

TABLE S1. Genetic organization of ICESp1116

BLASTP analysis ^c								
ORF ^a	Start (bp)	Stop (bp)	No. of aa ^b	Predicted function	Most significant database match	Accession no.	% aa identity (% aa similarity)	
orf1	116	277	53		hypothetical protein Gallo_0260 [<i>Streptococcus gallolyticus</i> UCN34]	YP_003429700.1	62 (79)	
orf2	280	1194	304	Replication initiator protein A	replication initiation protein Rep [<i>Streptococcus infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63101.1	61 (74)	
orf3	1181	1345	54		hypothetical protein STRINF_00903 [<i>S. infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102]	ZP_02920028.1	81 (87)	
orf4	1535	1909	124		hypothetical protein STRINF_00904 [<i>S. infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102]	ZP_02920029.1	64 (79)	
orf5	1920	2729	269		unnamed protein product [<i>Streptococcus macedonicus</i> ACA-DC 198]	YP_005095590.1	99 (99)	
orf6	2753	6148	1131	Adhesin isopeptide-forming domain, sspB-C2 type	unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095589.1	96 (98)	
orf7	6289	9651	1120	Peptidase family C39	unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095588.1	92 (94)	
orf8	9843	10070	75		unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095587.1	99 (100)	
orf9	10118	10693	191		unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095586.1	88 (97)	
orf10	10745	11497	250		hypothetical protein Gallo_0275 [<i>S. gallolyticus</i> UCN34]	YP_003429715.1	94 (99)	
orf11	11507	11968	153	Transcriptional regulator	putative transcriptional regulator [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63093.1	77 (82)	
orf12	12076	12432	118		hypothetical protein Sinf_1801 [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63092.1	98 (99)	
orf13	12377	14767	796	Type IV secretory pathway, VirB4 components	unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095583.1	99 (99)	
orf14	14804	17467	887	CHAP domain protein	surface antigen [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63090.1	97 (99)	
orf15	17483	18088	201		unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095586.1	95 (97)	

1	orf16	18101	18487	128	Single-strand DNA-binding protein	hypothetical protein STRINF_00915 [<i>S. infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102]	ZP_02920040.1	95 (97)
2								
3	orf17	18509	18784	91		unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095578.1	91 (97)
4	orf18	18784	19578	264		hypothetical protein Sinf_1795 [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63086.1	88 (93)
5	orf19	19590	20057	155		hypothetical protein STRINF_00919 [<i>S. infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102]	ZP_02920044.1	93 (96)
6								
7	orf20	20079	22148	689	TraG family protein	TraG family protein [<i>Streptococcus agalactiae</i> ATCC 13813]	EFV96646.1	97 (98)
8	orf21	22184	22327	47		hypothetical protein SGPB_1240 [<i>Streptococcus pasteurianus</i> ATCC 43144]	YP_004559376.1	91 (94)
9	orf22	22376	22870	164	Transcriptional regulator	XRE family transcriptional regulator [<i>Streptococcus sanguinis</i> ATCC 49296]	ZP_07887379.1	49 (66)
10	orf23*	22883	24664	593	DNA topoisomerase	topB gene product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095572.1	97 (99)
11	orf24	24680	29344	1554	Topoisomerase-primase, domain protein	hypothetical protein Sinf_1789 [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63080.1	91 (95)
12								
13	orf25	29402	29689	95		hypothetical protein, transposon associated [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63079.1	89 (96)
14								
15	orf26	30011	30385	124		mobilization protein [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63078.1	100 (100)
16	orf27	30357	31985	542	Relaxase	relaxase [<i>S. infantarius</i> subsp. <i>infantarius</i> CJ18]	AEZ63077.1	98 (99)
17	orf28	32021	32818	265		unnamed protein product [<i>S. macedonicus</i> ACA-DC 198]	YP_005095566.1	78 (83)
18	orf29	32927	33097	56		pSM19305 ORF alpha [<i>Streptococcus pyogenes</i>]	YP_232753.1	96 (100)
19	orf30	33111	33728	205	Site-specific recombinase	pSM19305 site-specific recombinase ORF beta [<i>S. pyogenes</i>]	YP_232754.1	99 (99)
20	orf31	33728	35827	699	DNA topoisomerase	pSM19305 DNA topoisomerase ORF gamma [<i>S. pyogenes</i>]	YP_232755.1	99 (99)
21	orf32	35975	36872	298	ParA protein	pSM19305 hypothetical protein ORF delta [<i>S. pyogenes</i>]	YP_232756.1	100 (100)
22	orf33*	36963	37178	71	Omega transcriptional repressor	pSM19305 transcriptional repressor ORF omega [<i>S. pyogenes</i>]	YP_232757.1	99 (100)
23	orf34	37195	37467	90	Bacterial epsilon antitoxin protein	pSM19035 antidote of epsilon-zeta postsegregational killing system [<i>S. pyogenes</i>]	YP_232758.1	100 (100)
24	orf35	37469	38332	287	Bacterial zeta toxin protein	pSM19035 toxin of epsilon-zeta postsegregational killing system [<i>S. pyogenes</i>]	YP_232759.1	99 (99)
25	erm(B)	39330	38593	245	rRNA methylase	ribosomal RNA adenine dimethylase [<i>Enterococcus faecalis</i> DS5]	ZP_05563514.1	100 (100)
26	orf37	39538	39455	27	rRNA methylase leader peptide	leader peptide [<i>S. pyogenes</i>]	YP_232760.1	100 (100)

1	<i>orf38</i>	40352	39666	228	IS1216 transposase	IS1216 transposase [<i>Enterococcus faecalis</i> V583]	NP_816937.1	99 (100)
2	<i>tet(M)</i> ^d	40421	41026	517	Tetracycline-resistance protein	tetracycline resistance protein [<i>Enterococcus gallinarum</i> EG2]	ZP_05648443.1	95 (96)
3	<i>orf40</i> *	42124	42261	45		conjugative transposon protein [<i>Clostridium difficile</i> 630]	YP_001086984.1	98 (100)
4	<i>orf41</i>	42673	42314	119	Transcriptional regulator	putative conjugative transposon regulatory protein [<i>C. difficile</i> 630]	YP_001086985.1	100 (100)
5	<i>orf42</i>	43175	43600	141	RNA polymerase sigma-70 region 4 family protein	putative conjugative transposon regulatory protein [<i>C. difficile</i> 630]	YP_001086987.1	100 (100)
6								
7	<i>orf43</i>	43597	43827	76		conjugative transposon protein [<i>C. difficile</i> 630]	YP_001086988.1	100 (100)
8	<i>orf44</i>	44404	46035	543	Site-specific recombinase	conjugative transposon site-specific recombinase [<i>C. difficile</i> 630]	YP_001086990.1	99 (99)
9	<i>orf45</i>	46512	47864	450		hypothetical protein [<i>S. agalactiae</i> ATCC 13813]	EFV96631.1	97 (99)

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11 ^a Asterisks indicate ORFs with unusual start codons, i.e. start codons other than ATG (GTG in *orf23* and *orf33*; and TTG in *orf40*).

12 ^b aa, amino acid(s).

13 ^c For each ORF, only the most significant homology detected is reported.

14 ^d Truncated *tet(M)* gene.

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