	dinF	2645829	2644471	452	10,92	48990	-	Na+-driven multidrug efflux pump	Na+-driven multidrug efflux pump	Na+ driven multidrug efflux pump	Multi antimicrobial extrusion protein MatE|Na+ c	V	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	+	

LC_02615	null	2647226	2646369	285	9,7	30325	-	Conserved protein	beta-propeller domains of methanol dehydrogen	Hypothetical membrane spanning protein	Protein of unknown function DUF477	R	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	+	
LC_02616	lemA	2647843	2647235	202	10,08	22071	-	LemA family protein	LemA family protein	LemA protein	LemA	S	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_02617	trpS	2649012	2647996	338	5,44	37702	-	Tryptophanyl-tRNA synthetase	tryptophanyl-tRNA synthetase II (Tryptophan-tR	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	Aminoacyl-tRNA synthetase, class I	Aminoacyl-	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02618	null	2650775	2649549	408	8,41	44750	-	Transporter, major facilitator superfamily MFS	predicted ORF	not_predicted_by_ERGO	Major facilitator superfamily MFS_1	GEPR	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02619	gshR	2652982	2651657	441	6,58	47050	-	Glutathione reductase	glutathione reductase (EC 1.6.4.2)	Glutathione reductase (EC 1.8.1.7)	Pyridine nucleotide-disulphide oxidoreductase, (	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02620	choQ	2653947	2652988	319	6,04	34906	-	ABC transporter, ATPase component	glycine betaine/carnitine/choline/proline ABC tra	Glycine betaine transport ATP-binding protein	Ribulose bisphosphate carboxylase, large chain	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02621	choS	2655479	2653947	510	10,07	55645	-	ABC transporter, permease protein	choline/proline/glycine betaine ABC transporter,	Glycine betaine transport system permease pr	Binding-protein-dependent transport systems in	M	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02622	null	2655726	2655508	72	12,25	8333	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02623	rep	2656171	2658459	762	4,72	85338	+	DNA helicase	superfamily I DNA and RNA helicase-like protei	ATP-dependent DNA helicase rep (EC 3.6.1.-	Helicase superfamily 1, UvrD-related	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02624	null	2658639	2659412	257	9,59	28551	+	Transcriptional regulator, LysR family	transcriptional regulator, LysR family	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR	LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02625	ydiA	2660450	2659479	323	10,16	35779	-	Tellurite resistance protein related permease	tellurite resistance protein related permease	Tellurite resistance protein	C4-dicarboxylate transporter/malic acid transpo	V	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02626	nodJ	2661756	2660992	254	9,76	28300	-	ABC transporter, permease protein	ABC-2 type transporter	ABC transporter permease protein	ABC-2|ABC-2 type transporter|ABC-2 transport	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02627	drrA	2662495	2661737	252	9,17	27944	-	ABC transporter, ATPase component	ABC transporter	ABC transporter ATP-binding protein	ABC transporter related	AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02628	ydfF	2662649	2663347	232	8,34	26357	+	Transcriptional regulator, ArsR family	transcriptional regulator, ArsR family	Transcriptional regulator, ArsR family	Bacterial regulatory protein, ArsR	Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02629	null	2664138	2663491	215	10,37	23821	-	Metal-dependent membrane protease	metal-dependent membrane protease	CAAX amino terminal protease family	Abortive infection protein	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	protease	+	
LC_02630	null	2666071	2664470	533	9,71	59323	-	ABC transporter, ATPase and permease com	predicted ORF	ABC transporter ATP-binding protein	ABC transporter, transmembrane region	ABC tr	V	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02631	yagB	2666927	2666283	214	7,1	23165	-	HD domain protein	hydrolase, HD-domain protein	Metal dependent hydrolase	Metal-dependent phosphohydrolase, HD region	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02632	null	2667079	2667495	138	8,44	15411	+	Transcriptional regulator, MarR family	transcriptional regulator	TRANSCRIPTIONAL REGULATOR, MarR/E	Bacterial regulatory protein, MarR	Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02633	uvrA3	2667664	2670192	842	7,28	90691	+	Excinuclease ABC, subunit A	excinuclease ABC subunit A-like protein	Excinuclease ABC subunit A	ABC transporter related	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02634	yghZ	2671309	2670302	335	6,09	37345	-	Aldo/keto reductase (oxidoreductase)	aldo/keto reductase, oxidoreductase	Oxidoreductase (EC 1.1.1.-)	Aldo/keto reductase	KCNAB voltage-gated K+ c	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02635	null	2672227	2671415	270	4,9	28223	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)	Cof protein	HAD-superfamily hydrolase, subfam	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02636	null	2672762	2672418	114	4,23	12749	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02637	null	2673142	2672921	73	12,75	8176	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02638	null	2673253	2673516	87	4,68	9759	+	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02639	null	2673806	2674495	229	10,25	24862	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Permease	Protein of unknown function DUF1275	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02640	gpm2	2675181	2674492	229	6,03	25372	-	Phosphoglycerate mutase family protein	phosphoglycerate mutase family protein	Phosphoglycerate mutase family protein	Phosphoglycerate/bisphosphoglycerate mutase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02641	folE	2676037	2675225	270	5,5	29760	-	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily, subfamily IIB, Cof	Hydrolase (HAD superfamily)	Cof protein	HAD-superfamily hydrolase, subfam	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02642	rnh	2676131	2676613	160	9,33	18447	+	Ribonuclease HI	RNase HI with double-stranded RNA/RNA-DN/	Ribonuclease HI (EC 3.1.26.4)	Ribonuclease H	Polynucleotidyl transferase, Rit	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02643	yoaU2	2677521	2676619	300	8,2	33164	-	Transcriptional regulator, LysR family	transcriptional regulators, LysR family	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR	LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02644	avtA	2677809	2679011	400	6,32	44147	+	Aminotransferase	Helix-turn-helix (HTH) containing DNA-binding	Aminotransferase class I family	Aminotransferase, class I and II	Pyridoxal phos	KE	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02645	null	2679277	2679432	51	10,88	5256	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02646	null	2679703	2679398	101	6,52	11501	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02647	null	2680059	2680391	110	8,81	12515	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02648	recA	2681784	2680597	395	5,61	42802	-	RecA recombinase	RecA/RadA recombinase	RecA protein	RecA bacterial DNA recombination	AAA+ ATPa	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02649	null	2682033	2682734	233	9,12	24455	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function DUF554	R	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02650	null	2683271	2682798	157	10,89	19011	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02651	null	2683857	2683603	84	11,36	9289	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02652	fruC	2686174	2684192	660	6,85	69283	-	PTS system, fructose-specific IIABC compon	PTS system, fructose specific IIABC componer	PTS system, fructose-specific IIABC compon	Phosphotransferase system, phosphoenolpyruv	G	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02653	fruK-1	2687107	2686178	309	4,75	33431	-	1-phosphofructokinase	fructose-1-phosphate kinase related fructose-6-	1-phosphofructokinase (EC 2.7.1.56)	PfkB	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02654	rpl	2687256	2688008	250	6,81	27821	+	Transcriptional regulator, RpiR family	phosphosugar-binding transcriptional regulator,	Transcriptional regulator, RpiR family	Helix-turn-helix protein RpiR	Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02655	glpK	2689602	2688070	510	5,3	55944	-	Glycerol kinase	ATP-dependent glycerol kinase	Glycerol kinase (EC 2.7.1.30)	Carbohydrate kinase, FGGY	Glycerol kinase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02656	ubiD	2690570	2692045	491	5,77	54322	+	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Vanillate decarboxylase VdcC protein (EC 4.1.	Carboxylyase-related protein	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02657	vdcB	2692055	2692627	190	6,8	20911	+	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	Vanillate decarboxylase VdcB protein (EC 4.1.	Flavoprotein	Phenylacrylic acid decarboxylase	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02658	null	2692624	2694015	463	9,69	49968	+	Sodium/sulphate symporter	transport protein	Sodium/sulfate symporter	Sodium/sulphate symporter	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02659	null	2695060	2694161	299	9,58	33163	-	Transcriptional regulator, LysR family	transcriptional regulator, LysR family	Transcriptional regulators, LysR family	Bacterial regulatory protein, LysR	LysR, substra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02660	null	2695090	2695521	143	6,6	15712	+	Conserved protein	conserved hypothetical protein	Putative vanillate decarboxylase subunit	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02661	rmaI	2696021	2695584	145	9,4	16576	-	Transcriptional regulator, MarR family	transcriptional regulator, MarR family	Transcriptional regulator, MarR family	Bacterial regulatory protein, MarR	Winged helix	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02662	yniG	2696154	2697536	460	9,43	49545	+	Transporter, major facilitator superfamily MFS	Drug resistance transporter, EmrB/QacA family	Multidrug resistance protein B	Tetracycline resistance protein TetB	Drug resis	GEPR	Yes	-	IMP	tmhmm:14	-	-	-	-	-	-	-	
LC_02663	null	2698496	2697768	242	4,91	27117	-	Class II aldolase/adducin domain protein	class II sugar-phosphate aldolase/adducin, N-te	L-fuculose phosphate aldolase (EC 4.1.2.17)	Class II aldolase/adducin, N-terminal	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02664	null	2698729	2698493	78	11,08	8673	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:1	-	-	-	-	-	-	-	
LC_02665	pts	2700290	2698722	522	7,94	57148	-	PTS system, galactitol-specific IIC componen	PTS system, Galactitol-specific IIC component	not_predicted_by_ERGO	Phosphotransferase system, galactitol-specific	G	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_02666	pts	2700683	2700363	106	7,51	11701	-	PTS system, galactitol-specific IIB component	PTS system, galactitol/lactose/cellobiose-specif	PTS system, galactitol-specific IIB component	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02667	pts	2701184	2700705	159	4,97	18221	-	PTS system, galactitol-specific IIA component	PTS system, galactitol-specific EIIA componen	PTS system, galactitol-specific IIA component	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02668	null	2701390	2702184	264	6,31	29660	+	Fucose operon repressor, DeoR family	transcription regulator	Transcriptional regulator, DeoR family	Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02669	null	2702540	2702277	87	9,84	9726	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02670	araD	2703690	2702821	289	5,81	32492	-	Rhamnulose-1-phosphate aldolase	L-rhamnulose-1-phosphate aldolase	Rhamnulose-1-phosphate aldolase (EC 4.1.2.	Class II aldolase/adducin, N-terminal|Rhamnulc	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02671	rhaA	2705020	2703740	426	5,58	48742	-	L-rhamnose isomerase	L-rhamnose isomerase	L-rhamnose isomerase (EC 5.3.1.14)	Rhamnose isomerase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02672	yulD	2705398	2705084	104	4,93	12400	-	L-rhamnose mutarotase	L-rhamnose 1-epimerase	L-rhamnose mutarotase (EC 5.1.3.-)	Rhamnose mutarotase|Dimeric alpha-beta barre	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02673	rhaB	2706879	2705401	492	5,14	54706	-	Rhamnulokinase	rhamnulokinase	Rhamnulokinase (EC 2.7.1.5)	Carbohydrate kinase, FGGY|Rhamnulokinase	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02674	proP	2708265	2706913	450	9,59	48695	-	Transporter, major facilitator superfamily MFS	L-rhamnose-proton tranport protein, MFS family	L-rhamnose-proton symport	Sugar transporter superfamily|Major facilitator s	GEPR	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_02675	null	2708388	2709410	340	7,18	39568	+	Transcriptional regulator, AraC family	transcriptional regulator, AraC family	Transcriptional regulator, AraC family	Helix-turn-helix, AraC type|Homeodomain-like|C	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02676	adhC	2709603	2710724	373	5,12	39796	+	Alcohol dehydrogenase	Zn-dependent alcohol dehydrogenase	Aryl-alcohol dehydrogenase (EC 1.1.1.90)	Alcohol dehydrogenase superfamily, zinc-conta	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02677	null	2711222	2710842	126	9,47	14483	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	Conserved hypothetical protein 1655	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02678	null	2712218	2711553	221	9,77	23775	-	Lipoprotein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02679	agl2	2712578	2714260	560	5,72	64393	+	Alpha,alpha-phosphotrehalase (GH13)	trehalose-6-phosphate hydrolase (alpha,alpha-p	Oligo-1,6-glucosidase (EC 3.2.1.10)	Glycosyl hydrolase, family 13, catalytic region|G	G	Yes	-	-	tmhmm:0	LC02679	-	-	-	-	-	+	
LC_02680	null	2717292	2715022	756	6,61	81628	-	Subtilisin-like serine protease	subtilisin-like serine protease	not_predicted_by_ERGO	Surface protein from Gram-positive cocci, anch	O	No	fibronectin	LPxTG	tmhmm:1	-	-	-	-	-	protease	-	
LC_02681	null	2718278	2717307	323	9,79	37214	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	R	No	-	Lipobox	tmhmm:0	-	-	-	-	-	-	-	
LC_02682	null	2720290	2718365	641	6,04	73535	-	Heparinase II/III-like	conserved hypothetical protein	not_predicted_by_ERGO	Heparinase II/III-like	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02683	null	2720576	2720229	115	7,87	12489	-	Preprotein translocase subunit YajC	preprotein translocase subunit YajC	not_predicted_by_ERGO	YajC	U	No	-	Sec	tmhmm:1	-	-	-	-	-	-	-	

LC_02684	AgaE	2721043	2720576	155	4,98	17246	-	PTS system, mannose-specific IIA componen	PTS system, mannose/fructose/sorbose IIA cor	not_predicted_by_ERGO		Phosphotransferase system, fructose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02685	pts	2721944	2721129	271	9,95	30035	-	PTS system, mannose-specific IID componen	PTS system, mannose-specific IID component	not_predicted_by_ERGO		Phosphotransferase system, mannose/fructose	G	No	-	IMP	tmhmm:4	-	-	-	-	-	-	-		
LC_02686	agaW	2722746	2721934	270	8,43	28618	-	PTS system, mannose-specific IIC componen	PTS system, N-acetylgalactosamine EIIC comp	not_predicted_by_ERGO		Phosphotransferase system, sorbose-specific I	GEPR	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-		
LC_02687	agaV	2723275	2722775	166	6,81	18536	-	PTS system, mannose-specific IIB componen	PTS system, mannose/fructose/N-acetylgalactc	not_predicted_by_ERGO		Phosphotransferase system, sorbose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02688	ugl	2724466	2723288	392	6,68	45030	-	Glucuronyl hydrolase	unsaturated glucuronyl hydrolase (UGL) (glycur	not_predicted_by_ERGO		Six-hairpin glycosidase-like|Glycosyl hydrolase,	M	No	-	-	tmhmm:0	LC02688	-	-	-	-	-	-		
LC_02689	null	2725293	2724463	276	5,49	31683	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO		Galactose-binding like	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02690	kdgR	2725517	2726284	255	9,46	28394	+	Transcriptional regulator, IclR family	transcriptional regulator, IclR family	not_predicted_by_ERGO		Transcriptional regulator IclR, N-terminal|Trans	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+		
LC_02691	kdul	2726516	2727361	281	6,12	32224	+	4-deoxy-L-threo-5-hexosulose-uronate ketol-is	4-deoxy-L-threo-5-hexosulose-uronate ketol-iso	not_predicted_by_ERGO		5-keto 4-deoxyuronate isomerase|Cupin, RmlC-	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02692	kduD	2727395	2728219	274	6,17	29963	+	2-deoxy-D-gluconate 3-dehydrogenase	2-deoxy-D-gluconate 3-dehydrogenase	not_predicted_by_ERGO		Short-chain dehydrogenase/reductase SDR|Gl	IQR	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02693	eda-1	2728339	2728992	217	8,81	22943	+	2-dehydro-3-deoxyphosphogluconate aldolase	2-dehydro-3-deoxy-6-phosphogluconate aldolas	not_predicted_by_ERGO		KDPG and KHG aldolase|Aldolase-type TIM ba	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02694	kdgK	2728997	2730016	339	4,99	37429	+	2-dehydro-3-deoxygluconokinase	2-dehydro-3- deoxygluconokinase (Ec 2.7.1.45)	not_predicted_by_ERGO		PfkB	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02695	rpiA	2730822	2730133	229	6,24	25152	-	Ribose-5-phosphate isomerase A	ribose-5-phosphate isomerase A (phosphoriboi	Ribose 5-phosphate isomerase (EC 5.3.1.6)		Ribose 5-phosphate isomerase|Bacterial regula	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02696	null	2734087	2731028	1019	8,08	112506	-	Polysaccharide lyase family 8	alpha-glucosidase, family 31 of glycosyl hydrola	not_predicted_by_ERGO		Surface protein from Gram-positive cocci, anch	G	No	fibronectin	LPxTG	tmhmm:1	LC02696	-	-	-	-	-	-		
LC_02697	null	2736487	2734367	706	6,32	80761	-	Glycoside hydrolase, family 36	conserved hypothetical protein	not_predicted_by_ERGO		Glycoside hydrolase, clan GH-D|Glycoside hydı	null	No	-	-	tmhmm:0	LC02697	-	-	-	-	-	-		
LC_02698	null	2736975	2736484	163	10,25	18312	-	PTS system, mannose-specific IIB componen	PTS system, sorbose IIB component	not_predicted_by_ERGO		Phosphotransferase system, sorbose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02699	null	2737846	2737007	279	10,23	29820	-	PTS system, mannose-specific IID componen	PTS system, IID component	not_predicted_by_ERGO		Phosphotransferase system, mannose/fructose	null	No	-	IMP	tmhmm:5	-	-	-	-	-	-	-		
LC_02700	null	2738645	2737839	268	9,47	28528	-	PTS system, mannose-specific IIC componen	PTS system, IIC component	not_predicted_by_ERGO		Phosphotransferase system, sorbose-specific I	null	No	-	IMP	tmhmm:6	-	-	-	-	-	-	-		
LC_02701	null	2739067	2738660	135	4,23	14833	-	PTS system, fructose-specific IIA component	predicted ORF	not_predicted_by_ERGO		Phosphotransferase system, fructose subfamily	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02702	araR	2739332	2740348	338	8,99	37854	+	Arabinose operon transcriptional regulator, Gn	arabinose operon transcriptional regulator, GntF	not_predicted_by_ERGO		Bacterial regulatory protein GntR, HTH|Winged	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+		
LC_02703	glvA	2742098	2740713	461	4,97	52091	-	Maltose-6'-phosphate glucosidase (GH4)	mannose-6-phosphate isomerase / maltose-6'-p	Maltose-6'-phosphate glucosidase (EC 3.2.1.1		Glycoside hydrolase, family 4|Lactate/malate de	G	Yes	-	IMP	tmhmm:1	LC02703	-	-	-	-	-	-		
LC_02704	glvC	2743714	2742110	534	9,35	58221	-	PTS system, maltose-specific IIBC componen	PTS system, glucose-like IIB component	PTS system, maltose and glucose-specific IIB		Phosphotransferase system, EIIB|Multicopper c	G	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-		
LC_02705	null	2745545	2743953	530	9,86	58695	-	ABC transporter, ATPase and permease com	multidrug ABC transporter, ATPase and permea	Multidrug resistance ABC transporter ATP-bir		ABC transporter related|AAA+ ATPase, core|At	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+		
LC_02706	null	2745677	2746543	288	7,2	32579	+	Transcriptional regulator, xre family	transcriptional regulator, MutR family	Transcriptional regulator		Helix-turn-helix type 3|Transcriptional activator f	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02707	null	2747352	2746609	247	4,79	27101	-	Transcriptional regulator, RpiR family	transcriptional regulator, RpiR family	Transcriptional regulator, RpiR family		Helix-turn-helix protein RpiR|Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02708	null	2747801	2747421	126	4,06	13117	-	PTS system, maltose-specific IIA component	PTS system, glucose/sucrose-specific IIABC c	PTS system, glucose-specific IIA component		Phosphotransferase system, sugar-specific per	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02709	null	2748318	2748473	51	10,88	5909	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02710	null	2749513	2748749	254	4,93	26826	-	4-hydroxy-2-oxoglutarate aldolase	4-hydroxy-2-oxoglutarate aldolase / 2-dehydro-3	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.1		Protein of unknown function DUF1341	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02711	selA	2750628	2749528	366	5,59	39766	-	Pyridoxal phosphate-dependent enzyme	selenocysteine synthase (seryl-tRNASer seleniu	L-seryl-tRNA selenium transferase family		Aromatic amino acid beta-eliminating lyase/thre	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02712	dho	2751746	2750625	373	5,02	40788	-	Amidohydrolase	dihydroorotase	Amidohydrolase family protein		Metal-dependent hydrolase, composite|Amidohy	F	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+		
LC_02713	null	2752719	2752024	231	7,52	23723	-	Conserved membrane protein	conserved hypothetical protein (inner membran	Hypothetical membrane spanning protein		no annotation	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-		
LC_02714	null	2753513	2752734	259	10,86	27180	-	Conserved membrane protein	conserved hypothetical protein	Permease		no annotation	null	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-		
LC_02715	null	2753883	2753515	122	10,07	13390	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein		no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-		
LC_02716	null	2754258	2753899	119	6,52	12443	-	Transcriptional regulator	transcriptional regulator	Transcriptional regulator		no annotation	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02717	null	2754701	2754345	118	5,13	13120	-	Transcriptional regulator, antiterminator bglG/I	transcriptional antiterminator, bglG	Transcriptional regulator		PRD	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02718	null	2756547	2754676	623	8,52	70062	-	Transcriptional antiterminator	transcriptional antiterminator	Transcription antiterminator, BglG family		PRD|Phosphotransferase system, EIIB compor	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02719	null	2757811	2757140	223	5,12	25167	-	Transaldolase	transaldolase family protein	Transaldolase (EC 2.2.1.2)		Transaldolase|Aldolase-type TIM barrel	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02720	pts	2758177	2757815	120	4,18	12985	-	PTS system, glucitol/sorbitol-specific IIA com	PTS system, glucitol/sorbitol-specific IIA compc	PTS system, glucitol/sorbitol-specific IIA com		Phosphotransferase system, glucitol/sorbitol-sp	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02721	pts	2759341	2758226	371	6,78	38982	-	PTS system, glucitol/sorbitol-specific, IIB com	PTS system, glucitol/sorbitol-specific IIBC com	PTS system, glucitol/sorbitol-specific IIBC cor		Sorbitol phosphotransferase enzyme II, N-termi	G	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-		
LC_02722	pts	2759963	2759394	189	9,34	21276	-	PTS system, glucitol/sorbitol-specific IIC com	PTS system, glucitol/sorbitol-specific IIC compc	PTS system, glucitol/sorbitol-specific IIC2 con		Phosphotransferase system, enzyme II sorbitol-	G	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	+		
LC_02723	srlM1	2760485	2759976	169	10,27	19557	-	Glucitol operon activator	glucitol/sorbitol operon activator	Glucitol operon activator protein		Glucitol operon activator	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	-		
LC_02724	null	2762354	2760486	622	6,52	71174	-	Sorbitol operon transcription regulator, BglG fa	sorbitol operon transcription regulator	Transcription antiterminator, BglG family		Phosphotransferase system, phosphoenolpyru	G	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+		
LC_02725	gutF	2763181	2762381	266	8,7	28227	-	Sorbitol-6-phosphate 2-dehydrogenase	D-sorbitol 6-phosphate 2-dehydrogenase	Short chain dehydrogenase/reductase family p		Short-chain dehydrogenase/reductase SDR|Gl	IQR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02726	null	2763807	2764076	89	4,68	10181	+	Prevent-host-death family protein	prevent-host-death family protein	not_predicted_by_ERGO		Protein of unknown function DUF172|Prevent-h	D	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02727	null	2764069	2764329	86	9,67	10486	+	Addiction module toxin, Txe/YoeB family	addiction module toxin, Txe/YoeB family protein	not_predicted_by_ERGO		Addiction module toxin, Txe/YoeB	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02728	araD	2765268	2764540	242	4,93	26681	-	L-ribulose-5-phosphate 4-epimerase	L-ribulose-5-phosphate 4-epimerase (Phosphor	L-ribulose-5-phosphate 4-epimerase (EC 5.1.1		Class II aldolase/adducin, N-terminal	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02729	yicB	2765465	2766286	273	5,91	30358	+	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily	Hydrolase (HAD superfamily)		Cof protein|HAD-superfamily hydrolase, subfam	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02730	sgbU	2767240	2766353	295	6,79	33047	-	L-xylulose 5-phosphate 3-epimerase	L-ribulose-5-phosphate 3-epimerase sgbU (L-x	L-xylulose 5-phosphate 3-epimerase (EC 5.3.1		Putative hexulose-6-phosphate isomerase|Xylos	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02731	null	2768198	2767425	257	8,93	28209	-	Lactose transport regulator, DeoR family	lactose transport regulator	Transcriptional regulator, DeoR family		Bacterial regulatory protein, DeoR N-terminal|Ba	KG	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-		
LC_02732	rmpD	2768913	2768272	213	4,7	22824	-	Hexulose-6-phosphate synthase	3-hexulose-6-phosphate synthase and related p	3-keto-L-gulonate-6-phosphate decarboxylase		Orotidine 5'-phosphate decarboxylase, core|Rib	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02733	null	2768963	2769136	57	11,91	6015	+	Conserved protein	predicted ORF	not_predicted_by_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02734	sgaB	2769418	2769125	97	10,03	11000	-	PTS system, ascorbate-specific IIB componer	PTS system, galactitol/ascorbate/lactose/cellobi	PTS system, 3-keto-L-gulonate specific IIB co		Phosphotransferase system, lactose/cellobiose	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02735	sgaT	2770987	2769491	498	9,51	55018	-	PTS system, ascorbate-specific IIC componer	PTS system, ascorbate-specific IIC component	PTS system, 3-keto-L-gulonate specific IIC co		Putative sugar-specific permease, SgaT/UlaA	S	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-		
LC_02736	null	2771489	2771031	152	4,07	16496	-	PTS system, ascorbate-specific IIA compone	PTS system, mannitol/fructose-specific IIA com	PTS system, 3-keto-L-gulonate specific IIA co		Phosphotransferase system, phosphoenolpyru	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02737	yjfR	2772583	2771513	356	6,01	40445	-	L-ascorbate-6-phosphate lactonase	L-ascorbate-6-phosphate lactonase ulaG (L-asc	Metal-dependent hydrolase (EC 3.-.-.-)		no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02738	prtR	2773439	2777923	1494	4,93	155717	+	Cell envelope-associated proteinase, lactocepi	cell envelope-associated proteinase PrtR (lactc	Endopeptidase lactocepin (EC 3.4.21.96)		Peptidase S8 and S53, subtilisin, kexin, sedolis	O	Yes	-	LPxTG	tmhmm:2	-	-	-	-	-	protease	+		
LC_02739	null	2777973	2778239	88	6,79	9933	+	Conserved protein	predicted ORF	no_function_in_ERGO		no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02740	null	2779336	2778440	298	10,02	31243	-	Transcriptional regulator / sugar kinase	transcriptional regulator / sugar kinase	Glucokinase (EC 2.7.1.2) / transcription regul		ROK	KG	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-		
LC_02741	asnA2	2780329	2779367	320	6,79	34402	-	Asparaginase	glycosylasparaginase precursor, threonine pept	N(4)-(beta-N-acetylglucosaminyl)-L-asparagin		Peptidase T2, asparaginase 2	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-		
LC_02742	null	2781645	2780326	439	7,01	48338	-	Dipeptidase, M20 family	dipeptidase	Exopeptidase, M20(A) family		ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|F	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-		
LC_02743	null	2782385	2781666	239	7,74	27317	-	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family		Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+		
LC_02744	null	2782747	2783949	400	8,79	43416	+	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Transporter, MFS superfamily		Major facilitator superfamily|Major facilitator sup	GEPR	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-		
LC_02745	null	2783975	2785009	344	4,96	39271	+	Alpha-L-fucosidase (GH29)	alpha-L-fucosidase	Alpha-L-fucosidase (EC 3.2.1.51)		Glycoside hydrolase, family 29 (alpha-L-fucosid	G	Yes	-	-	tmhmm:0	LC02745	-	-	-	-	-	-		
LC_02746	yjgM	2785575	2785075	166	6,74	18596	-	Acetyltransferase, GNAT family protein	acetyltransferase, GNAT family protein	Acetyltransferase yjgM (EC 2.3.1.-)		GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02747	yjhB	2786382	2785753	209	4,59	23393	-	Phosphohydrolase, MutT/nudix family	phosphohydrolase, MutT/nudix family protein	Phosphohydrolase (MutT/nudix family protein)		NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02748	null	2786720	2786508	70	11,45	7500	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO		no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-		
LC_02749	null	2787303	2786734	189	11,02	21152	-	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator		Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	IMP	tmhmm:4	-	-	-	-	regulator	-	-		
LC_02750	null	2793019	2787635	1794	6,57	195158	-	Alpha-glucosidase (GH31)	alpha-glucosidase/alpha-xylosidase, glycosyl hy	Alpha-glucosidase (EC 3.2.1.20)		Glycoside hydrolase, family 31|Coagulation fact	G	Yes	fibronectin	LPxTG	tmhmm:1	LC02750	-	-	-	-	-	+		
LC_02751	null	2794015	2794725	236	10,18	26659	+	ADP-ribose pyrophosphatase	ADP-ribose pyrophosphatase	Phosphohydrolase (MutT/nudix family protein)		NUDIX hydrolase|NUDIX	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		
LC_02752	pncA	2794838	2795398	186	5,87	20632	+	Isochorismatase family protein	bifunctional pyrazinamidase/nicotinamidase	Pyrazinamidase (EC 3.5.1.-) / Nicotinamidase		Isochorismatase hydrolase	Q	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+		

LC_02753	pncB	2795432	2796865	477	6,19	52347	+	Nicotinate phosphoribosyltransferase	nicotinate phosphoribosyltransferase related pro	Nicotinate phosphoribosyltransferase (EC 2.4.	Nicotinate phosphoribosyltransferase related|Ni	H	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02754	glpQ1	2797690	2796992	232	6,12	26541	-	Glycerophosphoryl diester phosphodiesterase	glycerophosphoryl diester phosphodiesterase fa	Glycerophosphoryl diester phosphodiesterase	Glycerophosphoryl diester phosphodiesterase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02755	arsC	2798163	2797747	138	8,67	15067	-	Arsenate reductase, tyrosine phosphatase	protein arsC, arsenate reductase, arsenical pun	Arsenate reductase (EC 1.20.4.1)	Low molecular weight phosphotyrosine protein p	T	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02756	null	2799625	2798252	457	9,73	49730	-	ABC transporter, glycerol-3-phosphate-bindin	glycerol-3-phosphate ABC transporter, glycerol-	Glycerol-3-phosphate-binding protein	Bacterial extracellular solute-binding protein, far	G	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	-	
LC_02757	null	2800437	2799622	271	10,32	30732	-	ABC transporter, glycerol-3-phosphate transpo	glycerol-3-phosphate ABC transporter, permeas	SN-glycerol-3-phosphate transport system per	Binding-protein-dependent transport systems in	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02758	ugpA	2801366	2800434	310	9,39	34282	-	ABC transporter, glycerol-3-phosphate transpo	glycerol-3-phosphate ABC transporter, permeas	SN-glycerol-3-phosphate transport system per	Binding-protein-dependent transport systems in	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02759	malK	2802471	2801356	371	4,5	41211	-	ABC transporter, ATP-biding protein	ABC transporter, ATPase component, TOBE	SN-glycerol-3-phosphate transport ATP-bindir	ABC transporter related|AAA+ ATPase, core|M	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02760	null	2803987	2802698	429	10,24	46188	-	Transporter, major facilitator superfamily MFS	permease of the major facilitator superfamily	Macrolide-efflux protein	Major facilitator superfamily MFS_1	null	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02761	null	2804933	2804148	261	8,24	29244	-	Beta-lactamase class A	beta-lactamase class A	Beta-lactamase (EC 3.5.2.6)	Penicillin-binding protein, transpeptidase fold	V	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+	
LC_02762	null	2806088	2805063	341	7,68	36927	-	Beta-lactamase class C related penicillin bindi	beta-lactamase class C related penicillin bindin	Beta-lactamase family protein	Beta-lactamase|Penicillin-binding protein, trans	V	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-	
LC_02763	murQ	2806992	2806072	306	5,89	31492	-	N-acetylmuramic acid 6-phosphate etherase	N-acetylmuramic acid 6-phosphate etherase (M	Glucokinase regulatory protein	Sugar isomerase (SIS)|Glucokinase regulatory p	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02764	null	2807848	2806901	315	9,17	34523	-	Transcriptional regulator, RpiR family	transcriptional regulator	Transcriptional regulator, RpiR family	Helix-turn-helix protein RpiR|Sugar isomerase (	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02765	pts	2808330	2807845	161	10,58	17327	-	PTS system, mannose/fructose/N-acetylgalac	PTS system, mannose/fructose/N-acetylgalactc	PTS system, mannose/fructose family IIB com	Phosphotransferase system, sorbose subfamily	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02766	levG	2809276	2808440	278	9,69	30510	-	PTS system, mannose/fructose/N-acetylgalac	PTS system, mannose/fructose/sorbose/N-acet	PTS system, mannose-specific IID componen	Phosphotransferase system, mannose/fructose	G	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02767	levF	2810099	2809269	276	8,73	29143	-	PTS system, mannose/fructose/N-acetylgalac	PTS system, mannose/fructose/N-acetylgalactc	PTS system, mannose-specific IIC componen	Phosphotransferase system, sorbose-specific I	G	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02768	yjhA	2811484	2810417	355	9,94	40096	-	Metal-dependent hydrolase	endonuclease/exonuclease/phosphatase family	Endonuclease/Exonuclease/phosphatase fami	Calcium-binding EF-hand|Endonuclease/exonu	K	Yes	invasin	Nterm	tmhmm:1	-	-	-	-	-	-	+	
LC_02769	rpmE2	2811632	2812564	310	5,04	33540	+	Phosphoesterase, DHH family protein	exopolyphosphatase-related proteins, DHH-fam	Phosphoesterase, DHH family protein	Phosphoesterase, RecJ-like|Phosphoesterase,	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02770	morA	2812773	2813630	285	5,7	31831	+	Oxidoreductase, aldo/keto reductase family	oxidoreductase, aldo/keto reductase of diketogu	Morphine 6-dehydrogenase (EC 1.1.1.218)	Aldo/keto reductase	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02771	yraB	2813681	2814112	143	9,77	16656	+	Transcriptional regulator, MerR family	transcriptional regulator, MerR family protein	Transcriptional regulator, MerR family	Bacterial regulatory protein, MerR|Putative DNA	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02772	null	2814986	2814240	248	4,92	28004	-	Methyltransferase	SAM-dependent methyltransferases	Methyltransferase (EC 2.1.1.-)	no annotation	QR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02773	sugE	2815478	2815161	105	10,57	11416	-	Small Multidrug Resistance protein	membrane transporter of cations and cationic di	Quaternary ammonium compound-resistance	Small multidrug resistance protein	P	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_02774	null	2816011	2815757	84	10,39	9669	-	Transcriptional regulator, AbrB family	predicted ORF	Transcriptional regulator, AbrB family	Transcriptional regulator AbrB|SpoVT/AbrB-like	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02775	null	2817911	2816298	537	9,43	59619	-	ABC transporter, drug efflux transporter ATPa	multidrug efflux ABC transport system, ATPase	not_predicted_by_ERGO	ABC transporter related|AAA+ ATPase, core|Al	V	No	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02776	ps105	2818728	2819057	109	7,88	12810	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02777	null	2819410	2819165	81	10,57	9262	-	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_02778	null	2820222	2819599	207	9,99	22717	-	Alpha/beta hydrolase	conserved hypothetical protein	Hydrolases of the alpha/beta superfamily	Alpha/beta hydrolase fold-1	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02779	null	2820919	2820419	166	8,91	18953	-	Acetyltransferase, GNAT family	acetyltransferase, GNAT family	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	KR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02780	null	2821456	2820923	177	8,6	19022	-	Histidinol phosphatase related phosphatase	histidinol phosphatase related phosphatase	not_predicted_by_ERGO	HAD-superfamily hydrolase, subfamily IIIA	E	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02781	ptp1	2822216	2821467	249	5,17	27684	-	Protein tyrosine/serine phosphatase	protein tyrosine/serine phosphatase	Protein tyrosine phosphatase (EC 3.1.3.48)	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02782	null	2822758	2822279	159	8,9	18406	-	Acetyltransferase, GNAT family	acetyltransferase, GNAT family	Acetyltransferase, GNAT family	GCN5-related N-acetyltransferase	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02783	null	2823482	2822811	223	6,79	25717	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02784	null	2824201	2823755	148	4,6	16044	-	Conserved protein	conserved hypothetical protein (cytoplasmic pro	Hypothetical protein	Protein of unknown function DUF984	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02785	null	2824724	2824245	159	9,74	17901	-	Conserved protein	conserved hypothetical protein (UPF0247-prote	Hypothetical cytosolic protein	Protein of unknown function DUF163	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02786	null	2824872	2825972	366	9,64	40923	+	Di-and tricarboxylate transporter	Di- and tricarboxylate transporter	Hypothetical membrane spanning protein	Divalent ion symporter	P	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	-	
LC_02787	null	2826222	2827079	285	4,59	30134	+	Putative protein without homology	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_02788	dapE	2828557	2827229	442	4,44	47944	-	Peptidase M20	ArgE/DapE/Acy1 family peptidase	Acetylornithine deacetylase/Succinyl-diaminop	ArgE/dapE/ACY1/CPG2/yscS|Peptidase M20|F	E	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	-	
LC_02789	oppA	2830192	2828582	536	9,98	58584	-	ABC transporter, oligopeptide transporter peri	oligopeptide ABC transport system, periplasmic	Oligopeptide-binding protein oppA	Bacterial extracellular solute-binding protein, far	E	Yes	-	Lipobox	tmhmm:0	-	-	-	-	-	-	+	
LC_02790	null	2831123	2832331	402	5,19	42127	+	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02791	null	2832574	2834646	690	6,37	78700	+	Glycoside hydrolase, family 43	glycosyl hydrolase family 43 protein	not_predicted_by_ERGO	Helix-turn-helix, AraC type|Glycoside hydrolase, K		No	-	-	tmhmm:0	LC02791	-	-	-	-	-	-	
LC_02792	uxuT	2836598	2834988	536	10,14	59786	-	Oligogalacturonide transporter	oligogalacturonide transporter	not_predicted_by_ERGO	Major facilitator superfamily MFS_1	G	No	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_02793	null	2838719	2836674	681	6,29	79000	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02794	cadA	2840840	2839014	608	4,8	64041	-	Heavy metal translocating P-type ATPase	ATPase, E1-E2 type:Heavy metal-(Cd/Co/Hg/P	Lead, cadmium, zinc and mercury transporting	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-t	P	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+	
LC_02795	hsp3	2841731	2841291	146	4,63	16654	-	Small heat shock protein, Hsp20 family	molecular chaperone, small heat shock protein,	Small heat shock protein	Heat shock protein Hsp20|HSP20-like chaperon	O	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02796	null	2842296	2841892	134	4,57	14499	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02797	htrA	2844222	2842888	444	6,06	45202	-	Serine protease	trypsin-like serine protease with PDZ domain	Endopeptidase degP (EC 3.4.21.-)	Peptidase S1 and S6, chymotrypsin/Hap|PDZ/I	O	Yes	-	IMP	tmhmm:1	-	-	-	-	-	protease	+	
LC_02798	phnP	2845471	2844662	269	5,99	29350	-	Metallo-beta-lactamase family protein	metal-dependent hydrolase of the beta-lactamas	Zn-dependent hydrolase (beta-lactamase supe	Beta-lactamase-like	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02799	null	2846350	2845553	265	9,69	29922	-	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02800	null	2847809	2846406	467	6,19	52574	-	Conserved protein	conserved hypothetical protein	hypothetical membrane protein yycH	YycH	null	Yes	-	Nterm	tmhmm:1	-	-	-	-	-	-	+	
LC_02801	hpk	2849709	2847799	636	4,94	71457	-	Two component sensor transduction histidine	PAS/PAC sensor signal transduction histidine k	Two-component sensor kinase yycG (EC 2.7.:	PAS|ATP-binding region, ATPase-like|Histidine	T	Yes	-	Cterm	tmhmm:2	-	-	-	HPK	-	-	+	
LC_02802	rrp	2850438	2849725	237	4,77	27086	-	Two-component response regulator	DNA-binding response regulator, OmpR family	Two-component response regulator yycF	Response regulator receiver|Transcriptional reg	TK	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	+	
LC_02803	null	2850807	2851481	224	7,33	24947	+	Alpha/beta superfamily hydrolase	alpha/beta superfamily hydrolase	Hydrolases of the alpha/beta superfamily	Alpha/beta hydrolase fold-1|Alpha/beta hydrolas	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02804	arpJ	2851575	2853023	482	10,22	52358	+	ABC transporter, amino acid transporter perm	amino acid ABC transporter, permease and per	Citrulline-binding protein / Citrulline transport s	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02805	argG	2853084	2854304	406	4,77	44672	+	Argininosuccinate synthase	argininosuccinate synthase, citrulline-aspartate	Argininosuccinate synthase (EC 6.3.4.5)	Argininosuccinate synthase|TonB box, N-termir	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02806	argH	2854297	2855700	467	5,74	51611	+	Argininosuccinate lyase	argininosuccinate lyase, arginosuccinase, ASAI	Argininosuccinate lyase (EC 4.3.2.1)	Fumarate lyase|Delta crystallin|L-Aspartase-like	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02807	ybhE	2856931	2855831	366	5,54	41149	-	Outer surface protein	outer surface protein	outer surface protein	Peptidyl-prolyl cis-trans isomerase, cyclophilin-t	S	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02808	null	2857368	2856949	139	10,21	16123	-	Conserved protein	conserved hypothetical protein	Transcriptional regulator	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02809	pts	2858769	2857408	453	10,11	49298	-	PTS system, cellobiose-specific IIC componer	PTS system, cellobiose-specific IIC component	PTS system, cellobiose-specific IIC componer	Aminoacyl-tRNA synthetase, class I|Phosphotra	G	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	+	
LC_02810	null	2859570	2858860	236	7,72	26428	-	Transcriptional regulator, GntR family	transcriptional regulator, GntR family	Transcriptional regulator, GntR family	Bacterial regulatory protein GntR, HTH|UbiC tra	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02811	pts	2859785	2860114	109	5,17	11850	+	PTS system, cellobiose-specific IIB componer	PTS system, cellobiose-specific IIB component	PTS system, cellobiose-specific IIB componer	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02812	pts	2860114	2860443	109	4,89	11894	+	PTS system, cellobiose-specific IIA componer	PTS system, cellobiose-specific IIA component	PTS system, diacetylchitobiose-specific IIA cc	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02813	wecD	2861121	2860570	183	4,76	21518	-	Acetyltransferase, gnat family	acetyltransferase, including N-acetylase of ribos	Acetyltransferase (EC 2.3.1.-)	GCN5-related N-acetyltransferase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02814	null	2861368	2862129	253	10,1	28075	+	Phosphohydrolase, MutT/nudix family	ADP-ribose phosphohydrolase, MutT/nudix fam	Phosphohydrolase (MutT/nudix family protein)	NUDIX hydrolase|NUDIX	LR	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02815	null	2862126	2862647	173	9,92	19634	+	Kinase	kinase	Putative kinase	no annotation	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02816	ycaC	2862904	2863527	207	5,01	22862	+	Isochorismatase hydrolase	isochorismatase hydrolase, cysteine hydrolase /	Hydrolase, isochorismatase family	Isochorismatase hydrolase	Q	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02817	null	2863683	2864183	166	11,8	18023	+	Transporter, major facilitator superfamily MFS	predicted ORF	not_predicted_by_ERGO	Major facilitator superfamily|Major facilitator sup	GEPF	No	-	IMP	tmhmm:5	-	-	-	-	-	-	-	
LC_02818	null	2864180	2865103	307	10,38	32503	+	Transporter, major facilitator superfamily MFS	predicted ORF	Efflux pump antibiotic resistance protein	Major facilitator superfamily|Major facilitator sup	GEPF	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02819	null	2865196	2865492	98	11,96	10620	+	Transporter, major facilitator superfamily MFS	predicted ORF	not_predicted_by_ERGO	Major facilitator superfamily|Major facilitator sup	P	No	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_02820	null	2865541	2866386	281	10,73	30144	+	Transporter, major facilitator superfamily MFS	predicted ORF	Transporter, MFS superfamily	Major facilitator superfamily|Major facilitator sup	P	Yes	-	IMP	tmhmm:8	-	-	-	-	-	-	-	
LC_02821	iolS	2866451	2867380	309	5,22	34115	+	Aldo/keto reductase	aryl-alcohol dehydrogenase related enzyme, oxi	IolS protein	Aldo/keto reductase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	

LC_02822	manO	2867861	2867496	121	10,99	14117	-	ManO-protein	ManO	Hypothetical cytosolic protein	Protein of unknown function DUF956	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02823	manN	2869096	2868185	303	9,98	33358	-	PTS system, mannose-specific IID componen	PTS system, mannose-specific IID component	PTS system, mannose-specific IID componen	Phosphotransferase system, mannose/fructose	G	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02824	manM	2869926	2869114	270	4,61	27545	-	PTS system, mannose-specific IIC componen	PTS system, mannose-specific IIC component	PTS system, mannose-specific IIC componen	Phosphotransferase system, sorbose-specific I	G	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02825	null	2870140	2869952	62	6,8	6975	-	PTS system, mannose-specific IIAB compone	PTS system, mannose-specific IIAB componen	not_predicted_by_ERGO	Phosphotransferase system, sorbose subfamily	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02826	manL	2870931	2870179	250	5,56	27166	-	PTS system, mannose-specific IIAB compone	PTS system, mannose-specific IIAB componen	PTS system, mannose-specific IIAB compone	Phosphotransferase system, fructose subfamily	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02827	upsA	2872437	2871166	423	10,45	45716	-	Transportation permease, UpsA	transport permease (UpsA)	Macrolide-efflux protein	no annotation	GEPF	Yes	-	IMP	tmhmm:10	-	-	-	-	-	-	+	
LC_02828	upsR	2872528	2873547	339	8,39	39599	+	Transcriptional regulator, xre family	transcriptional regulator, xre family (UpsR)	Transcriptional regulator	Transcriptional activator Rgg/GadR/MutR, C-te	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02829	null	2874572	2873724	282	10,47	31830	-	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator	Helix-turn-helix type 3|Lambda repressor-like, D	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02830	null	2875444	2874569	291	7,04	33735	-	Transcriptional regulator, xre family	transcriptional regulator, xre family	Transcriptional regulator	Helix-turn-helix type 3|Transcriptional activator f	K	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02831	null	2875594	2875938	114	10,47	12830	+	Conserved protein	conserved hypothetical protein	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:3	-	-	-	-	-	-	-	
LC_02832	null	2876536	2876847	103	9,32	11544	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02833	null	2877937	2878548	203	9,83	23650	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02834	bacA	2880639	2878534	701	4,81	74495	-	Peptidoglycan-binding protein	exported protein	Peptidoglycan-binding protein	Peptidoglycan-binding domain 1|Peptidoglycan	null	Yes	peptidoglucar	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02835	glnP	2881133	2882740	535	10,01	58656	+	ABC transporter, amino acid-binding protein	amino acid ABC transporter/signal transduction	ABC transporter amino acid-binding protein / A	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+	
LC_02836	glnQ2	2882744	2883490	248	5,33	27120	+	ABC transporter, amino acid transporter ATPa	polar amino acid ABC transporter, ATPase com	Amino acid transport ATP-binding protein	ABC transporter related|AAA+ ATPase, core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02837	null	2883878	2883603	91	10,75	10417	-	Conserved protein	predicted ORF	Hypothetical membrane spanning protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02838	malE2	2885183	2883906	425	10,13	46602	-	ABC transporter, sugar transporter periplasmi	sugar ABC transporter, periplasmic component	Sugar-binding protein	Bacterial extracellular solute-binding protein, far	G	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	+	
LC_02839	null	2885353	2885799	148	11,72	16388	+	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02840	null	2886432	2885716	238	9,16	27532	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane spanning protein	Protein of unknown function DUF975	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02841	null	2886841	2886503	112	8,48	12400	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02842	null	2886993	2887316	107	4,09	12029	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02843	null	2887561	2887731	56	11,34	6533	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02844	null	2887797	2888267	156	10,16	17890	+	Conserved protein	conserved hypothetical protein	Hypothetical membrane spanning protein	Protein of unknown function DUF304, prokaryot	S	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	+	
LC_02845	null	2888260	2889774	504	10,2	57329	+	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Protein of unknown function DUF304, prokaryot	null	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	-	
LC_02846	null	2889806	2890582	258	6,51	29214	+	ABC transporter, glutamine transporter ATPas	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein	AAA+ ATPase, core	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02847	null	2890693	2891559	288	5,06	32074	+	Fructosamine-3-kinase	aminoglycoside phosphotransferase, fructosam	Fructosamine-3-kinase (EC 2.7.1.-)	Aminoglycoside phosphotransferase|Protein kin	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02848	glnQ	2892438	2891698	246	5,15	26840	-	ABC transporter, glutamine transporter ATPas	amino acid ABC transporter, ATPase componer	Glutamine transport ATP-binding protein glnQ	ABC transporter related|AAA+ ATPase, core	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02849	glnP	2893889	2892435	484	10,28	52664	-	ABC transporter, glutamine-binding periplasm	amino acid ABC transporter/signal transduction	Glutamine-binding protein / Glutamine transpo	Binding-protein-dependent transport systems in	ET	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02850	glnP	2895632	2894172	486	10,23	52896	-	ABC transporter, glutamine-binding periplasm	amino acid ABC transporter/signal transduction	Glutamine-binding protein / Glutamine transpo	Binding-protein-dependent transport systems in	E	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02851	null	2895839	2896387	182	4,99	20293	+	Acetyltransferase, including N-acetylase of rib	acetyltransferase, including N-acetylase of ribos	Ribosomal-protein-serine acetyltransferase (E	GCN5-related N-acetyltransferase	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02852	null	2897187	2896564	207	9,03	22874	-	Conserved membrane protein	conserved hypothetical protein (membrane prot	Hypothetical membrane associated protein	Protein of unknown function DUF95, transmem	S	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02853	moxR	2897409	2898347	312	8,83	33828	+	ATPase associated with various cellular activit	magnesium chelatase, ChlI subunit:MoxR-like A	MoxR-like ATPases	AAA+ ATPase, core|ATPase associated with va	R	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02854	null	2898352	2899344	330	9,61	36569	+	Conserved protein	conserved hypothetical protein (membrane prot	Hypothetical membrane spanning protein	Peptidase S8 and S53, subtilisin, kexin, sedolis	R	Yes	-	IMP	tmhmm:2	-	-	-	-	-	protease	+	
LC_02855	null	2899337	2901502	721	10,3	80236	+	Membrane associated transglutaminase-like e	membrane associated transglutaminase-like en	Transglutaminase-like protein	Transglutaminase-like	E	Yes	-	IMP	tmhmm:8	-	-	-	-	-	protease	+	
LC_02856	null	2902048	2903157	369	5,19	41386	+	Glycosyl transferase, group 1	glycosyltransferase	Lipopolysaccharide N-acetylglucosaminyltrans	Glycosyl transferase, group 1	M	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02857	ansB	2904763	2903369	464	6,38	49758	-	Aspartate ammonia-lyase	aspartate ammonia-lyase (aspartase) gene anst	Aspartate ammonia-lyase (EC 4.3.1.1)	Fumarate lyase|L-Aspartase-like	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02858	null	2905810	2905562	82	10,62	9587	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02859	mae	2907209	2906031	392	5,28	41149	-	NAD-dependent malic enzyme	malate dehydrogenase (oxaloacetate-decarboxy	NAD-dependent malic enzyme (EC 1.1.1.39)	Regulator of chromosome condensation, RCC1	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02860	malP	2908571	2907246	441	9,51	46724	-	Citrate carrier protein	citrate carrier protein, CCS family / Na+/malate	Citrate/L-malate proton symporter	Citrate carrier protein	C	Yes	-	IMP	tmhmm:12	-	-	-	-	-	-	-	
LC_02861	dpiB	2908728	2910272	514	9,62	58423	+	Two component sensor transduction histidine	two-component sensor signal transduction histi	Sensor kinase dpiB (EC 2.7.3.-)	PAS|PAS fold	T	Yes	-	Cterm	tmhmm:2	-	-	-	HPK	-	-	-	
LC_02862	dpiA	2910250	2910939	229	9,49	26197	+	Two-component response regulator	response regulator of citrate/malate metabolism	Transcriptional regulatory protein dpiA	Response regulator receiver|Response regulato	C	Yes	-	-	tmhmm:0	-	-	-	RR	regulator	-	-	
LC_02863	null	2911671	2911123	182	10,82	20657	-	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	Sec	tmhmm:1	-	-	-	-	-	-	+	
LC_02864	serA	2911888	2912865	325	9,22	35970	+	D-isomer specific 2-hydroxyacid dehydrogena	Glycerate dehydrogenase	not_predicted_by_ERGO	D-isomer specific 2-hydroxyacid dehydrogenas	CHR	No	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02865	null	2914532	2913678	284	4,63	30157	-	3-hydroxyisobutyrate dehydrogenase related b	3-hydroxyisobutyrate dehydrogenase related bet	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.	Hydroxyacid dehydrogenase/reductase|6-phosp	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02866	null	2915239	2914841	132	7,67	14752	-	Conserved protein	conserved hypothetical protein	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02867	guaA	2916092	2915412	226	5,05	25391	-	Glutamine amidotransferase	GMP synthase - glutamine amidotransferase dc	GMP synthase [glutamine-hydrolyzing] (EC 6.:	Glutamine amidotransferase class-I|Glutamine a	F	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02868	null	2917200	2916271	309	6,52	33004	-	PEP phosphonomutase-like protein	PEP phosphonomutase-like protein	Hypothetical protein	Agrin NtA	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02869	null	2917577	2917747	56	10,47	6564	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02870	prsA	2918633	2917713	306	6,35	33615	-	Ribose-phosphate pyrophosphokinase	ribose-phosphate pyrophosphokinase 2 (RPPK	Ribose-phosphate pyrophosphokinase (EC 2.7	Phosphoribosyltransferase|Purine/pyrimidine ph	FE	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02871	ybcH	2918834	2919763	309	9,02	34900	+	Hydrolase of the alpha/beta superfamily protei	hydrolase, alpha/beta superfamily	Alpha/beta hydrolase	Alpha/beta hydrolase fold-1	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02872	null	2920884	2919931	317	4,69	35731	-	Esterase/lipase	esterase/lipase	Lipase (EC 3.1.1.3)	Alpha/beta hydrolase fold-3	I	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02873	mtlD	2922147	2920993	384	5,2	42575	-	Mannitol-1-phosphate 5-dehydrogenase	MtlD, mannitol-1-phosphate 5-dehydrogenase	Mannitol-1-phosphate 5-dehydrogenase (EC 1	Mannitol dehydrogenase, core|6-phosphoglucor	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02874	pts	2922594	2922151	147	4,32	16249	-	PTS system, mannitol-specific IIA component	PTS system, Mannitol/fructose-specific IIA com	PTS system, mannitol-specific IIA component	Phosphotransferase system, phosphoenolpyruv	GT	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02875	null	2924656	2922599	685	5,3	76088	-	Transcriptional regulator	transcriptional antiterminator	Transcriptional regulator, DeoR family	Phosphotransferase system, phosphoenolpyruv	null	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02876	pts	2926509	2924692	605	9,13	64195	-	PTS system, mannitol-specific IIBC compone	PTS system, mannitol-specific IIBC component	PTS system, mannitol-specific IIBC compone	Phosphotransferase system, EIIC|Phosphotran	G	Yes	-	IMP	tmhmm:7	-	-	-	-	-	-	+	
LC_02877	nagB	2926978	2927688	236	5,35	26098	+	Glucosamine-6-phosphate deaminase/isomer	glucosamine-6-phosphate deaminase (Glucosa	Glucosamine-6-phosphate isomerase (EC 3.5	Glucosamine-6-phosphate isomerase|Glucosam	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02878	null	2927967	2928752	261	4,67	28883	+	Hydrolase of the HAD superfamily	hydrolase, HAD superfamily, subfamily IIB, Cof	Hydrolase (HAD superfamily)	Cof protein|ATPase, P-type, K/Mg/Cd/Cu/Zn/Na	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02879	null	2929084	2929344	86	7,88	10553	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02880	null	2929355	2929531	58	10,78	6453	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-	
LC_02881	null	2929860	2930636	258	4,86	29099	+	Conserved protein	predicted ORF	Hypothetical protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02882	null	2930648	2931829	393	8,9	45965	+	Transcriptional regulator	transcriptional regulator	Transcriptional regulator	Helix-turn-helix type 3|Protein of unknown funct	E	Yes	-	-	tmhmm:0	-	-	-	-	regulator	-	-	
LC_02883	null	2932210	2933277	355	9,62	38772	+	Transporter, RND superfamily	efflux transporter, RND family, MFP subunit	Transporter, RND superfamily	Secretion protein HlyD	M	Yes	-	IMP	tmhmm:1	-	-	-	-	-	-	+	
LC_02884	as-48G	2933270	2933959	229	5,79	25199	+	ABC transporter, ATPase component	antimicrobial peptide ABC transporter, ATPase	ABC transporter ATP-binding protein	ABC transporter related|AAA+ ATPase, core	V	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+	
LC_02885	null	2933946	2935139	397	10,24	42136	+	ABC transporter, antimicrobial peptide transpo	antimicrobial peptide ABC transporter, permeas	ABC transporter permease protein	Protein of unknown function DUF214, permease	V	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	+	
LC_02886	null	2936071	2935154	305	9,77	33007	-	NADPH:quinone reductase related Zn-depend	NADPH:quinone reductase related Zn-depende	not_predicted_by_ERGO	Alcohol dehydrogenase superfamily, zinc-conta	CR	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02887	null	2936236	2937057	273	6,67	29912	+	Transcriptional regulator, xre family	transcriptional regulator, xre family	not_predicted_by_ERGO	Helix-turn-helix type 3|Lambda repressor-like, D	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	+	
LC_02888	null	2937129	2937560	143	4,44	16057	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-	
LC_02889	null	2937684	2938919	411	9,25	45393	+	Conserved protein	conserved hypothetical protein	Hypothetical protein	no annotation	null	Yes	-	IMP	tmhmm:4	-	-	-	-	-	-	-	
LC_02890	null	2945918	2939019	2299	4,38	237854	-	Adhesion exoprotein	predicted ORF	Gram positive anchor domain	Surface protein from Gram-positive cocci, anch	null	Yes	-	LPxTG	tmhmm:1	-	-	-	-	-	-	+	

LC_02891	null	2949173	2946015	1052	4,57	109190	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Bacterial Ig-like	null	No	iG	Sec	tmhmm:1	-	-	-	-	-	-	-
LC_02892	ykrV	2950608	2949439	389	4,95	42280	-	Aminotransferase	aminotransferase, class I and II	Aspartate aminotransferase (EC 2.6.1.1)	Aminotransferase, class I and II|Pyridoxal phos	E	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02893	cnhA	2951457	2950675	260	6,03	28900	-	Hydrolase, carbon-nitrogen family	amidohydrolase	Carbon-nitrogen hydrolase family protein	Nitrilase/cyanide hydratase and apolipoprotein N	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02894	metQ	2952326	2951487	279	10,24	30568	-	NLPA lipoprotein	glutelin / Lipoprotein YaeC family / NLPA lipopr	ABC transporter substrate-binding protein	NLPA lipoprotein	P	Yes	-	Lipobox	tmhmm:1	-	-	-	-	-	-	-
LC_02895	null	2953643	2953044	199	9,55	22925	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02896	ypjH	2953835	2954920	361	4,59	38443	+	Alcohol dehydrogenase, iron-containing	glycerol dehydrogenase and related enzymes	Glycerol dehydrogenase (EC 1.1.1.6)	Iron-containing alcohol dehydrogenase	C	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02897	null	2955162	2955347	61	4,93	7109	+	Putative protein without homology	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02898	null	2955301	2955477	58	10,57	6064	+	Conserved protein	predicted ORF	no_function_in_ERGO	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02899	amd	2957076	2955877	399	5,91	42829	-	Carboxypeptidase, M20(D)	N-acyl-L-amino acid amidohydrolase-like protei	Carboxypeptidase, M20(D) family	Peptidase M20|Peptidase M20D, amidohydrola	R	Yes	-	-	tmhmm:0	-	-	-	-	-	protease	+
LC_02900	null	2957561	2957073	162	11,4	17488	-	Integral membrane protein	conserved hypothetical protein (integral membr	Threonine/Serine Exporter	no annotation	S	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	-
LC_02901	labL	2958327	2957563	254	5,84	27168	-	Conserved membrane protein	conserved hypothetical protein (integral membr	Hypothetical membrane associated protein	Protein of unknown function DUF1212	S	Yes	-	IMP	tmhmm:6	-	-	-	-	-	-	+
LC_02902	null	2958738	2958532	68	10,64	7662	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	Cterm	tmhmm:2	-	-	-	-	-	-	-
LC_02903	null	2959099	2958878	73	10,46	8163	-	Conserved protein	predicted ORF	Hypothetical membrane associated protein	no annotation	null	Yes	-	IMP	tmhmm:2	-	-	-	-	-	-	-
LC_02904	null	2959396	2961015	539	9,93	60296	+	ABC transporter, ATPase and permease comp	ABC transporter, ATPase and permease compo	ABC transporter ATP-binding protein	ABC transporter, transmembrane region|ABC tr	V	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_02905	gidA	2963042	2961141	633	8,49	69929	-	tRNA uridine 5-carboxymethylaminomethyl mo	tRNA uridine 5-carboxymethylaminomethyl mod	Glucose inhibited division protein A	Pyridine nucleotide-disulphide oxidoreductase,	D	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02906	trmE	2964471	2963083	462	4,76	50197	-	tRNA modification GTPase MnmE	tRNA modification GTPase TrmE:Small GTP-b	tRNA (5-carboxymethylaminomethyl-2-thiourid	GTP-binding protein, HSR1-related|tRNA modi	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02907	null	2964529	2964906	125	11,71	13870	+	Conserved protein	predicted ORF	Hypothetical cytosolic protein	no annotation	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02908	null	2965712	2964945	255	10,1	28023	-	RNA-binding protein, jag protein	RNA-binding protein R3H	Jag protein	Single-stranded nucleic acid binding R3H|KH, t	R	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02909	oxaA2	2966566	2965730	278	10,77	31477	-	Stage III sporulation protein J	stage III sporulation protein J precursor	60 kDa inner membrane protein YIDC	60 kDa inner membrane insertion protein	U	Yes	-	IMP	tmhmm:5	-	-	-	-	-	-	+
LC_02910	rnpA	2966952	2966596	118	10,37	13797	-	Ribonuclease P protein component	Ribonuclease P protein component (RNaseP pr	Ribonuclease P protein component (EC 3.1.26	Bacterial ribonuclease P protein|Ribosomal prot	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
LC_02911	null	2967098	2967253	51	10,75	5683	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02912	null	2967443	2967592	49	9,88	5329	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
LC_02913	rpmH	2967853	2967713	46	13,11	5523	-	LSU/50S ribosomal protein L34P	ribosomal protein L34 (50S ribosomal protein L	LSU ribosomal protein L34P	Ribosomal protein L34	J	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00001	null	2969019	2970077	352	8,9	40386	+	Plasmid replication initiation protein RepA	plasmid replication initiation protein RepA	not_predicted_by_ERGO	Replication initiator A, N-terminal	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00002	null	2970067	2970645	192	10,19	22435	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00003	null	2970679	2971818	379	9,89	40754	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Cna B-type|Carboxypeptidase regulatory region	null	No	collagen	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00004	null	2971808	2972527	239	10,36	27361	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00005	null	2973108	2972908	66	12,38	7926	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00006	RepA2	2973130	2973330	66	10,55	7774	+	Replication protein A2	replication protein A2	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00007	null	2973336	2973599	87	5,57	10056	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00008	null	2973589	2974026	145	6,8	16510	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00009	PBCN11	2974019	2975263	414	10,18	48780	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00010	null	2975305	2975550	81	3,6	9104	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00011	null	2975537	2978083	848	8,62	95203	+	Conserved protein	conserved hypothetical protein (LtrC)	not_predicted_by_ERGO	Zinc finger, CHC2-type|Peptidase M, neutral zir	null	No	-	-	tmhmm:0	-	-	-	-	-	protease	+
pLC_00012	null	2979081	2978863	72	8,18	8357	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00013	null	2979236	2979084	50	4,14	5749	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00014	null	2979669	2979220	149	4,24	16859	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00015	null	2979973	2979683	96	4,34	10818	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00016	null	2980430	2979984	148	6,1	17051	-	Conserved protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00017	null	2980555	2980863	102	9,72	11993	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	High potential iron-sulfur protein	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00018	isldl4	2980917	2982116	399	10,2	45362	+	Transposase, IS116 family protein	transposase, IS111A/IS1328/IS1533/IS116/IS1	not_predicted_by_ERGO	Transposase, IS116/IS110/IS902	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00019	null	2982740	2983099	119	10,14	13740	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	Lambda repressor-like, DNA-binding	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00020	srtA	2983176	2983847	223	10,51	24952	+	Sortase	sortase (surface protein transpeptidase)	not_predicted_by_ERGO	Protein kinase|Peptidase C60, sortase A and B	null	No	-	Nterm	tmhmm:1	-	-	-	-	-	protease	+
pLC_00021	null	2983980	2984210	76	4,09	8650	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00022	null	2984280	2984465	61	10,3	6871	+	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00023	Icd	2984828	2986243	471	9,21	53965	+	Transposase, IS5 family protein	transposase, IS5	Transposase	Transposase, IS4-like	null	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00024	null	2986395	2988329	644	6,53	72756	+	PTS system, fructose-specific IIA component	PTS system, IIA component	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	null	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00025	frvA	2988329	2988766	145	4,32	15746	+	PTS system, fructose-specific IIA component	PTS system, fructose-specific IIA component	not_predicted_by_ERGO	Phosphotransferase system, phosphoenolpyruv	GT	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00026	frwB	2988780	2989100	106	9,93	11188	+	PTS system, fructose-specific IIB component	PTS system, fructose-specific IIBC component	not_predicted_by_ERGO	Phosphotransferase system, fructose-specific I	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00027	null	2989115	2990242	375	5,3	39199	+	PTS system, fructose-specific IIC component	PTS system, fructose-specific IIC component	not_predicted_by_ERGO	Phosphotransferase system, EIIC|Phosphotran	G	No	-	IMP	tmhmm:8	-	-	-	-	-	-	+
pLC_00028	null	2990245	2992839	864	4,73	97410	+	Glycoside hydrolase, family 38	glycosyl hydrolase, family 38	not_predicted_by_ERGO	Glycoside hydrolase, family 38|Glycosyl hydrola	G	No	-	-	tmhmm:0	pLC00028	-	-	-	-	-	+
pLC_00029	null	2992961	2993824	287	9,2	31012	+	Glucose uptake protein	glucose uptake protein	not_predicted_by_ERGO	Sugar transport	G	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-
pLC_00030	null	2994207	2993998	69	10,92	8306	-	Transposase, IS4 family protein	transposase, IS5	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00031	null	2994468	2994232	78	9,16	8229	-	Transposase, IS4 family protein	transposase	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00032	tnp4t	2994785	2994465	106	8,98	12937	-	Transposase, tnp4 family protein	transposase, tnp4	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00033	null	2994876	2995172	98	7,69	11263	+	LtrC-like protein	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00034	null	2995461	2995285	58	10,24	6644	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00035	hsdS	2996206	2995607	199	9,79	22843	-	Restriction modification system DNA specificit	HsdS	not_predicted_by_ERGO	Restriction modification system DNA specificity	V	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00036	hsdM1	2997791	2996169	540	4,87	60778	-	Type I restriction-modification system, M subu	Type I restriction modification system protein H	not_predicted_by_ERGO	N-6 Adenine-specific DNA methylase|N6 adenii	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00037	hsdR1	3000972	2997805	1055	7,32	120350	-	Type I restriction-modification system, restricti	type I restriction-modification system restrict	not_predicted_by_ERGO	Type I restriction modification system site-speci	V	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00038	null	3001288	3002037	249	10,43	28395	+	Transposase, IS30 family protein	predicted ORF	Transposase	Homeodomain-like	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00039	cysK	3002904	3003815	303	5,31	32612	+	Cystathionine beta-synthase	cysteine synthase (beta-pyrazolylalanine syntha	not_predicted_by_ERGO	Cysteine synthase/cystathionine beta-synthase	E	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00040	metC	3003837	3005021	394	5,6	43063	+	Cystathionine gamma-synthase	cystathionine beta-lyase/cystathionine gamma-s	not_predicted_by_ERGO	Cys/Met metabolism pyridoxal-phosphate-deper	E	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00041	cysE	3004987	3005544	185	11,19	19830	+	Serine O-acetyltransferase	serine O-acetyltransferase	not_predicted_by_ERGO	Bacterial transferase hexapeptide repeat|Trimer	E	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00042	tnp4t	3005702	3006022	106	8,98	12936	+	Transposase, tnp4 family protein	transposase, tnp4	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00043	null	3006112	3006489	125	10,32	14248	+	Transposase, IS4 family protein	transposase, IS1480	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00044	glcU	3007584	3006697	295	10,12	31950	-	Glucose uptake protein	putative glucose uptake protein glcU	not_predicted_by_ERGO	Sugar transport	GER	No	-	IMP	tmhmm:10	-	-	-	-	-	-	-
pLC_00045	null	3007772	3007638	44	7,54	5133	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	Putative rRNA methylase	QR	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00046	null	3007984	3007829	51	9,69	5675	-	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-

pLC_00047	null	3008379	3008167	70	10,03	8713	-	Conserved protein	transposase, IS1480b	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00048	null	3008803	3008411	130	8,4	14798	-	Galactokinase	predicted ORF	not_predicted_by_ERGO	Galactokinase|Ribosomal protein S5 domain 2-l	G	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00049	lacZ	3009009	3010889	626	4,55	72072	+	Beta-galactosidase (GH42)	beta-galactosidase, large subunit / lactase, larg	Beta-galactosidase (EC 3.2.1.23)	Glycoside hydrolase, family 2|Glycoside hydrola	G	Yes	-	-	tmhmm:0	pLC00049	-	-	-	-	-	+
pLC_00050	lacZ	3010873	3011832	319	4,46	35213	+	Beta-galactosidase small subunit	beta-galactosidase, small subunit / lactase, sma	not_predicted_by_ERGO	Glycoside hydrolase, family 42, domain 5|Glyco	G	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00051	galA	3012909	3011932	325	4,6	37060	-	Alpha-galactosidase	alpha-galactosidase	not_predicted_by_ERGO	Glycoside hydrolase, clan GH-D|Glycoside hydr	G	No	-	-	tmhmm:0	pLC00051	-	-	-	-	-	-
pLC_00052	tnp4t	3013007	3013327	106	8,98	12945	+	Transposase	transposase, tnp4	Transposase	no annotation	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00053	null	3013324	3013794	156	10,25	17586	+	Transposase, IS4 family protein	transposase, IS4	Transposase	Transposase, IS4-like	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00054	umuC	3014730	3013690	346	10,07	39573	-	ImpB/MucB/SamB family protein	ImpB/MucB/SamB family protein	not_predicted_by_ERGO	UMUC-like DNA-repair protein	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00055	null	3015097	3014921	58	9,27	6710	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00056	merA	3015524	3016873	449	6,73	49833	+	Pyridine nucleotide-disulfide oxidoreductase	pyridine nucleotide-disulfide oxidoreductase, Yk	not_predicted_by_ERGO	Mercuric reductase|Pyridine nucleotide-disulphi	F	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00057	null	3016948	3017109	53	10,37	6263	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00058	tnp4t	3017457	3017777	106	8,98	12937	+	Transposase, tnp4 family protein	transposase, tnp4	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00059	null	3017774	3018010	78	9,16	8229	+	Transposase, IS4 family protein	transposase	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00060	null	3018035	3018244	69	10,78	8232	+	Transposase, IS4 family protein	transposase, IS5	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00061	null	3018554	3018231	107	4,68	11700	-	Glycosyl transferase, group 2	glycosyltransferase	not_predicted_by_ERGO	Glycosyl transferase, family 2	M	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00062	lacT	3018897	3019775	292	6,81	33931	+	Transcription antiterminator lacT	Transcription antiterminator lacT	not_predicted_by_ERGO	Transcriptional antiterminator bgl|G|CAT RNA-b	K	No	-	-	tmhmm:0	-	-	-	-	regulator	-	-
pLC_00063	lacE	3019896	3021629	577	5,77	62399	+	PTS system, lactose-specific IIBC component	PTS system, lactose-specific IIBC component	not_predicted_by_ERGO	Phosphotransferase system, EIIC|Phosphotran	G	No	-	IMP	tmhmm:9	-	-	-	-	-	-	-
pLC_00064	lacG	3021656	3023080	474	4,92	53969	+	6-phospho-beta-galactosidase	6-phospho-beta-galactosidase (beta-D-phosphc	not_predicted_by_ERGO	Glycoside hydrolase, family 1|6-phospho-beta-g	G	No	-	-	tmhmm:0	pLC00064	-	-	-	-	-	+
pLC_00065	lacF	3023129	3023464	111	4,37	12365	+	PTS system, lactose-specific IIA component	PTS system, lactose-specific IIA component	PTS system, lactose-specific IIA component (	Phosphotransferase system, lactose/cellobiose-	G	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00066	null	3023783	3023956	57	4,43	6198	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00067	null	3024376	3023999	125	10,32	14232	-	Transposase, IS4 family protein	transposase, IS1480	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00068	null	3024666	3024466	66	8,5	8032	-	Transposase, tnp4 family protein	predicted ORF	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00069	null	3024781	3024629	50	9,52	6025	-	Transposase, IS1480 family protein	transposase, IS1480	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00070	null	3025127	3024843	94	10,77	10789	-	Conserved cytosolic protein	predicted ORF	Hypothetical cytosolic protein	no annotation	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00071	null	3025783	3025133	216	10,11	25128	-	Resolvase	Resolvase, N-terminal:Resolvase helix-turn-heli	DNA integration/recombination/inversion prote	Site-specific recombinase|Resolvase, N-termina	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	+
pLC_00072	tralSLpl:	3026125	3027036	303	10,42	35281	+	Transposase, IS30 family protein	transposase, IS30	Transposase	Integrase, catalytic core|Immunoglobulin/major I	L	Yes	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00073	nagZ	3029431	3027506	641	5,98	68564	-	Beta-N-acetylhexosaminidase (GH3)	beta-N-acetylhexosaminidase	Beta-N-acetylhexosaminidase (EC 3.2.1.52)	Glycoside hydrolase, family 3, N-terminal|Surfa	G	Yes	fibronectin	LPxTG	tmhmm:2	pLC00073	-	-	-	-	-	+
pLC_00074	null	3030135	3030296	53	7,7	5726	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00075	null	3030405	3030533	42	9,7	4573	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00076	null	3030526	3030759	77	8,67	9299	+	Putative protein without homology	predicted ORF	not_predicted_by_ERGO	no annotation	null	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00077	tnp4t	3030847	3031179	110	9,38	13099	+	Transposase, tnp4 family protein	transposase, tnp4	not_predicted_by_ERGO	no annotation	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00078	null	3031290	3031646	118	9,87	13410	+	Transposase, IS4 family protein	transposase, IS1480	not_predicted_by_ERGO	Transposase, IS4-like	L	No	-	-	tmhmm:0	-	-	-	-	-	-	-
pLC_00079	null	3032170	3031772	132	6,97	14821	-	Conserved protein	conserved hypothetical protein	not_predicted_by_ERGO	no annotation	J	No	-	-	tmhmm:0	-	-	-	-	-	-	+