Tablae S2. TYG1620 genome information with transcriptome analysis and Tn-mutants experiment.

S. intermedius TYG1620 genome annotation								RNA-seq (RPKM)			Expression ratio		in mouse subcutaneous	
Locus_tag ID	**gene**	**Chromosome region start**	**Chromosome region end**	**Product**	**aa length**	**COG**	**LPXTG motif (see Fig. 3)**	**Early-log phase (BHI-6h)**	**Stationaly phase (BHI-24h)**	**Subcutaneous-Abscess**	**Abscess / 6h**	**Abscess / 24h**	**Number of Tn-insertion sites (In vitro)**	**Vivo attenuated Tn-mutant**
SITYG_00010	*dnaA*	202	1546	chromosomal replication initiator protein DnaA	447	L		324.1	703.1	597.7			0	
SITYG_00020	*dnaN*	1701	2838	DNA polymerase III subunit beta	378	L		682.2	908.4	547.6			0	
SITYG_00030	-	2864	3035	hypothetical protein	56	S		0.0	0.0	0.0			0	
SITYG_00040	-	3057	3558	hypothetical protein	166	S		1357.9	1315.8	962.1			0	
SITYG_00050	-	3703	4819	GTP-binding protein	371	J		2698.5	748.2	1907.6			0	
SITYG_00060	*pth*	4890	5460	peptidyl-tRNA hydrolase	189	J		189.2	539.7	458.1			0	
SITYG_00070	*trcF*	5464	8959	transcription-repair coupling factor	1164	LK		200.6	653.9	324.7			4	vivo-attenuated
SITYG_00080	-	9038	9305	hypothetical protein	88	J		1786.7	411.5	714.6			0	
SITYG_00090	-	9297	9666	septum formation initiator	122	D		1090.4	119.1	353.8			0	
SITYG_00100	-	9668	9797	hypothetical protein	42			32.2	170.3	77.8			0	
SITYG_00110	-	9789	11070	beta-lactamase class A	426	V		349.7	411.7	384.1			1	alive in vivo
SITYG_00120	-	11066	12344	tRNA(Ile)-lysidine synthetase	425	D		1194.5	636.2	636.5			0	
SITYG_00130	*hpt*	12349	12892	hypoxanthine guanine phosphoribosyltransferase	180	F		3475.9	728.4	1941.8			2	vivo-attenuated
SITYG_00140	*ftsH*	12912	14883	cell division protein FtsH	656	O		1849.9	747.0	1462.2			1	vivo-attenuated
SITYG_00150	*nanA*	15856	18619	putative sialidase A	920	G	LPXTG	112.6	620.3	327.1	3.2		0	
SITYG_00160	-	18939	19413	competence-specific global transcription modulator	157			166.3	139.1	614.4	4.0	3.7	0	
SITYG_00170	-	26374	27181	putative cell shape-determining protein	268	M		467.8	272.3	373.3			0	
SITYG_00180	-	27182	27683	putative cell shape-determining protein	166	M		207.0	219.3	581.3	3.1		0	
SITYG_00190	-	27792	28974	putative stress protein	393	S		2091.6	446.2	1605.7			0	
SITYG_00200	-	29107	30076	ribose-phosphate pyrophosphokinase	322	FE		839.1	703.0	1254.0			0	
SITYG_00210	*araT*	30239	31427	aromatic-amino-acid transaminase	395	E		551.7	332.9	439.5			0	
SITYG_00220	*recO*	31404	32178	DNA repair protein RecO	257	L		428.8	425.9	376.2			0	
SITYG_00230	*plsX*	32174	33173	fatty acid/phospholipid synthesis protein PlsX	332	I		822.2	329.9	924.8			0	
SITYG_00240	-	33169	33415	acyl carrier protein	81	IQ		269.8	0.0	285.7			0	
SITYG_00250	-	33559	34267	phosphoribosylaminoimidazole-succinocarboxamide synthase	235	F		29.3	558.7	383.0	14.2		0	
SITYG_00260	-	34276	38002	putative phosphoribosylformylglycinamidine synthase	1241	F		77.9	513.1	215.6	3.0		1	alive in vivo
SITYG_00270	-	38023	38644	hypothetical protein	206	L		133.6	247.7	194.0			1	alive in vivo
SITYG_00280	*purF*	38669	40109	amidophosphoribosyltransferase	479	F		57.6	335.7	55.8			1	alive in vivo
SITYG_00290	*purM*	40358	41378	phosphoribosylformylglycinamidine cyclo-ligase	339	F		81.3	710.9	393.8	5.3		0	
SITYG_00300	*purN*	41377	41935	phosphoribosylglycinamide formyltransferase	185	F		59.5	196.9	287.9	5.3		0	
SITYG_00310	-	41967	42867	DNA polymerase III alpha subunit	299	L		46.1	488.3	234.3	5.5		0	
SITYG_00320	*purH*	43202	44753	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	516	F		13.4	212.5	142.4	11.6		1	vivo-attenuated
SITYG_00330	-	44804	46727	hypothetical protein	640	R		75.5	639.9	339.4	4.9		3	alive in vivo
SITYG_00340	-	47098	47563	hypothetical protein	154	V		142.7	141.8	129.6			0	
SITYG_00350	-	47779	47974	hypothetical protein	64	V		21.3	112.7	0.0			0	
SITYG_00360	-	48153	49419	hypothetical protein	421	R		920.7	711.7	1189.8			1	alive in vivo
SITYG_00370	-	49418	50030	hypothetical protein	203			826.9	754.0	672.7			0	
SITYG_00380	*purD*	50315	51575	phosphoribosylamine--glycine ligase	419	F		144.9	366.2	239.1			0	
SITYG_00390	-	51634	52816	hypothetical protein	393	I		228.1	520.5	203.9			3	vivo-attenuated
SITYG_00400	*purE*	53187	53625	phosphoribosylaminoimidazole carboxylase catalytic subunit PurE	145	F		161.0	501.7	45.9	-3.2	-13.1	1	vivo-attenuated
SITYG_00410	*purK*	53611	54703	phosphoribosylaminoimidazole carboxylase ATPase subunit PurK	363	F		102.6	261.6	312.7	3.3		0	
SITYG_00420	-	54702	55365	hypothetical protein	220			237.8	232.0	348.4			0	
SITYG_00430	-	55380	55608	hypothetical protein	75			272.9	867.4	88.1			0	
SITYG_00440	-	55612	56365	hypothetical protein	250			319.5	612.8	386.7			0	
SITYG_00450	-	56337	57066	-		M		102.4	271.3	261.7			1	alive in vivo
SITYG_00460	*purB*	57213	58509	adenylosuccinate lyase	431	F		227.3	457.8	170.5			0	
SITYG_00470	-	58773	59490	transcriptional regulators	238	K		1000.9	1134.0	644.3			1	alive in vivo
SITYG_00480	-	59639	61445	beta-galactosidase	601	G		156.2	571.9	417.0			0	
SITYG_00490	-	61441	61918	PTS system mannose-specific transporter subunit IIB	158	G		130.4	598.9	231.6			0	
SITYG_00500	-	61936	62830	PTS system mannose-specific transporter subunit IIC	297	G		41.8	467.0	89.9			1	alive in vivo
SITYG_00510	-	62801	63644	PTS system mannose-specific transporter subunit IID	280	G		54.1	312.8	214.4	4.3		1	alive in vivo
SITYG_00520	-	63661	64066	PTS system mannose-specific transporter subunit IIA	134	G		194.6	2767.2	818.2	4.6	-4.1	0	
SITYG_00530	-	64134	65388	putative galactosamine-6-phosphate isomerase	417	M		178.6	490.7	208.2			2	alive in vivo
SITYG_00540	*lacD*	65398	66400	tagatose 1,6-diphosphate aldolase	333	G		161.5	548.3	350.8			1	alive in vivo
SITYG_00550	*galM*	66442	67489	aldose-1-epimerase	348	G		447.7	566.7	489.2			2	alive in vivo
SITYG_00560	-	67584	68352	putative cell wall-binding protein	255	R		394.3	1831.2	405.3			0	
SITYG_00570	*ruvB*	68758	69757	holliday junction DNA helicase B	332	L		224.2	483.9	331.7			0	
SITYG_00580	-	69762	70329	hypothetical protein	188	S		168.3	542.6	425.1			0	
SITYG_00590	-	71003	71513	hypothetical protein	169			16.3	172.4	177.2	11.9		0	
SITYG_00600	-	71503	73000	hypothetical protein	498			69.3	367.0	167.7			2	alive in vivo
SITYG_00610	-	73110	73299	hypothetical protein	62			43.9	232.5	53.1			1	alive in vivo
SITYG_00620	-	73301	74099	putative D12 class N6 adenine-specific DNA methyltransferase	265	L		57.2	413.1	314.6	6.0		5	vivo-attenuated
SITYG_00630	-	74107	75154	putative C-5 cytosine methyltransferase	348	L		59.4	440.8	278.1	5.1		2	alive in vivo
SITYG_00640	-	75169	75721	putative membrane protein	183			52.6	437.9	181.9	3.8		1	alive in vivo
SITYG_00650	-	75717	75921	hypothetical protein	67			142.3	107.7	147.7			1	alive in vivo
SITYG_00660	-	75936	76368	hypothetical protein	143			38.4	254.3	93.0			1	alive in vivo
SITYG_00670	-	76354	76780	hypothetical protein	141	OC		29.2	206.3	94.3	3.5		0	
SITYG_00680	-	76772	76982	hypothetical protein	69			39.5	104.6	0.0			2	alive in vivo
SITYG_00690	-	76978	77992	hypothetical protein	337			61.4	260.1	366.4	6.5		2	alive in vivo
SITYG_00700	-	78103	78937	putative membrane protein	277			64.7	184.4	445.5	7.5		1	alive in vivo
SITYG_00710	-	79098	79413	hypothetical protein	104			92.2	209.3	63.8			0	
SITYG_00720	-	79857	80175	hypothetical protein	105			13.0	69.1	31.6			0	
SITYG_00730	-	80167	80500	hypothetical protein	110	RTKL		12.5	395.9	90.5	7.9	-5.3	0	
SITYG_00740	-	80515	81301	putative endonuclease	261			105.6	866.7	370.5	3.8		4	vivo-attenuated
SITYG_00750	-	81322	81781	hypothetical protein	152			36.1	191.5	153.1	4.6		0	
SITYG_00760	-	81792	84147	hypothetical protein	784			54.6	307.9	200.4	4.0		8	vivo-attenuated
SITYG_00770	-	84454	84970	hypothetical protein	171			88.4	383.3	155.7			2	alive in vivo
SITYG_00780	-	84996	85371	hypothetical protein	124			121.7	468.8	428.5	3.8		0	
SITYG_00790	-	85507	85768	hypothetical protein	86			111.3	168.4	0.0	<-111.3	<-168.4	1	alive in vivo
SITYG_00800	-	85788	89928	hypothetical protein	1379			77.2	498.9	254.7			10	vivo-attenuated
SITYG_00810	-	89898	90039	hypothetical protein	46			0.0	155.8	0.0			0	
SITYG_00820	-	90038	91793	DNA topoisomerase	584	L		125.3	513.4	337.6			3	alive in vivo
SITYG_00830	-	91789	93625	putative ATP-dependent Clp protease ATP-binding protein	611	O		31.6	287.3	229.7	7.9		0	
SITYG_00840	-	93725	94073	hypothetical protein	115			333.8	568.3	346.3			1	alive in vivo
SITYG_00850	-	94086	95154	hypothetical protein	355			62.1	226.3	150.4			1	vivo-attenuated
SITYG_00860	-	95172	95949	putative cell wall anchor protein	258		LPXTG	90.8	282.8	103.4			3	alive in vivo
SITYG_00870	-	95974	98176	putative glucan-binding protein	733		LPXTG	101.7	449.1	396.8	4.2		7	vivo-attenuated
SITYG_00880	-	98177	98600	putative single-stranded DNA-binding protein	140	L		98.1	571.4	403.6	4.5		0	
SITYG_00890	-	98861	99125	hypothetical protein	87			0.0	83.2	114.1	#DIV/0!		0	
SITYG_00900	-	99108	102258	putative conjugal transfer protein TraG	1049			63.2	334.9	290.1			5	vivo-attenuated
SITYG_00910	-	102382	102868	hypothetical protein	161			111.0	361.7	454.6	4.5		0	
SITYG_00920	-	102984	105114	putative membrane protein	709	U		64.3	412.7	424.3	7.2		3	vivo-attenuated
SITYG_00930	-	105118	105400	hypothetical protein	93	L		29.4	155.8	142.4	5.3		0	
SITYG_00940	-	105564	105873	hypothetical protein	102			53.7	355.6	292.5	5.9		0	
SITYG_00950	-	105872	106523	hypothetical protein	216			76.5	236.3	46.3			2	vivo-attenuated
SITYG_00960	-	106534	108484	hypothetical protein	649			48.9	371.9	154.5	3.4		6	alive in vivo
SITYG_00970	-	108495	109053	hypothetical protein	185			96.6	433.2	305.9	3.4		1	alive in vivo
SITYG_00980	-	109083	109356	hypothetical protein	90			76.0	241.5	36.8			1	alive in vivo
SITYG_00990	-	109371	110700	hypothetical protein	442	NU		31.2	148.8	188.9	6.6		1	alive in vivo
SITYG_01000	-	110723	111308	hypothetical protein	194			63.8	450.8	206.0	3.5		0	
SITYG_01010	-	111500	112319	hypothetical protein	272	D		121.6	161.0	134.9			1	alive in vivo
SITYG_01020	-	112386	112638	hypothetical protein	83			98.8	174.4	0.0			0	
SITYG_01030	-	112653	112986	hypothetical protein	110			49.8	395.9	663.4	14.5		1	alive in vivo
SITYG_01040	-	113126	114434	hypothetical protein	435			82.5	285.6	215.0			1	alive in vivo
SITYG_01050	-	114664	114793	hypothetical protein	42			0.0	0.0	0.0			1	alive in vivo
SITYG_01060	-	115028	115364	hypothetical protein	111			2370.4	1308.0	1942.6			0	
SITYG_01070	-	115495	116095	signal peptidase	199	U		1272.1	879.0	1338.9			2	alive in vivo
SITYG_01080	-	116265	119895	putative von Willebrand factor domain protein	1209	M	LPXTG	1645.6	793.0	1272.5			4	vivo-attenuated
SITYG_01090	-	120053	121436	putative Fimbrial isopeptide formation D2 domain protein	460		LPXTG	5093.0	1477.7	3761.2			0	
SITYG_01100	-	121650	122496	sortase	281	M		583.5	753.3	771.5			0	
SITYG_01110	-	122532	122907	sortase	124	M		752.2	527.4	1231.8			0	
SITYG_01120	-	123156	123585	putative phosphotyrosine protein phosphatase	142	T		1498.8	563.5	749.1			0	
SITYG_01130	-	123593	124007	hypothetical protein	137	S		861.7	530.8	970.2			1	vivo-attenuated
SITYG_01140	-	123996	125814	acyltransferase	605	I		778.1	1003.2	800.9			0	
SITYG_01150	*adhE*	126187	128839	bifunctional aldehyde/alcohol dehydrogenase	883	C		336.3	2568.7	526.3			2	vivo-attenuated
SITYG_01160	-	129137	129428	hypothetical protein	96	S		13285.6	528.6	6591.1			0	
SITYG_01170	-	129497	129956	type VII secretion protein EssA	152			162.7	239.4	371.9			2	vivo-attenuated
SITYG_01180	-	129918	130167	hypothetical protein	82			1232.8	264.8	443.6			1	alive in vivo
SITYG_01190	-	130186	131344	type VII secretion protein EssB	385	S		472.8	778.0	919.2			0	
SITYG_01200	-	131345	135791	type VII secretion protein EssC	1481	D		347.1	568.4	521.7			3	vivo-attenuated
SITYG_01210	-	135868	136279	hypothetical protein	136			857.9	1122.8	513.1			0	
SITYG_01220	-	136291	136576	hypothetical protein	94			858.7	539.7	422.8			0	
SITYG_01230	-	136572	137217	hypothetical protein	214			1517.8	1090.2	1012.0			1	alive in vivo
SITYG_01240	-	137218	138706	hypothetical protein	495			942.3	841.8	836.8			2	alive in vivo

SITYG_01250	-	138707	139511	hypothetical protein	267	S		247.7	519.3	312.3			2	vivo-attenuated
SITYG_01260	-	139510	139819	hypothetical protein	102	S		671.2	711.2	682.5			1	alive in vivo
SITYG_01270	-	139874	140246	hypothetical protein	123			167.3	767.9	243.0			2	vivo-attenuated
SITYG_01280	-	140340	141246	putative membrane protein	301			283.9	630.6	177.3			2	alive in vivo
SITYG_01290	-	141346	142258	putative membrane protein	303			213.8	746.9	693.7	3.5		0	
SITYG_01300	-	142244	142544	hypothetical protein	99	S		179.8	659.2	636.0	3.9		0	
SITYG_01310	-	142661	144059	hypothetical protein	465	R		213.6	455.8	280.1			1	alive in vivo
SITYG_01320	-	144055	144223	hypothetical protein	55			0.0	130.8	59.8			0	
SITYG_01330	-	144367	144757	hypothetical protein	129			159.5	563.5	618.0	4.2		1	alive in vivo
SITYG_01340	-	144780	145491	hypothetical protein	236			70.0	587.2	141.2			1	alive in vivo
SITYG_01350	-	145530	145827	hypothetical protein	98	S		69.8	591.9	67.6			0	
SITYG_01360	-	145926	146073	hypothetical protein	48			112.9	299.0	0.0	<-112.9	<-299	0	
SITYG_01370	-	146087	146600	putative membrane protein	170			153.6	299.8	665.6	4.7		1	alive in vivo
SITYG_01380	-	146608	147241	hypothetical protein	210			910.9	798.4	809.1			1	alive in vivo
SITYG_01390	-	147243	148065	hypothetical protein	273			434.0	294.1	281.0			3	vivo-attenuated
SITYG_01400	-	148064	148373	hypothetical protein	102	S		644.4	640.0	390.0			1	alive in vivo
SITYG_01410	-	148428	149538	hypothetical protein	369			504.5	534.5	1004.2			1	alive in vivo
SITYG_01420	-	149593	149749	hypothetical protein	51			26.6	140.9	0.0			2	alive in vivo
SITYG_01430	-	149898	150720	hypothetical protein	273			141.3	267.3	73.3			2	vivo-attenuated
SITYG_01440	-	150900	151221	hypothetical protein	106			206.8	136.9	93.9			0	
SITYG_01450	-	151419	152049	hypothetical protein	209			52.7	139.5	79.7			0	
SITYG_01460	-	152100	152403	hypothetical protein	100			41.1	72.5	132.6	3.5		0	
SITYG_01470	-	152423	153218	hypothetical protein	264			151.3	359.3	265.3			1	alive in vivo
SITYG_01480	-	153413	153605	hypothetical protein	63			64.8	0.0	0.0			0	
SITYG_01490	-	153607	154414	hypothetical protein	268			257.0	354.0	398.2			1	vivo-attenuated
SITYG_01500	-	154465	154771	hypothetical protein	101			122.0	71.8	295.4			1	alive in vivo
SITYG_01510	-	154785	155601	hypothetical protein	271			40.7	269.3	160.0	4.3		0	
SITYG_01520	-	155652	155973	hypothetical protein	106			51.7	410.7	93.9			0	
SITYG_01530	-	155981	156797	hypothetical protein	271			91.5	188.5	184.6			2	vivo-attenuated
SITYG_01540	-	157125	157962	hypothetical protein	278			69.4	78.8	180.0			1	alive in vivo
SITYG_01550	-	158091	158382	hypothetical protein	96			57.0	0.0	276.1	5.3	>276.1	1	alive in vivo
SITYG_01560	-	158384	159209	hypothetical protein	274			95.5	346.3	426.0	4.9		3	vivo-attenuated
SITYG_01570	-	159208	159517	hypothetical protein	102	S		201.4	497.8	97.5			1	alive in vivo
SITYG_01580	-	159691	162415	type VII secretion protein EsaA	907	S		787.3	355.0	637.8			0	
SITYG_01590	-	162411	162579	hypothetical protein	55			0.0	130.8	0.0			0	
SITYG_01600	*nanE*	162736	163441	N-acetylmannosamine-6-phosphate 2-epimerase	234	G		58.8	436.4	114.0			0	
SITYG_01610	-	163486	164812	sugar ABC transporter sugar-binding protein	441	G		75.1	580.0	45.4			0	
SITYG_01620	-	164944	165811	sugar ABC transporter permease protein	288	G		19.1	405.5	324.3	18.4		3	alive in vivo
SITYG_01630	-	165827	166658	sugar ABC transporter permease protein	276	G		69.9	502.4	338.4	5.3		0	
SITYG_01640	-	166671	167127	hypothetical protein	151	G		54.6	530.1	66.1			0	
SITYG_01650	-	167151	167799	hypothetical protein	215			51.2	847.8	46.5			1	alive in vivo
SITYG_01660	-	167824	168742	N-acetylneuraminate lyase	305	EM		67.8	718.1	229.7	3.7	-3.8	0	
SITYG_01670	-	168759	169644	putative glucokinase/N-acylmannosamine kinase	294	KG		51.6	819.4	22.7			1	vivo-attenuated
SITYG_01680	-	169712	170558	putative phosphosugar-binding transcriptional regulator	281	K		367.7	493.5	451.1			0	
SITYG_01690	-	170789	171845	hypothetical protein	351	S		82.5	437.0	180.7			1	alive in vivo
SITYG_01700	-	171828	173238	hypothetical protein	469	G		64.7	561.1	156.7			2	vivo-attenuated
SITYG_01710	-	173227	174154	N-acetylmuramic acid-6-phosphate etherase	308	R		138.7	1517.1	335.8			0	
SITYG_01720	-	174272	175097	hypothetical protein	274	K		346.9	799.1	413.9			0	
SITYG_01730	-	175549	175873	hypothetical protein	107			345.7	339.1	186.0			0	
SITYG_01740	*ntpI*	175862	177821	V-type sodium ATPase subunit I	652	C		315.5	639.4	430.6			3	vivo-attenuated
SITYG_01750	*ntpK*	177920	178400	V-type sodium ATPase subunit K	159	C		293.8	869.8	523.0			0	
SITYG_01760	*ntpE*	178455	179046	V-type sodium ATPase subunit E	196			231.6	483.4	220.9			0	
SITYG_01770	*ntpC*	179057	180068	V-type sodium ATPase subunit C	336	C		176.4	282.6	228.5			1	alive in vivo
SITYG_01780	-	180057	180381	V-type sodium ATPase subunit F	107	C		384.1	678.2	557.9			0	
SITYG_01790	*ntpA*	180393	182184	V-type sodium ATPase subunit A	596	C		199.2	601.2	207.5			2	vivo-attenuated
SITYG_01800	*ntpB*	182170	183562	V-type sodium ATPase subunit B	463	C		426.1	521.0	844.0			0	
SITYG_01810	*ntpD*	183574	184198	V-type sodium ATPase subunit D	207	C		624.9	704.3	595.4			1	alive in vivo
SITYG_01820	*thrC*	184500	185985	threonine synthase	494	E		296.1	621.5	324.6			0	
SITYG_01830	-	186094	187372	hypothetical protein	425	V		126.6	412.7	220.0			0	
SITYG_01840	-	187368	187980	hypothetical protein	203	R		325.3	287.3	278.9			0	
SITYG_01850	-	188132	188756	putative tetracycline transcriptional regulator	207			252.6	352.2	418.4			4	vivo-attenuated
SITYG_01860	-	188936	194684	putative fibrinogen-binding protein	1915	M	LPXTG	866.7	581.1	817.6			3	vivo-attenuated
SITYG_01870	-	195022	196159	hypothetical protein	378			197.0	869.7	680.1	3.8		1	alive in vivo
SITYG_01880	*ily*	196626	198225	intermedilysin	532			114.1	1291.8	364.2	3.5	-4.3	4	alive in vivo
SITYG_01890	-	198774	199218	putative transcriptional regulator	147	K		4409.8	494.9	3324.7			0	
SITYG_01900	*adcC*	199214	199919	putative zinc ABC transporter ATP-binding protein	234	P		659.0	467.5	655.2			1	alive in vivo
SITYG_01910	*adcB*	199911	200718	zinc ABC transporter permease protein	268	P		663.1	680.8	933.3			0	
SITYG_01920	*adcA*	200727	202230	zinc ABC transporter zinc-binding lipoprotein	500	P		720.3	438.6	781.7			0	
SITYG_01930	-	202497	202953	putative transcriptional regulator	151	K		109.2	337.3	110.1			0	
SITYG_01940	-	202972	205225	copper-translocating P-type ATPase	750	P		270.7	1014.4	361.0			0	
SITYG_01950	-	205237	205447	hypothetical protein	69	P		79.0	418.6	0.0			0	
SITYG_01960	-	205487	206357	putative ribosomal large subunit pseudouridine synthase	289	J		352.8	505.2	554.0			0	
SITYG_01970	-	206494	208714	penicillin-binding protein	739	M		463.4	544.4	601.6			0	
SITYG_01980	-	208763	208916	hypothetical protein	50	J		10031.5	1005.4	10632.7			0	
SITYG_01990	-	208925	209102	preprotein translocase subunit SecE	58	U		46.9	372.5	340.4	7.9		0	
SITYG_02000	*nusG*	209248	209785	transcription antitermination protein NusG	178	K		826.5	327.4	860.2			0	
SITYG_02010	-	209991	210777	hypothetical protein	261			285.0	223.7	319.4			0	
SITYG_02020	*rpsB*	211418	212201	30S ribosomal protein S2	260	J		3427.7	421.0	2270.0			0	
SITYG_02030	*tsf*	212283	213327	elongation factor Ts	347	J		1430.4	421.0	1260.1			0	
SITYG_02040	-	213402	213753	hypothetical protein	116			212.7	1502.5	57.2	-3.4	-31.5	1	alive in vivo
SITYG_02050	*ctsR*	214011	214473	transcriptional regulator ctsR	153	K		440.0	523.2	1152.0			1	alive in vivo
SITYG_02060	*clpC*	214476	216906	ATP-dependent Clp protease ATP-binding subunit	809	O		571.9	913.3	644.7			0	
SITYG_02070	-	216952	217393	putative acetyltransferase	146	R		761.9	1046.4	797.0			0	
SITYG_02080	-	217463	218519	dihydrouridine synthase TIM-barrel protein NifR3	351	J		282.8	457.8	313.8			0	
SITYG_02090	*hslO*	218421	219294	molecular chaperone Hsp33	290	O		346.9	377.6	920.2			1	alive in vivo
SITYG_02100	-	219502	220774	tellurite resistance protein	423	P		198.9	639.2	284.2			1	vivo-attenuated
SITYG_02110	-	220792	221611	hypothetical protein	272			410.3	992.7	490.5			1	alive in vivo
SITYG_02120	-	221852	222089	hypothetical protein	78	ER		0.0	0.0	42.4			0	
SITYG_02130	-	222446	223301	transcriptional regulator	284	K		145.5	282.7	340.6			0	
SITYG_02140	-	223316	223493	hypothetical protein	58			23.4	248.3	0.0			0	
SITYG_02150	-	223827	224640	hypothetical protein	270	R		96.9	459.5	197.6			3	alive in vivo
SITYG_02160	-	224626	225709	radical SAM protein	360	R		26.8	81.2	92.7	3.8		1	alive in vivo
SITYG_02170	-	225950	226847	putative ABC transporter	298	CP		69.4	343.0	156.7			1	alive in vivo
SITYG_02180	-	226870	227581	putative ABC transporter	236			52.5	401.8	42.4			2	alive in vivo
SITYG_02190	-	227573	228164	putative membrane protein	196			28.1	111.5	254.9	9.9		1	alive in vivo
SITYG_02200	-	228395	228953	acetyltransferase	185			171.0	236.3	234.0			0	
SITYG_02210	-	229222	229867	hypothetical protein	214	M		90.0	442.9	280.2	3.4		1	vivo-attenuated
SITYG_02220	*purA*	230096	231389	adenylosuccinate synthetase	430	F		657.7	934.7	598.0			0	
SITYG_02230	-	231643	232000	putative restriction endonuclease	118	V		290.5	61.6	309.4			0	
SITYG_02240	-	232011	232479	tRNA-specific adenosine deaminase	155	FJ		257.0	469.5	536.4			0	
SITYG_02250	-	232475	233018	hypothetical protein	180			236.8	809.4	665.8	3.1		0	
SITYG_02260	-	233243	234110	transcriptional regulator	288	K		488.0	506.9	335.9			0	
SITYG_02270	-	234313	235561	putative transporter protein	415	GEPR		99.7	616.3	603.5	6.6		0	
SITYG_02280	*pgi*	235799	237149	glucose-6-phosphate isomerase	449	G		1222.9	781.3	989.3			1	alive in vivo
SITYG_02290	*glpK*	237300	238812	glycerol kinase	503	C		161.9	436.0	318.8			1	alive in vivo
SITYG_02300	*rnpA*	239068	239428	ribonuclease P	119	J		380.2	61.0	167.4			0	
SITYG_02310	-	239411	240227	putative membrane protein insertase	271	U		625.3	403.9	590.7			0	
SITYG_02320	-	240239	241277	putative RNA-binding protein	345	R		955.1	486.9	919.1			0	
SITYG_02330	-	241332	241614	hypothetical protein	93			279.5	467.5	249.3			0	
SITYG_02340	-	241663	242296	hypothetical protein	210			249.0	173.6	1031.2	4.5	5.0	0	
SITYG_02350	*rpmH*	242433	242568	50S ribosomal protein L34	44	J		338.0	0.0	297.5			0	
SITYG_02360	*tatD*	242702	243479	putative deoxyribonuclease	258	L		1009.0	707.0	1085.6			1	alive in vivo
SITYG_02370	-	243478	244051	ribonuclease M5	190	L		637.1	958.8	508.2			0	
SITYG_02380	-	244366	244798	hypothetical protein	143			124.8	406.9	93.0			2	alive in vivo
SITYG_02390	-	245229	245490	hypothetical protein	86			79.5	0.0	500.2	6.9	>500.2	0	
SITYG_02400	-	245482	245983	hypothetical protein	166			149.0	570.2	340.7			2	alive in vivo
SITYG_02410	-	246176	246305	hypothetical protein	42			32.2	340.7	155.7	5.3		0	
SITYG_02420	*ksgA*	246323	247199	dimethyladenosine transferase	291	J		383.6	501.7	412.7			0	
SITYG_02430	-	247679	248558	ribosome small subunit-dependent GTPase A	292	R		641.8	425.0	594.1			0	
SITYG_02440	*rpe*	248570	249230	ribulose-phosphate 3-epimerase	219	G		182.3	266.4	304.3			0	
SITYG_02450	-	249222	249855	thiamine pyrophosphokinase	210	H		412.9	659.6	412.5			0	
SITYG_02460	*rmuC*	249856	251113	putative DNA recombination protein RmuC	418	S		511.5	419.6	623.1			0	
SITYG_02470	*cbf1*	251102	252047	hypothetical protein	314	R		219.5	116.3	170.0			0	
SITYG_02480	*purR*	252163	252958	purine operon repressor	264	F		615.7	497.5	694.7			0	
SITYG_02490	*rpsL*	253443	253857	30S ribosomal protein S12	137	J		7164.1	424.6	4487.4			0	
SITYG_02500	*rpsG*	253876	254347	30S ribosomal protein S7	156	J		2651.0	466.6	1897.5			0	
SITYG_02510	-	254495	256577	translation elongation factor G	693	J		1874.8	675.5	1345.7			0	
SITYG_02520	-	256936	257944	glyceraldehyde-3-phosphate dehydrogenase	335	G		5761.4	850.2	3427.0			0	
SITYG_02530	-	258098	259781	ribonuclease J	560	R		1750.0	574.5	1581.2			0	

SITYG_02540	-	259784	260015	hypothetical protein	76	S	502.8	380.5	608.6			0	
SITYG_02550	-	260291	260975	glycoprotein endopeptidase	227	O	315.4	642.5	381.7			0	
SITYG_02560	-	260971	261415	ribosomal protein-alanine acetyltransferase	147	R	364.4	445.4	588.0			1	alive in vivo
SITYG_02570	*gcp*	261404	262415	O-sialoglycoprotein endopeptidase	336	O	221.6	304.3	218.5			0	
SITYG_02580	-	262424	263120	branched-chain amino acid permease	231	E	286.1	726.2	274.1			0	
SITYG_02590	-	263109	263436	hypothetical protein	108	S	228.3	403.2	276.4			2	vivo-attenuated
SITYG_02600	-	263453	264365	putative transcriptional regulator	303	K	72.8	409.6	374.4	5.6		5	alive in vivo
SITYG_02610	-	264738	265965	hypothetical protein	408	GEPR	138.6	411.9	441.9	3.5		2	vivo-attenuated
SITYG_02620	-	266181	266367	hypothetical protein	61		289.9	236.3	431.9			0	
SITYG_02630	-	266401	267073	putative CAAX amino terminal protease	223	R	104.9	327.0	194.3			2	vivo-attenuated
SITYG_02640	-	267166	267907	putative transcriptional regulator	246	K	431.1	622.8	311.7			0	
SITYG_02650	-	267938	268394	MutT/NUDIX family protein	151	LR	63.7	96.4	110.1			0	
SITYG_02660	-	268438	269614	hypothetical protein	391	R	67.0	280.3	153.7			0	
SITYG_02670	-	269779	270274	hypothetical protein	164		1265.4	355.1	1541.8			0	
SITYG_02680	-	270286	271141	hypothetical protein	284	S	242.6	334.1	375.8			2	vivo-attenuated
SITYG_02690	-	271137	272892	glycerophosphoryl diester phosphodiesterase	584	C	120.5	450.8	217.4			0	
SITYG_02700	-	272942	273242	hypothetical protein	99	S	1106.2	586.0	1573.2			0	
SITYG_02710	-	273278	275558	x-prolyl-dipeptidyl aminopeptidase	759		407.5	616.8	665.1			1	alive in vivo
SITYG_02720	-	275665	276517	glycerol uptake facilitator protein	283	G	462.5	283.7	424.3			1	alive in vivo
SITYG_02730	-	276997	278260	hypothetical protein	420		203.6	609.0	413.4			0	
SITYG_02740	-	278341	279082	putative proteinase	246		2731.9	919.3	2154.8			0	
SITYG_02750	-	279078	280014	beta-lactamase	311	V	691.4	540.0	343.3			0	
SITYG_02760	-	280179	281058	mevalonate kinase	292	I	339.8	550.0	982.5	3.1		0	
SITYG_02770	*mvaD*	281039	281984	diphosphomevalonate decarboxylase	314	I	307.3	534.8	308.2			0	
SITYG_02780	-	281976	282975	phosphomevalonate kinase	332	I	431.8	835.9	733.8			0	
SITYG_02790	*fni*	282971	283988	isopentenyl pyrophosphate isomerase	338	C	575.1	561.8	454.2			0	
SITYG_02800	-	284016	285297	hydroxymethylglutaryl-CoA reductase	426	I	346.5	634.7	752.6			0	
SITYG_02810	*mvaS*	285298	286471	hydroxymethylglutaryl-CoA synthase	390	I	169.7	187.3	137.0			0	
SITYG_02820	-	286603	287053	hypothetical protein	149	S	83.0	341.8	44.6			0	
SITYG_02830	-	287056	287830	hypothetical protein	257	S	428.8	624.6	246.5			0	
SITYG_02840	-	287933	290249	pyruvate formate-lyase	771	C	1056.7	2277.2	854.2			0	
SITYG_02850	-	290477	291137	hypothetical protein	219		345.7	432.8	1156.3	3.6		0	
SITYG_02860	*dinP*	291155	292220	DNA polymerase IV	354	L	307.7	474.6	631.7			2	vivo-attenuated
SITYG_02870	-	292430	294785	exodeoxyribonuclease V alpha chain	784	L	246.6	597.2	315.5			0	
SITYG_02880	-	295010	295625	signal peptidase I	204	U	215.8	536.0	195.9			0	
SITYG_02890	*rnhC*	295628	296519	ribonuclease HIII	296	L	162.9	172.6	101.4			2	vivo-attenuated
SITYG_02900	-	296604	296910	hypothetical protein	101		3158.6	502.7	1673.7			0	
SITYG_02910	-	296906	297455	colicin V production protein	182	R	309.8	520.3	219.5			0	
SITYG_02920	*mutS2*	297514	299848	DNA mismatch repair protein	777	L	247.0	348.4	469.0			0	
SITYG_02930	*pepD*	299909	301331	dipeptidase A	473	E	242.1	309.1	254.2			0	
SITYG_02940	*trx*	301435	301750	thioredoxin	104	OC	2910.3	558.1	1657.7			0	
SITYG_02950	-	302018	303458	putative amino acid transporters	479	E	123.9	1724.4	174.3			0	
SITYG_02960	-	303605	304460	small-conductance mechanosensitive channel	284	M	242.6	436.9	176.2			0	
SITYG_02970	-	304834	305737	putative Zn-dependent protease	300	O	68.9	340.7	422.6	6.7		0	
SITYG_02980	-	305799	306168	hypothetical protein	122		123.7	178.7	136.1			0	
SITYG_02990	*gdhA*	306224	307571	glutamate dehydrogenase	448	E	194.0	407.8	201.3			2	vivo-attenuated
SITYG_03000	-	307907	308843	dihydroorotate dehydrogenase	311	F	217.2	399.1	450.6			2	vivo-attenuated
SITYG_03010	-	308960	309896	peptide methionine sulfoxide reductase	311	O	709.1	563.5	729.5			0	
SITYG_03020	-	310191	311460	chlorohydrolase	422	FR	758.4	710.0	553.9			4	vivo-attenuated
SITYG_03030	-	311705	311924	putative ABC transporter	72	V	18.9	802.7	137.6	7.9	-7.0	0	
SITYG_03040	-	312196	313375	ROK family protein	392	KG	246.3	521.9	468.5			0	
SITYG_03050	-	313547	314813	PTS system cellobiose-specific transporter subunit IIC	421	G	140.9	451.3	55.5			0	
SITYG_03060	-	314825	315722	hypothetical protein	298		87.9	759.4	67.2			0	
SITYG_03070	-	315736	317434	hypothetical protein	565	G	149.0	517.7	260.2			1	alive in vivo
SITYG_03080	-	317450	317771	PTS system cellobiose-specific transporter subunit IIB	106	G	1925.5	3149.0	1188.8			1	alive in vivo
SITYG_03090	-	317780	318098	PTS system lactose/cellobiose-specific transporter subunit IIA	105	G	574.0	552.8	600.0			0	
SITYG_03100	-	318311	318881	putative TetR family transcriptional regulator	189	K	414.8	385.5	229.0			1	alive in vivo
SITYG_03110	-	318943	320296	multi antimicrobial extrusion protein	450	V	153.3	341.1	207.8			0	
SITYG_03120	-	320878	321388	hypothetical protein	169		235.9	474.0	452.9			0	
SITYG_03130	-	321402	322272	putative AraC family transcriptional regulator	289	K	238.4	530.4	588.7			0	
SITYG_03140	-	322383	323823	6-phospho-beta-glucosidase	479	G	328.4	549.4	265.0			0	
SITYG_03150	-	323812	323947	hypothetical protein	44		553.1	325.6	148.8	-3.4		0	
SITYG_03160	-	323969	324194	glyoxalase family protein	74	E	0.0	97.7	0.0			0	
SITYG_03170	-	324472	325624	hypothetical protein	383	E	54.0	286.1	313.8	6.3		1	alive in vivo
SITYG_03180	-	325837	326572	histidinol-phosphatase	244	ER	163.7	597.9	286.9			0	
SITYG_03190	-	326571	327951	putative endonuclease	459	V	162.3	748.4	465.7	3.1		0	
SITYG_03200	-	327937	329275	hypothetical protein	445	V	241.8	837.6	487.8			1	alive in vivo
SITYG_03210	-	329271	329814	putative acetyltransferase	180	R	282.7	526.1	240.4			0	
SITYG_03220	-	329934	330327	glucosidase	130	G	137.2	279.6	51.1			0	
SITYG_03230	-	330363	330495	glucosidase	43	G	94.3	332.9	0.0			1	alive in vivo
SITYG_03240	-	330837	331515	putative response regulator	225	TK	232.5	615.8	474.0			0	
SITYG_03250	-	331517	332384	histidine kinase A	288	T	196.2	278.8	498.0			0	
SITYG_03260	-	332709	333468	ABC-2 family transporter protein	252		142.1	665.9	370.5			0	
SITYG_03270	-	333481	334390	ABC transporter ATP-binding protein	302	V	36.5	531.8	209.9	6.3	-3.0	1	alive in vivo
SITYG_03280	-	334613	336221	glucan 1,6-alpha-glucosidase	535	G	332.8	519.3	324.7			0	
SITYG_03290	-	336289	336943	hypothetical protein	217		69.8	470.4	92.1			0	
SITYG_03300	-	336939	338274	hypothetical protein	444	P	87.0	609.0	270.8	3.4		1	alive in vivo
SITYG_03310	-	338275	338836	ABC transporter permease	186	S	66.5	352.5	125.3			0	
SITYG_03320	-	339260	341513	5-methyltetrahydropteroyltriglutamate- homocysteine methyltransferase	750	E	46.0	360.9	200.6	4.7		0	
SITYG_03330	-	341959	343105	hypothetical protein	381		709.5	1323.1	701.0			0	
SITYG_03340	-	343133	343943	CDP-diacylglycerol diphosphatase	269	I	788.7	1139.4	582.7			0	
SITYG_03350	-	343932	344448	hypothetical protein	171	OC	747.6	1703.5	642.2			0	
SITYG_03360	-	344631	344850	hypothetical protein	72	R	37.9	301.0	0.0			0	
SITYG_03370	-	345099	345528	hypothetical protein	142		29.0	358.6	140.4	5.3	-3.1	0	
SITYG_03380	-	345502	346408	hypothetical protein	301	G	105.3	509.3	166.3			1	alive in vivo
SITYG_03390	-	346404	347448	glycosyltransferase	347	M	75.5	378.9	192.4			0	
SITYG_03400	*rpsF*	347724	348015	30S ribosomal protein S6	96	J	4533.1	302.1	2588.1			0	
SITYG_03410	-	348026	348497	single-strand binding protein	156	L	2448.4	279.9	1556.4			0	
SITYG_03420	*rpsR*	348533	348773	30S ribosomal protein S18	79	J	172.8	457.8	83.7			0	
SITYG_03430	-	349181	349691	acetyltransferase	169	KR	667.0	517.1	886.1			0	
SITYG_03440	-	349842	350520	hypothetical protein	225	S	354.9	324.1	518.4			0	
SITYG_03450	-	350535	351480	magnesium and cobalt transporter	314	P	623.3	255.8	595.1			0	
SITYG_03460	*uvrA*	351593	354428	excinuclease ATPase subunitA	944	L	471.2	550.3	644.7			2	vivo-attenuated
SITYG_03470	-	354465	355221	hypothetical protein	251		268.9	436.0	411.8			0	
SITYG_03480	*pepP*	355368	356430	aminopeptidase P	353	E	273.4	351.8	463.3			1	alive in vivo
SITYG_03490	*efp*	356488	357049	elongation factor P	186	J	2735.9	548.4	1485.7			0	
SITYG_03500	-	357158	357548	hypothetical protein	129	S	1212.5	338.1	618.0			0	
SITYG_03510	*nusB*	357525	357966	nitrogen utilization substance protein NusB	146	K	677.3	99.7	523.7			0	
SITYG_03520	-	357977	358481	competence-specific sigma factor	167		82.3	741.2	557.9	7.4		0	
SITYG_03530	*lysC*	364140	365490	aspartate kinase	449	E	218.2	390.7	275.2			1	alive in vivo
SITYG_03540	*phaB*	365656	366448	enoyl-CoA hydratase	263	I	906.1	388.4	1128.5			0	
SITYG_03550	-	366538	366973	putative transcriptional regulator	144	K	2937.1	404.1	1893.0			0	
SITYG_03560	*fabH*	366972	367947	3-oxoacyl-(acyl-carrier-protein) synthase III	324	I	1280.6	608.5	1534.6			1	vivo-attenuated
SITYG_03570	-	368000	368225	acyl carrier protein	74	IQ	81654.5	2344.0	79487.8			0	
SITYG_03580	*fabK*	368490	369465	enoyl-acyl carrier protein reductase	324	R	1178.5	405.7	1184.4			0	
SITYG_03590	*fabD*	369457	370396	malonyl-CoA-acyl carrier protein transacylase	312	I	455.0	421.2	759.3			0	
SITYG_03600	*fabG*	370385	371117	3-ketoacyl-(acyl carrier protein) reductase	243	IQR	923.7	420.3	699.6			0	
SITYG_03610	*fabF*	371197	372430	3-oxoacyl-(acyl carrier protein) synthase	410	IQ	360.0	338.6	390.9			0	
SITYG_03620	*accB*	372430	372910	acetyl-CoA carboxylase	159	I	164.2	137.3	104.6			0	
SITYG_03630	*fabZ*	372906	373329	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase	140	I	627.6	467.5	308.6			0	
SITYG_03640	*accC*	373344	374712	biotin carboxylase	455	I	600.4	562.2	778.1			0	
SITYG_03650	*accD*	374731	375595	acetyl CoA carboxylase carboxyltransferase subunit beta	287	I	638.5	406.9	836.8			0	
SITYG_03660	*accA*	375591	376362	acetyl CoA carboxylase subunit alpha	256	I	2270.5	1111.6	1966.7			0	
SITYG_03670	*dedA*	376697	377357	DedA protein	219	S	226.3	399.5	334.7			1	alive in vivo
SITYG_03680	*serS*	377397	378675	seryl-tRNA synthetase	425	J	366.8	601.8	550.0			0	
SITYG_03690	-	378887	379259	hypothetical protein	123	S	412.6	236.3	243.0			0	
SITYG_03700	*manN*	379542	380454	PTS system mannose-specific transporter subunit IID	303	G	491.2	457.8	539.5			0	
SITYG_03710	*manM*	380473	381277	PTS system mannose-specific transporter subunit IIC	267	G	1460.1	1721.9	1049.2			0	
SITYG_03720	*manL*	381294	382284	PTS system mannose-specific transporter subunit IIAB	329	G	1043.3	443.9	811.5			4	vivo-attenuated
SITYG_03730	-	382555	383578	alcohol dehydrogenase	340	R	498.8	8420.4	746.0			1	alive in vivo
SITYG_03740	-	383800	384613	putative hydrolase	270	R	2137.9	432.5	1469.9			0	
SITYG_03750	-	384719	385319	hypothetical protein	199	S	269.6	622.6	937.3	3.8		1	alive in vivo
SITYG_03760	-	385436	386876	putative xanthine/uracil permease	479	R	164.2	335.7	258.0			1	alive in vivo
SITYG_03770	-	387240	387654	putative hydrolase	137	R	2114.2	743.1	1261.3			0	
SITYG_03780	-	387646	388168	putative N-acetyltransferase	173	KR	818.5	547.3	538.7			0	
SITYG_03790	-	388175	389279	putative transcriptional regulator LytR	367	K	1303.8	517.5	1209.8			0	
SITYG_03800	-	389322	389610	hypothetical protein	95		158.4	534.1	278.9			2	vivo-attenuated
SITYG_03810	-	389619	390030	Histidine triad protein	136	FGR	302.8	106.9	293.2			0	
SITYG_03820	-	390098	390830	ABC type multidrug transport system ATPase component	243	V	408.0	390.3	260.7			0	

SITYG_03830	-	390826	391873	ABC transporter permease	348	U	277.3	713.6	354.9			0	
SITYG_03840	-	391923	392721	hypothetical protein	265	M	1200.8	660.9	767.6			0	
SITYG_03850	-	392717	393353	tRNA [guanine-N (7)-] methyltransferase	211	R	1213.1	552.8	963.1			1	vivo-attenuated
SITYG_03860	-	393759	394452	hypothetical protein	230	S	389.1	475.6	594.1			2	vivo-attenuated
SITYG_03870	-	394663	395152	ribosome maturation protein RimP	162	S	856.8	629.1	1006.3			0	
SITYG_03880	*nusA*	395203	396397	transcription termination factor NusA	397	K	434.3	773.0	395.3			0	
SITYG_03890	-	396407	396704	hypothetical protein	98	K	363.1	296.0	371.9			0	
SITYG_03900	-	396696	396996	ribosomal protein L7A family protein	99	J	705.2	366.2	702.9			0	
SITYG_03910	*infB*	397012	399850	translation initiation factor IF-2	945	J	575.9	464.6	594.5			0	
SITYG_03920	*rbfA*	399928	400279	ribosome-binding factor A	116	J	118.2	62.6	0.0	<-118.2		0	
SITYG_03930	-	400437	402069	hypothetical protein	543	P	998.9	727.1	910.7			1	alive in vivo
SITYG_03940	-	402260	403412	N-acetylglucosamine-6-phosphate deacetylase	383	G	237.7	496.0	374.8			0	
SITYG_03950	-	403687	408151	putative serine protease	1487	O	74.3	502.1	155.2			5	vivo-attenuated
SITYG_03960	-	408406	408559	hypothetical protein	50		27.1	430.9	0.0			0	
SITYG_03970	-	408696	409113	hypotheticcal protein	138		179.1	263.5	602.0	3.7		0	
SITYG_03980	-	409109	409568	transcriptional regulator	152	K	72.3	335.1	350.0	5.3		0	
SITYG_03990	-	409560	409971	hypothetical protein	136		70.7	213.9	146.6			0	
SITYG_04000	*glyQ*	410248	411163	glycyl-tRNA synthetase subunit alpha	304	J	389.9	360.2	406.1			0	
SITYG_04010	*glyS*	411165	413205	glycyl-tRNA synthetase subunit beta	679	J	862.2	624.8	536.6			0	
SITYG_04020	-	413220	413478	hypothetical protein	85	S	852.1	425.9	1012.0			0	
SITYG_04030	-	413529	414195	Trk system potassium uptake protein TrkA	221	P	859.5	593.9	738.8			0	
SITYG_04040	-	414205	415561	potassium uptake protein TrkH	451	P	569.0	583.4	518.4			0	
SITYG_04050	-	415639	415807	hypothetical protein	55		74.1	130.8	836.8	12.3	5.3	0	
SITYG_04060	-	415827	416025	putative transcriptional regulator	65	K	125.7	0.0	50.7			0	
SITYG_04070	*mraW*	416173	417124	S-adenosyl-methyltransferase mraW	316	M	1487.4	462.1	802.5			0	
SITYG_04080	*ftsL*	417132	417450	Cell division protein FtsL	105	D	1239.2	414.6	1073.7			0	
SITYG_04090	-	417453	419712	penicillin-binding protein 2X	752	M	653.7	593.4	875.7			0	
SITYG_04100	*mraY*	419713	420697	Phospho-N-acetylmuramoyl-pentapeptide- transferase	327	M	737.7	558.3	489.9			0	
SITYG_04110	-	421098	423057	putative extracellular solute-binding protein	652	E	789.8	493.6	671.5			1	alive in vivo
SITYG_04120	-	423413	423911	CTP synthase	165	F	866.3	706.0	887.2			0	
SITYG_04130	-	423961	424372	hypothetical protein	136	S	1453.4	267.3	952.9			0	
SITYG_04140	-	424784	425666	fructose biphosphate aldolase	293	G	3155.8	2690.8	2539.0			0	
SITYG_04150	-	426104	426551	LytR/AlgR family transcriptional regulator	148	KT	306.2	295.0	269.6			0	
SITYG_04160	-	426556	427219	hypothetical protein	220		519.3	265.2	242.3			0	
SITYG_04170	*rpmB*	427353	427542	50S ribosomal protein L28	62	J	4148.2	348.8	3187.9			0	
SITYG_04180	-	427716	428082	alkaline-shock protein	121	S	2436.8	420.3	2167.5			0	
SITYG_04190	-	428084	429752	hypothetical protein	555	R	1238.5	606.0	1149.9			0	
SITYG_04200	-	430143	431019	ABC transporter, ATP-binding protein	291	V	104.2	351.2	332.4	3.5		4	vivo-attenuated
SITYG_04210	-	431029	431764	putative kinase	244	V	79.0	478.4	259.6	3.6		0	
SITYG_04220	-	431768	432869	histidine kinase	366	T	165.8	359.3	209.8			1	vivo-attenuated
SITYG_04230	-	432865	433465	two-component system transcriptional regulator	199	TK	269.6	512.7	485.4			0	
SITYG_04240	-	433594	434482	hypothetical protein	295	O	733.4	866.1	497.6			0	
SITYG_04250	-	434590	434806	hypothetical protein	71		96.0	203.5	186.0			0	
SITYG_04260	-	435172	435913	amino acid transport ATP-binding protein	246	E	375.1	563.5	230.4			1	alive in vivo
SITYG_04270	-	435909	437475	glutamine ABC transporter substrate-binding protein	521	ET	389.4	364.8	371.9			1	alive in vivo
SITYG_04280	-	437600	439490	hypothetical protein	629		338.0	465.1	632.3			1	alive in vivo
SITYG_04290	*bacA*	439556	440399	undecaprenyl diphosphatase	280	V	506.8	573.5	440.8			0	
SITYG_04300	-	440367	440496	hypothetical protein	42		32.2	170.3	1556.9	52.7	7.6	0	
SITYG_04310	*mecA*	440525	441275	negative regulator of genetic competence MecA	249	OTN	1393.8	468.8	1472.8			0	
SITYG_04320	*rgpG*	441271	442438	putative glycosyl transferase	388	M	1105.5	753.2	851.9			2	vivo-attenuated
SITYG_04330	-	442528	443299	feS assembly ATPase SufC	256	O	672.5	370.5	1250.4			0	
SITYG_04340	-	443338	444601	feS assembly protein SufD	420	O	443.4	591.6	787.1			0	
SITYG_04350	-	444617	445850	cysteine desulfurase, SufS subfamily	410	E	249.0	427.7	57.0	-4.0	-9.0	0	
SITYG_04360	-	445836	446286	SUF system FeS assembly protein, NifU family	149	C	101.4	293.0	267.8			0	
SITYG_04370	-	446373	447615	D-alanyl-D-alanine carboxypeptidase	413	M	230.5	460.0	202.1			1	alive in vivo
SITYG_04380	-	447771	449115	ATP-dependent RNA helicase	447	LKJ	450.6	245.3	291.4			1	vivo-attenuated
SITYG_04390	-	449275	450085	amino acid ABC transporter permease	269	E	394.3	488.3	557.9			2	alive in vivo
SITYG_04400	-	450084	450828	amino acid ABC transporter ATP-binding protein	247	E	384.7	827.0	499.4			1	alive in vivo
SITYG_04410	-	450922	451147	hypothetical protein	74		1567.1	586.0	490.9			0	
SITYG_04420	*trxB*	451209	452121	thioredoxin reductase	303	O	732.3	385.5	924.9			0	
SITYG_04430	-	452299	453676	amino acid permease	458	E	295.2	367.0	401.1			0	
SITYG_04440	-	453863	454208	hypothetical protein	114		120.2	764.3	640.4	5.8		1	vivo-attenuated
SITYG_04450	-	454207	454690	hypothetical protein	160		51.5	455.0	228.7	4.8		0	
SITYG_04460	-	454792	456253	nicotinate phosphoribosyltransferase	486	H	885.9	481.3	762.9			0	
SITYG_04470	*nadE*	456249	457074	NAD synthetase	274	H	588.3	319.6	486.9			0	
SITYG_04480	*pepC*	457221	458559	aminopeptidase C	445	E	781.3	344.9	555.4			1	alive in vivo
SITYG_04490	*pbp1a*	458728	460900	penicillin-binding protein 1A	723	M	420.2	404.7	508.6			1	alive in vivo
SITYG_04500	*recU*	460892	461495	holliday junction resolvase RecU	200	R	350.8	145.8	682.8			0	
SITYG_04510	-	461575	462085	hypothetical protein	169	S	97.6	215.4	196.9			0	
SITYG_04520	-	462160	462502	cell division initiation protein	113	D	933.9	192.8	880.9			0	
SITYG_04530	-	462563	462668	hypothetical protein	34		3871.6	6278.5	2295.3			0	
SITYG_04540	-	462711	462801	hypothetical protein	29		92.2	0.0	111.6			0	
SITYG_04550	-	462939	464094	predicted N6-adenine-specific DNA methylase	384	L	535.1	494.7	417.3			3	alive in vivo
SITYG_04560	-	464106	465549	hypothetical protein	480		457.1	380.7	487.1			2	alive in vivo
SITYG_04570	*ahpC*	465652	466219	alkyl hydroperoxidase	188	O	1565.6	1162.7	1257.5			0	
SITYG_04580	-	466230	467763	NADH oxidase	510	O	990.4	759.7	648.5			0	
SITYG_04590	*luxS*	467812	468295	S-ribosylhomocysteine lyase	160	T	249.1	364.0	665.3			0	
SITYG_04600	-	468510	470118	hypothetical protein	535	R	2324.3	451.0	1536.3			2	alive in vivo
SITYG_04610	*gmk*	470299	470926	guanylate kinase	208	F	1541.5	665.9	1665.7			0	
SITYG_04620	*rpoZ*	470954	471266	DNA-directed RNA polymerase subunit omega	103	K	2433.1	422.6	1899.0			0	
SITYG_04630	*priA*	471324	473706	primosomal protein N'	793	L	247.3	498.2	366.8			0	
SITYG_04640	*fmt*	473766	474702	methionyl-tRNA formyltransferase	311	J	505.2	328.7	472.1			0	
SITYG_04650	-	474691	476005	ribosomal RNA small subunit methyltransferase B	437	J	350.4	551.9	397.4			0	
SITYG_04660	*pppL*	476023	476764	phosphoprotein phosphatase	246	T	1125.2	741.4	975.7			1	vivo-attenuated
SITYG_04670	*pkn_1*	476760	478635	putative serine/threonine protein kinase	624	RTKL	867.2	586.0	551.6			0	
SITYG_04680	*pkn_2*	478585	478708	hypothetical protein	40		134.9	357.3	163.3			0	
SITYG_04690	-	478897	479596	hypothetical protein	232	S	308.6	503.0	459.7			3	vivo-attenuated
SITYG_04700	-	479592	480588	putative histidine kinase	331	T	324.9	485.4	594.9			0	
SITYG_04710	-	480589	481222	two component response transcriptional regulator	210	TK	380.1	1006.7	475.9			1	alive in vivo
SITYG_04720	-	481261	482662	cyclophilin type peptidyl-prolyl cis-trans isomerase	466	R	544.8	298.0	716.8			0	
SITYG_04730	-	482663	483056	S1 RNA binding domain protein	130	J	1688.8	1062.4	1303.2			0	
SITYG_04740	-	483175	483493	hypothetical protein	105		1721.9	414.6	1136.8			0	
SITYG_04750	-	483612	484146	hypothetical protein	177	J	1204.1	535.0	1410.4			0	
SITYG_04760	*recX*	484232	485009	regulatory protein recX	258	R	170.8	339.4	232.6			0	
SITYG_04770	-	485072	485849	putative aminoglycoside 3'-phosphotransferase	258	J	331.0	650.5	685.0			2	alive in vivo
SITYG_04780	-	485905	487285	putative RNA methyltransferase	459	J	438.9	684.7	451.2			0	
SITYG_04790	-	487649	487883	hypothetical protein	77		195.0	93.9	214.6			0	
SITYG_04800	-	487882	489244	hypothetical protein	453	S	624.4	1032.6	567.7			1	alive in vivo
SITYG_04810	-	489254	489509	hypothetical protein	84		748.3	430.9	315.0			0	
SITYG_04820	-	489759	490479	hypothetical protein	239		201.6	366.2	320.8			4	vivo-attenuated
SITYG_04830	-	490631	491291	hypothetical protein	219		408.5	566.0	471.7			0	
SITYG_04840	-	491333	491909	putative acetyltransferase	191	J	223.3	267.1	174.3			0	
SITYG_04850	-	491905	493192	hypothetical protein	428		238.5	273.2	351.1			4	alive in vivo
SITYG_04860	*valS*	493213	495865	valyl-tRNA synthetase	883	J	200.2	348.0	200.7			0	
SITYG_04870	-	495966	497250	hypothetical protein	427	L	345.7	308.1	438.0			4	alive in vivo
SITYG_04880	-	497251	499150	putative nucleoside triphosphate hydrolase	632		799.5	486.0	772.1			8	vivo-attenuated
SITYG_04890	-	499151	499754	hypothetical protein	200		715.4	328.0	799.4			3	alive in vivo
SITYG_04900	-	499746	500733	hypothetical protein	328		617.8	289.4	447.7			6	vivo-attenuated
SITYG_04910	-	501262	501409	hypothetical protein	48	JD	395.1	299.0	409.9			0	
SITYG_04920	-	501658	501805	hypothetical	48	D	28.2	0.0	0.0			0	
SITYG_04930	-	501833	501950	hypothetical protein	38		70.9	0.0	0.0			0	
SITYG_04940	*cysK*	502225	503155	cysteine synthase	309	E	1075.0	70.9	723.5			0	
SITYG_04950	-	503254	503890	hypothetical protein	211	S	260.9	172.8	284.2			1	alive in vivo
SITYG_04960	*comFA*	503946	505248	putative ATP-dependent RNA helicase	433	L	76.5	371.3	61.7			4	alive in vivo
SITYG_04970	*comFC*	505244	505910	putative competence protein	221	R	81.0	231.0	301.6	4.1		0	
SITYG_04980	-	505988	506531	30S ribosomal interface protein S30EA	180	J	3437.7	7001.1	2681.6			3	vivo-attenuated
SITYG_04990	-	506663	507269	RNA methyltransferase, RsmD family	201	L	2820.2	580.2	1458.2			0	
SITYG_05000	-	507258	507756	phosphopantetheine adenyltransferase	165	H	524.8	485.4	524.3			0	
SITYG_05010	-	507736	508792	hypothetical protein	351	T	628.5	561.9	504.0			0	
SITYG_05020	-	509073	509637	hypothetical protein	187	S	595.7	350.7	445.1			0	
SITYG_05030	-	509670	510753	ribosomal RNA large subunit methyltransferase N	360	R	390.7	669.6	621.2			1	alive in vivo
SITYG_05040	-	510745	511264	VanZ-like protein	172	V	327.7	508.1	328.9			0	
SITYG_05050	*pilD*	511249	511933	prepilin type IV endopeptidase	227	NOU	151.6	803.2	440.4	3.2		0	
SITYG_05060	*dps*	512084	512612	putative DNA-binding ferritin-like protein	175	P	13379.4	8198.9	9433.4			0	
SITYG_05070	-	512874	513099	hypothetical protein	74	S	6692.4	1367.3	5846.7			0	
SITYG_05080	-	513092	513473	rhodanese-like protein	126	P	1589.6	173.0	1001.6			0	
SITYG_05090	-	513493	514219	putative 16srRNA pseudouridylate synthase	241	J	80.0	272.4	152.2			2	alive in vivo
SITYG_05100	*typA*	514399	516241	GTP-binding protein TypA	613	T	1400.7	489.1	1112.1			0	
SITYG_05110	-	516303	516588	hypothetical protein	94		611.3	385.5	352.4			1	alive in vivo

SITYG_05120	*murD*	516661	518014	UDP-N-acetylmuramoylalanine--D-glutamate ligase	450	M		312.7	633.4	348.8			0	
SITYG_05130	*murG*	518015	519086	N-acetylglucosaminyl transferase	356	M		197.5	328.3	393.8			0	
SITYG_05140	-	519082	520132	putative cell division protein	349	M		568.9	376.7	430.4			0	
SITYG_05150	*ftsA*	520254	521640	cell division protein FtsA	461	D		1912.5	1094.0	1717.1			0	
SITYG_05160	*ftsZ*	521657	522932	cell division protein FtsZ	424	D		1330.7	413.6	1023.9			0	
SITYG_05170	-	522933	523605	pyridoxal 5'-phosphate-dependent enzymes class III	223	R		679.0	425.1	478.2			0	
SITYG_05180	-	523614	524160	putative cell division protein sepF	181	S		873.7	281.7	919.6			0	
SITYG_05190	-	524164	524428	hypothetical genome	87	S		2466.9	499.4	1141.1			0	
SITYG_05200	-	524431	525223	RNA binding protein	263	S		2236.5	693.6	1724.4			0	
SITYG_05210	*divIVA*	525232	526018	cell division protein DivIVA	261	D		2491.0	363.4	1558.7			0	
SITYG_05220	*ileS*	526283	529076	isoleucyl-tRNA synthetase	930	J		298.5	354.0	327.2			0	
SITYG_05230	-	530065	531190	hypothetical protein	374	R		475.7	449.3	589.1			0	
SITYG_05240	*pckA*	531412	533059	phosphoenolpyruvate carboxykinase	548	C		143.6	520.3	262.2			2	alive in vivo
SITYG_05250	*hlyX*	533147	534488	putative hemolysin	446	R		730.0	573.5	816.2			2	vivo-attenuated
SITYG_05260	*treR*	534543	535257	trehalose operon transcriptional repressor	237	K		87.1	615.5	337.5	4.2		0	
SITYG_05270	-	535435	537448	PTS system trehalose-specific transporter subunit IIABC	670	G		651.2	884.2	758.3			2	vivo-attenuated
SITYG_05280	-	537615	539259	putative trehalose-6-phosphate hydrolase	547	G		681.3	748.5	623.0			0	
SITYG_05290	-	539406	541581	putative nuclease	724	R	LPXTG	158.3	485.0	337.0			0	
SITYG_05300	*pflA*	541749	542547	pyruvate formate lyase activating enzyme	265	O		1143.6	578.3	943.8			0	
SITYG_05310	*ppaC*	542691	543627	manganese dependent inorganic pyrophosphatase	311	C		1076.9	586.9	1223.1			0	
SITYG_05320	-	544127	544640	hypothetical protein	170			121.3	428.4	97.9			0	
SITYG_05330	-	544623	545307	hypothetical protein	227			97.0	449.8	264.3			0	
SITYG_05340	-	545638	546397	hypothetical protein	252			131.2	608.0	145.5			0	
SITYG_05350	*murE*	546520	547966	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6- diaminopimelate ligase	481	M		424.6	395.1	388.9			0	
SITYG_05360	-	548051	549680	polysaccharide biosynthesis protein	542	R		285.2	485.6	604.1			0	
SITYG_05370	-	549898	550018	hypothetical protein	39			0.0	0.0	0.0			0	
SITYG_05380	-	550118	550286	hypothetical protein	55	E		49.4	130.8	0.0			0	
SITYG_05390	-	550471	551638	betaC-S lyase	388	E		191.9	376.6	172.1			0	
SITYG_05400	-	552109	554764	translocating P-type ATPase	884	P		293.7	496.6	472.8			1	alive in vivo
SITYG_05410	-	554861	555491	uracil phosphoribosyltransferase	209	F		3173.7	697.6	2199.7			4	vivo-attenuated
SITYG_05420	-	555603	556194	ATP-dependent Clp protease proteolytic subunit	196	OU		589.6	334.6	611.7			1	vivo-attenuated
SITYG_05430	-	556284	556554	hypothetical protein	89	S		460.9	81.4	186.0			0	
SITYG_05440	-	556636	557800	hypothetical protein	387	E		245.9	302.1	405.5			1	alive in vivo
SITYG_05450	-	558128	559052	branched-chain amino acid ABC transporter permease	307	E		166.1	475.6	826.0	5.4		1	alive in vivo
SITYG_05460	-	559055	560006	branched-chain amino acid ABC transporter permease	316	E		104.7	415.9	337.9	3.5		1	alive in vivo
SITYG_05470	-	560005	560770	branched-chain amino acid ABC transporter	254	E		222.3	459.6	354.4			0	
SITYG_05480	-	560769	561480	amino acid ABC transporter ATPase	236	E		250.9	309.1	155.4			0	
SITYG_05490	-	561627	562284	hypothetical protein	218	R		606.1	1605.5	259.8			0	
SITYG_05500	-	562348	563212	hypothetical protein	287	S		139.2	254.3	93.0			0	
SITYG_05510	-	563270	563384	hypothetical protein	37			0.0	192.8	88.1	>88.1		0	
SITYG_05520	-	563364	564003	thymidylate kinase	212	F		1324.3	515.8	1823.0			0	
SITYG_05530	-	563999	564893	DNA polymerase III subunit delta	297	L		1039.4	860.3	1235.6			0	
SITYG_05540	-	564915	565245	initiation-control protein yabA	109	S		942.8	732.5	1704.1			1	alive in vivo
SITYG_05550	-	565247	566111	putative tetrapyrrole methylase	287	R		667.4	1119.1	720.6			0	
SITYG_05560	-	566122	566632	methylated DNA-protein cysteine methyltransferase	169	L		1236.3	517.1	1083.0			0	
SITYG_05570	-	566649	567003	arsenate reductase	117	P		105.5	186.2	141.8			0	
SITYG_05580	-	567138	567768	endonuclease III	209	L		256.8	104.6	159.4			0	
SITYG_05590	-	567795	568182	putative endonuclease	128	E		107.2	170.3	77.8			2	vivo-attenuated
SITYG_05600	-	568193	569021	putative glyoxalase	275	L		210.4	238.9	327.5			1	alive in vivo
SITYG_05610	-	569500	570409	CAAX amino terminal protease	302	R		95.8	290.1	176.8			1	alive in vivo
SITYG_05620	-	570386	570668	hypothetical protein	93	K		73.5	389.6	462.9	6.9		1	alive in vivo
SITYG_05630	-	570654	571290	putative membrane protein	211	S		150.0	241.9	205.3			1	alive in vivo
SITYG_05640	-	571417	571873	hypothetical protein	151			181.9	241.0	22.0	-7.6	-13.1	0	
SITYG_05650	-	571869	572502	hypothetical protein	210	S		222.8	381.9	618.7	3.0		0	
SITYG_05660	-	572870	573131	hypothetical protein	86			63.6	84.2	115.4			1	alive in vivo
SITYG_05670	-	573377	575375	methionyl-tRNA synthetase	665	J		840.8	461.9	914.7			0	
SITYG_05680	-	575464	576646	hypothetical protein	393			136.9	409.0	288.9			0	
SITYG_05690	-	576737	577424	putative response regulator	228	TK		1853.7	671.7	1271.7			1	alive in vivo
SITYG_05700	-	577407	578388	histidine kinase	326	T		321.4	134.4	348.0			0	
SITYG_05710	-	578510	579269	hypothetical protein	252			16.4	289.5	291.1	19.3		1	alive in vivo
SITYG_05720	-	579237	579375	hypothetical protein	45			0.0	0.0	0.0			0	
SITYG_05730	-	579486	580266	putative ABC transporter ATP-binding protein	259	V		53.2	676.1	141.6			0	
SITYG_05740	-	580246	582226	ABC-type bacitracin resistance protein permease	659	V		163.4	665.9	390.5			0	
SITYG_05750	-	582374	583241	ABC transporter protein	288	V		47.8	329.5	127.4			0	
SITYG_05760	-	583242	584106	putative ABC transporter protein	287	V		91.2	483.2	488.2	5.8		1	alive in vivo
SITYG_05770	-	584150	584588	LytTr family transcriptional regulator	145	KT		75.8	250.9	298.0	4.3		0	
SITYG_05780	-	584600	584990	hypothetical protein	129			138.3	676.1	103.0			0	
SITYG_05790	-	585061	586027	hypothetical protein	321			313.5	273.0	239.1			0	
SITYG_05800	-	586533	586662	hypothetical protein	42			0.0	0.0	0.0			0	
SITYG_05810	-	586801	587569	ABC-type antimicrobial peptide transport system ATPase component	255	V		64.8	429.2	91.5			0	
SITYG_05820	-	587561	589550	ABC-type antimicrobial peptide transport system permease	662	V		54.2	331.4	151.5	3.0		0	
SITYG_05830	-	589721	591110	putative amino acid permease transporter	462	E		262.8	411.3	643.4			0	
SITYG_05840	-	591178	591607	putative acyl-CoA N-acetyl transferase	142	KR		270.7	409.8	468.2			0	
SITYG_05850	-	591619	592081	putative acyl-CoA N-acetyl transferase	153			215.5	380.5	195.6			0	
SITYG_05860	-	592077	592716	hypothetical protein	212	G		175.3	447.1	110.0			0	
SITYG_05870	-	592861	593065	putative major cold shock protein	67	K		589.7	0.0	443.0			0	
SITYG_05880	-	593259	593496	hypothetical protein	78			1137.7	370.9	847.4			0	
SITYG_05890	-	593488	594187	3-ketoacyl-ACP reductase	232	IQR		178.0	628.7	387.9			0	
SITYG_05900	-	594198	594945	putative acetyltransferase	248			177.7	470.7	295.7			0	
SITYG_05910	-	594941	595274	hypothetical protein	110			286.5	593.9	301.6			0	
SITYG_05920	-	595283	595682	hypothetical protein	132			239.1	385.5	402.7			0	
SITYG_05930	-	595717	596167	hypothetical protein	149	S		165.9	634.8	66.9			0	
SITYG_05940	*glmU*	596251	597631	N-acetylglucosamine-1-phosphate uridyltransferase	459	M		742.5	302.5	749.5			0	
SITYG_05950	-	597639	598191	hypothetical protein	183	LR		804.1	915.6	545.8			0	
SITYG_05960	-	598195	598510	hypothetical protein	104			750.6	488.3	669.5			0	
SITYG_05970	*pfs*	598563	599256	5'-methylthioadenosine S-adenosylhomocysteine nucleosidase	230	F		670.4	697.6	652.1			0	
SITYG_05980	-	599273	599582	hypothetical protein	102			1423.0	640.0	650.0			0	
SITYG_05990	-	599694	601236	putative ABC transporter ATP-binding protein	513	R		242.1	327.8	254.0			1	alive in vivo
SITYG_06000	-	601562	602366	peptidyl-prolyl cis-trans isomerase	267	O		593.3	574.0	512.1			1	alive in vivo
SITYG_06010	-	602853	603063	putative phage shock protein	69	KT		1896.3	209.3	1243.3			0	
SITYG_06020	*ftsK*	603152	605450	putative cell division protein	765	D		525.3	564.2	760.4			1	vivo-attenuated
SITYG_06030	-	605796	608166	cation transport ATPase	789	P		253.8	296.7	326.3			3	vivo-attenuated
SITYG_06040	-	608185	608539	putative membrane protein	117			82.0	248.3	56.7			1	alive in vivo
SITYG_06050	-	608492	608621	hypothetical protein	42			0.0	0.0	0.0			0	
SITYG_06060	*rplK*	608700	609126	50S ribosomal protein L11	141	J		4995.3	515.8	2758.0			0	
SITYG_06070	*rplA*	609215	609905	50S ribosomal protein L1	229	J		1334.6	191.1	1091.5			0	
SITYG_06080	*pyrH*	610189	610930	uridylate kinase	246	F		979.7	415.2	1029.9			0	
SITYG_06090	-	610933	611491	ribosome recycling factor	185	J		1174.6	433.2	683.9			0	
SITYG_06100	-	611603	612458	hypothetical protein	284	S		436.6	359.8	246.6			0	
SITYG_06110	-	612517	613555	DNA polymerase III subunit delta	345	L		627.4	529.3	551.4			0	
SITYG_06120	*sodA*	613625	614231	manganese-dependent superoxide dismutase	201	P		1553.9	689.0	1425.1			0	
SITYG_06130	-	614303	614678	hypothetical protein	124			66.4	234.4	107.1			0	
SITYG_06140	-	615158	617309	putative ABC-type bacteriocin transporter	716	V		40.5	459.7	359.5	9.7		0	
SITYG_06150	-	617319	618681	putative bacteriocin secretion accessory protein	453			85.3	419.5	331.8	4.2		1	alive in vivo
SITYG_06160	-	618777	618927	hypothetical protein	49			0.0	146.5	0.0			0	
SITYG_06170	-	618971	619565	putative histidine kinase	197	T		244.4	369.9	186.0			1	alive in vivo
SITYG_06180	-	619616	620288	putative histidine kinase	223	T		246.9	163.5	164.4			2	alive in vivo
SITYG_06190	-	620289	621042	putative response regulator	250	KT		121.2	437.7	53.3			1	alive in vivo
SITYG_06200	-	621204	621918	hypothetical protein	237	R		29.0	123.1	84.4	3.2		1	alive in vivo
SITYG_06210	-	622149	622374	putative bacteriocin, class IIb	74			55.3	390.7	89.3			0	
SITYG_06220	-	622395	622782	hypothetical protein	128			32.2	56.8	0.0			0	
SITYG_06230	-	622789	623011	putative bacteriocin, class IIb	73			0.0	0.0	0.0			0	
SITYG_06240	-	623296	623479	putative bacteriocin class IIb	60			22.7	120.1	54.9			1	alive in vivo
SITYG_06250	-	623514	623835	hypothetical protein	106			38.8	410.7	281.6	7.9		0	
SITYG_06260	-	624064	624280	putative bacteriocin class IIb	71			38.4	101.7	0.0			0	
SITYG_06270	-	624508	624802	putative enterocin A immunity	97			0.0	0.0	34.2			0	
SITYG_06280	-	624969	625221	hypothetical protein	83			0.0	87.2	318.8	#DIV/0!	3.0	1	alive in vivo
SITYG_06290	-	625431	625662	putative bacteriocin class IIb	76			53.9	190.3	652.1	13.2		0	
SITYG_06300	-	625679	625793	hypothetical protein	37			0.0	0.0	0.0			0	
SITYG_06310	-	626114	627164	putative cell wall anchor protein	349	OC	LPXTG	31.6	83.7	162.6	5.6		0	
SITYG_06320	-	627268	628330	hypothetical protein	353			277.3	662.1	321.5			0	
SITYG_06330	-	628463	629150	hypothetical protein	228	T		422.7	447.8	555.5			0	
SITYG_06340	*arcA*	629457	630687	arginine deiminase	409	E		1281.5	30675.2	1249.1			0	
SITYG_06350	-	630710	631727	ornithine carbamoyltransferase	338	E		1072.7	8513.3	997.3			0	
SITYG_06360	*arcC*	631942	632890	carbamate kinase	315	E		210.0	2155.7	370.7			0	
SITYG_06370	-	633127	634630	putative C4-dicarboxylate anaerobic carrier	500	S		218.0	1125.8	574.6			1	alive in vivo
SITYG_06380	*arcT*	634650	635991	acetylornithine deacetylase	446	E		188.7	721.0	299.5			1	alive in vivo
SITYG_06390	-	636299	636773	arginine repressor	157	K		201.3	463.6	105.9			0	
SITYG_06400	*queA*	636783	637812	S-adenosylmethionine tRNA ribosyltransferase-isomerase	342	J		213.7	469.8	409.9			0	

SITYG_06410	*nagB*	638118	638826	glucosamine-6-phosphate deaminase	235	G		152.3	248.3	312.0			1	vivo-attenuated
SITYG_06420	-	638942	640301	putative D-alanyl-D-alanine carboxypeptidase	452	M		653.2	258.7	657.6			1	alive in vivo
SITYG_06430	-	640379	641549	hypothetical protein	389	GEPR		177.3	507.1	240.3			1	alive in vivo
SITYG_06440	-	641845	643279	6-phospho-beta-glucosidase	477	G		63.6	735.6	252.1	4.3	-3.5	1	alive in vivo
SITYG_06450	-	643367	643607	hypothetical protein	79	S		17.3	640.9	418.4	26.4		0	
SITYG_06460	-	643722	644037	PTS system, IIB component	104	G		13.2	139.5	159.4	13.2		0	
SITYG_06470	*celR*	644092	646084	putative transcriptional regulator	663	K		54.1	319.9	216.8	4.4		2	vivo-attenuated
SITYG_06480	-	646096	646414	putative PTS system, cellobiose-specific IIA component	105	G		130.4	1174.7	284.2			0	
SITYG_06490	-	646436	646943	hypothetical protein	168			24.5	303.4	0.0			0	
SITYG_06500	-	646982	648326	PTS system cellobiose transporter subunit IIC	447	G		83.3	523.2	306.3	4.0		0	
SITYG_06510	*coiA*	648414	649446	putative competence protein CoiA	343	R		44.2	149.1	165.4	4.1		2	alive in vivo
SITYG_06520	-	649397	651200	oligoendopeptidase F	600	E		1120.4	499.7	690.6			2	vivo-attenuated
SITYG_06530	-	651201	651885	O-methyltransferase	227	R		357.8	417.6	205.5			0	
SITYG_06540	-	651991	652930	foldase protein PrsA	312	O		5190.7	444.6	2577.3			0	
SITYG_06550	-	653154	653640	hypothetical protein	161	S		367.0	180.9	289.3			0	
SITYG_06560	*alaS*	653685	656304	alanyl-tRNA synthetase	872	J		402.3	495.0	460.1			0	
SITYG_06570	-	656366	657905	ABC transporter, ATP-binding protein	512	V		113.2	471.2	195.8			0	
SITYG_06580	-	657966	659205	putative femAB family protein	412	V		294.6	372.5	437.7			0	
SITYG_06590	*murM*	659217	660432	putative femAB family protein	404	V		433.6	560.7	479.4			0	
SITYG_06600	-	660431	661241	cof family protein	269	R		199.7	352.7	545.5			0	
SITYG_06610	-	661230	662625	hypothetical protein	464	R		315.2	378.1	230.4			0	
SITYG_06620	-	662673	663060	hypothetical protein	128			235.8	170.3	233.5			0	
SITYG_06630	-	663423	666117	putative calcium-translocating P-type ATPase	897	P		477.3	301.8	484.6			1	alive in vivo
SITYG_06640	-	666137	666296	hypothetical protein	52			26.1	0.0	0.0			0	
SITYG_06650	*prfB*	666774	667752	peptide chain release factor 2	325	J		1234.3	606.7	862.5			0	
SITYG_06660	*ftsE*	667853	668546	cell division ATP-binding protein FtsE	230	D		706.3	222.0	681.1			0	
SITYG_06670	*ftsX*	668538	669465	cell division protein FtsX	308	D		1230.6	568.9	974.9			0	
SITYG_06680	-	669499	670135	hypothetical protein	211	R		215.2	276.4	315.8			0	
SITYG_06690	*dinG*	670244	672731	putative ATP-dependent DNA helicase DinG	828	KL		205.2	265.1	105.0			0	
SITYG_06700	-	672851	673832	hypothetical protein	326	S		473.6	515.2	368.5			0	
SITYG_06710	*rodA*	673868	675101	rod-shaped determining protein	410	D		242.2	695.1	407.2			0	
SITYG_06720	*thiJ*	675113	675662	4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis protein	182	R		959.6	480.3	621.9			1	alive in vivo
SITYG_06730	-	675789	676353	putative HAD superfamily hydrolase	187	R		1500.4	662.4	1210.7			0	
SITYG_06740	*gyrB*	676365	678312	DNA gyrase subunit B	648	L		718.0	485.3	557.0			0	
SITYG_06750	*ezrA*	678399	680124	septation ring formation regulator EzrA	574	D		988.3	318.5	809.2			2	vivo-attenuated
SITYG_06760	-	680243	681257	hypothetical protein	337	G		511.4	260.1	435.7			0	
SITYG_06770	-	681645	682302	putative two-component response regulator	218	TK		669.3	367.9	489.1			1	alive in vivo
SITYG_06780	-	682298	683675	putative two component system histidine kinase	458	T		1027.3	766.0	787.6			4	alive in vivo
SITYG_06790	-	683999	684644	hypothetical protein	214			430.9	340.7	435.9			1	alive in vivo
SITYG_06800	*thrS*	684636	686601	threonyl-tRNA synthetase	654	J		576.3	469.7	659.2			0	
SITYG_06810	-	686824	687379	putative transcriptional regulator	184	K		127.1	118.8	72.4			0	
SITYG_06820	-	687514	688216	ABC transporter, ATP-binding protein	233	V		242.3	438.2	529.3			0	
SITYG_06830	-	688226	691592	hypothetical protein	1121	V		382.0	633.3	429.6			0	
SITYG_06840	-	691683	692514	putative metallo-dependent phosphatase	276	T		259.6	396.7	217.5			1	alive in vivo
SITYG_06850	-	692585	692950	-		K		875.1	602.0	577.8			0	
SITYG_06860	-	693065	693842	putative glycyl-radical enzyme activating protein	258	O		37.4	424.2	155.1	4.5	-3.3	1	alive in vivo
SITYG_06870	-	693819	693942	hypothetical protein	40			0.0	0.0	0.0			0	
SITYG_06880	-	693974	694718	transcriptional regulator, DeoR family	247	KG		245.3	502.1	580.4			0	
SITYG_06890	-	694736	695699	transcriptional regulator	320	K		202.5	387.9	156.4			0	
SITYG_06900	-	695943	696267	PTS system, IIA component	107	G		64.0	542.6	124.0			1	alive in vivo
SITYG_06910	-	696287	696599	PTS system, cellobiose-specific IIB component	103	G		13.3	281.7	32.2			0	
SITYG_06920	-	696610	697912	PTS system, cellobiose-specific IIC component	433	G		95.6	590.7	254.5			3	alive in vivo
SITYG_06930	-	698076	700524	pyruvate formate lyase	815	C		64.4	475.8	176.4			2	alive in vivo
SITYG_06940	-	700538	701207	putative fructose-6-phosphate aldolase	222	G		24.8	98.5	165.1	7.2		0	
SITYG_06950	*gldA*	701319	702408	glycerol dehydrogenase	362	C		91.4	464.1	691.6	8.2		1	alive in vivo
SITYG_06960	-	702726	703350	hypothetical protein	207			146.2	422.6	434.5	3.2		0	
SITYG_06970	-	703340	703682	hypothetical protein	113			12.1	64.3	29.4			0	
SITYG_06980	-	703759	704371	hypothetical protein	203			542.2	502.7	672.7			0	
SITYG_06990	-	704361	704703	hypothetical protein	113			48.5	192.8	117.5			0	
SITYG_07000	-	704780	705392	hypothetical protein	203			704.9	323.2	918.9			0	
SITYG_07010	-	705382	706705	hypothetical protein	440			692.9	548.1	759.0			1	alive in vivo
SITYG_07020	-	706719	707025	hypothetical protein	101			745.6	359.1	262.5			0	
SITYG_07030	-	707026	707344	hypothetical protein	105			978.3	1382.1	757.9			0	
SITYG_07040	-	707688	711171	endo-beta-N-acetylglucosaminidase	1160	G	LPXTG	51.2	441.6	196.1	4.2		2	alive in vivo
SITYG_07050	-	711399	713478	putative alpha-1,2-mannosidase	692	G		99.8	644.8	323.6	3.5		0	
SITYG_07060	-	713645	714935	putative glycosyl hydrolase	429	S		57.9	425.9	451.5	8.5		0	
SITYG_07070	-	714936	717570	putative alpha-mannosidase	877	G		50.4	308.7	87.7			4	vivo-attenuated
SITYG_07080	-	717635	718514	ROK family protein	292	KG		89.7	500.0	125.7			0	
SITYG_07090	-	718498	720382	N-acetyl-beta-D-glucosaminidase	627			81.5	571.5	191.9			1	alive in vivo
SITYG_07100	-	720526	721489	ABC sugar transporter permease protein	320	G		51.7	365.1	312.8	6.6		1	vivo-attenuated
SITYG_07110	-	721502	722435	ABC sugar transporter membrane spanning permease	310	G		53.4	447.5	258.3	5.3		3	vivo-attenuated
SITYG_07120	-	722523	724005	putative transporter protein	493	G		58.8	578.3	203.3	3.8	-3.4	0	
SITYG_07130	-	724266	724887	hypothetical protein	206	S		86.8	106.2	242.6	3.0		1	alive in vivo
SITYG_07140	-	724883	726527	putative histidine kinase	547	T		196.8	441.1	458.1			0	
SITYG_07150	-	726537	727830	putative response regulator	430	T		80.2	390.9	201.9			1	alive in vivo
SITYG_07160	-	727920	728487	hypothetical protein	188	S		109.7	348.8	53.1			2	alive in vivo
SITYG_07170	-	728573	730082	DNA methyltransferase	502	V		285.9	597.1	519.1			1	alive in vivo
SITYG_07180	-	730068	730617	putative restriction endonuclease	182	V		113.3	480.3	237.8			0	
SITYG_07190	-	730601	731156	putative restriction endonuclease subunit S	184	V		164.4	0.0	36.2	-4.2		0	
SITYG_07200	-	731227	732214	putative phage integrase	328	L		369.8	467.5	437.5			0	
SITYG_07210	-	732224	733313	putative type I restriction enzyme	362	V		331.4	726.4	359.6			0	
SITYG_07220	-	733349	733904	hypothetical protein	184			59.8	158.4	199.0	3.6		0	
SITYG_07230	-	733929	734826	hypothetical protein	298			203.5	367.5	526.2			2	vivo-attenuated
SITYG_07240	-	734839	737932	type I deoxyribonuclease HsdR	1030	V		299.1	426.3	263.0			3	vivo-attenuated
SITYG_07250	*lysS*	738158	739646	lysyl-tRNA synthetase	495	J		1017.5	310.1	668.1			0	
SITYG_07260	-	739728	740370	phosphoglycerate mutase	213	G		684.9	616.1	453.6			0	
SITYG_07270	-	740394	740871	putative prolyl-tRNA synthetase	158	S		774.0	414.6	757.9			0	
SITYG_07280	-	740870	741713	hypothetical protein	280	S		295.2	417.1	345.5			0	
SITYG_07290	-	741868	744211	cation transport ATPase	780	P		286.8	384.5	274.3			2	alive in vivo
SITYG_07300	-	744341	745082	1-acyl-sn-glycerol-3-phosphate acyltransferase	246	I		526.2	326.2	284.6			0	
SITYG_07310	-	745212	745854	putative glutamine amidotransferase	213	R		96.9	239.6	125.1			1	alive in vivo
SITYG_07320	-	746054	748061	putative dipeptidase	668	E	LPXTG	90.9	1335.8	230.2			1	alive in vivo
SITYG_07330	-	748599	748728	hypothetical protein	42			192.9	0.0	155.7			0	
SITYG_07340	-	748823	749525	CAAX amino terminal protease	233	R		537.7	344.3	486.4			1	alive in vivo
SITYG_07350	*nrdF*	749651	750611	ribonucleotide-diphosphate reductase subunit beta	319	F		423.5	412.0	272.0			1	vivo-attenuated
SITYG_07360	-	750621	751008	hypothetical protein	128	S		653.8	340.7	467.1			0	
SITYG_07370	*nrdE*	751037	753197	ribonucleotide-diphosphate reductase subunit alpha	719	F		389.9	295.0	451.0			0	
SITYG_07380	-	753296	753515	glutaredoxin	72	O		2462.4	100.3	962.9			0	
SITYG_07390	-	753897	754161	phosphocarrier protein HPr	87	G		7762.1	1664.7	3879.9			0	
SITYG_07400	-	754162	755896	phosphoenolpyruvate-protein kinase	577	G		3141.0	849.1	2125.4			0	
SITYG_07410	-	755929	756055	hypothetical protein	41			32.9	0.0	0.0			0	
SITYG_07420	*uvrC*	756047	757856	excinuclease ABC subunit C	602	L		233.9	425.2	283.1			0	
SITYG_07430	-	757964	758570	putative nitroreductase	201	C		657.1	580.2	596.6			2	vivo-attenuated
SITYG_07440	*pepV*	758598	759999	dipeptidase PepV	466	E		701.7	533.3	802.8			0	
SITYG_07450	-	760230	760527	hypothetical protein	98	MG		97.8	813.9	371.9	4.1		1	alive in vivo
SITYG_07460	-	760623	760752	hypothetical protein	42			32.2	0.0	389.2	13.2	>389.2	0	
SITYG_07470	-	760761	761346	putative uracil DNA glycosylase	194	L		70.9	300.5	206.0	3.2		1	alive in vivo
SITYG_07480	-	761448	761901	putative MarR family transcriptional regulator	150	K		293.0	145.5	687.2			1	alive in vivo
SITYG_07490	-	761897	763430	putative ABC transporter	510	M		414.0	401.4	589.5			1	alive in vivo
SITYG_07500	-	763426	764146	putative ABC transporter, ATP-binding protein	239	E		363.0	427.3	320.8			1	vivo-attenuated
SITYG_07510	-	764747	766421	putative cell wall protein	557			86.7	301.9	299.9	3.8		0	
SITYG_07520	-	766858	767698	lysozyme M1	279	M		696.3	209.3	478.2			0	
SITYG_07530	-	767993	769226	cell division protein FtsW	410	D		397.0	427.7	325.8			0	
SITYG_07540	*ppc*	769264	771964	phosphoenolpyruvate carboxylase	899	C		417.9	447.6	479.8			1	alive in vivo
SITYG_07550	-	772089	772560	RNA polymerase sigma factor	156	K		26.4	140.0	191.9	7.9		0	
SITYG_07560	-	772546	773611	putative sigma factor regulator	354			77.9	577.7	424.3	5.9		1	alive in vivo
SITYG_07570	*tuf*	773734	774931	translation elongation factor EF-Tu	398	J		6518.6	1376.9	4286.9			0	
SITYG_07580	*tpiA*	775087	775846	triosephosphate isomerase	252	G		6104.8	723.8	3453.2			0	
SITYG_07590	-	775912	779668	hypothetical protein	1251	R		178.9	444.6	320.8			0	
SITYG_07600	-	779833	780685	putative CAAX amino terminal protease	283	R		1178.2	1521.7	1190.4			0	
SITYG_07610	-	780897	781143	putative transposase	81	L		16.9	357.3	326.6	21.1		0	
SITYG_07620	-	781281	782655	tRNA modification GTPase	457	R		338.1	431.8	365.4			1	vivo-attenuated
SITYG_07630	-	783014	783698	ribose 5-phosphate isomerase A	227	G		818.7	578.3	396.4			0	
SITYG_07640	-	783918	784728	purine nucleoside phosphorylase	269	F		399.5	434.1	359.5			0	
SITYG_07650	-	784855	785629	purine nucleoside phosphorylase	257	F		284.0	653.0	376.2			0	
SITYG_07660	-	785628	786384	putative histidine protein kinase	251			230.5	523.2	371.9			0	
SITYG_07670	-	786445	788620	putative phosphoglycerol transferase	724	M		825.8	394.0	687.9			0	
SITYG_07680	-	788821	790021	putative methyltransferase	399	R		522.0	531.1	468.6			0	
SITYG_07690	*aroD*	790017	790695	3-dehydroquinate dehydratase	225	E		110.1	64.8	74.1			0	

SITYG_07700	*aroE*	790684	791539	shikimate 5-dehydrogenase	284	E	184.4	154.2	176.2			0	
SITYG_07710	*aroB*	791549	792617	3-dehydroquinate synthase	355	E	337.9	473.2	413.7			1	alive in vivo
SITYG_07720	*aroC*	792650	793817	chorismate synthase	388	E	280.8	320.1	120.5			0	
SITYG_07730	-	793816	794653	putative transport protein	278	R	302.3	577.6	443.9			0	
SITYG_07740	-	794649	795030	hypothetical protein	126	S	261.3	634.4	263.6			0	
SITYG_07750	-	795040	796147	prephenate dehydrogenase	368	E	191.1	476.4	408.2			0	
SITYG_07760	-	796158	796497	hypothetical protein	112	S	232.5	194.5	118.5			2	vivo-attenuated
SITYG_07770	*aroA*	796937	798233	3-phosphoshikimate 1-carboxyvinyltransferase	431	E	371.3	610.4	612.1			0	
SITYG_07780	*aroK*	798225	798702	shikimate kinase	158	E	147.8	460.7	357.9			0	
SITYG_07790	*pheA*	798698	799532	prephenate dehydratase	277	E	184.0	474.3	590.0	3.5		0	
SITYG_07800	-	799544	800882	putative transcriptional attenuator	445	K	927.0	821.2	848.1			1	alive in vivo
SITYG_07810	-	800955	802326	RNA methyltransferase	456	J	111.9	336.6	271.0			0	
SITYG_07820	-	802643	803549	transcriptional regulator	301	K	91.6	824.7	199.5			0	
SITYG_07830	-	803678	805034	putative drug resistance transporter	451	GEPR	88.7	615.8	466.6	5.7		0	
SITYG_07840	-	805068	805512	hypothetical protein	147	S	84.1	346.4	45.2			0	
SITYG_07850	-	805606	806047	hypothetical protein	146		37.6	249.1	45.5			0	
SITYG_07860	-	806103	806961	putative oxidoreductase	285	R	48.3	332.9	117.0			0	
SITYG_07870	-	807127	807697	hypothetical protein	189	S	72.8	347.0	352.4	5.3		0	
SITYG_07880	-	807929	808736	putative alpha/beta hydrolase family protein	268	R	51.4	81.7	174.2	3.7		1	alive in vivo
SITYG_07890	-	808747	808876	putative ADP-ribosylglycohydrolase	42	O	64.3	681.4	1012.0	17.1		0	
SITYG_07900	-	809098	810625	ABC transporter, ATP-binding protein	508	V	73.3	460.5	197.3			2	alive in vivo
SITYG_07910	-	811527	812253	putative cyclase	241	V	40.0	302.7	276.6	7.5		0	
SITYG_07920	-	812252	812987	hypothetical protein	244		28.2	59.8	368.9	14.2	5.1	0	
SITYG_07930	-	813476	813845	hypothetical protein	122	O	123.7	476.4	81.6			0	
SITYG_07940	-	814034	814721	putative response regulator	228	TK	471.0	223.9	423.9			0	
SITYG_07950	-	814713	816057	hypothetical protein	447	T	271.6	392.4	269.0			1	alive in vivo
SITYG_07960	-	816335	817015	-		V	79.3	387.8	162.4			0	
SITYG_07970	-	817016	817745	hypothetical protein	242		45.5	150.7	399.5	9.6		1	alive in vivo
SITYG_07980	-	817731	818379	hypothetical protein	215		6.4	305.2	124.0	21.1		0	
SITYG_07990	-	818710	819049	hypothetical protein	112		24.5	194.5	148.1	6.6		0	
SITYG_08000	-	819033	819153	hypothetical protein	39		0.0	0.0	0.0			0	
SITYG_08010	-	819536	819671	hypothetical protein	44	K	0.0	0.0	0.0			0	
SITYG_08020	-	819669	819933	hypothetical protein	87	C	0.0	0.0	152.2	>152.2	>152.2	0	
SITYG_08030	-	820398	821094	glycosyltransferase	231	M	1281.4	947.2	1269.7			0	
SITYG_08040	-	821101	821443	hypothetical protein	113		133.4	64.3	0.0	<-133.4		1	alive in vivo
SITYG_08050	-	821426	822710	polysaccharide biosynthesis protein	427	R	646.1	462.1	531.8			0	
SITYG_08060	-	822699	823695	putative glycosyl transferase	331	M	962.1	330.9	806.6			1	alive in vivo
SITYG_08070	-	823738	825283	putative membrane protein	514	S	534.3	369.8	292.5			0	
SITYG_08080	-	825308	825959	calcium-binding protein	216		1013.1	303.8	956.4			0	
SITYG_08090	-	826060	826987	putative glycosyl transferase	308	M	590.7	308.2	736.6			1	alive in vivo
SITYG_08100	-	827060	827912	hypothetical protein	283	M	1124.7	180.5	1025.4			0	
SITYG_08110	*rgpA*	828014	829163	putative glycosyl transferase	382	M	942.3	286.9	690.4			0	
SITYG_08120	*rgpB*	829159	830095	putative glycosyl transferase	311	M	580.6	305.2	515.0			0	
SITYG_08130	*rgpC*	830097	830904	ABC-2 type transporter	268	GM	945.8	708.0	709.3			0	
SITYG_08140	-	830903	832124	ABC transporter, ATP-binding protein	406	GM	604.7	521.9	534.6			0	
SITYG_08150	-	832149	833901	putative glycosyltransferase	583	M	707.9	627.1	521.6			1	vivo-attenuated
SITYG_08160	-	833897	835658	putative rhamnan synthesis protein F	586	M	803.3	262.0	741.3			0	
SITYG_08170	-	835771	838230	-		M	158.6	205.5	130.7			2	alive in vivo
SITYG_08180	-	838410	839100	SAM-dependent methyltransferase	229	R	553.1	414.0	392.9			1	alive in vivo
SITYG_08190	-	839086	839884	hypothetical protein	265	S	285.9	716.0	339.8			2	vivo-attenuated
SITYG_08200	-	839969	840440	putative phosphohydrolase	156	LR	378.7	513.2	916.8			1	alive in vivo
SITYG_08210	*rmlA*	840580	841450	glucose-1-phosphate thymidylyltransferase	289	M	1659.3	732.5	1581.3			0	
SITYG_08220	-	841453	842047	putative dTDP-4-dehydrorhamnose 3,5-epimerase	197	M	761.2	406.9	591.7			0	
SITYG_08230	-	842080	843127	dTDP-glucose 4,6-dehydratase	348	M	903.3	440.8	815.3			0	
SITYG_08240	-	843161	844181	UDP-glucose 4-epimerase	339	M	1545.4	797.1	1634.3			1	vivo-attenuated
SITYG_08250	-	844499	845081	putative methyltransferase	193	QR	156.8	490.8	138.0			4	vivo-attenuated
SITYG_08260	*pepQ*	845347	846430	putative proline dipeptidase	360	E	425.2	547.8	278.2			2	vivo-attenuated
SITYG_08270	*ccpA*	846693	847698	catabolite control protein A	334	K	1155.7	393.6	999.2			0	
SITYG_08280	-	847772	848789	putative glycosyl transferase	338	M	770.9	777.9	849.2			1	alive in vivo
SITYG_08290	-	848790	850104	glycosyltransferase	437	M	334.6	434.8	366.8			0	
SITYG_08300	-	850130	850472	hypothetical protein	113		315.4	321.3	411.1			1	alive in vivo
SITYG_08310	-	850770	851472	putative response transcriptional regulator	233	TK	555.5	532.1	586.5			0	
SITYG_08320	-	851464	852817	putative histidine sensory kinase	450	T	604.0	487.2	764.5			4	vivo-attenuated
SITYG_08330	*vicX*	852818	853622	zinc-dependent hydrolase	267	R	660.4	246.0	711.9			0	
SITYG_08340	-	853630	853990	hypothetical protein	119	S	172.8	0.0	27.9	-5.7		0	
SITYG_08350	-	854378	855077	ribonuclease III	232	K	255.2	157.2	244.2			1	alive in vivo
SITYG_08360	*smc*	855067	858601	structural maintenance of chromosomes protein	1177	D	476.6	466.4	568.3			0	
SITYG_08370	-	858602	859397	HAD hydrolase, IIB family protein	264	R	537.4	525.2	656.8			2	alive in vivo
SITYG_08380	-	859396	860209	putative hydrolase	270	R	326.5	324.3	741.1			1	vivo-attenuated
SITYG_08390	*ftsY*	860221	861691	cell division protein	489	U	1021.5	792.3	724.1			0	
SITYG_08400	-	861757	862189	hypothetical protein	143		1546.0	1169.9	1162.3			1	alive in vivo
SITYG_08410	*ppdK*	862389	864999	pyruvate phosphate dikinase	869	G	42.9	235.7	103.9			1	alive in vivo
SITYG_08420	-	865179	865809	hypothetical protein	209	R	131.7	34.9	15.9	-7.6		0	
SITYG_08430	-	865821	866646	hypothetical protein	274	S	120.7	319.6	426.0	3.8		3	vivo-attenuated
SITYG_08440	-	866681	868604	firmicute fructose-1,6-bisphosphatase	640	G	161.8	422.8	323.8			4	vivo-attenuated
SITYG_08450	-	868727	869870	putative cysteine desulfurase	380	E	225.0	211.5	228.4			4	vivo-attenuated
SITYG_08460	*thiI*	869873	871088	thiamine biosynthesis protein	404	H	273.1	307.5	264.5			1	alive in vivo
SITYG_08470	-	871109	871631	hypothetical protein	173	O	333.8	505.2	673.3			2	alive in vivo
SITYG_08480	*rplU*	871849	872164	50S ribosomal protein L21	104	J	7282.3	558.1	3666.1			0	
SITYG_08490	-	872180	872525	hypothetical protein	114	J	14007.6	955.4	8673.9			0	
SITYG_08500	*rpmA*	872542	872836	50S ribosomal protein L27	97	J	10187.0	373.7	5943.2			0	
SITYG_08510	-	873350	875006	NAD(FAD)-dependent dehydrogenase	551	R	155.3	451.2	212.2			3	alive in vivo
SITYG_08520	-	875101	875284	hypothetical protein	60	P	22.7	120.1	0.0			0	
SITYG_08530	-	875416	875905	hypothetical protein	162	S	644.7	1977.3	1252.7			1	alive in vivo
SITYG_08540	-	876470	877325	hypothetical protein	284	R	116.4	179.9	328.9	3.1		2	vivo-attenuated
SITYG_08550	-	877461	878370	transcriptional regulator	302	K	1268.6	797.8	1115.8			0	
SITYG_08560	*lspA*	878366	878840	putative signal peptidase II	157	MU	927.7	695.4	699.1			0	
SITYG_08570	*rluD*	878817	879714	23S rRNA pseudouridine synthase	298	J	323.7	416.5	212.7			0	
SITYG_08580	-	879861	880203	glutamate 5-kinase	113	E	121.3	449.8	58.7			0	
SITYG_08590	-	880247	881216	hypothetical protein	322	R	154.1	498.9	310.9			0	
SITYG_08600	*phnA*	881300	881642	PhnA protein	113	P	2001.3	128.5	1086.4			1	alive in vivo
SITYG_08610	-	881649	882285	hypothetical protein	211		156.5	380.1	284.2			0	
SITYG_08620	-	882482	882941	hypothetical protein	152		81.3	383.0	284.4	3.8		3	vivo-attenuated
SITYG_08630	-	882971	883325	hypothetical protein	117		140.6	620.8	340.4			1	alive in vivo
SITYG_08640	-	883363	883627	chorismate mutase	87	E	691.4	416.2	722.7			0	
SITYG_08650	-	883642	884860	putative permease, chloride channel	405	P	214.6	523.2	494.7			0	
SITYG_08660	*thyA*	884945	885785	thymidylate synthase	279	F	775.3	235.4	693.4			0	
SITYG_08670	-	885787	886003	hypothetical protein	71		153.6	406.9	46.5	-3.0	-10.5	0	
SITYG_08680	-	886069	886582	dihydrofolate reductase	170	H	3646.8	1028.1	2427.3			0	
SITYG_08690	-	886581	886755	hypothetical protein	57		262.2	0.0	865.7	3.6	>865.7	0	
SITYG_08700	*clpX*	886808	888041	ATP-dependent Clp protease, ATP-binding subunit ClpX	410	O	440.7	196.0	390.9			1	alive in vivo
SITYG_08710	-	888053	888641	putative ribosome biogenesis GTP-binding protein YsxC	195	R	910.1	411.1	956.4			0	
SITYG_08720	-	888763	889471	putative autolysin/N-acetylmuramidase	235	NU	1997.9	434.5	1588.6			0	
SITYG_08730	-	889640	890444	formate-nitrate transporter	267	P	87.7	382.6	162.4			0	
SITYG_08740	-	890640	892398	putative ABC transporter, ATP-binding protein	585	V	108.5	987.5	228.5			3	alive in vivo
SITYG_08750	-	892387	894136	putative multidrug ABC transporter permease/ATPase	582	V	125.7	490.0	241.1			0	
SITYG_08760	-	894254	895790	putative ABC transporter ATPase	511	R	124.2	643.8	804.1	7.0		2	vivo-attenuated
SITYG_08770	-	896164	896905	ABC transporter, ATP-binding protein	246	E	481.4	415.2	487.9			0	
SITYG_08780	-	896904	899082	ABC transporter, permease protein	725	ET	596.1	292.6	516.4			3	alive in vivo
SITYG_08790	*uvrB*	899697	901686	excinuclease ABC subunit B	662	L	173.1	408.8	434.2			0	
SITYG_08800	-	901791	902568	hypothetical protein	258		165.5	141.4	542.8	3.6	3.2	0	
SITYG_08810	-	902599	903097	GNAT family acetyltransferase	165	KR	216.6	353.0	60.5	-3.3	-7.0	0	
SITYG_08820	-	903132	903684	hypothetical protein	183	S	172.8	238.9	36.4	-4.4	-7.9	0	
SITYG_08830	-	903786	904917	coproporphyrinogen III oxidase	376	H	447.5	446.9	426.2			0	
SITYG_08840	-	904920	905661	acyl-ACP thioesterase	246	I	302.3	474.5	338.8			1	alive in vivo
SITYG_08850	-	905647	906274	putative ADP-ribose pyrophosphatase	208	F	628.5	630.9	848.8			1	alive in vivo
SITYG_08860	-	906356	907130	putative hydrolase	257	G	455.5	653.0	454.1			1	alive in vivo
SITYG_08870	-	907119	907758	putative membrane protein	212	S	590.7	790.9	314.3			1	alive in vivo
SITYG_08880	-	907757	908708	hypothetical protein	316	R	458.0	600.8	612.4			1	vivo-attenuated
SITYG_08890	*ndk*	908785	909205	nucleoside diphosphate kinase	139	F	148.1	418.6	191.3			0	
SITYG_08900	-	909357	910248	hypothetical protein	296	R	363.1	320.6	225.4			0	
SITYG_08910	-	910244	911225	hypothetical protein	326	S	355.2	403.2	286.6			0	
SITYG_08920	-	911221	912133	hypothetical protein	303	S	204.7	481.9	352.4			0	
SITYG_08930	*inlA*	912349	914845	putative internalin A precursor	831		226.0	246.5	169.0			7	vivo-attenuated
SITYG_08940	*pyrR*	915077	915599	pyrimidine regulatory protein PyrR	173	F	715.2	378.9	750.3			2	vivo-attenuated
SITYG_08950	*pyrP*	915603	916872	xanthinge/uracil permease	422	F	212.5	450.2	553.9			4	alive in vivo
SITYG_08960	*pyrB*	916933	917854	aspartate carbamoyltransferase	306	F	373.8	214.7	479.7			0	
SITYG_08970	-	917896	918985	carbamoyl-phosphate synthase small subunit	362	EF	323.8	262.3	405.7			1	alive in vivo
SITYG_08980	*carB*	919165	922345	carbamoyl phosphate synthase large subunit	1059	EF	152.6	428.4	378.9			0	

SITYG_08990	-	922440	923400	glucokinase	319	KG	1447.5	961.4	1380.8			0	
SITYG_09000	*rplS*	923549	923897	50S ribosomal protein L19	115	J	1406.6	189.4	606.0			0	
SITYG_09010	-	924280	925135	putative DNA adenine methylase	284	L	480.3	411.2	434.6			2	vivo-attenuated
SITYG_09020	-	925138	926449	hypothetical protein	436		329.1	167.6	444.3			2	alive in vivo
SITYG_09030	-	926821	926989	hypothetical protein	55	H	24.7	130.8	59.8			0	
SITYG_09040	-	927411	927573	hypothetical protein	53		25.6	406.9	0.0			0	
SITYG_09050	-	927790	927916	hypothetical protein	41		131.7	523.2	79.7			0	
SITYG_09060	-	927932	928109	integrase	58	L	70.3	124.2	0.0			2	alive in vivo
SITYG_09070	-	928367	929108	putative alpha/beta hydrolase	246		16.8	296.6	27.1			0	
SITYG_09080	-	929406	929850	hypothetical protein	147		1401.4	346.4	655.9			0	
SITYG_09090	*ciaR*	930111	930786	two-component response transcriptional regulator	224	TK	878.8	293.0	1011.6			0	
SITYG_09100	*ciaH*	930775	932122	putative sensor histidine kinase	448	T	535.8	375.2	402.6			4	vivo-attenuated
SITYG_09110	*amy*	932397	933846	cytoplasmic alpha-amylase	482	G	111.6	409.5	187.1			2	alive in vivo
SITYG_09120	*flaR*	934215	934725	topology modulation protein	169	F	97.6	344.7	177.2			1	alive in vivo
SITYG_09130	*rpsT*	934789	935026	30S ribosomal protein S20	78	J	2327.9	0.0	1949.1			0	
SITYG_09140	*coaA*	935094	936015	pantothenate kinase	306	H	85.6	71.6	21.8	-3.6	-3.9	0	
SITYG_09150	-	936116	936701	ribosomal RNA small subunit methyltransferase C	194	J	241.1	450.8	566.5			0	
SITYG_09160	*pdp*	936697	937975	pyrimidine-nucleoside phosphorylase	425	F	162.3	292.3	322.2			0	
SITYG_09170	*deoC*	937993	938656	deoxyribose-phosphate aldolase	220	F	1989.6	1325.8	1332.9			0	
SITYG_09180	-	938642	939032	cytidine deaminase	129	F	574.4	450.8	463.5			0	
SITYG_09190	-	939103	940159	putative lipoprotein	351	R	3272.2	1290.2	2215.7			0	
SITYG_09200	-	940288	941824	ABC transporter, ATP-binding protein	511	R	734.6	643.8	830.3			0	
SITYG_09210	-	941816	942881	putative ABC transporter, permease protein	354	R	331.1	639.6	471.5			0	
SITYG_09220	-	942882	943839	putative ABC transporter, permease protein	318	R	1339.4	574.1	1280.2			0	
SITYG_09230	-	943949	944597	hemolysin III-like membrane protein	215	R	1882.0	610.4	1456.7			1	alive in vivo
SITYG_09240	-	944580	945039	hypothetical protein	152		1699.0	335.1	1400.2			0	
SITYG_09250	-	945152	945878	hypothetical protein	241	S	257.1	363.2	166.0			0	
SITYG_09260	-	945927	946479	hypothetical protein	183	R	285.6	199.0	436.6			0	
SITYG_09270	-	946545	946992	transcriptional regulator	148	K	111.4	147.5	134.8			0	
SITYG_09280	-	947139	947565	hypothetical protein	141	S	973.7	515.8	495.0			0	
SITYG_09290	-	947561	948743	aspartate aminotransferase	393	E	494.8	539.1	577.7			3	vivo-attenuated
SITYG_09300	-	948742	949101	-		E	762.6	367.3	811.2			2	alive in vivo
SITYG_09310	-	949084	950476	asparaginyl-tRNA synthetase	463	J	1192.0	457.8	800.8			7	vivo-attenuated
SITYG_09320	*pmrB*	950587	951787	putative transport protein	399	GEPR	131.4	402.9	393.3	3.3		3	vivo-attenuated
SITYG_09330	-	952006	952732	-		ER	154.3	363.2	207.5			1	alive in vivo
SITYG_09340	-	953124	953577	hypothetical protein	150	S	796.7	291.1	532.0			0	
SITYG_09350	-	953679	954222	hypothetical protein	180	Q	5454.5	445.2	3384.3			0	
SITYG_09360	*eno*	954588	955893	enolase	434	G	5238.5	2643.7	3070.3			0	
SITYG_09370	-	955970	956714	NAD-dependent deacetylase	247	K	200.7	443.0	566.9	3.1		0	
SITYG_09380	-	956866	957544	putative satD protein	225		183.5	291.7	370.3			0	
SITYG_09390	-	957536	958268	putative satE protein	243		334.3	150.1	397.8			0	
SITYG_09400	-	958526	959372	hypothetical protein	281	S	858.1	441.6	569.8			0	
SITYG_09410	-	959504	960089	putative transcriptional regulator	194	K	78.0	112.7	51.5			0	
SITYG_09420	-	960078	960573	putative deoxycytidylate deaminase	164	F	108.9	133.2	243.4			0	
SITYG_09430	-	960620	961238	hypothetical protein	205	R	483.3	888.9	910.0			1	alive in vivo
SITYG_09440	-	961414	961531	hypothetical protein	38		0.0	0.0	0.0			0	
SITYG_09450	-	961661	962309	putative glycerol-3-phosphate acyltransferase	215	S	1325.1	542.6	1177.8			1	alive in vivo
SITYG_09460	*parE*	962481	964425	DNA topoisomerase IV, B subunit	647	L	529.2	395.6	413.3			0	
SITYG_09470	-	964443	965271	hypothetical protein	275		135.3	159.2	133.4			1	alive in vivo
SITYG_09480	-	965467	966202	hypothetical protein	244		570.0	119.6	423.5			0	
SITYG_09490	-	966221	967043	putative streptomycin adenylyltransferase	273		247.3	240.6	256.5			2	alive in vivo
SITYG_09500	-	967017	967131	hypothetical protein	37		109.2	192.8	0.0	<-109.2	<-192.8	0	
SITYG_09510	*parC*	967430	969869	DNA topoisomerase IV subunit A	812	L	472.8	378.4	732.9			0	
SITYG_09520	-	970012	971032	branched-chain amino acid aminotransferase	339	EH	97.6	150.8	98.5			0	
SITYG_09530	-	971135	971366	hypothetical protein	76		1382.7	95.1	869.4			0	
SITYG_09540	*rpsA*	971774	972974	30S ribosomal protein S1	399	J	2945.2	311.3	1590.0			1	vivo-attenuated
SITYG_09550	-	973252	973612	hypothetical protein	119	LR	357.2	305.2	278.9			0	
SITYG_09560	-	973744	974764	L-lactate dehydrogenase	339	C	1338.0	366.2	620.2			0	
SITYG_09570	*gyrA*	974926	977374	DNA gyrase subunit A	815	L	781.2	386.0	598.9			0	
SITYG_09580	*srtA*	977394	978138	sortase A	247	M	457.2	472.6	377.9			0	
SITYG_09590	-	978197	979541	pyridine nucleotide-disulfide oxidoreductase	447	C	756.2	490.5	597.7			0	
SITYG_09600	-	979757	980135	large conductance mechanosensitive channel protein	125	M	3138.6	348.8	1594.0			0	
SITYG_09610	*dnaG*	980295	982071	DNA primase	591	L	1076.7	284.6	644.6			0	
SITYG_09620	*rpoD*	982073	983186	RNA polymerase sigma factor RpoD	370	K	1237.4	335.6	821.0			0	
SITYG_09630	-	983203	983533	hypothetical protein	109	R	1433.0	199.8	1186.8			0	
SITYG_09640	-	983683	985012	branched-chain amino acid transport system II carrier protein	442	E	162.3	281.1	219.1			2	vivo-attenuated
SITYG_09650	-	985152	985863	cytochrome C-type biogenesis protein	236	O	40.8	432.7	155.4	4.1	-3.3	0	
SITYG_09660	-	985879	986464	thiol-disulfide oxidoreductase	194	OC	56.7	413.2	51.5			1	alive in vivo
SITYG_09670	-	986476	987586	putative peptide methionine sulfoxide reductase	369	O	71.0	415.7	72.4			1	alive in vivo
SITYG_09680	-	987643	988378	putative two-component response transcriptional regulator	244	T	237.0	418.6	382.6			0	
SITYG_09690	-	988374	990084	putative histidine kinase	569	T	169.8	385.5	252.5			2	vivo-attenuated
SITYG_09700	-	990111	990891	putative ABC transporter permease	259	R	95.7	309.9	218.9			6	vivo-attenuated
SITYG_09710	-	990893	991673	putative ABC transporter permease	259	R	164.9	535.3	553.6	3.7		1	alive in vivo
SITYG_09720	-	991665	992649	ABC transporter, ATP-binding protein	327	R	118.0	357.3	173.5			1	alive in vivo
SITYG_09730	-	992798	994043	oxidoreductase	414	R	223.2	476.6	290.4			2	vivo-attenuated
SITYG_09740	-	994058	994667	flavin reductase	202	R	149.9	288.7	263.8			1	alive in vivo
SITYG_09750	-	994686	995616	thiamine biosynthesis	309	H	240.9	496.2	388.7			1	alive in vivo
SITYG_09760	-	995913	997287	NADH oxidase	457	R	256.6	207.9	372.7			2	alive in vivo
SITYG_09770	-	997427	998987	voltage-gated chloride channel family protein	519	P	186.1	493.0	392.7			3	alive in vivo
SITYG_09780	-	999100	999877	hypothetical protein	258		160.2	311.1	232.6			0	
SITYG_09790	-	999876	1001061	hypothetical protein	394		259.0	482.1	449.1			1	alive in vivo
SITYG_09800	-	1001441	1002425	guanosine monophosphate reductase	327	F	307.7	178.7	255.1			0	
SITYG_09810	-	1002612	1003194	xanthine phosphoribosyltransferase	193	F	92.7	264.3	362.3	4.3		0	
SITYG_09820	-	1003193	1004459	xanthine permease	421	F	91.7	399.2	214.2			2	alive in vivo
SITYG_09830	-	1004556	1005894	matE efflux family protein	445	V	136.4	377.7	525.4	4.2		0	
SITYG_09840	-	1005970	1006153	4-oxalocrotonate tautomerase	60	R	181.3	360.2	1097.5	6.6		0	
SITYG_09850	*tdk*	1006275	1006881	thymidine kinase	201	F	492.9	580.2	447.4			0	
SITYG_09860	*prfA*	1006877	1007957	peptide chain release factor 1	359	J	541.6	284.9	455.6			0	
SITYG_09870	*hemK*	1007956	1008787	HemK protein	276	J	414.3	396.7	386.7			1	alive in vivo
SITYG_09880	-	1008779	1009382	putative tranlsation factor	200	J	557.2	364.4	549.6			1	alive in vivo
SITYG_09890	*glyA*	1009388	1010675	serine hydroxymethyltransferase	428	E	222.4	239.0	234.1			0	
SITYG_09900	-	1010676	1011651	hypothetical protein	324		234.0	563.5	206.0			1	vivo-attenuated
SITYG_09910	-	1011654	1012257	putative PvaA-like protein	200	M	316.4	291.5	333.1			0	
SITYG_09920	-	1012368	1013217	hydrolase	282	R	1895.7	258.8	1277.4			1	vivo-attenuated
SITYG_09930	*guaA*	1013544	1015104	GntR family transcriptional regulator	519	F	406.8	295.8	405.5			0	
SITYG_09940	-	1015245	1015944	hypothetical protein	232	K	290.8	125.7	215.5			0	
SITYG_09950	-	1016059	1016392	hypothetical protein	110	S	759.9	264.0	542.8			3	vivo-attenuated
SITYG_09960	*ffh*	1016452	1018027	signal recognition particle protein	524	U	553.1	306.9	497.3			0	
SITYG_09970	-	1018222	1019293	tyrosine recombinase XerC	356	L	263.4	615.5	346.9			1	vivo-attenuated
SITYG_09980	-	1019785	1020946	hypothetical protein	386		35.7	151.4	224.9	6.9		1	alive in vivo
SITYG_09990	-	1020973	1021714	putative esterase	246	S	56.0	207.6	176.2	3.4		1	alive in vivo
SITYG_10000	-	1021732	1022581	putative esterase	282	R	122.1	465.9	260.2			0	
SITYG_10010	-	1022663	1023998	tRNA:M(5)U-54 methyltransferase	444	J	186.4	329.2	293.4			0	
SITYG_10020	-	1024091	1024586	phosphoribosylanthranilate isomerase	164		259.8	177.6	101.4			0	
SITYG_10030	*topA*	1024644	1026729	DNA topoisomerase I	694	L	266.6	295.1	399.8			0	
SITYG_10040	-	1026823	1027666	DNA protecting protein DprA	280	LU	78.7	338.9	119.1			0	
SITYG_10050	-	1027780	1027927	hypothetical protein	48		0.0	0.0	0.0			0	
SITYG_10060	-	1027923	1028079	hypothetical protein	51		319.1	422.6	450.6			1	alive in vivo
SITYG_10070	-	1028513	1029203	hypothetical protein	229		156.3	318.5	262.0			0	
SITYG_10080	-	1029248	1029599	hypothetical protein	116		23.6	187.8	0.0			0	
SITYG_10090	-	1029883	1030216	hypothetical protein	110		99.7	132.0	542.8	5.9	3.4	0	
SITYG_10100	-	1030218	1030944	hypothetical protein	241		68.6	60.5	138.3			2	alive in vivo
SITYG_10110	-	1030989	1031300	-			26.7	212.0	193.7	7.9		0	
SITYG_10120	-	1031535	1031718	hypothetical protein	60		22.7	0.0	54.9			1	alive in vivo
SITYG_10130	-	1031807	1032359	hypothetical protein	183		30.1	159.2	54.6			1	alive in vivo
SITYG_10140	-	1032404	1032761	hypothetical protein	118		58.1	184.7	56.3			1	alive in vivo
SITYG_10150	-	1032779	1033127	hypothetical protein	115		95.4	252.6	230.9			0	
SITYG_10160	-	1033113	1033278	hypothetical protein	54		0.0	0.0	121.7	>121.7	>121.7	0	
SITYG_10170	-	1033401	1033533	hypothetical protein	43		188.6	832.4	152.2			0	
SITYG_10180	-	1033545	1033896	hypothetical protein	116		354.5	313.0	143.0			0	
SITYG_10190	-	1033916	1034267	hypothetical protein	116		330.9	438.2	886.9			1	alive in vivo
SITYG_10200	-	1034545	1034704	hypothetical protein	52		234.8	1105.6	189.5			1	alive in vivo
SITYG_10210	-	1034870	1035200	hypothetical protein	109		150.8	466.1	334.7			0	
SITYG_10220	-	1035203	1035539	hypothetical protein	111		271.6	65.4	119.5			1	alive in vivo
SITYG_10230	-	1035539	1035692	hypothetical protein	50		108.4	287.3	131.3			0	
SITYG_10240	-	1035846	1036176	hypothetical protein	109		339.4	133.2	334.7			0	
SITYG_10250	-	1036172	1036724	hypothetical protein	183	S	443.4	398.1	454.8			0	
SITYG_10260	-	1036910	1037261	hypothetical protein	116		496.4	125.2	343.3			1	alive in vivo
SITYG_10270	-	1037280	1037631	hypothetical protein	116		165.5	250.4	200.3			0	

SITYG_10280	-	1037617	1039666	hypothetical protein	682			477.8	450.4	485.2			3	alive in vivo
SITYG_10290	-	1039649	1040297	hypothetical protein	215			531.3	406.9	418.4			1	alive in vivo
SITYG_10300	-	1040365	1040656	hypothetical protein	96			1126.1	151.0	931.7			0	
SITYG_10310	-	1040670	1041078	hypothetical protein	135	O		630.4	269.3	541.5			0	
SITYG_10320	-	1041186	1041954	ribonuclease HII	255	L		237.7	372.0	209.2			2	alive in vivo
SITYG_10330	-	1041940	1042792	ribosome biogenesis GTP-binding protein YlqF	283	R		467.4	515.8	400.7			0	
SITYG_10340	*rpsU*	1043196	1043373	30S ribosomal protein S21	58	J		1101.5	124.2	794.3			1	vivo-attenuated
SITYG_10350	-	1043521	1043860	putative ribonucleotide reductase	112			1272.6	194.5	977.5			0	
SITYG_10360	-	1044108	1046397	putative cell wall anchor protein	762	D	LPXTG	592.6	460.8	583.5			0	
SITYG_10370	-	1046631	1047903	putative transcriptional regulator	423	KE		150.0	328.2	276.3			0	
SITYG_10380	-	1047932	1049675	ABC transporter, ATP-binding protein	580	V		152.3	416.0	236.2			2	vivo-attenuated
SITYG_10390	-	1049674	1051417	ABC transporter, permease/ATP-binding protein	580	V		169.0	327.8	190.1			1	alive in vivo
SITYG_10400	-	1051512	1052184	hypothetical protein	223	S		253.1	425.1	254.0			0	
SITYG_10410	*cutC*	1052196	1052829	copper homeostasis protein CutC	210	P		347.3	416.6	618.7			0	
SITYG_10420	-	1052884	1053738	-		M		97.1	360.2	352.8	4.0		0	
SITYG_10430	-	1053880	1054405	hypothetical protein	174			31.6	251.1	57.4			4	vivo-attenuated
SITYG_10440	-	1054443	1054953	putative transcriptional regulator	169	R		276.5	344.7	590.7			0	
SITYG_10450	-	1055011	1055251	RNA-binding protein	79	R		414.8	91.6	251.0			0	
SITYG_10460	*rpsP*	1055269	1055542	30S ribosomal protein S16	90	J		10195.7	80.5	5112.9			0	
SITYG_10470	-	1055658	1057962	pullulanase	767	G		507.7	648.6	710.4			0	
SITYG_10480	-	1057972	1058932	lipid kinase	319	IR		358.6	343.4	334.7			2	vivo-attenuated
SITYG_10490	*ligA*	1058940	1060899	NAD-dependent DNA ligase	652	L		228.7	302.9	405.0			0	
SITYG_10500	-	1061203	1062151	2-dehydropantoate 2-reductase	315	H		1479.0	602.7	1313.5			0	
SITYG_10510	-	1062175	1063225	putative membrane protein, putative toxin regulator	349	R		158.0	272.1	325.2			1	alive in vivo
SITYG_10520	-	1063281	1063791	putative transporter	169	S		593.8	430.9	413.5			0	
SITYG_10530	-	1063926	1064370	GtrA family protein	147	S		65.4	247.5	248.8	4.1		0	
SITYG_10540	-	1065110	1065818	hypothetical protein	235	S		298.8	527.6	638.3			2	vivo-attenuated
SITYG_10550	-	1065828	1066278	transcriptional regulator	149	K		110.6	390.7	133.9			0	
SITYG_10560	-	1066347	1067256	putative ribonuclease BN	302	S		146.0	217.6	563.4	4.2		4	vivo-attenuated
SITYG_10570	*map*	1067306	1068164	methionine aminopeptidase	285	J		1087.8	717.1	1439.6			0	
SITYG_10580	-	1068188	1069466	hypothetical protein	425	K		240.2	240.7	157.2			0	
SITYG_10590	-	1069458	1070010	acetyltransferase	183	J		864.2	318.5	654.9			2	vivo-attenuated
SITYG_10600	-	1070088	1071348	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	419	M		859.3	366.2	733.2			7	vivo-attenuated
SITYG_10610	*metK*	1071683	1072874	S-adenosylmethionine synthetase	396	H		365.7	627.3	489.0			0	
SITYG_10620	*pyrC*	1073139	1074414	dihydroorotase	424	F		211.5	224.1	307.2			1	vivo-attenuated
SITYG_10630	*mutX*	1074425	1074896	mutator mutT protein	156	LR		660.5	513.2	298.5			0	
SITYG_10640	*ung*	1074922	1075576	uracil-DNA glycosylase	217	L		380.6	302.4	276.4			0	
SITYG_10650	-	1075600	1076587	oxidoreductase, NAD-binding domain protein	328	R		479.1	334.0	468.0			0	
SITYG_10660	-	1077026	1077740	hypothetical protein	237	S		2318.1	338.5	2700.4			0	
SITYG_10670	-	1077817	1080052	competence protein	744	R		52.0	383.5	260.6	5.5		2	vivo-attenuated
SITYG_10680	-	1080035	1080740	competence protein ComEA	234	L		17.7	187.0	71.2	4.4	-3.1	0	
SITYG_10690	-	1080711	1080834	hypothetical protein	40			0.0	0.0	0.0			0	
SITYG_10700	*smpB*	1080907	1081375	SsrA-binding protein	155	O		647.0	93.9	643.7			0	
SITYG_10710	*vacB*	1081337	1083677	ribonuclease R	779	K		489.3	422.6	484.9			5	vivo-attenuated
SITYG_10720	*secG*	1083767	1084001	putative preprotein translocase subunit SecG	77	U		620.5	93.9	386.2			0	
SITYG_10730	-	1084050	1084179	hypothetical protein	42			32.2	0.0	0.0			1	alive in vivo
SITYG_10740	-	1084409	1085717	hypothetical protein	435			101.5	252.0	307.1	3.3		2	vivo-attenuated
SITYG_10750	-	1085857	1086190	hypothetical protein	110			224.2	461.9	422.2			1	alive in vivo
SITYG_10760	-	1086205	1086457	hypothetical protein	83			197.5	348.8	358.6			0	
SITYG_10770	-	1086524	1087343	hypothetical protein	272	D		136.8	1100.1	355.6			1	alive in vivo
SITYG_10780	-	1087535	1088120	hypothetical protein	194			99.3	488.3	120.2			1	vivo-attenuated
SITYG_10790	-	1088143	1089472	hypothetical protein	442	NU		87.4	463.0	272.0	3.4		1	alive in vivo
SITYG_10800	-	1089487	1089760	hypothetical protein	90			15.2	161.0	36.8			1	alive in vivo
SITYG_10810	-	1089790	1090348	hypothetical protein	185			74.3	630.1	323.9	4.7		1	alive in vivo
SITYG_10820	-	1090359	1092309	hypothetical protein	649			42.5	304.3	159.6	4.1		5	alive in vivo
SITYG_10830	-	1092320	1092971	hypothetical protein	216			31.9	270.0	77.1			2	vivo-attenuated
SITYG_10840	-	1092970	1093279	hypothetical protein	102			120.8	497.8	162.5			0	
SITYG_10850	-	1093443	1093725	hypothetical protein	93	L		0.0	155.8	71.2			0	
SITYG_10860	-	1093729	1095859	putative membrane protein	709	U		70.1	484.9	386.6	6.0		1	alive in vivo
SITYG_10870	-	1095975	1096461	hypothetical protein	161			1246.2	316.5	640.5			0	
SITYG_10880	-	1096585	1099735	putative conjugal transfer protein TraG	1049			101.4	690.6	325.2	3.5		7	vivo-attenuated
SITYG_10890	-	1099718	1099982	hypothetical protein	87			31.4	249.7	38.0			0	
SITYG_10900	-	1100243	1100666	putative single-stranded DNA-binding protein	140	L		49.0	103.9	308.6	6.8		0	
SITYG_10910	-	1100667	1102869	putative glucan-binding protein	733		LPXTG	96.1	299.4	337.5	3.8		7	vivo-attenuated
SITYG_10920	-	1102894	1103671	putative cell wall anchor protein	258		LPXTG	69.4	254.5	142.2			3	vivo-attenuated
SITYG_10930	-	1103689	1104757	hypothetical protein	355			66.0	267.5	94.0			0	
SITYG_10940	-	1104770	1105118	hypothetical protein	115			357.6	568.3	259.7			1	alive in vivo
SITYG_10950	-	1105218	1107054	putative ATP-dependent Clp protease ATP-binding protein	611	O		81.3	825.8	235.2	3.1	-4.2	0	
SITYG_10960	-	1107050	1108805	DNA topoisomerase	584	L		118.2	450.8	354.8	3.3		5	vivo-attenuated
SITYG_10970	-	1108804	1108945	hypothetical protein	46			0.0	155.8	71.2			0	
SITYG_10980	-	1108915	1113055	hypothetical protein	1379			82.2	504.2	553.0	7.3		8	vivo-attenuated
SITYG_10990	-	1113075	1113336	hypothetical protein	86			31.8	84.2	38.5			1	alive in vivo
SITYG_11000	-	1113472	1113847	hypothetical protein	124			143.8	644.6	669.5	5.1		0	
SITYG_11010	-	1113873	1114389	hypothetical protein	171			72.4	425.9	97.3			3	vivo-attenuated
SITYG_11020	-	1114696	1117051	hypothetical protein	784			44.0	186.6	149.2	3.7		8	vivo-attenuated
SITYG_11030	-	1117062	1117521	hypothetical protein	152			63.3	287.3	196.9	3.4		0	
SITYG_11040	-	1117542	1118328	putative endonuclease	261			121.4	475.3	383.3	3.4		4	alive in vivo
SITYG_11050	-	1118343	1118676	hypothetical protein	110	RTKL		0.0	329.9	90.5			0	
SITYG_11060	-	1118668	1118986	hypothetical protein	105			13.0	69.1	0.0			0	
SITYG_11070	-	1119430	1119745	hypothetical protein	104			65.8	69.8	31.9			0	
SITYG_11080	-	1119906	1120740	putative membrane protein	277			139.3	553.3	493.7	3.9		1	alive in vivo
SITYG_11090	-	1120851	1121865	hypothetical protein	337			36.8	260.1	9.9	-3.4	-31.4	2	alive in vivo
SITYG_11100	-	1121861	1122071	hypothetical protein	69			19.8	418.6	47.8			2	vivo-attenuated
SITYG_11110	-	1122063	1122489	hypothetical protein	141	OC		19.5	51.6	165.0	9.2		0	
SITYG_11120	-	1122475	1122907	hypothetical protein	143			28.8	50.9	186.0	7.0	3.0	1	alive in vivo
SITYG_11130	-	1122922	1123126	hypothetical protein	67			40.7	323.2	344.6	9.2		1	alive in vivo
SITYG_11140	-	1123122	1123674	putative membrane protein	183			90.2	398.1	382.0	4.6		1	alive in vivo
SITYG_11150	-	1123689	1124736	putative C-5 cytosine methyltransferase	348	L		79.2	251.9	249.4	3.4		2	alive in vivo
SITYG_11160	-	1124744	1125536	putative D12 class N6 adenine-specific DNA methyltransferase	263	L		83.8	443.9	393.1	5.1		3	alive in vivo
SITYG_11170	-	1125544	1125733	hypothetical protein	62			87.8	0.0	0.0			1	alive in vivo
SITYG_11180	-	1125843	1127340	hypothetical protein	498			97.0	778.0	127.5			1	alive in vivo
SITYG_11190	-	1127330	1127840	hypothetical protein	169			0.0	86.2	275.7	#DIV/0!		0	
SITYG_11200	-	1128040	1128190	50S ribosomal protein L33	49	J		27.7	146.5	66.9			1	alive in vivo
SITYG_11210	-	1128173	1129319	multidrug transporter	381	GEPR		325.8	479.4	595.9			1	alive in vivo
SITYG_11220	*coaE*	1129395	1129989	dephospho-CoA kinase	197	H		384.1	296.0	456.5			0	
SITYG_11230	*mutM*	1129992	1130817	formamidopyrimidine-DNA glycosylase	274	L		266.5	532.7	596.4			0	
SITYG_11240	-	1130954	1131395	hypothetical protein	146			94.1	299.0	250.5			0	
SITYG_11250	-	1131438	1131915	phosphohydrolase	158	LR		426.1	414.6	231.6			0	
SITYG_11260	-	1131975	1132350	putative competence protein	124			354.0	468.8	214.2			3	vivo-attenuated
SITYG_11270	*era*	1132398	1133298	GTP-binding protein Era	299	R		709.8	756.9	513.3			0	
SITYG_11280	-	1133357	1133762	diacylglycerol kinase	134	M		204.8	379.8	223.2			0	
SITYG_11290	-	1133742	1134240	hypothetical protein	165	R		791.3	529.5	927.6			0	
SITYG_11300	-	1134358	1136095	ABC-type transport system, ATPase and permease component	578	V		114.6	316.3	196.6			1	alive in vivo
SITYG_11310	-	1136091	1137822	ABC-type transport system, ATPase and permease component	576	V		117.4	304.7	272.7			2	alive in vivo
SITYG_11320	-	1138030	1138198	hypothetical protein	55	C		24.7	0.0	0.0			0	
SITYG_11330	-	1138318	1138450	hypothetical protein	43			0.0	166.5	0.0			0	
SITYG_11340	-	1139071	1139638	acetyltransferases	188	J		512.1	465.1	336.5			0	
SITYG_11350	*ald*	1139767	1140880	alanine dehydrogenase	370	E		879.6	691.0	848.1			3	vivo-attenuated
SITYG_11360	-	1141096	1141417	TfoX N-terminal domain protein	106	K		749.5	684.6	1720.6			0	
SITYG_11370	-	1141419	1141920	acetyltransferase	166	KR		1142.6	965.0	681.5			0	
SITYG_11380	-	1141932	1142172	hypothetical protein	79			259.3	366.2	83.7			0	
SITYG_11390	-	1142149	1143220	PhoH family protein	356	T		646.8	430.9	778.2			0	
SITYG_11400	-	1143295	1143511	hypothetical protein	71	S		153.6	305.2	418.4			0	
SITYG_11410	*pyrE*	1144291	1144921	orotate phosphoribosyltransferase	209	F		513.6	383.7	637.6			1	alive in vivo
SITYG_11420	-	1144931	1145159	hypothetical protein	75	C		400.3	867.4	308.3			0	
SITYG_11430	*pyrF*	1145250	1145946	orotidine-5'-phosphate decarboxylase	231	F		298.0	442.0	331.8			0	
SITYG_11440	*pyrD*	1146316	1147255	dihydroorotate dehydrogenase	312	F		194.4	280.8	117.6			0	
SITYG_11450	-	1147264	1148071	dihydroorotate dehydrogenase electron transfer subunit	268	HC		61.7	163.4	99.5			1	alive in vivo
SITYG_11460	-	1148261	1149170	LysR family transcriptional regulator	302	K		314.9	314.3	353.5			3	vivo-attenuated
SITYG_11470	-	1149462	1150701	major facilitator transporter	412	GEPR		200.9	443.4	291.8			0	
SITYG_11480	-	1151176	1152019	hypothetical protein	280	R		241.1	260.7	655.2			0	
SITYG_11490	-	1152011	1153340	phospotransferase system component protein	442	G		109.2	248.0	128.5			0	
SITYG_11500	-	1153490	1154420	hypothetical protein	309			744.9	638.0	777.4			1	alive in vivo
SITYG_11510	*thrB*	1154530	1155397	homoserine kinase	288	E		296.6	380.2	590.7			0	
SITYG_11520	-	1155398	1156691	homoserine dehydrogenase	430	E		734.7	373.9	683.4			1	vivo-attenuated
SITYG_11530	-	1156869	1157820	putative deacetylase	316	G		244.3	323.5	274.5			0	
SITYG_11540	-	1157852	1158014	hypothetical protein	53			51.2	135.6	248.0	5.3		0	
SITYG_11550	-	1158028	1159339	putative GTPase	436	R		604.3	368.8	237.5			0	
SITYG_11560	-	1159396	1159531	hypothetical protein	44			891.1	0.0	892.6			0	

SITYG_11570	-	1159785	1161267	galactose-1-phosphate-uridylyltransferase	493	G	70.0	385.5	88.1			0	
SITYG_11580	*galK*	1161339	1162518	galactokinase	392	G	158.3	391.4	238.5			1	alive in vivo
SITYG_11590	*galR*	1162755	1163757	galactose operon transcriptional regulator GalR	333	K	414.0	636.0	972.1			2	alive in vivo
SITYG_11600	-	1163759	1164695	biotin-(acetyl-CoA-carboxylase) ligase	311	H	208.3	375.6	375.5			1	vivo-attenuated
SITYG_11610	-	1164842	1164965	hypothetical protein	40		0.0	0.0	0.0			2	alive in vivo
SITYG_11620	-	1165156	1165813	hypothetical protein	218	S	202.0	301.0	275.1			0	
SITYG_11630	-	1165816	1166491	hypothetical protein	224	S	971.0	293.0	490.9			1	vivo-attenuated
SITYG_11640	-	1166637	1168026	putative dipeptidase	462	E	74.7	522.1	115.7			2	alive in vivo
SITYG_11650	-	1168093	1169233	cystathionine beta-lyase	379	E	94.6	462.6	475.7	5.5		0	
SITYG_11660	-	1169229	1169613	putative endoribonuclease L-PSP	127	J	64.8	572.3	653.8	11.0		0	
SITYG_11670	-	1169629	1171009	putative amino acid permease	459	E	75.1	636.9	356.6	5.2		2	alive in vivo
SITYG_11680	-	1171016	1171781	glutamine amidotransferase	254	R	81.3	258.5	354.4	4.7		0	
SITYG_11690	-	1172004	1173669	DNA polymerase III subunits gamma and tau	554	L	637.8	343.1	373.9			0	
SITYG_11700	-	1173668	1174286	GAF domain-containing protein	205	T	349.0	426.7	552.5			0	
SITYG_11710	-	1174313	1174943	putative SAM-dependent methyltransferases	209	QR	105.4	348.8	302.9	3.1		0	
SITYG_11720	-	1174939	1175566	hypothetical protein	208		145.5	175.2	96.1			1	alive in vivo
SITYG_11730	-	1175881	1178455	histidine triad protein	857		557.6	563.5	737.3			1	alive in vivo
SITYG_11740	-	1178465	1179389	metal binding lipoprotein	307	P	422.0	404.3	728.2			1	vivo-attenuated
SITYG_11750	*trmD*	1179508	1180243	tRNA [Guanine-N(1)-]-methyltransferase	244	J	496.7	209.3	464.5			0	
SITYG_11760	*rimM*	1180232	1180751	16S rRNA processing protein RimM	172	J	591.5	254.0	328.9			0	
SITYG_11770	-	1180990	1182565	ABC transporter, ATP-binding protein	524	V	263.4	320.9	312.4			1	alive in vivo
SITYG_11780	-	1182724	1182874	hypothetical protein	49		0.0	146.5	0.0			0	
SITYG_11790	-	1182870	1183032	hypothetical protein	53		128.0	406.9	743.9	6.3		0	
SITYG_11800	*rplL*	1183346	1183715	50S ribosomal protein L7/L12	122	J	19290.7	1905.7	7565.5			0	
SITYG_11810	*rplJ*	1183786	1184287	50S ribosomal protein L10	166	J	3278.8	87.7	2064.5			0	
SITYG_11820	-	1184614	1185457	AraC family transcriptional regulator	280	S	172.2	495.3	321.6			1	alive in vivo
SITYG_11830	-	1185544	1186471	putative NlpC/p60-like transpeptidase	308		44.7	474.1	108.3			1	alive in vivo
SITYG_11840	-	1186895	1187345	hypothetical protein	149		285.8	244.2	89.3			0	
SITYG_11850	*dapA*	1187547	1188429	dihydrodipicolinate synthase	293	EM	32.9	473.4	125.2	4.1	-4.5	0	
SITYG_11860	*asd*	1188474	1189551	aspartate-semialdehyde dehydrogenase	358	E	104.0	530.5	317.0	3.3		0	
SITYG_11870	-	1189685	1189865	hypothetical protein	59		0.0	0.0	0.0			0	
SITYG_11880	*potD*	1189931	1191002	spermidine/putrescine-binding periplasmic protein	356	E	546.1	492.4	581.3			0	
SITYG_11890	*potC*	1190998	1191772	ABC transporter, permease protein	257	E	268.0	369.1	181.6			0	
SITYG_11900	*potB*	1191768	1192575	ABC transporter, permease protein	268	E	313.6	626.3	224.0			0	
SITYG_11910	*potA*	1192555	1193713	spermidine/putrescine transport ATP-binding protein	385	E	465.7	436.5	485.6			1	alive in vivo
SITYG_11920	-	1193705	1193822	hypothetical protein	38		35.5	0.0	85.8			0	
SITYG_11930	*murB*	1193808	1194711	UDP-N-acetylenolpyruvoylglucosamine reductase	300	M	266.4	413.7	355.9			0	
SITYG_11940	-	1195106	1195199	hypothetical protein	30		0.0	0.0	0.0			0	
SITYG_11950	*lepA*	1195430	1197254	GTP-binding protein LepA	607	M	514.0	421.7	600.1			0	
SITYG_11960	-	1197198	1198206	putative hydrolase	335	R	218.1	370.6	288.9			0	
SITYG_11970	*hemH*	1198811	1199909	ferrochelatase	365	H	222.9	420.3	365.8			0	
SITYG_11980	-	1200040	1200160	hypothetical protein	39		0.0	183.1	0.0			1	vivo-attenuated
SITYG_11990	*pepT*	1200284	1201508	peptidase T	407	E	267.7	430.9	172.3			0	
SITYG_12000	*udk*	1201996	1202632	uridine kinase	211	F	423.9	483.7	805.3			0	
SITYG_12010	-	1202736	1203726	oxidoreductase	329	R	192.7	554.9	192.7			0	
SITYG_12020	-	1203712	1204798	DEAD/DEAH box helicase	361	LKJ	156.6	445.2	277.4			0	
SITYG_12030	-	1204849	1206217	putative polysaccharide deacetylase	455	G	430.6	353.4	359.7			3	alive in vivo
SITYG_12040	*lguL*	1206448	1206835	lactoylglutathione lyase	128	E	1339.8	397.5	726.6			0	
SITYG_12050	*rplT*	1207114	1207474	50S ribosomal protein L20	119	J	1624.7	244.2	1087.9			0	
SITYG_12060	*rpmI*	1207520	1207721	50S ribosomal protein L35	66	J	6026.2	656.0	3946.8			0	
SITYG_12070	-	1207754	1208312	translation initiation factor IF-3	185	J	2460.7	275.7	2285.5			0	
SITYG_12080	-	1208456	1209134	cytidylate kinase	225	F	1168.6	1102.0	1022.0			0	
SITYG_12090	-	1209143	1209596	hypothetical protein	150		750.9	339.6	620.7			0	
SITYG_12100	-	1209635	1209839	putative Ferredoxin	67	C	935.4	107.7	246.1	-3.5		0	
SITYG_12110	-	1209825	1210320	hypothetical protein	164		335.2	355.1	527.5			0	
SITYG_12120	-	1210535	1211648	glycerate kinase	370	G	96.9	335.6	261.7			0	
SITYG_12130	*serB*	1211651	1212302	phosphoserine phosphatase SerB	216	E	133.8	168.8	169.7			2	vivo-attenuated
SITYG_12140	*glmM*	1212408	1213761	phosphoglucosamine mutase	450	G	1542.2	779.6	1699.6			0	
SITYG_12150	-	1213785	1214514	hypothetical protein	242	S	506.4	361.7	537.2			0	
SITYG_12160	-	1214500	1215358	hypothetical protein	285	S	1213.5	358.6	772.5			0	
SITYG_12170	-	1215466	1216810	Mur ligase family protein	447	M	145.1	327.0	179.3			0	
SITYG_12180	-	1216809	1217595	putative glutamine amidotransferase	261	R	174.2	363.4	166.1			0	
SITYG_12190	-	1217625	1217883	hypothetical protein	85		80.4	340.7	311.4	4.2		0	
SITYG_12200	-	1217986	1219882	ABC transporter, ATP-binding protein	631	R	100.6	312.9	143.0			1	alive in vivo
SITYG_12210	-	1219955	1220321	hypothetical protein	121		79.3	300.2	54.9			2	alive in vivo
SITYG_12220	-	1220322	1221024	Zn-dependent protease	233	O	797.7	438.2	600.8			0	
SITYG_12230	*estA*	1221167	1221959	putative esterase	263	R	471.4	638.2	646.6			2	vivo-attenuated
SITYG_12240	-	1222063	1223725	hypothetical protein	553	R	611.5	409.9	561.9			1	alive in vivo
SITYG_12250	-	1224153	1224192	hypothetical protein	12		0.0	563.5	0.0			0	
SITYG_12260	-	1224420	1225707	putative protease	428	O	1005.6	358.6	795.9			0	
SITYG_12270	-	1225834	1226764	putative protease	309	O	767.2	448.9	442.7			0	
SITYG_12280	-	1226902	1227196	hypothetical protein	97		338.6	149.5	649.0			0	
SITYG_12290	-	1227282	1227750	hypothetical protein	155		1081.4	563.5	965.6			0	
SITYG_12300	-	1227765	1228149	hypothetical protein	127	R	334.9	228.9	287.7			0	
SITYG_12310	*lgt*	1228166	1228940	prolipoprotein diacylglyceryl transferase	257	M	343.0	369.1	272.5			1	alive in vivo
SITYG_12320	-	1228932	1229865	HPr kinase/phosphorylase	310	T	560.2	282.6	742.7			0	
SITYG_12330	-	1229975	1230518	NTP pyrophosphohydrolases	180	LR	603.5	202.3	536.3			0	
SITYG_12340	-	1230546	1230825	hypothetical protein	92	KT	3494.0	315.0	2591.5			0	
SITYG_12350	-	1230919	1231357	putative Zn-dependent metalloprotease	145	S	303.1	451.5	435.6			0	
SITYG_12360	-	1231343	1233473	putative transcriptional accessory protein	709	K	570.6	443.6	622.3			0	
SITYG_12370	-	1233592	1233733	hypothetical protein	46		764.9	0.0	427.3			0	
SITYG_12380	-	1233729	1234635	putative permease	301	R	448.7	921.7	742.6			0	
SITYG_12390	-	1234631	1235447	putative membrane protein	271	S	894.7	727.1	726.1			0	
SITYG_12400	-	1235561	1236926	putative transporter	454	GEPR	112.4	402.5	103.0			1	alive in vivo
SITYG_12410	-	1236973	1238461	glucose-6-phosphate dehydrogenase	495	G	407.0	236.3	492.7			3	vivo-attenuated
SITYG_12420	-	1239035	1239728	hypothetical protein	230		209.5	570.8	420.2			0	
SITYG_12430	-	1239975	1240608	hypothetical protein	210	R	340.8	694.3	507.7			1	alive in vivo
SITYG_12440	-	1240591	1242286	putative ABC transporter, ATP-binding protein	564	V	217.8	285.2	432.5			1	alive in vivo
SITYG_12450	-	1242303	1243569	putative lanthionine synthetase C-like protein	421		147.4	329.8	261.8			1	alive in vivo
SITYG_12460	-	1243546	1244266	putative NADPH-dependent FMN reductase	239	R	265.0	305.2	195.3			2	alive in vivo
SITYG_12470	-	1244386	1244596	hypothetical protein	69		434.6	11615.2	669.5			0	
SITYG_12480	-	1244652	1247652	putative lantibiotic dehydratase	999		225.4	380.9	217.6			2	alive in vivo
SITYG_12490	-	1249488	1249620	hypothetical protein	43		0.0	166.5	76.1			1	alive in vivo
SITYG_12500	-	1249793	1250738	putative permease	314	R	188.8	348.8	159.4			0	
SITYG_12510	-	1250751	1252374	malate dehydrogenase	540	C	222.4	1015.5	253.7			1	alive in vivo
SITYG_12520	-	1252547	1252904	putative transcriptional regulator	118	K	127.8	369.3	168.8			0	
SITYG_12530	-	1253027	1253918	putative transcriptional regulator	296	K	46.6	197.3	157.8	3.7		1	alive in vivo
SITYG_12540	-	1254081	1254744	DNA alkylation repair enzyme	220	L	112.6	198.9	166.6			0	
SITYG_12550	-	1254745	1255288	acetyltransferase	180	M	160.4	768.9	332.9			0	
SITYG_12560	*fhs*	1255391	1257062	formate--tetrahydrofolate ligase	556	F	372.4	420.8	607.0			0	
SITYG_12570	-	1257213	1257780	hypothetical protein	188		58.5	155.0	53.1			1	alive in vivo
SITYG_12580	-	1257883	1258576	phosphopantothenate-cysteine ligase	230	H	287.3	380.5	246.3			0	
SITYG_12590	-	1258572	1259124	phosphopantothenoylcysteine decarboxylase	183	H	473.4	358.3	345.6			0	
SITYG_12600	-	1259107	1259671	putative membrane protein	187	S	58.8	272.7	997.1	18.5	3.0	0	
SITYG_12610	*pgm*	1259849	1261568	phosphoglucomutase	572	G	1805.0	779.8	1238.5			1	alive in vivo
SITYG_12620	*bta*	1261891	1262239	bacteriocin transport accesory protein	115	OC	1311.2	505.2	634.8			0	
SITYG_12630	*mutY*	1262413	1263589	A/G-specific adenine glycosylase	391	L	356.3	373.7	452.6			3	vivo-attenuated
SITYG_12640	*pta*	1263654	1264632	phosphate acetyltransferase	325	C	415.7	404.4	297.8			0	
SITYG_12650	-	1264635	1265532	23S rRNA pseudouridine synthase	298	J	744.5	930.9	828.4			0	
SITYG_12660	*ppnK*	1265528	1266347	inorganic polyphosphate/ATP-NAD kinase	272	G	212.7	295.1	404.6			0	
SITYG_12670	-	1266330	1267002	GTP pyrophosphokinase	223	S	956.8	523.2	747.2			0	
SITYG_12680	-	1267097	1267658	hypothetical protein	186	S	199.6	548.4	179.0			1	alive in vivo
SITYG_12690	-	1267729	1268701	ribose-phosphate pyrophosphokinase	323	FE	247.5	339.1	309.9			0	
SITYG_12700	-	1268710	1269826	putative aminotransferase	371	E	732.2	669.5	944.8			0	
SITYG_12710	-	1269830	1270178	hypothetical protein	115		417.2	378.9	173.1			0	
SITYG_12720	-	1270358	1271003	redox-sensing transcriptional repressor REX	214	R	83.6	340.7	140.1			0	
SITYG_12730	-	1271021	1271192	putative glutamine amidotransferase	56	R	169.8	514.0	352.4			0	
SITYG_12740	*radC*	1271654	1272335	putative DNA repair protein	226	L	42.6	355.0	294.9	7.5		2	alive in vivo
SITYG_12750	*phoU*	1272420	1273074	phosphate transport system regulatory protein	217	P	323.5	168.0	429.9			0	
SITYG_12760	*pstB1*	1273154	1273913	phosphate ABC transporter, ATP-binding protein	252	P	327.9	231.6	568.9			0	
SITYG_12770	*pstB2*	1273952	1274756	phosphate ABC transporter, ATP-binding protein	267	P	252.8	328.0	724.4	3.1		0	
SITYG_12780	-	1274767	1275652	phosphate ABC transporter, permease PstA	294	P	225.0	422.1	272.3			0	
SITYG_12790	-	1275641	1276553	phosphate ABC transporter, permease PstC	303	P	354.8	481.9	231.2			3	alive in vivo
SITYG_12800	*pstS*	1276573	1277440	ABC transporter, phosphate-binding protein	288	P	535.9	557.6	637.0			0	
SITYG_12810	-	1277546	1278851	putative RNA methylase	434	J	149.4	437.8	192.4			0	
SITYG_12820	-	1278860	1279625	putative inositol monophosphatase	254	G	379.6	316.0	341.3			0	
SITYG_12830	-	1279608	1279902	hypothetical protein	97	S	98.8	224.2	102.5			0	
SITYG_12840	-	1279894	1280296	transcriptional regulator Spx	133	P	794.6	437.3	974.2			0	
SITYG_12850	-	1280416	1281349	riboflavin biosynthesis protein RibF	310	H	489.1	659.5	688.8			0	

SITYG_12860	*truB*	1281374	1282253	tRNA pseudouridine synthase B	292	J	325.6	450.0	365.6			0	
SITYG_12870	-	1282256	1283063	putative alpha/beta hydrolase family protein	268	R	154.2	245.1	435.5	3.1		0	
SITYG_12880	-	1283214	1283601	hypothetical protein	128		182.2	227.1	337.3			0	
SITYG_12890	-	1283606	1284875	hypothetical protein	422	S	310.5	381.0	237.4			4	vivo-attenuated
SITYG_12900	-	1285068	1286082	putative alpha/beta hydrolase family protein	337	R	77.7	390.1	158.5			1	alive in vivo
SITYG_12910	-	1286087	1286576	hypothetical protein	162		93.3	763.9	595.5	7.0		0	
SITYG_12920	-	1286685	1288431	ABC transporter, ATP-binding protein	581	V	83.2	528.6	281.8	3.7		1	alive in vivo
SITYG_12930	-	1288423	1290190	putative ABC transporter, ATP-binding protein	588	V	96.3	323.3	505.8	5.7		2	vivo-attenuated
SITYG_12940	-	1290208	1290820	putative TetR/AcrR family transcriptional regulator	203	K	54.2	359.1	131.3			0	
SITYG_12950	-	1290882	1291029	hypothetical protein	48		0.0	0.0	0.0			0	
SITYG_12960	-	1291686	1292088	putative NUDIX family hydrolase	133	LR	650.1	874.6	849.3			0	
SITYG_12970	*pcrA*	1292113	1294396	ATP-dependent DNA helicase PcrA	760	L	388.8	385.0	457.5			4	vivo-attenuated
SITYG_12980	-	1294545	1295745	putative cation efflux family protein	399	P	197.0	457.8	259.4			0	
SITYG_12990	-	1296037	1296169	hypothetical protein	43	E	0.0	166.5	76.1			0	
SITYG_13000	-	1296409	1296967	signal peptidase I	185	U	4326.6	512.0	2843.4			0	
SITYG_13010	-	1297129	1298632	pyruvate kinase	500	G	2831.7	321.7	1570.1			0	
SITYG_13020	-	1298690	1299701	6-phosphofructokinase	336	G	4394.4	586.9	3496.3			0	
SITYG_13030	*dnaE*	1299783	1302885	DNA-polymerase III subunit alpha	1033	L	204.6	389.6	339.9			0	
SITYG_13040	-	1303016	1303211	GntR family transcriptional regulator	64	K	63.8	225.4	0.0			0	
SITYG_13050	-	1303231	1303426	putative ABC transporter, ATP-binding protein	64	V	0.0	0.0	51.5			0	
SITYG_13060	*recJ*	1303723	1305958	single-stranded-DNA-specific exonuclease RecJ	744	L	293.2	491.6	278.6			0	
SITYG_13070	-	1306056	1306464	putative GNAT-family acetyltransferase	135	KR	172.8	646.3	566.1	3.6		0	
SITYG_13080	-	1306447	1307179	methyltransferase	243	QR	345.7	510.3	260.7			1	alive in vivo
SITYG_13090	-	1307188	1307944	putative short chain dehydrogenase	251	R	351.2	377.9	385.2			0	
SITYG_13100	-	1307953	1308565	putative phosphoglycerate mutase	203	G	427.0	718.1	295.4			0	
SITYG_13110	-	1308607	1309537	ribonuclease Z	309	R	615.5	661.6	647.9			0	
SITYG_13120	-	1309547	1310177	hypothetical protein	209		368.7	523.2	494.1			0	
SITYG_13130	*hflX*	1310169	1311408	GTP-binding protein HflX	412	R	328.1	532.1	397.1			0	
SITYG_13140	*miaA*	1311400	1312285	tRNA delta(2)-isopentenylpyrophosphate transferase	294	J	389.0	347.6	408.5			0	
SITYG_13150	-	1312362	1312533	hypothetical protein	56		1091.6	385.5	1409.4			0	
SITYG_13160	-	1312673	1312811	putative macrolide ABC transporter permease	45	V	0.0	0.0	0.0			0	
SITYG_13170	-	1313120	1314470	glutathione reductase	449	C	500.9	358.1	386.8			0	
SITYG_13180	-	1314909	1315446	putative biotin synthase	178	R	455.8	327.4	243.1			0	
SITYG_13190	-	1315646	1316111	hypothetical protein	154	J	0.0	94.5	0.0			0	
SITYG_13200	*pheT*	1315958	1318364	phenylalanyl-tRNA synthetase subunit beta	801	J	317.2	337.9	409.0			0	
SITYG_13210	-	1318500	1319028	acetyltransferase	175	KR	298.5	332.9	551.5			0	
SITYG_13220	*pheS*	1319032	1320145	phenylalanyl-tRNA synthetase subunit alpha	370	J	402.5	414.6	550.4			0	
SITYG_13230	-	1320384	1322250	putative ABC transporter ATP-binding protein	621	R	351.2	423.9	382.1			1	alive in vivo
SITYG_13240	*papS*	1322246	1323446	tRNA CCA-pyrophosphorylase	399	J	252.3	183.1	217.6			0	
SITYG_13250	*dapB*	1323442	1324210	dihydrodipicolinate reductase	255	E	399.7	228.9	287.7			0	
SITYG_13260	-	1324220	1325069	hypothetical protein	282	S	395.8	336.5	343.0			0	
SITYG_13270	-	1325072	1325447	hypothetical protein	124	S	3550.8	234.4	1928.1			0	
SITYG_13280	*fruA*	1325607	1327557	putative PTS system, fructose-specific enzyme IIABC component	649	G	338.2	405.7	448.0			0	
SITYG_13290	*fruB*	1327553	1328465	1-phosphofructokinase	303	G	463.9	168.7	528.5			0	
SITYG_13300	*fruR*	1328461	1329124	transcriptional regulators of sugar metabolism	220	KG	394.2	530.3	530.1			0	
SITYG_13310	*pepN*	1329361	1331905	aminopeptidase N	847	E	432.1	311.0	280.3			1	alive in vivo
SITYG_13320	-	1332036	1333005	thioredoxin reductase	322	O	342.5	340.2	217.6			0	
SITYG_13330	-	1333065	1334757	putative phosphoglucomutase/phosphomannomutase protein	563	G	1076.3	545.5	753.7			4	vivo-attenuated
SITYG_13340	*dnaD*	1335262	1335937	putative DNA replication protein	224	L	393.3	227.9	208.3			0	
SITYG_13350	-	1335987	1336269	homoserine O-succinyltransferase	93	E	117.7	233.8	249.3			0	
SITYG_13360	-	1336522	1336639	putative homoserine O-succinyltransferase	38	E	248.2	0.0	85.8			0	
SITYG_13370	*apt*	1336940	1337453	adenine phosphoribosyltransferase	170	F	1916.4	428.4	2075.0			0	
SITYG_13380	-	1337576	1338272	hypothetical protein	231	M	160.9	378.9	245.3			0	
SITYG_13390	-	1338264	1338645	putative effector of murein hydrolase LrgA	126	R	130.7	288.4	105.4			0	
SITYG_13400	-	1339117	1339243	hypothetical protein	41		1514.4	3313.6	1195.5			0	
SITYG_13410	-	1339372	1340374	hypothetical protein	333	S	53.8	372.8	120.3			0	
SITYG_13420	-	1340746	1342516	putative ABC transporter ATP-binding/permease protein	589	V	138.3	173.8	164.5			2	vivo-attenuated
SITYG_13430	-	1342525	1344262	putative ABC transporter ATP-binding/permease protein	578	V	382.1	506.0	560.8			1	alive in vivo
SITYG_13440	*endA*	1344415	1345261	putative DNA-entry endonuclease	281		505.0	363.6	747.8			1	alive in vivo
SITYG_13450	-	1345323	1345500	DNA-directed RNA polymerase subunit beta	58		281.2	124.2	113.5			0	
SITYG_13460	-	1345492	1346773	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	426	M	1169.0	617.6	956.4			1	vivo-attenuated
SITYG_13470	-	1346810	1347041	hypothetical protein	76		1436.6	285.4	1347.6			0	
SITYG_13480	-	1347142	1347562	ATP synthase subunit epsilon	139	C	1659.3	313.9	1338.9			0	
SITYG_13490	-	1347572	1348979	ATP synthase subunit beta	468	C	890.4	374.8	606.7			0	
SITYG_13500	-	1349013	1349892	ATP synthase subunit gamma	292	C	854.2	175.0	628.3			0	
SITYG_13510	-	1349907	1351413	ATP synthase subunit alpha	501	C	818.1	277.2	573.4			0	
SITYG_13520	-	1351428	1351965	ATP synthase subunit delta	178	C	115.9	81.8	74.8			0	
SITYG_13530	-	1351964	1352459	proton-translocating ATPase subunit b	164	C	1843.6	621.5	872.3			0	
SITYG_13540	-	1352473	1353187	ATP synthase subunit A	237	C	1899.8	800.2	1153.3			0	
SITYG_13550	-	1353226	1353427	ATP synthase subunit C	66	C	12258.8	546.6	6145.1			0	
SITYG_13560	*glgP*	1353740	1356140	glycogen phosphorylase	799	G	155.6	631.8	292.9			1	vivo-attenuated
SITYG_13570	*glgA*	1356161	1357595	glycogen synthase	477	G	112.8	536.3	364.1	3.5		2	vivo-attenuated
SITYG_13580	*glgD*	1357591	1358731	glucose-1-phosphate adenylyltransferase, GlgD subunit	379	G	141.9	1811.9	308.3			0	
SITYG_13590	*glgC*	1358720	1359863	glucose-1-phosphate adenylyltransferase	380	G	105.2	1384.2	289.9			0	
SITYG_13600	*glgB*	1359866	1361777	1,4-alpha-glucan branching enzyme	636	G	256.1	977.4	446.7			4	vivo-attenuated
SITYG_13610	*rexA*	1362290	1365971	ATP-dependent nuclease subunit A	1226	L	220.9	507.4	234.6			0	
SITYG_13620	*rexB*	1365967	1369240	ATP-dependent nuclease subunit B	1090	L	176.2	476.7	411.1			1	alive in vivo
SITYG_13630	-	1369361	1370576	putative ABC transporter, permease component	404	CP	331.2	560.7	231.4			0	
SITYG_13640	-	1370572	1371466	putative ABC transporter ATP-binding protein	297	R	607.8	368.7	763.8			1	alive in vivo
SITYG_13650	-	1371546	1371660	hypothetical protein	37		0.0	192.8	0.0			0	
SITYG_13660	-	1371670	1371964	hypothetical protein	97		254.0	224.2	273.3			0	
SITYG_13670	-	1371941	1372343	hypothetical protein	133		980.3	983.9	1648.7			0	
SITYG_13680	-	1372324	1373593	hypothetical protein	422		326.9	588.8	292.8			0	
SITYG_13690	-	1373594	1373990	hypothetical protein	131		544.7	166.5	557.9			0	
SITYG_13700	-	1374026	1374275	hypothetical protein	82		183.3	0.0	40.3	-4.2		0	
SITYG_13710	-	1374276	1374597	hypothetical protein	106		25.8	342.3	0.0			0	
SITYG_13720	-	1374738	1374948	hypothetical protein	69		118.5	0.0	0.0	<-118.5		0	
SITYG_13730	-	1374947	1375340	hypothetical protein	130		95.0	111.8	51.1			1	vivo-attenuated
SITYG_13740	-	1375881	1376040	hypothetical protein	52		78.3	414.6	189.5			0	
SITYG_13750	-	1376290	1376710	hypothetical protein	139		187.7	157.0	167.4			0	
SITYG_13760	-	1376916	1377129	hypothetical protein	70	S	116.8	103.2	94.3			0	
SITYG_13770	-	1377230	1377557	hypothetical protein	108		1522.3	336.0	614.2			0	
SITYG_13780	-	1377569	1378328	ABC transporter, ATP-binding protein	252	R	49.2	202.7	172.0	3.8		1	alive in vivo
SITYG_13790	-	1378324	1379191	ABC transporter permease	288	R	124.4	709.7	324.3			0	
SITYG_13800	-	1379234	1380239	peptide ABC transporter substrate-binding protein	334	R	111.4	262.4	259.8			0	
SITYG_13810	-	1380403	1380619	hypothetical protein	71		288.1	0.0	325.4			0	
SITYG_13820	-	1380724	1382374	fibronectin-binding protein A	549	K	211.2	532.7	225.2			1	alive in vivo
SITYG_13830	*aldB*	1382689	1383409	alpha-acetolactate decarboxylase	239	Q	351.4	244.2	237.1			0	
SITYG_13840	-	1383452	1385117	acetolactate synthase	554	EH	535.6	580.7	591.1			0	
SITYG_13850	-	1385199	1386447	hypothetical protein	415	R	275.9	528.2	579.3			1	alive in vivo
SITYG_13860	-	1386415	1387594	hypothetical protein	392	R	348.3	652.3	562.1			2	vivo-attenuated
SITYG_13870	-	1387857	1389243	FeS assembly protein SufB	461	O	1146.3	475.6	1007.1			0	
SITYG_13880	-	1389375	1389819	flavodoxin	147	C	9828.6	1187.8	8481.4			0	
SITYG_13890	-	1389964	1390903	hypothetical protein	312	R	388.8	351.0	406.4			1	alive in vivo
SITYG_13900	-	1390899	1391025	hypothetical protein	41		131.7	174.4	159.4			0	
SITYG_13910	*rpmE*	1391007	1391253	50S ribosomal protein L31	81	J	5986.2	357.3	4000.5			0	
SITYG_13920	-	1391486	1392233	hypothetical protein	248	R	327.6	382.4	470.5			1	alive in vivo
SITYG_13930	-	1392186	1392486	putative endonuclease	99	L	677.5	586.0	334.7			0	
SITYG_13940	-	1392825	1393359	hypothetical protein	177	S	69.9	329.2	150.4			0	
SITYG_13950	*lacG*	1393537	1394944	6-phospho-beta-galactosidase	468	G	109.1	374.8	306.9	3.1		0	
SITYG_13960	*lacE*	1394945	1396649	phosphotransferase system cellobiose-specific component IIC	567	G	85.2	425.6	335.9	4.3		0	
SITYG_13970	*lacF*	1396645	1396966	phosphotransferase system cellobiose-specific component IIA	106	G	155.1	753.0	187.7			0	
SITYG_13980	-	1397002	1397836	transcriptional antiterminator	277	K	213.9	368.9	662.2	3.4		0	
SITYG_13990	-	1398092	1404755	beta-galactosidase	2220	G	62.9	504.6	197.4	3.4	-3.1	7	vivo-attenuated
SITYG_14000	*lacC*	1404907	1405840	fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	310	G	231.2	329.7	365.9			2	alive in vivo
SITYG_14010	-	1405915	1407391	putative PTS system, IIC component	491	G	109.6	1071.9	136.1			1	alive in vivo
SITYG_14020	-	1407521	1407827	putative PTS system, IIB component	101	G	94.9	1723.5	65.6			0	
SITYG_14030	-	1407850	1408333	putative PTS system, galactose-specific IIA component	160	GT	68.7	682.4	207.9	3.3	-3.9	2	alive in vivo
SITYG_14040	-	1408497	1408929	putative galactose-6-phosphate isomerase subunit LacA	143	G	220.9	508.7	209.2			0	
SITYG_14050	*lacB*	1408948	1409467	putative galactose-6-phosphate isomerase subunit LacB	172	G	127.9	1143.2	367.6	3.1	-3.7	0	
SITYG_14060	-	1409593	1410340	transcriptional regulator, DeoR family	248	KG	855.2	2588.7	658.7			0	
SITYG_14070	-	1410508	1411456	tagatose 1,6-diphosphate aldolase	315	G	192.5	185.4	360.2			0	
SITYG_14080	-	1411736	1413281	ATP-dependent RNA helicase	514	LKJ	1006.8	469.4	845.0			0	
SITYG_14090	-	1413574	1413697	hypothetical protein	40		33.7	178.7	0.0			0	
SITYG_14100	-	1413784	1413979	hypothetical protein	64		21.3	225.4	51.5			0	
SITYG_14110	-	1413997	1414906	CorA-like magnesium transporter	302	P	146.0	241.7	243.0			0	
SITYG_14120	*prfC*	1415085	1416630	peptide chain release factor 3	514	J	287.3	512.0	396.5			0	
SITYG_14130	-	1416820	1417141	hypothetical protein	106		64.6	342.3	250.3	4.2		0	
SITYG_14140	-	1417152	1417560	putative transcriptional regulator	135	K	233.8	592.5	246.1			1	alive in vivo

SITYG_14150	-	1417827	1418025	hypothetical protein	65		188.6	222.0	0.0	<-188.6	<-222.0	1	vivo-attenuated
SITYG_14160	-	1418017	1418443	hypothetical protein	141		136.3	103.2	94.3			2	vivo-attenuated
SITYG_14170	-	1418435	1418852	hypothetical protein	138		218.8	263.5	289.0			1	alive in vivo
SITYG_14180	-	1418848	1419439	hypothetical protein	196	K	252.7	223.1	203.9			0	
SITYG_14190	-	1419484	1419835	hypothetical protein	116		59.1	313.0	28.6			0	
SITYG_14200	-	1419821	1420013	hypothetical protein	63		172.8	457.8	889.1	5.6		0	
SITYG_14210	-	1420249	1420600	hypothetical protein	116		23.6	250.4	200.3	9.2		1	alive in vivo
SITYG_14220	-	1420619	1420970	hypothetical protein	116		47.3	313.0	28.6			0	
SITYG_14230	-	1420956	1421187	hypothetical protein	76		53.9	380.5	217.4	4.4		1	alive in vivo
SITYG_14240	-	1421384	1421735	hypothetical protein	116		1997.3	375.6	915.5			0	
SITYG_14250	-	1421755	1422106	hypothetical protein	116		709.1	313.0	1487.7			0	
SITYG_14260	-	1422092	1424141	hypothetical protein	682		510.2	343.2	377.4			3	alive in vivo
SITYG_14270	-	1424388	1425066	putative membrane protein	225		379.3	388.9	325.8			2	vivo-attenuated
SITYG_14280	-	1425069	1425774	putative membrane protein	234		276.5	592.2	213.7			0	
SITYG_14290	-	1425780	1426329	hypothetical protein	182	S	309.8	280.2	493.9			0	
SITYG_14300	*murF*	1426318	1427689	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate--D-alanyl-D-alanine ligase	456	M	1391.8	609.1	1084.0			0	
SITYG_14310	-	1427942	1428995	D-alanyl-alanine synthetase A	350	M	1024.2	542.6	839.2			0	
SITYG_14320	*recR*	1429119	1429716	recombination protein RecR	198	L	479.4	625.7	740.1			0	
SITYG_14330	*pbp2b*	1429726	1431787	putative penicillin-binding protein 2B	686	M	408.6	469.1	550.6			0	
SITYG_14340	*gpmA*	1431943	1432636	phosphoglycerate mutase	230	G	2322.5	475.6	2057.7			0	
SITYG_14350	-	1432773	1433235	putative Fe/Zn uptake regulation protein	153	P	826.0	998.8	1021.6			1	alive in vivo
SITYG_14360	-	1433403	1433679	transcriptional regulator HU subunit beta	91	L	7033.9	477.7	4256.9			0	
SITYG_14370	-	1433807	1434641	hypothetical protein	277	S	1009.7	395.2	445.5			0	
SITYG_14380	-	1434876	1435830	putative iron compound ABC transporter permease protein	317	P	126.1	391.6	189.5			2	vivo-attenuated
SITYG_14390	-	1435861	1436785	putative ABC transporter permease	307	P	139.2	665.9	619.5	4.8		2	alive in vivo
SITYG_14400	-	1436785	1437538	iron complex transport system ATP-binding protein	250	P	275.4	992.2	466.8			0	
SITYG_14410	-	1437559	1438531	putative ABC transporter, periplasmic component	323	P	102.4	429.5	423.6	4.5		0	
SITYG_14420	*pphA*	1438593	1439325	serine/threonine protein phosphatase 1	243	T	549.7	420.3	685.9			0	
SITYG_14430	*recN*	1439636	1441295	putative DNA repair protein RecN	552	L	417.6	410.6	550.8			0	
SITYG_14440	-	1441302	1441734	transcriptional regulator	143	K	585.7	254.3	278.9			0	
SITYG_14450	-	1441726	1442542	putative rRNA methylase	271	J	254.2	350.1	196.9			1	alive in vivo
SITYG_14460	-	1442507	1443410	putative geranylgeranyl pyrophosphate synthase	300	H	803.9	608.4	656.1			0	
SITYG_14470	-	1443406	1443619	exodeoxyribonuclease VII small subunit	70	L	331.1	722.2	235.7			0	
SITYG_14480	*xseA*	1443596	1444937	exodeoxyribonuclease VII large subunit	446	L	665.1	491.6	426.8			0	
SITYG_14490	-	1445218	1445680	putative transcriptional regulator	153	K	134.7	142.7	65.2			2	vivo-attenuated
SITYG_14500	-	1445726	1446956	hypothetical protein	409	R	114.7	178.7	236.8			1	alive in vivo
SITYG_14510	-	1447064	1448528	putative beta-fructosidase	487	G	31.2	315.2	109.7	3.8	-3.4	1	alive in vivo
SITYG_14520	-	1448535	1449387	sugar ABC transporter permease	283	G	63.3	464.3	212.2	3.7		0	
SITYG_14530	-	1449388	1450273	ABC transporter permease	294	G	75.0	546.3	295.0	4.3		0	
SITYG_14540	-	1450361	1451675	sugar ABC transporter substrate-binding protein	437	G	31.6	234.1	22.9			2	vivo-attenuated
SITYG_14550	-	1451806	1452802	putative transcriptional regulator	331	K	437.3	286.8	453.7			1	alive in vivo
SITYG_14560	-	1452885	1453719	putative carbohydrate kinase	277	G	388.0	658.7	301.0			1	alive in vivo
SITYG_14570	*folD*	1453824	1454679	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase	284	H	242.6	334.1	223.2			0	
SITYG_14580	-	1454948	1456241	hypothetical protein	430	V	166.8	254.9	101.0			1	alive in vivo
SITYG_14590	-	1456252	1456900	putative ABC transporter, ATP binding protein	215	V	204.8	610.4	248.0			2	vivo-attenuated
SITYG_14600	-	1456923	1458312	putative ABC transporter permease	462	V	149.3	221.5	195.2			1	alive in vivo
SITYG_14610	-	1458367	1458517	hypothetical protein	49		0.0	293.0	0.0			0	
SITYG_14620	-	1458755	1459298	hypothetical protein	180	S	152.8	283.3	74.0			0	
SITYG_14630	-	1459429	1459564	hypothetical protein	44		153.6	0.0	223.2			0	
SITYG_14640	-	1459572	1461717	ferrous iron transport protein B	714	P	201.1	491.7	365.2			3	alive in vivo
SITYG_14650	-	1461713	1462190	ferrous iron transport protein A	158	P	121.7	414.6	526.3	4.7		0	
SITYG_14660	-	1462358	1462589	hypothetical protein	76	S	915.8	0.0	1521.5			0	
SITYG_14670	*clpE*	1462828	1465096	putative ATP-dependent Clp protease subunit	755	O	287.2	1308.0	314.4			1	vivo-attenuated
SITYG_14680	-	1465142	1465748	hypothetical protein	201	S	75.3	471.4	16.6	-4.2	-34.1	1	alive in vivo
SITYG_14690	-	1465807	1466701	putative transcriptional regulator	297	K	157.8	467.0	280.8			2	vivo-attenuated
SITYG_14700	-	1466857	1467307	hypothetical protein	149	LR	525.4	439.5	602.5			0	
SITYG_14710	-	1467370	1467670	hypothetical protein	99		470.1	0.0	234.3			0	
SITYG_14720	-	1467743	1469798	putative transport protein	684	P	181.7	524.0	322.5			5	vivo-attenuated
SITYG_14730	-	1469809	1470064	hypothetical protein	84		146.4	172.4	78.8			0	
SITYG_14740	-	1470076	1470625	methyltransferase	182	QR	302.2	440.3	439.0			0	
SITYG_14750	-	1470618	1471554	Fe-S oxidoreductase	311	R	217.2	258.2	118.0			0	
SITYG_14760	-	1471603	1471927	methylated DNA-protein-cysteine methyltransferase	107	L	76.8	610.4	650.9	9.2		0	
SITYG_14770	-	1471948	1472599	membrane-associated phospholipid phosphatase	216	I	102.0	303.8	339.4	3.6		1	alive in vivo
SITYG_14780	-	1472588	1473152	putative membrane protein	187	S	514.8	389.6	373.9			4	vivo-attenuated
SITYG_14790	-	1473296	1473449	hypothetical protein	50		406.7	0.0	131.3			0	
SITYG_14800	-	1473584	1474097	putative RNA methyltransferase	170	J	549.9	171.3	704.7			0	
SITYG_14810	*trkA*	1474420	1475770	potassium transporter peripheral membrane component	449	P	1010.9	586.0	565.3			2	vivo-attenuated
SITYG_14820	-	1475773	1477213	potassium transporter	479	P	279.4	579.9	418.4			2	vivo-attenuated
SITYG_14830	-	1477245	1477500	putative membrane protein insertion efficiency factor	84	S	113.9	258.5	196.9			0	
SITYG_14840	-	1477499	1478225	ribosomal large subunit pseudouridine synthase B	241	J	394.2	575.1	345.8			0	
SITYG_14850	-	1478211	1478778	segregation and condensation protein B	188	K	709.7	542.6	921.0			0	
SITYG_14860	-	1478770	1479481	segregation and condensation protein A	236	S	455.1	710.9	974.5			1	alive in vivo
SITYG_14870	-	1479480	1480212	tyrosine recombinase XerD	243	L	294.7	270.2	178.3			0	
SITYG_14880	-	1480208	1480670	hypothetical protein	153	R	502.8	332.9	499.9			0	
SITYG_14890	-	1480666	1481188	phosphoesterase	173	R	1033.1	1010.3	1308.2			2	vivo-attenuated
SITYG_14900	-	1481163	1482189	hypothetical protein	341	F	731.8	471.2	714.5			0	
SITYG_14910	*murI*	1482146	1482941	glutamate racemase	264	M	365.2	414.6	265.3			0	
SITYG_14920	-	1483033	1483282	hypothetical protein	82	S	249.9	176.5	201.6			0	
SITYG_14930	*lysA*	1483336	1484587	diaminopimelate decarboxylase	416	E	215.5	421.6	305.0			0	
SITYG_14940	-	1484695	1485379	putative membrane protein	227	R	2498.6	1188.7	1982.0			2	vivo-attenuated
SITYG_14950	-	1485404	1485896	predicted HD superfamily hydrolase	163	R	1618.8	670.0	1306.3			0	
SITYG_14960	-	1485941	1486682	putative rRNA methylase	246	J	436.6	326.2	474.3			0	
SITYG_14970	-	1486712	1486991	acylphosphatase	92	C	133.8	315.0	467.9	3.8		1	alive in vivo
SITYG_14980	*yidC*	1487070	1487988	60Kd inner membrane protein	305	U	605.5	885.7	470.4			0	
SITYG_14990	-	1488119	1488584	putative mutT like protein	154	LR	1302.4	850.6	734.3			0	
SITYG_15000	*greA*	1488660	1489143	transcription elongation factor GreA	160	K	876.0	409.5	623.7			1	vivo-attenuated
SITYG_15010	-	1489346	1490951	hypothetical protein	534	R	2592.3	698.3	1564.2			0	
SITYG_15020	-	1490943	1491063	hypothetical protein	39		69.1	366.2	167.4			0	
SITYG_15030	-	1491059	1491557	GNAT family acetyltransferase	165	KR	141.6	132.4	665.4	5.1	4.2	0	
SITYG_15040	-	1491553	1491928	putative acetyltransferase	124	KR	243.4	293.0	1044.4	4.7		0	
SITYG_15050	-	1491909	1492077	putative acetyltransferase	55		172.8	130.8	119.5			0	
SITYG_15060	*murC*	1492066	1493398	UDP-N-acetylmuramate--L-alanine ligase	443	M	685.1	478.4	278.9			0	
SITYG_15070	-	1493480	1494113	hypothetical protein	210		360.4	381.9	428.3			0	
SITYG_15080	-	1494154	1497265	putative DNA/RNA helicase	1036	KL	390.7	522.7	619.8			3	vivo-attenuated
SITYG_15090	*engA*	1497477	1498788	GTP-binding protein engA	436	R	477.8	385.5	758.3			0	
SITYG_15100	-	1498915	1499362	hypothetical protein	148		556.8	393.3	921.1			0	
SITYG_15110	-	1499363	1499795	hypothetical protein	143		835.4	1169.9	906.6			0	
SITYG_15120	-	1499823	1500546	putative membrane protein	240		321.3	364.7	388.9			0	
SITYG_15130	-	1500560	1501271	putative membrane protein	236		198.4	618.1	211.9			0	
SITYG_15140	-	1501270	1502878	hypothetical protein	535		647.5	792.6	643.2			3	alive in vivo
SITYG_15150	*dnaI*	1502909	1503809	primosomal protein DnaI	299	L	373.3	415.1	323.6			0	
SITYG_15160	-	1503809	1504961	putative replication initiation and membrane attachment protein	383	L	514.9	286.1	592.8			0	
SITYG_15170	*nrdR*	1504961	1505435	transcriptional repressor NrdR	157	K	743.9	649.0	1186.4			0	
SITYG_15180	-	1505633	1506116	hypothetical protein	160		42.9	546.0	249.5	6.3		0	
SITYG_15190	-	1506166	1506982	hypothetical protein	271	R	71.2	565.5	443.0	6.8		0	
SITYG_15200	-	1506999	1509189	PTS system glucose-specific transporter subunit IIABC	729	G	314.4	923.1	559.4			1	alive in vivo
SITYG_15210	-	1509400	1509964	PTS system glucose-specific transporter subunit IIABC	187	G	242.7	467.5	178.0			1	alive in vivo
SITYG_15220	-	1510150	1510840	DNA-binding response regulator	229	TK	1857.7	923.6	1731.9			1	vivo-attenuated
SITYG_15230	*gnd*	1510848	1512273	6-phosphogluconate dehydrogenase	474	G	2628.6	1079.5	1754.7			0	
SITYG_15240	-	1512364	1512901	hypothetical protein	178	R	610.3	736.6	280.5			0	
SITYG_15250	-	1513093	1514320	putative membrane protein	408	GEPR	98.0	537.3	253.7			0	
SITYG_15260	*htpX*	1514422	1515319	putative heat shock protein	298	O	1290.2	514.5	1220.3			0	
SITYG_15270	-	1515320	1515881	putative membrane protein	186	S	1249.6	195.9	1145.6			3	vivo-attenuated
SITYG_15280	-	1515883	1516015	hypothetical protein	43		0.0	332.9	0.0			0	
SITYG_15290	-	1516028	1516742	ribosomal RNA small subunit methyltransferase G	237	M	470.6	338.5	337.5			0	
SITYG_15300	-	1516793	1517105	hypothetical protein	103	M	212.7	281.7	418.4			0	
SITYG_15310	-	1517174	1517615	hypothetical protein	146	M	235.2	249.1	364.3			0	
SITYG_15320	-	1517633	1518386	putative short chain dehydrogenase	250	R	292.0	466.9	573.4			1	alive in vivo
SITYG_15330	-	1518418	1519255	ABC transporter permease protein	278	P	342.0	446.3	407.9			0	
SITYG_15340	-	1519247	1520927	cobalt ABC transporter, ATP-binding protein	559	P	276.5	470.9	358.6			4	alive in vivo
SITYG_15350	-	1520938	1521700	putative uridine phosphorylase	253		277.6	547.9	803.9	3.2		2	vivo-attenuated
SITYG_15360	-	1522058	1522538	hypothetical protein	159		155.6	137.3	62.8			0	
SITYG_15370	-	1522565	1523045	hypothetical protein	159		388.9	1190.3	1213.4	3.4		0	
SITYG_15380	-	1523058	1523535	putative membrane protein	158		313.1	645.0	589.5			0	
SITYG_15390	-	1523524	1523737	predicted transcriptional regulators	70	K	136.3	206.3	141.4			2	vivo-attenuated
SITYG_15400	-	1524072	1524618	putative membrane protein	181	S	539.4	442.7	423.0			0	
SITYG_15410	-	1524632	1525481	S-adenosyl-l-methionine hydroxide adenosyltransferase	282	S	889.2	673.0	828.0			0	
SITYG_15420	-	1526079	1526247	hypothetical protein	55		74.1	523.2	119.5			0	
SITYG_15430	-	1532773	1532986	hypothetical protein	70		77.9	206.3	0.0			0	

SITYG_15440	-	1533056	1533749	methionine ABC transporter permease protein	230	P		131.7	253.7	231.8			2	vivo-attenuated
SITYG_15450	-	1533749	1534811	methionine ABC transporter ATP-binding protein	353	P		164.1	538.0	661.9	4.4		0	
SITYG_15460	-	1534803	1536177	putative succinyl-diaminopimelate desuccinylase	457	E		114.7	335.9	307.0			0	
SITYG_15470	-	1536266	1537118	putative lipoprotein	283	P		277.5	696.4	660.0			0	
SITYG_15480	-	1537272	1538097	ABC transporter, substrate-binding protein	274	ET		1282.2	772.4	1278.1			1	alive in vivo
SITYG_15490	-	1538279	1539416	hypothetical protein	378			62.0	231.9	194.3	3.4		0	
SITYG_15500	-	1539566	1540283	hypothetical protein	238	S		2615.0	704.9	2198.9			0	
SITYG_15510	-	1540397	1541489	hypothetical protein	363	R		281.1	281.7	606.9			2	vivo-attenuated
SITYG_15520	-	1541490	1542228	S-adenosylmethionine-dependent methyltransferase	245	QR		354.1	595.5	408.2			0	
SITYG_15530	-	1542439	1542793	hypothetical protein	117	S		1031.2	496.6	851.0			0	
SITYG_15540	-	1542793	1543306	isochorismatase family protein	170	Q		929.9	856.7	665.6			0	
SITYG_15550	-	1543302	1543899	predicted HD superfamily hydrolase	198	H		715.7	441.7	773.8			0	
SITYG_15560	*nadD*	1543888	1544527	nicotinate-nucleotide adenylyltransferase	212	H		207.7	343.9	141.4			0	
SITYG_15570	-	1544539	1544851	RNA-binding protein	103	J		372.3	493.0	257.5			0	
SITYG_15580	-	1544914	1546021	GTP-binding protein YqeH	368	R		580.8	377.2	644.1			0	
SITYG_15590	-	1546023	1546551	HAD superfamily phosphatase	175	R		942.8	582.7	779.8			0	
SITYG_15600	-	1546700	1547327	hypothetical protein	208	S		383.7	280.4	496.5			0	
SITYG_15610	-	1547357	1548269	putative membrane protein	303	GER		377.5	313.2	671.7			0	
SITYG_15620	-	1548363	1549410	putative butanediol dehydrogenase	348	ER		344.7	902.5	259.0			2	vivo-attenuated
SITYG_15630	*gatB*	1549538	1550972	aspartyl/glutamyl-tRNA amidotransferase subunit B	477	J		422.3	459.7	483.2			0	
SITYG_15640	*gatA*	1550971	1552438	aspartyl/glutamyl-tRNA amidotransferase subunit A	488	J		254.5	419.4	410.7			0	
SITYG_15650	*gatC*	1552437	1552740	aspartyl/glutamyl-tRNA amidotransferase subunit C	100	J		657.1	362.6	331.4			0	
SITYG_15660	-	1552804	1554553	aspartyl-tRNA synthetase	582	J		71.2	314.1	172.2			0	
SITYG_15670	-	1554932	1555508	isochorismatase family protein	191	Q		439.3	343.4	383.5			0	
SITYG_15680	-	1555507	1556296	GTP-sensing transcriptional pleiotropic repressor	262	K		1146.1	306.4	750.9			0	
SITYG_15690	-	1556457	1557672	putative aminotransferase AlaT	404	E		399.5	524.5	586.8			0	
SITYG_15700	-	1557824	1558277	universal stress protein UspA	150	T		1309.5	7082.3	1307.9			0	
SITYG_15710	-	1558322	1559711	predicted hydrolases of the HAD superfamily	462	R		421.1	379.7	412.1			3	vivo-attenuated
SITYG_15720	*ansB*	1559775	1560738	asparaginase	320	EJ		409.2	502.0	406.7			1	alive in vivo
SITYG_15730	*recG*	1561228	1563244	ATP-dependent DNA helicase RecG	671	LK		444.4	654.0	642.6			0	
SITYG_15740	*alr*	1563347	1564454	alanine racemase	368	M		419.7	615.4	353.8			0	
SITYG_15750	-	1564440	1564842	Holo-[acyl-carrier-protein] synthase	133	I		175.4	273.3	174.9			0	
SITYG_15760	-	1564847	1565888	putative phospho-2-dehydro-3-deoxyheptonate aldolase	346	E		1773.2	464.4	1321.6			0	
SITYG_15770	*secA*	1565908	1568428	preprotein translocase subunit SecA	839	U		1822.2	575.5	1542.2			0	
SITYG_15780	-	1568554	1570402	amino acid permease	615	E		473.6	570.8	336.9			1	alive in vivo
SITYG_15790	-	1570658	1571603	mannose-6-phosphate isomerase, class I	314	G		588.2	1139.4	786.4			0	
SITYG_15800	-	1571630	1572356	GentR family transcriptional regulator	241	K		771.4	454.0	622.4			0	
SITYG_15810	-	1572389	1573658	phosphotransferase system cellobiose-specific component IIC	422	G		163.4	346.3	166.2			0	
SITYG_15820	-	1573800	1575198	beta-galactosidase	465	G		32.6	314.4	143.7	4.8		0	
SITYG_15830	-	1575231	1575369	hypothetical protein	45			0.0	0.0	0.0			2	vivo-attenuated
SITYG_15840	-	1575346	1575760	hypothetical protein	137			110.2	318.5	121.3			0	
SITYG_15850	-	1575844	1577605	putative ABC transporter	586	V		497.0	524.1	444.8			1	alive in vivo
SITYG_15860	-	1577594	1579361	ABC multidrug transporter	588	V		605.7	559.6	676.3			3	alive in vivo
SITYG_15870	-	1579353	1579812	MarR family transcriptional regulator	152	K		1934.0	191.5	1531.5			0	
SITYG_15880	-	1579983	1581171	putative NADH-dependent oxidoreductase	395	C		380.6	628.9	583.2			2	alive in vivo
SITYG_15890	-	1581437	1581848	peptide deformylase	136	J		181.7	427.7	390.9			0	
SITYG_15900	*scrK*	1581913	1582813	putative fructokinase	299	KG		124.4	244.2	156.2			0	
SITYG_15910	*scrA*	1582952	1584851	PTS system, sucrose-specific IIABC component	632	G		72.1	509.2	312.0	4.7		0	
SITYG_15920	*scrB*	1585042	1586497	sucrose-6-phosphate hydrolase	484	G		65.6	287.0	214.0	3.6		0	
SITYG_15930	*scrR*	1586477	1587443	transcriptional regulator	321	K		77.3	364.0	197.5			0	
SITYG_15940	-	1587528	1588347	hypothetical protein	272	R		455.8	590.3	429.1			1	alive in vivo
SITYG_15950	-	1588473	1589397	oligopeptide ABC transporter ATP-binding protein	307	E		888.9	380.5	608.6			1	vivo-attenuated
SITYG_15960	-	1589407	1590475	oligopeptide ABC transporter ATP-binding protein AmiE	355	EP		761.3	535.0	959.1			0	
SITYG_15970	-	1590483	1591410	oligopeptide transport system permease protein AmiD	308	EP		711.5	450.4	790.8			1	vivo-attenuated
SITYG_15980	-	1591409	1592906	oligopeptide transport system permease	498	EP		817.4	484.4	851.9			2	vivo-attenuated
SITYG_15990	*aliA*	1593279	1595259	oligopeptide-binding protein AliA	659	E		142.5	643.7	481.8	3.7		0	
SITYG_16000	-	1595455	1597432	oligopeptide-binding protein AmiA	658	E		1200.2	555.8	1112.4			0	
SITYG_16010	-	1597590	1598277	hypothetical protein	228	S		259.6	447.8	175.4			0	
SITYG_16020	-	1598501	1600115	CTP synthetase	537	F		1053.7	612.7	1007.9			0	
SITYG_16030	*rpoE*	1600357	1600945	DNA-directed RNA polymerase subunit delta	195	K		4776.0	710.1	3586.4			0	
SITYG_16040	-	1601182	1602466	trigger factor	427	O		3728.2	907.1	2971.9			0	
SITYG_16050	-	1602583	1603147	hypothetical protein	187	S		456.0	584.4	623.2			0	
SITYG_16060	-	1603360	1603909	putative membrane protein	182	S		1072.9	480.3	1079.2			0	
SITYG_16070	*thiD*	1603811	1604585	phosphomethylpyrimidine kinase	257	H		348.4	340.7	544.9			0	
SITYG_16080	*truA*	1604574	1605324	tRNA pseudouridine synthase A	249	J		2284.3	410.2	1566.5			0	
SITYG_16090	-	1605445	1605919	NUDIX family hydrolase	157	LR		122.5	278.2	296.6			0	
SITYG_16100	*dnaJ*	1605948	1607085	chaperone protein DnaJ	378	O		193.4	367.2	247.3			0	
SITYG_16110	*dnaK*	1607534	1609367	chaperone protein DnaK	610	O		1210.7	4951.2	1068.3			0	
SITYG_16120	*grpE*	1609651	1610188	heat shock protein GrpE	178	O		672.1	1063.9	635.8			1	alive in vivo
SITYG_16130	*hrcA*	1610223	1611258	heat-inducible transcription repressor HrcA	344	K		821.6	1146.5	844.1			0	
SITYG_16140	-	1611421	1612150	ABC multidrug transporter permease component	242			227.6	934.4	592.3			0	
SITYG_16150	-	1612142	1612982	ABC-type multidrug transport system, ATPase component	279	V		222.2	470.9	382.6			0	
SITYG_16160	-	1613023	1613596	hypothetical protein	190			217.2	421.9	105.2			1	alive in vivo
SITYG_16170	-	1613595	1613919	PadR family transcriptional regulator	107	K		845.0	678.2	433.9			0	
SITYG_16180	-	1614135	1614600	D-alanyl-D-alanine carboxypeptidase	154	M		294.4	567.1	583.1			0	
SITYG_16190	-	1614897	1615596	putative phosphoglycerate mutase	232	G		1376.8	2829.4	1178.0			0	
SITYG_16200	-	1615910	1616453	hypothetical protein	180	G		99.3	566.6	684.3	7.5		0	
SITYG_16210	-	1616644	1617982	hypothetical protein	445	S		648.0	558.4	848.1			0	
SITYG_16220	-	1617994	1618261	hypothetical protein	88	T		683.6	164.6	1090.7			0	
SITYG_16230	-	1618371	1619376	putative sugar binding transcriptional regulator	334	K		111.4	546.6	589.5	5.8		0	
SITYG_16240	-	1619458	1621357	hypothetical protein	632			120.1	636.4	565.8	5.1		2	vivo-attenuated
SITYG_16250	-	1621619	1621928	preprotein translocase YajC subunit	102	U		214.8	640.0	97.5			0	
SITYG_16260	-	1621927	1622743	PTS system, N-acetylgalactosamine-specific IID component	271	G		482.9	781.0	713.8			0	
SITYG_16270	-	1622729	1623509	PTS system, N-acetylgalactosamine-specific IIC component	259	G		356.3	1436.8	708.1			0	
SITYG_16280	-	1623524	1624016	PTS system, N-acetylgalactosamine-specific IIB component	163	G		252.9	1116.6	489.9			0	
SITYG_16290	-	1624026	1625217	glucuronyl hydrolase	396			289.1	1125.5	758.8			2	vivo-attenuated
SITYG_16300	-	1625230	1625665	PTS system transporter subunit IIA	144	G		171.6	353.6	92.3			0	
SITYG_16310	-	1625955	1626771	gluconate 5-dehydrogenase	271	IQR		76.3	296.2	36.9			0	
SITYG_16320	-	1626786	1627428	putative ribose/galactose isomerase	213	G		239.1	650.3	140.8			0	
SITYG_16330	-	1627459	1628461	2-keto-3-deoxygluconate kinase	333	G		211.1	657.9	270.6			1	alive in vivo
SITYG_16340	-	1628470	1629100	keto-hydroxyglutarate-aldolase	209	G		164.6	383.7	302.9			0	
SITYG_16350	-	1629250	1631278	putative fibrinogen-binding protein	675	M	LPXTG	441.8	563.5	356.5			0	
SITYG_16360	-	1631518	1634710	putative hyaluronate lyase protein	1063		LPXTG	133.9	502.6	512.8	4.2		1	alive in vivo
SITYG_16370	-	1635021	1635498	glutathione peroxidase	158	O		173.9	414.6	147.4			0	
SITYG_16380	-	1636775	1640042	putative collagen-binding protein	1088	M	LPXTG	174.0	302.7	276.6			2	vivo-attenuated
SITYG_16390	-	1640668	1640827	hypothetical protein	52			0.0	0.0	0.0			0	
SITYG_16400	-	1641209	1641578	hypothetical protein	122	S		2720.5	357.3	1986.6			0	
SITYG_16410	-	1641564	1641840	putative transcriptional regulator	91	K		150.3	398.1	181.9			0	
SITYG_16420	-	1642267	1642420	hypothetical protein	50			108.4	143.6	0.0	<-108.4	<-143.6	0	
SITYG_16430	-	1642627	1642741	hypothetical protein	37			0.0	0.0	0.0			0	
SITYG_16440	-	1643003	1643765	hypothetical protein	253	R		76.2	576.8	382.2	5.5		2	alive in vivo
SITYG_16450	-	1643766	1644693	ABC transporter, ATP-binding protein	308	V		89.5	853.4	173.3			0	
SITYG_16460	-	1644743	1646798	hypothetical protein	684	V		82.8	684.4	332.3	4.4		1	alive in vivo
SITYG_16470	-	1647000	1647171	hypothetical protein	56			0.0	1413.6	117.5	#DIV/0!	-14.4	0	
SITYG_16480	-	1647455	1647956	hypothetical protein	166			1258.5	921.1	761.7			0	
SITYG_16490	-	1647956	1649066	hypothetical protein	369	E		381.2	316.8	488.5			2	alive in vivo
SITYG_16500	-	1649936	1650728	hypothetical protein	263	S		78.6	388.4	393.1	5.4		0	
SITYG_16510	-	1650740	1650866	hypothetical protein	41	S		32.9	174.4	0.0			0	
SITYG_16520	-	1651263	1651452	hypothetical protein	62			21.9	116.3	531.3	26.4	3.8	0	
SITYG_16530	-	1651432	1651927	transposase	164	L		117.3	621.5	284.0			0	
SITYG_16540	-	1652062	1654126	P-type ATPase-metal/cation transporter	687	P		978.8	660.1	924.4			0	
SITYG_16550	-	1654127	1654406	hypothetical protein	92			26702.9	7009.8	16448.7			0	
SITYG_16560	-	1654586	1655168	transposase	193	L		49.9	415.3	224.3	4.9		1	vivo-attenuated
SITYG_16570	-	1655541	1656552	putative ABC transporter permease	336	V		935.5	717.3	814.5			0	
SITYG_16580	-	1656548	1657259	ABC transporter, ATP-binding protein	236	V		670.9	896.3	381.3			2	alive in vivo
SITYG_16590	-	1657258	1658023	hypothetical protein	254	O		694.1	545.8	367.5			1	alive in vivo
SITYG_16600	-	1658031	1658844	hypothetical protein	270	R		545.9	594.6	592.9			0	
SITYG_16610	-	1658857	1660081	hypothetical protein	407	IQ		1206.5	1310.6	1575.2			0	
SITYG_16620	-	1660073	1661327	3-oxoacyl-ACP synthase	417	IQ		1740.0	1472.0	1097.1			2	vivo-attenuated
SITYG_16630	-	1661329	1662253	hypothetical protein	307			767.7	689.7	641.2			0	
SITYG_16640	-	1662254	1662662	hypothetical protein	135			406.7	484.7	1230.6	3.3		1	alive in vivo
SITYG_16650	-	1662700	1663702	hypothetical protein	333	MG		658.2	965.0	410.9			0	
SITYG_16660	-	1663903	1664359	transposase	151	L		354.8	2650.5	418.4			2	alive in vivo
SITYG_16670	-	1664405	1664552	hypothetical protein	48			366.8	448.5	204.9			0	
SITYG_16680	-	1664754	1664928	hypothetical protein	57			1954.9	1136.6	2308.5			0	
SITYG_16690	-	1665209	1666076	putative transcriptional regulator	288	K		578.9	228.1	532.8			2	vivo-attenuated
SITYG_16700	-	1666559	1666907	hypothetical protein	115			739.0	442.0	461.7			2	vivo-attenuated
SITYG_16710	-	1667011	1667512	transposase	166	L		99.4	1096.5	60.1			0	
SITYG_16720	-	1667487	1668327	putative transposase	279	L		74.1	392.4	167.4			0	

SITYG_16730	-	1668328	1668574	putative transcriptional regulator	81	K		16.9	268.0	0.0			0	
SITYG_16740	-	1668624	1669068	hypothetical protein	147	D		46.7	297.0	22.6			1	alive in vivo
SITYG_16750	-	1669348	1669768	-				49.4	261.6	0.0			1	alive in vivo
SITYG_16760	-	1669773	1670508	replication initiation factor	244	L		56.4	179.4	136.6			0	
SITYG_16770	-	1670631	1670802	hypothetical protein	56			24.3	0.0	0.0			0	
SITYG_16780	-	1670861	1671122	putative transcriptional regulator	86			15.9	252.6	0.0			2	vivo-attenuated
SITYG_16790	-	1671193	1672429	integrase	411	L		80.5	337.8	178.7			0	
SITYG_16800	*rpsI*	1672520	1672913	30S ribosomal protein S9	130	J		3726.0	559.2	3194.0			0	
SITYG_16810	*rplM*	1672932	1673379	50S ribosomal protein L13	148	J		10588.5	1524.0	7188.9			0	
SITYG_16820	-	1673560	1674430	hypothetical protein	289	S		190.7	353.6	230.9			2	vivo-attenuated
SITYG_16830	-	1674572	1674725	hypothetical protein	50			108.4	143.6	131.3			0	
SITYG_16840	*trmH*	1674863	1675592	RNA methyltransferase	242	J		386.9	512.4	330.6			1	vivo-attenuated
SITYG_16850	-	1675748	1676879	Multiple sugar ABC transporter, ATP-binding protein	376	G		542.8	2059.5	461.7			0	
SITYG_16860	-	1676989	1677862	including PucR C-terminal helix-turn-helix domain; pfam13556	290	TQ		185.3	604.1	138.0			0	
SITYG_16870	-	1677848	1678253	hypothetical protein	134	S		891.1	922.4	694.3			1	alive in vivo
SITYG_16880	*cysS*	1678245	1679589	cysteinyl-tRNA synthetase	447	J		237.7	327.0	358.6			0	
SITYG_16890	-	1679606	1680128	dihydrofolate reductase	173	H		206.6	126.3	57.7	-3.3		0	
SITYG_16900	-	1680136	1680901	putative uridine phosphorylase	254			254.9	287.3	236.3			0	
SITYG_16910	*cysE*	1680944	1681529	serine O-acetyltransferase	194	E		283.6	788.8	789.6	3.0		0	
SITYG_16920	*pnpA*	1681578	1683759	polyribonucleotide nucleotidyltransferase	726	J		475.5	574.3	372.9			0	
SITYG_16930	-	1684157	1685957	oligoendopeptidase F	599	E		336.5	586.0	585.8			0	
SITYG_16940	-	1686120	1686876	hypothetical protein	251			137.2	465.1	239.1			0	
SITYG_16950	*rpsO*	1687772	1688102	ribosomal protein S15	109	J		264.0	133.2	273.9			0	
SITYG_16960	-	1688171	1688903	pseudouridylate synthase	243	J		447.7	510.3	466.4			0	
SITYG_16970	-	1688889	1690062	hypothetical protein	390	GEPR		290.0	580.7	333.9			0	
SITYG_16980	-	1690191	1691565	hypothetical protein	457			609.8	367.8	811.3			1	alive in vivo
SITYG_16990	-	1691578	1692250	hypothetical protein	223			321.0	555.9	388.5			0	
SITYG_17000	-	1692268	1693012	hypothetical protein	247			172.8	502.1	445.4			0	
SITYG_17010	-	1692989	1694762	spore coat protein CotH	590	M		311.2	433.8	407.8			0	
SITYG_17020	-	1694754	1696200	putative membrane protein	481	S		220.9	668.7	361.1			2	alive in vivo
SITYG_17030	-	1696199	1697606	glycosyltransferase	468	M		265.3	1436.9	635.2			0	
SITYG_17040	-	1697621	1699454	hypothetical protein	610	S		138.0	287.7	301.3			0	
SITYG_17050	-	1699466	1700366	hypothetical protein	299			359.5	830.2	323.6			1	alive in vivo
SITYG_17060	-	1700372	1702152	-		MG		212.1	308.6	321.6			1	alive in vivo
SITYG_17070	*def*	1702447	1703062	peptide deformylase	204	J		876.8	750.4	783.8			0	
SITYG_17080	-	1703123	1703354	transglycosylase associated protein	76	S		413.0	95.1	173.9			0	
SITYG_17090	*pepS*	1703436	1704678	putative aminopeptidase	413	E		150.3	336.2	331.5			0	
SITYG_17100	-	1704697	1704850	hypothetical protein	50			0.0	0.0	0.0			0	
SITYG_17110	*polC*	1704869	1709264	DNA polymerase III subunit alpha, Gram-positive type	1464	L		197.3	355.0	242.2			0	
SITYG_17120	-	1709547	1710402	5'-nucleotidase	284	R		388.1	719.6	434.6			0	
SITYG_17130	-	1710590	1714298	putative alkaline amylopullulanase	1235	G	LPXTG	136.5	604.5	281.7			7	vivo-attenuated
SITYG_17140	*leuS*	1715073	1717575	leucine-tRNA ligase	833	J		412.8	474.3	469.6			1	alive in vivo
SITYG_17150	-	1717715	1719611	putative endopeptidase O	631	O		566.7	452.0	550.8			0	
SITYG_17160	-	1719786	1720506	putative ABC transporter, ATP-binding protein	239	P		2915.2	305.2	2050.2			1	alive in vivo
SITYG_17170	-	1720507	1721362	ABC transporter, permease component	284	P		1314.8	514.0	1491.6			0	
SITYG_17180	-	1721390	1722320	putative metal ABC transporter substrate-binding lipoprotein	309	P		3091.1	1275.9	2580.7			0	
SITYG_17190	-	1722474	1723125	putative transcriptional regulator	216	K		1650.3	607.6	1234.0			0	
SITYG_17200	*dtd*	1723188	1723632	D-tyrosyl-tRNA(Tyr) deacylase	147	J		588.6	346.4	384.5			0	
SITYG_17210	*relA*	1723711	1725928	GTP pyrophosphokinase	738	TK		368.6	376.7	588.8			26	vivo-attenuated
SITYG_17220	-	1726546	1727290	ribosomal RNA small subunit methyltransferase E	247	S		239.7	502.1	377.9			0	
SITYG_17230	*prmA*	1727290	1728244	ribosomal protein L11 methyltransferase	317	J		352.2	506.8	463.2			0	
SITYG_17240	-	1728385	1728856	GNAT family acetyltransferase	156	KR		343.5	326.6	511.7			2	alive in vivo
SITYG_17250	-	1728852	1729305	MutT/NUDIX family protein	150	LR		283.9	339.6	243.8			0	
SITYG_17260	-	1729314	1729785	hypothetical protein	156			220.2	373.2	191.9			1	alive in vivo
SITYG_17270	-	1729872	1731144	recombination factor protein RarA	423	L		185.9	380.1	292.1			1	alive in vivo
SITYG_17280	-	1732043	1732157	putative deoxyribonucleoside kinase	37	F		0.0	0.0	0.0			0	
SITYG_17290	-	1732311	1733079	hypothetical protein	255	S		502.3	600.9	549.2			0	
SITYG_17300	-	1733172	1733334	hypothetical protein	53			0.0	0.0	0.0			0	
SITYG_17310	*groEL*	1733459	1735082	chaperonin GroEL	540	O		904.8	5158.6	1020.9			0	
SITYG_17320	*groES*	1735114	1735396	co-chaperonin GroES	93	O		3927.5	16286.2	2172.2			0	
SITYG_17330	-	1735540	1735831	hypothetical protein	96			313.6	302.1	483.1			0	
SITYG_17340	-	1735845	1736676	PTS system mannose-specific transporter subunit IID	276	G		1063.3	449.5	495.5			2	alive in vivo
SITYG_17350	-	1736677	1737526	PTS system mannose-specific transporter subunit IIC	282	G		796.4	957.7	721.5			0	
SITYG_17360	-	1737558	1738053	PTS system mannose-specific transporter subunit IIB	164	G		385.5	266.4	202.9			0	
SITYG_17370	-	1738076	1738514	PTS system mannose-specific transporter subunit IIA	145	G		1430.1	1003.4	2063.4			0	
SITYG_17380	-	1738761	1740048	putative sugar-binding periplasmic protein	428	G		235.3	546.4	647.6			0	
SITYG_17390	-	1740044	1740728	putative transcriptional regulator	227	TK		218.3	546.2	337.7			0	
SITYG_17400	-	1740720	1742043	histidine kinase	440	T		250.8	797.3	660.4			1	alive in vivo
SITYG_17410	-	1742033	1743020	putative periplasmic sugar-binding protein	328	G		340.4	534.3	478.2			1	vivo-attenuated
SITYG_17420	-	1743236	1743632	single-stranded DNA-binding protein	131	L		83.8	166.5	380.4	4.9		0	
SITYG_17430	-	1743703	1744330	phenylalanyl-tRNA synthetase subunit beta	208	R		1137.9	700.9	896.9			2	vivo-attenuated
SITYG_17440	-	1744346	1744664	thioredoxin	105	OC		678.3	276.4	252.6			0	
SITYG_17450	-	1744660	1744948	hypothetical protein	95			2491.8	228.9	1534.2			0	
SITYG_17460	*pepA*	1745067	1746132	glutamyl aminopeptidase	354	G		268.8	433.3	377.2			0	
SITYG_17470	-	1746268	1746619	hypothetical protein	116			94.5	438.2	257.5			0	
SITYG_17480	-	1747267	1747426	hypothetical protein	52			26.1	0.0	0.0			1	alive in vivo
SITYG_17490	-	1747592	1747922	hypothetical protein	109			25.1	133.2	486.9	21.1	3.0	0	
SITYG_17500	-	1747925	1748255	hypothetical protein	109			364.5	865.7	121.7			1	alive in vivo
SITYG_17510	-	1748576	1748864	hypothetical protein	95			43.2	381.5	69.7			0	
SITYG_17520	-	1749273	1749849	hypothetical protein	191			180.0	267.1	244.1			0	
SITYG_17530	-	1749845	1750427	hypothetical protein	193			64.1	188.8	327.8	5.6		1	alive in vivo
SITYG_17540	-	1750436	1750592	hypothetical protein	51			79.8	281.7	0.0			0	
SITYG_17550	-	1750748	1750934	hypothetical protein	61			66.9	708.9	54.0			0	
SITYG_17560	-	1751399	1751624	hypothetical protein	74			184.4	195.3	89.3			0	
SITYG_17570	-	1751723	1752056	hypothetical protein	110			199.3	329.9	331.7			0	
SITYG_17580	-	1752052	1754203	hypothetical protein	716			478.3	551.7	508.9			3	vivo-attenuated
SITYG_17590	-	1754336	1754894	hypothetical protein	185	S		646.8	433.2	575.9			0	
SITYG_17600	-	1755075	1756401	dihydrofolate synthetase	441	H		168.9	546.9	204.5			2	alive in vivo
SITYG_17610	-	1756581	1757220	putative membrane protein	212			71.4	275.1	157.2			0	
SITYG_17620	-	1757496	1757793	hypothetical protein	98			572.6	148.0	574.8			0	
SITYG_17630	-	1757809	1758202	hypothetical protein	130			1646.6	1174.2	1149.8			0	
SITYG_17640	-	1758183	1759515	hypothetical protein	443			576.1	725.9	573.0			1	alive in vivo
SITYG_17650	-	1759507	1759894	hypothetical protein	128			1318.4	965.3	622.8			1	alive in vivo
SITYG_17660	-	1760134	1760527	hypothetical protein	130			179.4	335.5	306.6			0	
SITYG_17670	-	1760546	1760771	hypothetical protein	74			73.7	586.0	133.9			0	
SITYG_17680	-	1760773	1761160	hypothetical protein	128			192.9	283.9	596.8	3.4		0	
SITYG_17690	-	1761340	1763200	prolyl-tRNA synthetase	619	J		368.0	378.1	448.1			0	
SITYG_17700	-	1763233	1764505	zinc metalloprotease	423	M		300.0	431.9	521.0			2	alive in vivo
SITYG_17710	*cdsA*	1764656	1765460	phosphatidate cytidylyltransferase	267	I		706.8	738.0	849.3			0	
SITYG_17720	*uppS*	1765468	1766218	undecaprenyl pyrophosphate synthetase	249	I		663.7	322.3	696.2			0	
SITYG_17730	*yajC*	1766685	1767024	preprotein translocase subunit YajC	112	U		8675.7	583.4	5243.2			1	alive in vivo
SITYG_17740	-	1767426	1767606	hypothetical protein	59	S		599.2	366.2	390.5			0	
SITYG_17750	*tkt*	1767701	1769678	transketolase	658	G		352.5	611.3	665.4			0	
SITYG_17760	-	1769818	1770910	putative L-ascorbate 6-phosphate lactonase	363	R		53.2	382.3	101.2			0	
SITYG_17770	-	1771071	1772742	hypothetical protein	556	K		136.5	486.6	270.4			0	
SITYG_17780	-	1772945	1773653	putative L-ribulose-5-phosphate 4-epimerase	235	G		35.2	279.3	496.4	15.4		0	
SITYG_17790	-	1773655	1774519	L-ribulose-5-phosphate 3-epimerase	287	G		33.6	330.6	139.5	4.5		0	
SITYG_17800	-	1774524	1775190	putative 3-keto-L-gulonate-6-phosphate decarboxylase	221	G		112.1	989.8	316.6	3.1	-3.8	0	
SITYG_17810	-	1775235	1775721	putative phosphotransferase system sugar-specific EII component	161	GT		76.8	271.3	0.0			0	
SITYG_17820	-	1775922	1776204	putative phosphotransferase system sugar-specific EII component	93	G		117.7	311.7	35.6	-3.0	-10.5	0	
SITYG_17830	-	1776234	1777695	PTS system ascorbate-specific transporter subunit IIC	486	S		76.7	571.6	178.7			0	
SITYG_17840	*clpL*	1777862	1779992	ATP-dependent Clp protease ATP-binding subunit	709	O		467.4	9336.6	650.6			2	alive in vivo
SITYG_17850	-	1780369	1780675	hypothetical protein	101			1559.0	359.1	1476.8			0	
SITYG_17860	-	1780674	1781085	hypothetical protein	136			1281.8	588.1	1417.1			0	
SITYG_17870	-	1781066	1782326	hypothetical protein	419			250.2	575.5	215.2			0	
SITYG_17880	-	1782322	1782715	Protein of unknown function DUF1310 (IPR010738)	130			358.9	1565.6	383.3			0	
SITYG_17890	-	1782769	1782952	hypothetical protein	60			181.3	480.3	109.7			0	
SITYG_17900	-	1782954	1783341	hypothetical protein	128			578.8	908.5	285.4			0	
SITYG_17910	-	1783383	1783566	hypothetical protein	60			68.0	360.2	0.0			0	
SITYG_17920	-	1783570	1783879	hypothetical protein	102			147.7	355.6	325.0			0	
SITYG_17930	-	1783832	1783958	hypothetical protein	41			98.8	0.0	0.0			0	
SITYG_17940	-	1784001	1784184	hypothetical protein	60			22.7	0.0	54.9			0	
SITYG_17950	-	1784180	1784573	hypothetical protein	130			116.1	279.6	102.2			0	
SITYG_17960	-	1784807	1785194	hypothetical protein	128			235.8	567.8	363.3			0	
SITYG_17970	*glmS*	1785390	1787205	Glucosamine-fructose-6-phosphate aminotransferase	604	M		841.1	448.0	724.8			0	
SITYG_17980	*ackA*	1787586	1788786	acetate kinase	399	C		598.0	347.9	803.4			2	vivo-attenuated
SITYG_17990	-	1788832	1789786	adenine-specific DNA methylase	317	L		182.6	345.5	389.5			1	alive in vivo
SITYG_18000	-	1789876	1790173	hypothetical protein	98			55.9	517.9	304.3	5.9		0	
SITYG_18010	-	1790183	1790621	Competence operon G, ComGF	145	U		94.7	752.6	68.8			0	

SITYG_18020	-	1790604	1790898	hypothetical protein	97	NU		28.2	74.7	136.6	5.3		0	
SITYG_18030	*comYD*	1790869	1791298	competence protein ComYD	142	NU		67.7	409.8	93.6			0	
SITYG_18040	*comYC*	1791257	1791575	competence protein ComYC	105	U		39.1	276.4	63.2			0	
SITYG_18050	*comYB*	1791571	1792657	competence protein ComYB	361	NU		87.9	768.9	295.9	3.7	-3.1	1	vivo-attenuated
SITYG_18060	*comYA*	1792535	1793477	competence protein ComYA	313	NU		26.4	303.3	117.3	4.8	-3.1	0	
SITYG_18070	-	1793545	1793911	hypothetical protein	121	S		816.0	300.2	411.6			1	alive in vivo
SITYG_18080	-	1794039	1794756	hypothetical protein	238			225.6	459.7	112.0			0	
SITYG_18090	-	1794730	1796347	hypothetical protein	538			436.1	557.2	428.5			5	vivo-attenuated
SITYG_18100	*glnA*	1796542	1797889	glutamine synthetase type I	448	E		1478.2	636.2	1110.8			0	
SITYG_18110	*glnR*	1797927	1798287	putative transcription regulator	119	K		2730.9	305.2	2175.8			0	
SITYG_18120	-	1798363	1798894	hypothetical protein	176	S		359.4	496.6	453.9			0	
SITYG_18130	-	1799068	1799749	hypothetical protein	226	R		1011.2	968.0	634.1			3	alive in vivo
SITYG_18140	-	1800155	1804088	putative glucan-binding protein	1310		LPXTG	2319.3	681.6	1807.7			2	vivo-attenuated
SITYG_18150	*pgk*	1804418	1805615	phosphoglycerate kinase	398	G		4383.8	1266.7	2860.7			0	
SITYG_18160	*rpoC*	1805746	1809385	DNA-directed RNA polymerase subunit beta	1212	K		874.3	766.9	888.6			0	
SITYG_18170	*rpoB*	1809423	1812990	DNA-directed RNA polymerase I subunit beta	1188	K		853.6	548.3	771.4			0	
SITYG_18180	-	1813276	1815619	putative membrane carboxypeptidase	780	M		394.8	365.8	518.6			2	alive in vivo
SITYG_18190	*tyrS*	1815800	1817057	tyrosyl-tRNA synthetase	418	J		841.5	489.5	711.0			0	
SITYG_18200	*rrmA*	1817300	1818137	rRNA (guanine-N1-)-methyltransferase A	278	QR		163.5	446.3	347.9			1	alive in vivo
SITYG_18210	-	1818194	1818875	peptidase S54	226	R		170.6	580.8	162.2			1	alive in vivo
SITYG_18220	-	1818867	1819395	5-formyltetrahydrofolate cyclo-ligase	175	H		204.3	624.3	285.3			0	
SITYG_18230	*hipO*	1819440	1820571	putative N-acetyldiaminopimelate deacetylase	376	R		542.8	796.6	515.0			0	
SITYG_18240	*dapD*	1820583	1821282	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	232	E		468.8	785.9	517.2			0	
SITYG_18250	*gltX*	1821399	1822857	glutamyl-tRNA synthetase	485	J		1448.2	512.4	1164.0			0	
SITYG_18260	*radA*	1823065	1824481	DNA repair protein RadA	471	O		149.4	388.0	361.7			0	
SITYG_18270	-	1824438	1824909	hypothetical protein	156	Q		158.5	46.7	149.2			0	
SITYG_18280	-	1824918	1825362	deoxyuridine 5'-triphosphate nucleotidohydrolase	147	F		317.7	247.5	384.5			0	
SITYG_18290	-	1825455	1826490	putative LD-carboxypeptidase	344	V		160.3	615.7	126.1			0	
SITYG_18300	*gpsA*	1827553	1828570	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	338	C		240.7	540.2	760.3	3.4		0	
SITYG_18310	*galU*	1828595	1829495	UTP-glucose-1-phosphate uridylyltransferase	299	M		470.1	317.4	457.5			0	
SITYG_18320	-	1829591	1829954	hypothetical protein	120	L		57.1	363.2	55.3			0	
SITYG_18330	-	1829964	1830099	hypothetical protein	44			30.7	162.8	0.0			0	
SITYG_18340	-	1830786	1831194	hypothetical protein	135	S		691.4	484.7	1058.3			0	
SITYG_18350	-	1831223	1831541	predicted transcriptional regulators	105	K		287.0	414.6	31.6	-8.4	-15.7	0	
SITYG_18360	-	1831821	1832115	putative integrase	97	L		56.4	149.5	102.5			1	alive in vivo
SITYG_18370	-	1838589	1839063	putative transcriptional regulator	157			131.3	1066.3	233.0			0	
SITYG_18380	*rplQ*	1839992	1840379	50S ribosomal protein L17	128	J		6313.4	851.7	3866.3			0	
SITYG_18390	*rpoA*	1840390	1841329	DNA-directed RNA polymerase subunit alpha	312	K		2924.5	561.7	2342.1			0	
SITYG_18400	*rpsK*	1841373	1841757	30S ribosomal protein S11	127	J		1220.7	286.1	993.7			0	
SITYG_18410	*rpsM*	1841776	1842142	30S ribosomal protein S13	121	J		5270.2	480.3	3292.5			0	
SITYG_18420	*rpmJ*	1842157	1842274	50S ribosomal protein L36	38	J		815.5	375.6	944.1			0	
SITYG_18430	-	1842298	1842517	translation initiation factor IF-1	72	J		4754.3	301.0	3347.3			0	
SITYG_18440	*adk*	1842632	1843271	adenylate kinase	212	F		1337.3	653.4	927.2			0	
SITYG_18450	*secY*	1843480	1844788	preprotein translocase subunit SecY	435	U		1604.7	806.4	1190.0			0	
SITYG_18460	*rplO*	1844800	1845241	50S ribosomal protein L15	146	J		705.5	299.0	592.0			0	
SITYG_18470	-	1845400	1845583	50S ribosomal protein L30	60	J		1972.1	240.2	1810.8			0	
SITYG_18480	*rpsE*	1845596	1846091	30S ribosomal protein S5	164	J		4131.4	1553.8	2454.7			0	
SITYG_18490	*rplR*	1846109	1846466	50S ribosomal protein L18	118	J		708.8	430.9	534.4			0	
SITYG_18500	*rplF*	1846547	1847084	50S ribosomal protein L6	178	J		741.6	409.2	766.7			0	
SITYG_18510	*rpsH*	1847279	1847678	30S ribosomal protein S8	132	J		4283.3	716.0	3422.8			0	
SITYG_18520	*rpsN*	1847859	1848045	30S ribosomal protein S14	61	J		1672.7	118.1	863.8			0	
SITYG_18530	*rplE*	1848062	1848605	50S ribosomal protein L5	180	J		886.2	971.3	1183.6			0	
SITYG_18540	*rplX*	1848628	1848934	50S ribosomal protein L24	101	J		1870.7	359.1	1476.8			0	
SITYG_18550	*rplN*	1849010	1849379	50S ribosomal protein L14	122	J		1090.4	952.8	898.1			0	
SITYG_18560	*rpsQ*	1849404	1849665	30S ribosomal protein S17	86	J		683.4	673.6	846.5			0	
SITYG_18570	*rpmC*	1849688	1849895	50S ribosomal protein L29	68	J		2044.0	636.9	873.2			0	
SITYG_18580	*rplP*	1849904	1850318	50S ribosomal protein L16	137	J		3607.1	796.2	3007.7			0	
SITYG_18590	*rpsC*	1850321	1850975	30S ribosomal protein S3	217	J		608.9	403.2	506.7			0	
SITYG_18600	*rplV*	1850987	1851332	50S ribosomal protein L22	114	J		3991.9	1146.5	2939.8			0	
SITYG_18610	-	1851346	1851625	30S ribosomal protein S19	92	J		6095.9	393.8	3059.4			0	
SITYG_18620	*rplB*	1851726	1852560	50S ribosomal protein L2	277	J		1517.0	553.3	1264.3			0	
SITYG_18630	*rplW*	1852577	1852874	50S ribosomal protein L23	98	J		8128.7	2367.6	5680.3			0	
SITYG_18640	*rplD*	1852873	1853497	50S ribosomal protein L4	207	J		850.9	387.4	563.3			0	
SITYG_18650	*rplC*	1853521	1854148	50S ribosomal protein L3	208	J		3638.7	806.1	3283.3			0	
SITYG_18660	*rpsJ*	1854232	1854541	30S ribosomal protein S10	102	J		1933.1	284.5	1462.4			0	
SITYG_18670	-	1854846	1855589	-				362.9	532.4	432.5			0	
SITYG_18680	*tgt*	1855515	1856658	queuine tRNA-ribosyltransferase	380	J		413.7	499.9	307.5			0	
SITYG_18690	-	1856843	1857689	hypothetical protein	281	S		916.9	753.3	973.3			0	
SITYG_18700	-	1857946	1858441	hypothetical protein	164			460.9	177.6	547.7			0	
SITYG_18710	-	1858441	1858879	putative CoA-binding protein	145	R		113.6	200.7	45.9			0	
SITYG_18720	*polA*	1859044	1861690	DNA polymerase I	881	L		316.7	606.3	463.0			4	vivo-attenuated
SITYG_18730	-	1861790	1862333	phosphoglycerate mutase	180	G		152.8	283.3	462.3	3.3		0	
SITYG_18740	-	1862510	1862669	hypothetical protein	52			208.7	829.2	126.3			0	
SITYG_18750	-	1862675	1862891	hypothetical protein	71			499.3	406.9	325.4			0	
SITYG_18760	-	1862958	1863726	putative HAD-superfamily hydrolase	255	R		270.1	400.6	300.7			0	
SITYG_18770	-	1863728	1865423	putative phosphotransferase system IIB components	564	G		384.2	324.1	319.9			1	alive in vivo
SITYG_18780	-	1865579	1866338	transcriptional regulator	252	K		174.9	608.0	344.0			0	
SITYG_18790	-	1866379	1867411	signal transduction histidine kinase	343	T		124.6	319.4	262.7			1	alive in vivo
SITYG_18800	-	1867412	1868099	DNA-binding response regulator	228	TK		271.7	543.8	321.6			2	vivo-attenuated
SITYG_18810	-	1868197	1870741	putative fibronectin-binding protein	847		LPXTG	94.6	501.0	378.9	4.4		0	
SITYG_18820	-	1871020	1871191	hypothetical protein	56			194.1	642.5	293.6			0	
SITYG_18830	-	1871571	1872966	putative polysaccharide biosynthesis protein	464			496.6	897.9	655.1			1	alive in vivo
SITYG_18840	-	1872976	1873954	hypothetical protein	325			687.1	741.5	862.5			1	alive in vivo
SITYG_18850	-	1873962	1875027	hypothetical protein	354			506.3	474.6	688.3			0	
SITYG_18860	-	1875023	1876001	glycosyl transferase 2 family protein	325	M		772.0	651.6	708.5			0	
SITYG_18870	-	1876039	1877173	putative glycosyl transferase	377	M		534.1	562.0	628.7			2	alive in vivo
SITYG_18880	-	1877169	1877787	putative Acyltransferase	205	R		637.7	391.1	991.2			0	
SITYG_18890	-	1877779	1878409	sugar transferase	209	M		737.5	732.5	669.5			0	
SITYG_18900	-	1878431	1879685	aminotransferase DegT	417	M		1108.2	963.8	1177.2			1	alive in vivo
SITYG_18910	-	1879725	1881534	hypothetical protein	602	MG		1112.1	741.0	1021.4			0	
SITYG_18920	-	1881558	1882251	tyrosine kinase	230	D		610.6	507.4	565.1			0	
SITYG_18930	-	1882261	1882957	capsular polysaccharide biosynthesis protein	231	M		417.2	410.4	418.4			0	
SITYG_18940	-	1882965	1883703	capsular polysaccharide biosynthesis protein	245	GM		393.5	416.9	244.9			1	alive in vivo
SITYG_18950	-	1883699	1885145	transcriptional regulator	481	K		490.6	607.9	826.4			1	alive in vivo
SITYG_18960	*nrdG*	1885319	1885925	anaerobic ribonucleoside-triphosphate reductase activating protein	201	O		787.2	761.5	679.4			0	
SITYG_18970	-	1885929	1886436	acetyltransferase	168	R		1587.3	823.5	1525.1			0	
SITYG_18980	-	1886439	1886943	putative acetyltransferase	167	R		716.1	784.8	916.5			2	alive in vivo
SITYG_18990	-	1886999	1887143	hypothetical protein	47			288.1	152.6	278.9			0	
SITYG_19000	-	1887151	1889362	anaerobic ribonucleoside-triphosphate reductase	736	F		919.3	695.7	772.1			0	
SITYG_19010	-	1889468	1891010	putative membrane protein	513			575.7	555.8	521.0			2	vivo-attenuated
SITYG_19020	-	1891071	1891200	hypothetical protein	42			64.3	340.7	0.0			0	
SITYG_19030	-	1891264	1892797	cardiolipin synthetase	510	I		284.1	444.4	196.5			0	
SITYG_19040	-	1893132	1893570	hypothetical protein	145			710.3	1003.4	435.6			0	
SITYG_19050	-	1893615	1894857	dihydrofolate synthase	413	H		918.5	796.2	929.8			0	
SITYG_19060	-	1895055	1895361	hypothetical protein	101	S		5449.6	1364.4	3872.4			0	
SITYG_19070	-	1895378	1895789	holliday junction resolvase-like protein	136	L		4380.3	1871.3	4593.4			0	
SITYG_19080	-	1895797	1896106	hypothetical protein	102	S		5557.7	1351.2	5134.7			0	
SITYG_19090	-	1896369	1896927	hypothetical protein	185			609.6	1654.0	395.9			0	
SITYG_19100	-	1897440	1897575	hypothetical protein	44			0.0	0.0	74.4			0	
SITYG_19110	-	1897656	1898055	transcriptional regulator Spx	132	P		39755.9	1707.3	19253.4			0	
SITYG_19120	*recA*	1898140	1899286	recombinase A	381	L		2037.9	1323.1	1603.6			0	
SITYG_19130	*cinA*	1899334	1900603	competence damage-inducible protein A	422	R		389.0	640.7	1092.0	3.1		0	
SITYG_19140	-	1900705	1900912	hypothetical protein	68			60.1	424.6	339.6	6.1		0	
SITYG_19150	*tag*	1900916	1901471	3-methyladenine DNA glycosylase	184	L		201.8	316.8	307.6			0	
SITYG_19160	*ruvA*	1901480	1902071	ATP-dependent DNA helicase RuvA	196	L		196.5	148.7	101.9			0	
SITYG_19170	-	1902240	1902747	putative transcriptional regulator	168	K		40.9	346.7	198.1	5.3		0	
SITYG_19180	-	1902721	1903240	hypothetical protein	172			55.9	84.7	483.7	9.4	4.8	0	
SITYG_19190	*hexB*	1903385	1905332	DNA mismatch repair protein	648	L		481.5	564.3	577.7			3	alive in vivo
SITYG_19200	-	1905573	1906014	DNA-binding protein	146	KT		122.3	299.0	113.9			0	
SITYG_19210	-	1906010	1906469	hypothetical protein	152			235.0	1244.8	240.7			0	
SITYG_19220	*hexA*	1906609	1909168	DNA mismatch repair protein MutS	852	L		338.8	420.8	470.9			1	alive in vivo
SITYG_19230	*argR*	1909330	1909771	arginine repressor	146	K		630.2	498.3	933.6			0	
SITYG_19240	*argS*	1909874	1911563	arginyl-tRNA synthetase	562	J		400.3	429.3	338.9			0	
SITYG_19250	-	1911614	1912070	ribonucleotide reductase	151	F		400.3	337.3	264.3			0	
SITYG_19260	-	1912145	1912655	hypothetical protein	169			1594.2	474.0	866.4			0	
SITYG_19270	-	1912998	1915260	glucan phosphorylase	753	G		253.1	602.3	284.1			0	
SITYG_19280	*malQ*	1915297	1916809	4-alpha-glucanotransferase	503	G		249.7	842.9	358.6			0	
SITYG_19290	-	1917137	1918400	maltose/maltodextrin-binding protein	420	G		748.8	4227.9	938.2			1	alive in vivo
SITYG_19300	-	1918473	1919769	ABC transporter, permease protein	431	G		144.0	457.8	217.0			0	

SITYG_19310	-	1919770	1920613	ABC transporter, permease protein	280	G	83.7	312.8	95.3			1	alive in vivo
SITYG_19320	*malA*	1920710	1921523	putative membrane protein	270	S	117.4	162.2	172.9			0	
SITYG_19330	*malR*	1921533	1922520	transcriptional regulators	328	K	138.7	356.2	213.7			0	
SITYG_19340	-	1922533	1924609	pullulanase, type I	691	G	171.8	550.4	314.4			1	alive in vivo
SITYG_19350	-	1924820	1925756	hypothetical protein	311	S	1369.4	493.0	976.3			0	
SITYG_19360	*aspS*	1925742	1927485	aspartyl-tRNA synthetase	580	J	540.2	491.7	414.8			0	
SITYG_19370	-	1927615	1927822	hypothetical protein	68		20.0	0.0	0.0			0	
SITYG_19380	*hisS*	1927894	1929175	histidyl-tRNA synthetase	426	J	534.3	463.2	486.0			0	
SITYG_19390	*rpmF*	1929401	1929584	50S ribosomal protein L32	60	J	7095.0	600.4	4719.2			0	
SITYG_19400	-	1929599	1929749	50S ribosomal protein L33	49	J	110.6	0.0	0.0	<-110.6		0	
SITYG_19410	-	1929836	1931120	hypothetical protein	427	MG	145.4	273.8	156.4			0	
SITYG_19420	-	1931198	1932694	-		L	77.6	587.6	322.2	4.5		1	alive in vivo
SITYG_19430	-	1932713	1932962	hypothetical protein	82		16.7	88.3	40.3			0	
SITYG_19440	-	1933023	1934040	putative replication initiation factor	338	L	85.7	432.1	464.1	5.9		1	alive in vivo
SITYG_19450	-	1934044	1934464	hypothetical protein	139		39.5	209.3	167.4	4.6		0	
SITYG_19460	-	1934733	1935831	cell division protein FtsK	365	D	83.1	560.4	503.0	6.6		2	vivo-attenuated
SITYG_19470	-	1936122	1936344	hypothetical protein	73		74.7	0.0	0.0			0	
SITYG_19480	-	1936390	1936714	hypothetical protein	107		25.6	271.3	217.0	9.2		1	alive in vivo
SITYG_19490	-	1936902	1937409	hypothetical protein	168		1472.7	346.7	1564.7			0	
SITYG_19500	-	1937866	1939108	hypothetical protein	413	GEPR	43.4	230.0	40.4			2	alive in vivo
SITYG_19510	-	1939110	1941020	-		RTKL	89.0	563.7	199.8			3	alive in vivo
SITYG_19520	-	1941542	1942412	transcriptional activator	289	K	400.5	833.5	531.0			1	alive in vivo
SITYG_19530	-	1942611	1942734	hypothetical protein	40		33.7	178.7	979.7	31.6	4.6	0	
SITYG_19540	-	1942991	1944899	cadmium-translocating P-type ATPase	635	P	258.7	541.3	394.7			0	
SITYG_19550	-	1945212	1945368	hypothetical protein	51		26.6	140.9	386.2	15.8		0	
SITYG_19560	-	1945532	1945655	hypothetical protein	40	KR	0.0	0.0	979.7	>979.7	>979.7	0	
SITYG_19570	-	1945674	1945788	hypothetical protein	37		145.5	192.8	0.0	<-145.5	<-192.8	0	
SITYG_19580	-	1945824	1946694	putative cation diffusion facilitator family transporter	289	P	276.5	1086.1	450.2			2	vivo-attenuated
SITYG_19590	-	1946864	1947386	transcriptional regulator, TetR family	173	K	71.5	84.2	192.4			0	
SITYG_19600	-	1947450	1948620	major facilitator superfamily transporter	389	P	425.5	619.8	557.9			0	
SITYG_19610	-	1948840	1949437	DNA-3-methyladenine glycosylase	198	L	194.6	294.5	201.8			0	
SITYG_19620	-	1949693	1950440	transcriptional regulator, DeoR family	248	KG	405.4	823.7	403.3			1	alive in vivo
SITYG_19630	-	1950458	1951286	hypothetical protein	275	R	305.6	743.1	218.3			1	alive in vivo
SITYG_19640	-	1951524	1952016	putative acetyltransferase	163	KR	404.7	312.6	183.7			0	
SITYG_19650	*dltD*	1952068	1953337	D-alanyl-lipoteichoic acid biosynthesis DltD	422	M	405.3	363.6	284.9			0	
SITYG_19660	-	1953329	1953569	D-alanine--poly(phosphoribitol) ligase subunit 2	79	IQ	2730.9	1007.2	1799.2			0	
SITYG_19670	*dltB*	1953583	1954828	D-alanyl-lipoteichoic acid biosynthesis protein DltB	414	M	859.6	776.6	1169.5			0	
SITYG_19680	*dltA*	1954824	1956375	D-alanine--poly(phosphoribitol) ligase subunit 1	516	Q	829.1	396.7	822.3			0	
SITYG_19690	-	1956384	1956516	D-Ala-teichoic acid biosynthesis protein	43		2734.0	665.9	3119.1			0	
SITYG_19700	-	1956808	1957135	transcriptional regulator, PadR family	108	K	329.8	403.2	859.9			0	
SITYG_19710	-	1957121	1958123	hypothetical protein	333	S	414.0	943.0	501.1			2	alive in vivo
SITYG_19720	-	1958132	1958753	HAD superfamily hydrolase	206	R	400.8	1026.2	388.1			1	alive in vivo
SITYG_19730	-	1958980	1960435	hypothetical protein	484		225.2	573.9	179.4			0	
SITYG_19740	-	1960448	1961129	hypothetical protein	226		91.4	451.8	280.2	3.3		0	
SITYG_19750	-	1961109	1961844	hypothetical protein	244		440.2	209.3	273.3			0	
SITYG_19760	-	1962001	1962391	hypothetical protein	129	GEPR	191.5	676.1	978.4	5.6		0	
SITYG_19770	-	1962484	1962649	hypothetical protein	54		100.6	133.2	1338.9	14.5	8.4	0	
SITYG_19780	-	1962803	1963322	bacteriocin transport accessory protein	172	OC	55.9	423.4	561.1	10.9		0	
SITYG_19790	-	1963251	1963539	hypothetical protein	95		0.0	0.0	34.9			0	
SITYG_19800	-	1963563	1963899	hypothetical protein	111		185.2	1635.0	179.3			0	
SITYG_19810	-	1964118	1964439	hypothetical protein	106	K	116.3	410.7	657.0	6.1		0	
SITYG_19820	-	1964340	1965102	hypothetical protein	253	K	54.4	461.4	237.2	4.7		0	
SITYG_19830	-	1965102	1965876	HAD-superfamily hydrolase, subfamily IIB	257	R	139.3	425.9	246.5			0	
SITYG_19840	-	1965989	1968662	putative membrane protein	890	S	79.1	542.6	488.4	6.7		1	alive in vivo
SITYG_19850	-	1968836	1969370	transcriptional regulator, TetR family	177	K	101.0	205.8	94.0			0	
SITYG_19860	*rpsD*	1969558	1970170	30S ribosomal protein S4	203	J	840.5	215.4	705.6			0	
SITYG_19870	-	1970372	1971005	HAD hydrolase, subfamily IA	210	R	563.6	833.2	1189.8			0	
SITYG_19880	-	1971043	1971316	hypothetical protein	90	S	668.6	724.4	367.8			0	
SITYG_19890	*dnaB*	1971319	1972672	replicative DNA helicase	450	L	558.0	487.2	556.7			0	
SITYG_19900	*rplI*	1972704	1973157	50S ribosomal protein L9	150	J	613.5	194.0	687.2			0	
SITYG_19910	-	1973153	1975130	hypothetical protein	658	T	715.5	766.9	833.0			0	
SITYG_19920	-	1975378	1977295	glucose inhibited division protein A	638	D	1099.3	664.9	1100.1			0	
SITYG_19930	-	1977427	1978549	tRNA (5-methylaminomethyl-2-thiouridylate)- methyltransferase	373	J	569.4	430.9	572.8			0	
SITYG_19940	-	1978908	1979415	hypothetical protein	168		2364.5	390.1	1683.6			0	
SITYG_19950	*sdaB*	1979672	1980344	Iron-sulphur-dependent L-serine dehydratase beta subunit	223	E	166.7	523.2	508.1	3.3		0	
SITYG_19960	*sdaA*	1980352	1981225	L-serine dehydratase alpha subunit	290	E	123.5	402.7	80.5			0	
SITYG_19970	-	1981452	1982097	putative phosphoglycolate phosphatase	214	R	321.6	647.3	280.2			0	
SITYG_19980	-	1982273	1982870	hypothetical protein	198		736.5	478.5	622.4			0	
SITYG_19990	-	1983024	1983819	cobalt transport protein	264	P	360.0	469.9	606.3			0	
SITYG_20000	-	1983811	1984651	cobalt ABC transporter, ATP-binding protein	279	P	666.7	967.9	657.5			0	
SITYG_20010	-	1984635	1985463	ABC transporter ATP-binding protein	275	P	465.9	345.0	776.2			0	
SITYG_20020	*pgsA*	1985464	1986004	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	179	I	960.2	529.0	539.3			0	
SITYG_20030	-	1986014	1986827	hypothetical protein	270	S	326.5	297.3	271.7			0	
SITYG_20040	-	1986885	1988181	putative peptidase	431	R	428.9	508.7	402.9			0	
SITYG_20050	-	1988180	1989428	putative zinc-dependent peptidase	415	R	388.9	316.9	354.0			0	
SITYG_20060	-	1989603	1989984	hypothetical protein	126	S	1676.7	519.1	1317.8			0	
SITYG_20070	*recF*	1989985	1991083	DNA replication and repair protein RecF	365	L	411.8	700.5	411.6			0	
SITYG_20080	*guaB*	1991913	1993395	inosine-5'-monophosphate dehydrogenase	493	F	926.5	860.0	738.6			0	
SITYG_20090	*trpS*	1993532	1994558	tryptophanyl-tRNA synthetase	341	J	752.0	385.5	802.6			0	
SITYG_20100	-	1994639	1995635	UDP-glucose 4-epimerase	331	M	108.3	198.6	110.9			0	
SITYG_20110	-	1995652	1996342	triose-phosphate isomerase	229	G	138.3	318.5	291.1			0	
SITYG_20120	-	1996354	1996894	hypothetical protein	179	R	161.3	488.3	297.5			0	
SITYG_20130	-	1997048	1998671	ABC transporter, ATP-binding protein	540	R	329.7	487.4	420.7			0	
SITYG_20140	-	1998744	2001321	hypothetical protein	858	S	117.5	196.1	187.0			1	alive in vivo
SITYG_20150	-	2001644	2002394	response regulator	249	KT	453.5	234.4	562.4			1	alive in vivo
SITYG_20160	-	2002393	2003536	histidine kinase	380	T	424.6	615.2	702.9			0	
SITYG_20170	-	2003735	2003882	hypothetical protein	48		56.4	0.0	204.9	4.0	>204.9	0	
SITYG_20180	-	2004158	2004638	ribosomal RNA large subunit methyltransferase H	159	S	164.2	183.1	83.7			2	alive in vivo
SITYG_20190	-	2004841	2006032	putative serine protease	396	O	1839.0	442.8	1543.0			1	alive in vivo
SITYG_20200	-	2006068	2006854	hypothetical protein	261	K	865.5	559.2	779.3			2	alive in vivo