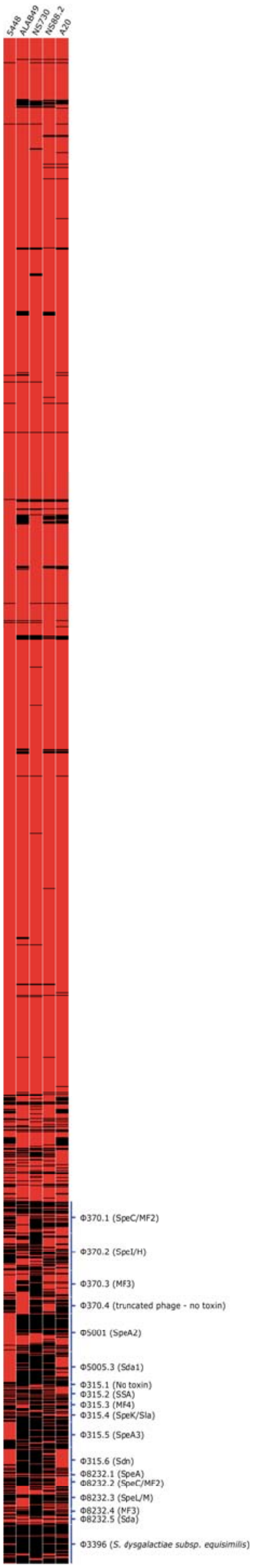

Supplementary fig. 1. DNA microarray analysis highlighting the core genome of the non-M1 GAS strains used in this study. Heat map generated from an oligonucleotide microarray with probes representing M1 core ORFeome in addition to ORFs representing various M1, M3, M18, and *S. dysgalactiae subsp. equisimilis* prophages (phage, and corresponding genes, are indicated; see Supplementary table 1). Strains under examination are designated at the top of each column. Red indicates gene present, based on median-normalised fluorescence units exceeding a threshold value, and black indicates gene absent.

Supplementary table 1. DNA microarray data for the *S. pyogenes* isolates 5448 (M1T1), ALAB49 (M53), NS730 (M90), NS88.2 (M98.1) and A20 (M23). Oligonucleotide probes represent M1 core ORFeome in addition to ORFs representing various M1, M3, M18, and *S. dysgalactiae subsp. equisimilis* prophages. Phage (Φ) or loci of interest are given. Fluorescence intensities have been normalised to the median and a mean hybridisation score calculated for each gene. An average threshold of 40 median-normalised fluorescence units was selected; genes of fluorescence intensity less than threshold were designated absent (black) and those exceeding threshold designated present (red).

Gene Annotation	**Notes**	**5448**	**ALAB49**	**NS730**	**NS88.2**	**A20**
Hypothetical protein		72.0	81.8	80.3	61.1	56.1
SPy0002 chromosomal replication initiator protein DnaA		114.4	109.0	147.8	100.3	112.9
SPy0003 DNA polymerase III, beta chain		148.7	120.8	129.2	133.9	132.4
SPy0004 conserved hypothetical protein		102.8	163.6	113.9	118.3	112.3
Hypothetical protein		81.7	99.3	104.8	101.3	105.6
Hypothetical protein		134.2	167.6	118.5	128.8	136.1
SPy0006 conserved hypothetical protein, GTP-binding protein YchF		179.2	185.9	209.6	154.7	161.0
SPy0007 peptidyl-tRNA hydrolase		98.2	127.5	108.7	89.1	66.1
SPy0008 transcription-repair coupling factor		229.3	177.9	198.0	182.7	181.4
SPy0009 S4 domain protein		77.2	99.2	103.3	82.7	84.3
SPy0010 DivIC homolog, putative		73.3	114.9	99.1	105.0	105.3
Pyruvate formate-lyase TnpC		118.3	118.9	105.4	76.3	102.3
SPy0012 hypothetical protein		141.1	156.1	163.2	114.2	144.1
SPy0013 conserved hypothetical protein		132.5	118.5	134.7	74.3	57.1
Hypoxanthine phosphoribosyltransferase		96.8	132.1	102.4	88.4	97.5
SPy0015 cell division protein FtsH		130.8	140.9	129.5	125.9	129.8
SPy0016 amino acid permease, putative		149.4	217.7	194.5	245.4	260.7
Hypothetical protein		282.3	316.2	268.7	231.3	181.8
SPy0019 P54 protein, putative; pcsB homolog GBS putative autolysin		247.9	191.2	243.5	184.2	186.7
SPy0020 ribose-phosphate pyrophosphokinase		203.3	263.1	268.2	214.5	237.1
SPy0021 unknown conserved protein, putative		117.3	140.9	122.0	108.4	108.7
SPy0022 fatty acid/phospholipid synthesis protein PlsX		176.3	189.1	195.0	231.5	218.0
SPy0023 acyl carrier protein		98.4	100.3	96.6	115.1	158.1

SPy0024 phosphoribosylaminoimidazole-succinocarboxamide synthase	121.7	154.1	157.2	185.4	166.5
SPy0025 phosphoribosylformylglycinamidine synthase, putative	208.1	155.3	213.0	148.4	93.7
SPy0026 amidophosphoribosyltransferase	152.9	147.2	281.6	166.6	145.5
SPy0027 phosphoribosylformylglycinamidine cyclo-ligase	212.2	204.2	189.2	140.0	179.8
SPy0028 phosphoribosylglycinamide formyltransferase	116.3	119.1	120.5	113.5	127.0
Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	180.5	213.6	262.4	222.7	256.4
SPy0032 phosphoribosylamine--glycine ligase	291.6	209.2	321.9	281.7	240.9
SPy0033 phosphoribosylaminoimidazole carboxylase, catalytic subunit	166.7	166.1	231.4	97.6	57.9
SPy0034 phosphoribosylaminoimidazole carboxylase, PurK protein	158.9	317.1	324.7	239.1	293.0
SPy0035 hypothetical protein	99.1	8.0	10.8	20.2	21.1
SPy0036 adenylosuccinate lyase	164.7	196.2	203.8	205.0	196.0
SPy0038 Holliday junction DNA helicase RuvB	217.6	168.6	254.3	191.0	170.6
SPy0040 Unknown	127.0	114.6	185.0	109.2	113.7
SPy0041 Unknown	156.1	111.2	126.5	132.7	132.6
Hypothetical protein	31.2	49.1	33.2	38.4	34.6
Hypothetical protein	83.7	111.1	93.8	53.5	54.6
SPy0044 alcohol dehydrogenase	118.4	158.7	178.0	83.9	83.0
SPy0045 unknown conserved protein, putative	174.0	165.5	162.9	147.3	177.7
SPy0047 ribosomal protein S10	89.7	72.6	89.5	71.0	76.1
SPy0049 Ribosomal protein L3P	129.1	149.1	142.0	102.0	108.5
SPy0051 Ribosomal protein L23	96.1	85.0	91.5	85.8	76.5
SPy0052 ribosomal protein L2	116.7	100.0	130.6	79.6	88.2
SPy0053 ribosomal protein S19	90.2	93.9	103.7	62.4	62.9
SPy0055 ribosomal protein L22	110.9	99.9	112.5	82.0	102.8
SPy0056 ribosomal protein S3	124.3	122.1	133.0	130.8	144.8
SPY0059 ribosomal protein L29	107.7	72.6	95.7	75.6	72.2
SPy0061 ribosomal protein L14	176.2	180.7	158.8	168.3	202.9
SPy0062 ribosomal protein L24	78.4	68.4	75.0	98.9	107.9

SPy0063 ribosomal protein L5	140.7	129.7	155.5	169.1	155.1
SPy0065 Ribosomal protein S8	56.4	68.5	69.4	83.6	64.1
SPy0066 Ribosomal protein L6	94.1	84.2	94.5	59.4	70.8
SPy0067 ribosomal protein L18	138.8	151.8	161.6	140.6	203.1
SPy0069 ribosomal protein S5	389.5	267.5	309.0	362.0	486.2
SPy0071 Ribosomal protein L30p/L7e	131.4	120.9	104.8	173.0	180.9
SPy0073 preprotein translocase, SecY subunit	102.0	90.1	124.5	104.8	110.2
SPy0074 adenylate kinase	99.3	97.5	106.3	106.3	122.9
SPy0075 initiation factor IF-1-related protein	119.4	98.0	102.4	89.9	95.3
SPy0076 ribosomal protein L36	76.0	62.0	60.4	51.6	55.4
SPy0077 Ribosomal protein S13/S18	122.0	118.4	124.3	120.3	143.7
SPy0080 DNA-directed RNA polymerase, alpha subunit	141.3	177.1	166.4	162.6	168.0
Ribosomal protein L17	99.1	94.4	114.4	82.0	86.6
SPy0084 hypothetical protein	171.8	189.1	263.4	185.6	243.2
Hypothetical protein	136.9	158.6	162.0	183.6	158.2
Unknown conserved protein	254.9	225.9	211.1	385.5	374.2
Unknown conserved protein	120.1	130.7	152.2	126.6	130.7
SPy0092 AdcR protein, putative	126.0	124.8	134.8	142.6	169.2
SPy0093 ABC transporter, ATP-binding protein, putative	130.3	126.4	135.8	111.7	145.6
SPy0094 zinc ABC transporter, permease protein, putative	156.8	160.8	257.0	213.7	234.7
SPy0096 tyrosyl-tRNA synthetase	164.2	140.5	162.4	152.8	200.3
SPy0097 penicillin-binding protein 1, putative	143.4	130.4	198.8	132.6	156.0
SPy0098 DNA-directed RNA polymerase, beta subunit	146.6	151.0	287.9	219.3	233.8
SPy0099 dna-directed rna polymerase beta chain	152.3	165.5	230.5	197.1	214.4
SPy0100 putative DNA binding protein	127.7	111.3	120.4	119.6	155.9
SPy0102 comG operon protein 2	133.0	154.1	130.4	140.8	174.1
SPy0103 comG operon protein 3	70.9	66.5	84.8	63.9	65.6
SPy0104 comG operon protein 4	115.6	128.1	215.5	114.8	157.9
SPy0105 conserved hypothetical protein	69.5	70.9	82.3	58.3	72.8
SPy0106 comG operon protein 6	62.8	58.8	58.5	72.5	81.5
SPy0108 conserved hypothetical protein	195.4	209.9	159.5	204.1	295.2
SPy0109 acetate kinase	158.0	157.4	204.9	123.1	128.0

SPy0110 hypothetical protein		96.5	116.8	141.8	105.5	94.0
SPy0112 pyrroline-5-carboxylate reductase		353.9	277.2	287.4	371.1	359.1
SPy0115 glutamyl-aminopeptidase (pepA)		251.7	225.4	290.5	245.1	265.1
SPy0116 hypothetical protein		123.6	162.0	206.3	186.5	175.1
SPy0117 conserved hypothetical protein		84.3	131.9	155.9	113.5	73.8
Phenylalanyl-tRNA synthetase, beta chain		164.0	138.8	176.8	114.5	110.7
Single-strand binding protein		149.2	124.9	204.8	158.7	125.3
SPy0121 similar to Lactobacillus acidophilus dA/dG-kinase		187.0	159.1	175.4	150.3	126.9
SPy0122 NifR3/Smm1 family protein		185.4	183.0	243.2	191.1	208.5
SPy0123 33 kda chaperoni		185.7	220.1	256.3	309.4	208.7
SPy0124 RofA		195.6	39.9	225.6	69.9	198.3
Hypothetical protein	FCT/Pilus locus	47.1	4.9	72.6	18.3	36.6
Cpa	FCT/Pilus locus	175.2	13.1	18.1	26.6	21.3
Hypothetical protein	FCT/Pilus locus	166.9	24.5	26.8	40.1	25.3
SPy0127 LepA	FCT/Pilus locus	97.2	4.2	8.4	22.7	3.2
SPy0128 LPXTG-motif cell wall anchor domain protein	FCT/Pilus locus	85.7	6.5	10.0	19.0	14.4
SPy0129 conserved hypothetical protein	FCT/Pilus locus	92.4	10.1	14.1	33.5	16.2
SPy0130 LPXTG-motif cell wall anchor domain protein	FCT/Pilus locus	131.9	33.0	37.6	38.5	33.5
SPy0131 conserved hypothetical protein	FCT/Pilus locus	287.8	31.9	39.1	64.5	313.1
Conserved hypothetical protein	FCT/Pilus locus	178.8	4.5	8.0	11.0	117.0
SPy0133 conserved hypothetical protein	FCT/Pilus locus	502.3	157.9	230.4	391.0	659.9
Hypothetical protein	FCT/Pilus locus	140.3	11.0	12.5	23.9	194.6
SPy0135 alternative sortase gene B; Tim Barnett	FCT/Pilus locus	174.4	13.5	25.3	24.6	306.2
SPy0136 hypothetical protein		97.9	99.8	107.1	91.5	39.0
SPy0137 conserved hypothetical protein TIGR00366		108.4	128.5	132.7	100.6	77.2
Transcriptional regulator, putative		123.6	142.3	180.0	132.9	112.6
Transcriptional regulator, LysR family, putative		123.5	146.5	143.6	135.4	120.6
SPy0140 acetyl-CoA acetyltransferase		113.5	112.4	139.8	121.2	108.9
SPy0142 butyrate-acetoacetate coa-transferase subunit b		162.1	119.7	131.6	113.6	103.7
SPy0144 conserved hypothetical protein		90.0	104.4	125.7	59.3	41.2
SPy0145 endoribonuclease L-PSP, putative		72.6	160.2	124.0	113.5	124.3
SPy0146 transcriptional regulatory protein pfoR		257.5	192.7	247.7	279.2	310.9

SPy0147 hypothetical protein		92.9	122.1	125.2	119.9	110.3
SPy0149 ATP synthase, subunit K		219.8	231.3	272.7	254.6	202.2
SPy0151 ATP synthase (C/AC39) subunit		159.5	133.8	145.5	114.9	104.3
ATP synthase (F/14-kDa) subunit		168.4	121.1	214.5	175.8	171.1
Hypothetical protein		123.6	159.6	172.2	188.2	157.2
SPy0155 ATP synthase archaeal, B subunit		384.4	350.4	478.3	358.6	328.7
SPy0157 V-type ATPase, subunit D		117.9	155.9	168.2	136.7	81.0
SPy0158 surface-located membrane protein 1 (lmp1), putative		157.4	190.5	201.3	153.0	134.8
SPy0159 hypothetical protein		130.5	139.1	149.7	144.3	128.4
SPy0160 adenylosuccinate synthetase		169.1	215.6	255.4	182.8	211.2
SPy0163 basic membrane protein D, putative		125.9	113.3	149.3	128.8	110.8
SPy0164 transcription antitermination protein NusG		87.9	81.6	79.9	70.1	64.5
SPy0165 nicotine adenine dinucleotide glycohydrolase, nga	SLO/Nga locus in SF370	134.4	115.2	131.6	143.3	119.0
SPy0166 hypothetical protein	SLO/Nga locus in SF370	46.2	63.5	56.8	50.2	51.3
SPy0167 streptolysin o precursor	SLO/Nga locus in SF370	110.8	109.5	107.0	122.3	108.0
SPy0169 hypothetical protein	SLO/Nga locus in SF370	32.5	17.2	25.9	44.4	37.3
SPy0170 hypothetical protein	SLO/Nga locus in SF370	112.2	110.2	117.0	84.3	76.3
SPy0171 hypothetical protein		256.0	199.4	191.9	200.9	196.8
SPy0172 cystathionine gamma-synthase		152.1	163.0	195.1	250.2	199.0
SPy0173 leucyl-tRNA synthetase		132.2	115.0	107.1	133.2	119.0
SPy0174 SgaT protein		118.4	145.6	158.3	170.1	122.7
SPy0175 SgaT protein, putative		120.7	97.6	105.6	94.8	94.3
SPy0176 PTS system, IIA component		149.8	175.1	201.4	175.8	150.4
SPy0177 hexulose-6-phosphate synthase SgbH, putative		173.0	139.9	194.5	201.6	155.4
SPy0178 hexulose-6-phosphate isomerase, putative		121.5	89.8	87.1	114.2	85.6
SPy0180 hypothetical protein		139.5	105.8	138.8	137.1	119.0
SPy0181 putative cel operon regulator		92.0	105.4	100.8	84.9	73.5
SPy0182 conserved hypothetical protein		153.7	147.3	185.5	176.4	154.2
SPy0183 glycine betaine transport ATP-binding protein		101.6	103.9	109.5	127.3	106.6
SPy0184 glycine betaine-binding protein/glycine betaine transport system		121.4	111.1	108.0	132.8	121.5
SPy0186 unknown conserved protein		183.1	161.9	277.9	194.5	214.7

SPy0187 zinc uptake regulation protein, putative fur-like regulator	158.2	166.9	251.2	166.0	163.8
SPy0188 VirR positive regulator; mga-like	94.8	92.0	106.4	23.3	20.0
SPy0189 conserved hypothetical protein	81.0	76.5	75.2	34.0	28.5
SPy0191 sortase family protein	118.2	154.1	173.2	24.2	16.1
Transposase for insertion sequence elemen	95.3	141.6	135.9	90.5	77.3
SPy0196 putative dicarboxylate carrier protein, putative	93.0	201.1	145.0	96.9	101.1
SPy0197 nicotinate-nucleotide pyrophosphorylase	141.3	270.6	197.5	152.9	175.3
SPy0198 IS861, transposase OrfB	162.5	169.2	88.9	104.8	228.4
Hypothetical protein	146.7	159.7	163.6	221.2	188.8
Hypothetical protein	95.6	86.6	133.4	114.7	125.8
SPy0203 queuine tRNA-ribosyltransferase	133.4	130.0	158.0	141.9	132.8
SPy0205 conserved hypothetical protein	151.7	196.0	203.8	162.4	183.3
SPy0207 BioY family protein, putative	213.0	188.3	242.3	236.5	251.2
Cytidine/deoxycytidylate deaminase family protein	197.0	158.7	174.6	182.6	172.9
SPy0210 hypothetical protein	125.9	109.9	138.4	120.7	108.1
Hypothetical protein	102.5	108.4	124.6	101.1	119.8
SPy0212 exotoxin G precursor	87.4	85.3	95.7	93.5	81.1
Hypothetical protein	116.3	91.2	96.0	149.1	114.8
Hypothetical protein	61.0	46.9	45.3	60.5	49.5
SPy0215 Phosphoglucose isomerase	145.4	128.8	98.6	185.3	161.4
SPy0216 RofA, putative, RALP-4	146.7	176.0	188.5	172.3	145.1
H repeat-associated protein in rhsc-phrb intergenic region (orf-h2)	458.3	612.4	14.3	216.2	85.9
H repeat-associated protein in rhsc-phrb intergenic region (orf-h2), putative	833.8	1275.6	22.9	338.3	161.0
SPy0219 hypothetical protein	451.6	701.7	101.9	190.6	123.2
Hypothetical protein	119.8	87.6	93.5	92.3	78.7
Hypothetical protein	255.5	245.8	224.8	226.1	244.7
SPy0223 Rhomboid family protein	198.9	180.8	296.0	231.3	208.8
SPy0224 UTP-glucose-1-phosphate uridylyltransferase	129.4	129.2	164.8	45.8	32.3
SPy0226 glycerol-3-phosphate dehydrogenase (NAD+)	234.7	221.1	250.6	273.6	212.1
SPy0227 hypothetical protein	83.3	107.9	106.4	103.9	98.4
SPy0228 hypothetical transcriptional regulator in cotf-tetb intergenic region, putative	108.0	151.8	171.8	164.9	137.0

SPy0229 ABC transporter, ATP-binding protein, putative	144.3	142.1	155.6	119.5	126.8
SPy0230 transport ATP-binding protein MsbA, putative	138.0	110.3	186.4	126.1	107.7
Hypothetical protein	117.5	114.0	138.1	77.7	65.8
SPy0233 Uncharacterized BCR, COG1636 superfamily	153.3	199.6	160.8	159.7	150.2
SPy0235 deoxyuridine 5`-triphosphate nucleotidohydrolase	176.4	176.9	193.7	143.9	125.7
Hypothetical protein	197.1	242.9	257.2	223.2	199.2
SPy0236 DNA repair protein RadA	203.8	187.5	220.6	288.7	247.4
SPy0237 conserved hypothetical protein	153.3	158.2	227.8	174.6	154.4
SPy0238 conserved hypothetical protein TIGR00266	133.7	153.1	153.4	151.6	134.3
SPy0239 glutamyl-tRNA synthetase	197.4	155.4	228.6	186.3	162.7
Hypothetical protein	86.7	105.5	95.5	118.1	77.6
SPy0242 ComD, histidine kinase spt1S1	122.6	150.5	193.3	186.5	133.1
SPy0244 ComD, histidine kinase spt1S2	120.1	147.4	142.1	225.9	166.1
SPy0245 response regulator spt1R	123.8	122.9	110.6	107.4	61.4
Effector RNA gene X for fasSystem	50.1	81.2	71.3	38.8	32.7
SPy0246 ribonuclease P protein component	203.3	186.3	190.8	158.6	172.1
SPy0247 inner membrane protein, 60 kDa	155.8	184.3	236.9	228.8	199.3
SPy0248 jag protein	78.2	103.9	93.3	102.9	80.9
SPy0250 ribosomal protein L34	114.6	101.7	102.0	73.2	51.6
SPy0251 putative N-acetylmannosamine-6-P epimerase	209.4	169.4	177.7	8.2	0.2
Hypothetical protein	95.4	151.9	182.6	125.9	126.8
SPy0252 conserved hypothetical protein	124.3	120.9	116.9	133.1	151.4
SPy0254 sugar ABC transporter, permease protein, putative	100.4	123.5	137.5	154.9	111.8
SPy0256 hypothetical protein	148.6	167.7	200.2	213.7	107.1
SPy0258 ROK family protein, putative	171.7	182.1	151.2	179.5	169.2
SPy0259 rpir protei, putative	100.7	99.4	114.7	128.4	111.3
SPy0260 hydrolase, putative	154.1	151.7	156.6	243.9	151.7
SPy0262 dimethyladenosine transferase	171.3	159.0	195.9	144.9	89.4
SPy0263 conserved hypothetical protein TIGR00157	176.0	163.6	214.2	164.0	98.9
SPy0264 ribulose-phosphate 3-epimerase	137.7	111.8	143.3	129.3	105.5
SPy0265 conserved hypothetical protein	195.9	199.4	231.3	249.3	209.5
SPy0266 unnamed protein product	133.4	143.6	167.5	137.6	106.7

SPy0268 transcriptional regulator, purine operon repressor	223.4	285.1	276.6	232.8	215.2
SPy0271 ribosomal protein S12	194.5	162.0	240.1	199.3	198.5
SPy0272 ribosomal protein S7	118.0	98.6	127.6	114.8	84.8
SPy0273 translation elongation factor G	145.3	127.3	134.7	174.9	164.0
Hypothetical protein	46.2	42.4	41.7	37.4	27.1
SPy0276 amino acid ABC transporter, ATP-binding protein	144.6	155.0	157.0	123.8	134.0
SPy0277 amino acid ABC transporter, permease protein, putative	137.3	137.1	159.2	132.7	162.0
SPy0278 hypothetical protein	147.2	194.7	203.4	206.9	201.0
SPy0280 undecaprenol kinase, putative	166.0	213.8	226.2	286.5	286.4
SPy0282 undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase	122.8	104.8	130.7	120.0	99.2
Hypothetical protein	54.8	50.1	45.5	51.4	42.9
SPy0285 ABC transporter, ATP-binding protein	152.8	163.3	194.9	168.6	145.4
SPy0287 Uncharacterized protein family (UPF0051), putative	165.1	142.4	168.4	172.5	165.7
SPy0288 aminotransferase, class V	167.2	145.7	174.7	144.7	140.5
SPy0290 ABC transporter membrane protein	138.3	109.2	168.8	133.4	116.6
D-alanyl-D-alanine carboxypeptidase, putative	140.2	132.3	147.1	155.8	135.5
SPy0292 D-alanyl-D-alanine carboxypeptidase, putative	74.4	60.9	66.5	60.9	60.2
Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	93.0	82.3	98.5	119.9	79.4
SPy0294 oligopeptidepermease	173.2	151.6	167.2	199.4	184.4
SPy0296 oligopeptide ABC transporter, ATP-binding protein	195.8	164.9	223.3	210.9	193.8
SPy0297 oligopeptide ABC transporter, ATP-binding protein	105.2	122.0	137.7	133.3	104.3
Conserved hypothetical protein	66.7	90.9	90.5	84.9	55.0
Hypothetical protein	108.6	113.2	89.8	139.0	95.3
SPy0300 ComX1	224.6	261.1	229.6	317.6	331.7
SPy0305 conserved hypothetical protein	133.4	151.2	170.5	136.6	133.7
SPy0306 GTPase of unknown function subfamily, putative	148.6	148.5	152.1	142.1	141.8
SPy0307 conserved hypothetical protein TIGR00253	83.2	99.4	110.2	90.6	103.4
SPy0308 conserved hypothetical protein TIGR00482	92.9	106.8	116.8	109.8	115.5
SPy0310 iojap-related protein	212.2	243.7	186.8	250.3	281.4
SPy0312 methlytransferase, UbiE/COQ5 family superfamily	127.9	144.2	204.4	170.5	182.7
SPy0314 conserved hypothetical protein	143.1	137.1	156.3	131.6	163.1

SPy0316 conserved hypothetical protein TIGR01033	65.1	76.9	77.1	63.5	90.4
SPy0317 amino acid ABC transporter, periplasmic amino acid-binding portion	86.2	95.4	97.8	73.0	86.7
SPy0320 ABC transporter, ATP-binding protein	153.4	203.5	196.6	201.8	228.8
SPy0321 ABC transporter, permease protein	90.7	109.1	111.5	109.7	131.9
SPy0323 branched-chain amino acid transport system II carrier protein	230.2	210.6	261.7	261.3	322.0
SPy0324 sodium/dicarboxylate symporter	119.5	130.8	170.4	129.9	147.9
SPy0326 potassium uptake protein KtrA, putative	94.5	81.6	84.8	89.9	96.0
SPy0329 glucose-inhibited division protein B	180.7	191.6	167.7	240.8	270.8
SPy0330 LemA-like protein	123.3	133.7	134.2	103.0	93.5
SPy0331 heat shock protein HtpX	131.8	191.9	153.6	117.0	95.1
Hypothetical protein	199.7	229.8	202.5	191.9	177.3
SPy0334 YlbN-like protein	88.8	106.0	141.9	88.0	93.7
Hypothetical protein	56.8	54.7	73.6	76.0	68.2
SPy0336 DNA-binding response regulator CovR, spt2R	177.1	165.1	161.9	131.9	171.4
SPy0337 sensory transduction histidine kinase, putative	102.2	103.6	119.3	84.3	66.0
SPy0338 conserved hypothetical protein TIGR00244	122.7	150.7	168.4	108.9	91.8
SPy0339 hypothetical protein	180.2	164.7	176.5	187.5	172.9
SPy0340 primosomal protein DNAi	277.0	321.7	324.6	336.7	402.7
SPy0341 GTP-binding protein	209.0	311.1	286.3	362.9	343.0
SPy0342 helicase, Snf2 family	300.1	341.2	410.6	362.4	445.8
SPy0343 CG1326 gene product, putative	127.0	114.9	146.1	102.2	89.4
Hypothetical protein	92.2	94.8	93.7	73.3	69.2
SPy0345 UDP-N-acetylmuramate--alanine ligase	164.1	175.5	210.3	161.9	167.6
SPy0346 putative arylalkylamine n-acetyltransferase	139.2	175.4	136.9	166.4	187.0
SPy0348 aminodeoxychrorismate lyase homolog, putative	145.4	190.8	153.8	152.1	189.4
SPy0349 transcription elongation factor GreA	95.2	118.4	135.9	164.2	155.2
Hypothetical protein	122.2	104.0	125.9	100.0	89.1
SPy0351 membrane protein homolog, putative	108.0	109.9	133.9	118.3	106.3
SPy0352 Acylphosphatase	126.9	125.2	127.8	148.9	128.9
SPy0356 rRNA methylase, putative	219.5	227.8	245.6	239.1	189.3

SPy0357 hypothetical protein	188.5	194.2	242.3	233.2	186.8
SPy0358 conserved hypothetical integral membrane protein	175.4	183.4	240.9	383.5	323.0
SPy0359 conserved hypothetical protein	176.6	124.9	174.5	136.4	107.1
Hypothetical protein	60.4	97.4	93.9	66.6	36.1
SPy0361 glutamate racemase	92.2	124.6	151.3	120.9	125.4
SPy0362 HAM1 protein	213.7	162.1	232.7	264.8	242.4
SPy0363 conserved hypothetical protein TIGR00040	181.8	257.7	234.5	224.4	246.2
SPy0365 hypothetical protein	86.8	98.5	76.6	86.6	55.7
SPy0367 conserved hypothetical protein TIGR00281	147.8	203.0	194.4	204.3	265.2
SPy0369 ribosomal large subunit pseudouridine synthase B	174.2	170.7	143.9	292.0	264.3
SPy0370 conserved hypothetical protein TIGR00278	218.7	226.7	230.5	294.3	314.3
SPy0373 conserved hypothetical protein	103.3	125.2	124.5	108.9	104.2
SPy0374 histidine kinase, putative	108.3	187.1	152.4	104.3	82.5
SPy0376 conserved hypothetical protein TIGR01212	157.5	128.8	181.2	162.3	143.5
SPy0377 unknown conserved protein	211.8	186.7	225.6	328.1	342.3
SPy0378 CBS domain protein	134.4	147.8	142.9	160.6	162.4
SPy0380 inorganic pyrophosphatase, manganese-dependent	128.3	119.2	155.6	99.8	95.5
SPy0382 conserved hypothetical protein	175.9	182.0	156.3	131.4	141.4
SPy0383 streptococcal iron uptake permease subunit G	135.7	158.9	143.2	146.1	148.3
SPy0384 streptococcal iron uptake permease subunit B	223.4	204.6	244.1	250.4	267.6
SPy0385 streptococcal iron uptake substrate binding protein D	225.9	292.1	296.8	387.9	381.2
SPy0388 UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	146.1	124.5	49.6	165.1	140.7
SPy0392 uracil phosphoribosyltransferase	140.8	122.9	145.4	123.3	158.7
SPy0393 hypothetical protein	63.6	59.9	53.7	74.7	66.3
SPy0395 ATP-dependent Clp protease, proteolytic subunit	141.1	113.8	172.9	143.1	136.3
SPy0397 unknown conserved protein in B. subtilis, putative	104.4	115.9	129.6	118.8	117.4
SPy0399 thymidylate kinase	144.9	132.3	151.9	148.1	175.8
SPy0400 DNA polymerase III, subunits gamma and tau, putative	122.9	111.1	123.3	116.9	124.0
SPy0401 signal peptidase-like protein	92.4	90.6	104.8	99.9	102.9
Signal peptidase-like protein	116.6	109.1	94.7	144.0	141.2
SPy0405 unknown conserved protein in B. subtilis	72.0	77.8	79.0	77.6	73.7
SPy0406 conserved hypothetical protein TIGR00096	104.0	126.5	120.9	109.8	143.8

SPy0407 hypothetical protein	197.4	227.1	250.6	231.3	252.9
SPy0408 copper homeostasis protein	147.6	127.3	138.2	154.1	181.1
Hypothetical protein	93.2	121.8	91.1	108.7	101.1
SPy0412 exodeoxyribonuclease III	113.2	90.5	124.4	126.3	111.2
SPy0414 L-lactate dehydrogenase, putative	107.2	97.8	81.3	104.0	92.5
Hypothetical protein	94.2	63.6	73.4	95.4	88.2
SPy0416 cell envelope proteinase	124.0	100.5	122.4	186.6	165.5
Hypothetical protein	96.8	88.3	100.3	119.2	126.2
Hypothetical protein	135.9	109.4	163.3	107.3	107.8
SPy0421 hypothetical protein	195.5	187.7	224.1	290.7	323.8
SPy0422 methionyl-tRNA synthetase	94.1	105.2	100.6	74.1	85.6
SPy0425 Ribonucleotide reductases	201.1	167.4	204.1	232.8	235.8
SPy0427 Ribonucleotide reductase	237.7	257.4	247.1	334.8	400.8
SPy0428 Exotoxin SpyA; ADP-ribosylating toxin targeting host actin cytoskel.	147.8	137.7	160.1	146.2	128.3
SPy0430 hypothetical protein	119.7	126.1	261.3	119.0	135.7
SPy0432 hypothetical protein	171.5	135.1	320.6	162.4	195.5
SPy0433 hypothetical protein	132.7	4.6	6.0	32.2	37.0
SPy0436 exotoxin type c precursor; SpeJ	73.8	5.1	7.6	94.6	12.1
SPy0437 hypothetical protein	81.0	11.5	18.3	45.4	37.4
SPy0439 hypothetical protein	234.4	289.9	344.7	241.8	325.4
SPy0440 3-oxoacyl-(acyl carrier protein) reductase, putative	415.0	478.7	586.4	640.3	697.5
SPy0441 unknown conserved protein	106.5	88.3	103.3	110.2	116.7
SPy0442 glycerol-3-phosphate transporter, putative	256.8	242.1	190.5	203.6	241.5
SPy0443 UDP-N-acetylglucosamine pyrophosphorylase	223.8	221.7	261.0	372.5	351.3
SPy0444 MutT/nudix family protein	116.8	93.1	135.8	122.6	112.6
SPy0446 hypothetical protein	123.4	104.2	120.7	114.9	123.2
SPy0447 MTA/SAH nucleosidase	98.1	99.0	108.4	105.4	94.6
SPy0448 hypothetical protein	78.4	45.3	55.4	50.6	53.7
SPy0450 streptococcal metal-dependent transcriptional repressor, MtsR	128.4	114.7	128.6	116.8	118.3
Hypothetical protein	63.7	52.6	53.4	68.2	56.3

SPy0453 manganese-binding protein	100.8	111.5	119.2	100.2	85.1
SPy0454 manganese transport system ATP-binding protein	101.0	112.9	115.5	123.7	123.4
SPy0456 manganese transport system membrane protein	241.3	299.5	289.9	339.4	305.3
SPy0457 peptidyl-prolyl cis-trans isomerase	136.8	145.7	182.7	159.3	130.8
SPy0458 cell division protein FtsK	350.9	417.6	444.0	553.3	367.2
SPy0459 hypothetical protein	156.7	219.3	191.7	222.0	190.3
SPy0460 Ribosomal protein L11	83.8	92.6	104.9	73.7	64.1
SPy0461 ribosomal protein L1	157.4	169.2	191.6	166.7	96.1
Hypothetical protein	70.2	112.1	69.5	81.0	66.1
SPy0462 uridylate kinase	150.4	154.4	184.5	145.9	110.5
SPy0463 ribosome recycling factor	128.0	151.6	164.1	156.2	117.2
SPy0464 conserved hypothetical protein	113.3	140.4	148.9	136.7	99.6
SPy0466 peptide methionine sulfoxide reductase	189.2	191.3	266.4	261.4	220.4
SPy0467 conserved hypothetical protein	71.0	83.3	76.3	89.2	78.4
SPy0469 LysM domain protein protein	196.1	160.2	210.7	181.4	184.1
Hypothetical protein	98.9	131.9	125.1	113.5	99.1
SPy0470 antigen, 67 kDa (myosin-crossreactive)	143.2	182.6	176.0	197.6	152.4
SPy0471 phoH family protein	138.4	156.4	230.0	164.0	107.3
SPy0472 conserved hypothetical protein	86.5	110.6	101.0	90.7	78.1
SPy0473 conserved hypothetical protein TIGR00043	273.5	286.2	280.3	371.3	338.4
SPy0475 diacylglycerol kinase	199.7	223.2	143.7	245.8	226.1
SPy0476 GTP-binding protein Era	178.6	143.0	236.2	212.5	191.0
SPy0477 MutT/nudix family protein	110.1	124.1	127.8	163.6	161.5
SPy0479 bacteriocin-related protein	354.1	349.4	93.8	577.9	541.1
SPy0480 hypothetical protein	214.4	159.8	45.5	199.6	174.9
IS1553, transposase	117.5	144.1	20.2	104.6	67.9
IS1553, transposase, putative	202.3	375.7	13.4	372.0	231.8
BlpM protein	191.5	160.9	36.6	290.0	261.7
SPy0484 conserved hypothetical protein	127.9	129.1	31.5	167.1	184.2
SPy0488 hypothetical protein	126.6	112.9	160.4	152.4	126.0
SPy0489 hypothetical protein	143.6	135.8	138.4	122.2	115.0
SPy0492 hypothetical protein	91.3	82.5	105.6	133.8	138.5

Hypothetical protein	108.6	110.7	125.2	122.7	122.1
Hypothetical protein	159.1	149.2	154.4	249.3	203.7
Hypothetical protein	118.8	130.2	138.0	174.4	154.2
SPy0496 MutR, putative	256.1	290.8	347.4	284.4	255.4
SPy0497 formamidopyrimidine-DNA glycosylase	182.5	204.3	228.8	235.3	193.1
SPy0498 kinase, putative	254.6	259.8	211.4	306.9	259.2
SPy0500 conserved hypothetical protein	155.0	127.7	157.4	190.7	192.7
SPy0501 multi-drug resistance efflux pump	278.0	327.6	307.8	403.5	349.3
Hypothetical protein	145.2	257.7	254.9	295.3	266.4
SPy0502 preprotein translocase, SecG subunit	125.6	132.8	133.2	129.5	120.0
SPy0503 exoribonuclease, VacB/Rnb family	233.0	318.9	340.8	190.2	235.2
SPy0504 SsrA-binding protein	131.0	119.2	168.0	191.4	138.7
SPy0505 glutamine cyclotransferase	95.9	82.4	81.7	96.8	106.8
SPy0508 conserved hypothetical protein	114.2	76.3	104.9	126.6	127.8
SPy0510 probable glycosyl transferase	111.7	120.7	144.7	150.9	150.7
SPy0511 lactoylglutathione lyase	72.2	71.7	63.8	70.1	73.2
SPy0512 NAD(P)H-flavin oxidoreductase	120.4	124.0	147.2	168.8	155.0
SPy0513 proline dipeptidase	148.4	148.2	129.0	237.3	228.7
SPy0515 lipopolysaccharide biosynthesis protein-related protein	104.5	122.2	142.7	141.1	131.1
SPy0516 hypot N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein,	78.7	71.5	69.2	76.8	77.0
Spy0517 threonyl-tRNA synthetase	83.4	83.6	82.7	82.0	81.6
Spy0518 ABC transporter, ATP-binding protein	173.5	174.2	210.2	228.6	226.6
Spy0519 conserved hypothetical protein	116.8	130.7	137.9	196.0	198.2
Hypothetical protein	105.2	106.1	90.5	113.2	122.1
Hypothetical protein	58.5	56.4	62.8	51.0	72.5
Spy0524 acetyl-coa acetyltransferase	136.3	115.6	129.2	133.7	148.3
Spy0526 bacitracin synthetase , putative	115.4	100.5	108.6	152.8	125.4
Spy0527 hypothetical protein	163.8	138.7	194.9	217.1	184.4
SPy0529 histidine kinase PnpS	143.6	115.5	130.1	148.4	135.5
SPy0530 VicX protein	112.5	116.3	119.0	121.3	136.3
SPy0531 ribonuclease III	102.2	86.4	82.3	103.0	104.2

SPy0532 chromosome segregation SMC protein, putative	97.2	85.9	93.2	125.3	118.0
SPy0533 MutR, putative	45.5	44.9	42.4	62.3	58.1
SPy0535 hypothetical protein	49.8	52.0	50.5	54.3	69.2
SPy0536 nitroreductase family protein	73.7	69.8	80.7	89.5	103.7
SPy0537 hypothetical protein	89.8	96.0	112.2	78.3	92.2
SPy0538 S-adenosylmethionine synthetase; Ado-Met	69.8	74.9	72.7	62.9	62.6
SPy0539 hypothetical protein	68.9	57.5	55.6	63.3	57.5
SPy0540 Glycosyl transferases domain protein	66.3	76.0	52.3	81.9	84.9
Hypothetical protein	91.1	105.6	82.4	70.7	89.7
SPy0542 UDP-glucose 6-dehydrogenase	48.5	61.2	55.0	56.4	50.3
SPy0543 macrolide-efflux protein	96.7	150.5	147.6	112.4	143.0
SPy0544 repressor protein, putative	78.0	80.5	80.6	63.0	66.7
SPy0545 hypothetical protein	134.3	133.9	126.5	128.7	128.0
SPy0546 hypothetical protein	127.3	128.1	116.2	147.5	164.2
SPy0547 hypothetical protein	86.2	79.0	75.5	90.6	79.6
SPy0549 hypothetical protein	119.0	84.4	99.7	114.7	112.4
SPy0550 DNA-damage-inducible protein J, putative	94.2	102.8	109.8	101.1	106.9
SPy0552 hypothetical protein	102.9	103.6	119.3	153.0	134.9
SPy0553 hypothetical protein	119.8	123.2	131.9	212.9	171.5
SPy0555 putative portal protein-related	214.7	14.9	218.5	41.8	343.0
SPy0556 hypothetical protein	152.0	10.4	207.1	34.3	137.5
SPy0558 hypothetical protein	80.4	2.7	126.8	12.3	74.4
SPy0559 asparaginyl-tRNA synthetase, putative	89.4	8.3	106.8	22.5	83.5
SPy0560 hypothetical protein	86.0	2.3	102.8	11.8	63.6
SPy0561 microcin immunity protein MccF	92.4	5.3	58.1	23.0	122.4
Hypothetical protein	92.6	4.9	66.2	15.0	113.4
SPy0563 hypothetical protein	81.6	17.5	120.8	25.2	81.1
SPy0565 transposase OrfAB, subunit B, putative	66.9	67.4	77.2	62.3	53.5
SPy0567 haloacid dehalogenase-like hydrolase superfamily	209.0	199.7	205.8	220.1	212.9
SPy0568 f270, putative	224.3	222.7	244.6	259.2	279.6
SPy0569 cell division protein FtsY	161.2	184.3	165.9	209.3	160.3
SPy0570 drug transporter, putative	162.9	215.0	214.0	178.6	184.0

SPy0571 beta-glucoside operon antiterminator	140.8	160.9	186.3	139.3	116.0
SPy0572 pts system, beta-glucosides-specific iiabc component	177.6	215.6	209.3	191.1	178.3
SPy0574 6-phospho-beta-glucosidase	214.0	231.8	250.8	287.1	264.4
SPy0575 conserved hypothetical protein	208.0	284.0	194.2	227.4	221.1
SPy0576 conserved hypothetical protein	121.9	180.2	140.1	141.6	127.8
SPy0577 hypothetical protein	81.9	145.4	102.0	135.7	98.9
SPy0578 hypothetical protein	62.7	62.1	68.5	64.8	53.4
SPy0580 transcriptional accessory protein Tex, putative	143.4	122.8	167.5	157.6	131.2
SPy0581 sprt protein, putative	124.4	123.3	141.9	140.5	128.1
SPy0583 conserved hypothetical protein	170.3	177.2	200.5	188.9	186.8
SPy0584 HPr(Ser) kinase/phosphatase	119.8	131.0	130.3	207.4	133.0
SPy0585 prolipoprotein diacylglyceryl transferase	170.8	166.0	212.4	265.1	254.0
SPy0587 conserved hypothetical protein	92.2	118.6	89.3	86.6	73.5
SPy0588 conserved hypothetical protein	88.3	106.6	125.7	107.8	100.9
SPy0589 hypothetical protein	114.2	136.7	126.7	132.8	118.9
SPy0591 protease, putative	165.5	161.7	125.6	180.4	153.9
Hypothetical protein	54.9	82.9	59.4	87.3	85.7
SPy0593 conserved hypothetical protein	106.3	91.2	111.2	102.6	54.1
Hypothetical protein	231.1	283.7	229.8	263.0	130.1
SPy0595 lysyl-tRNA synthetase	157.1	186.1	178.5	204.4	200.8
SPy0596 haloacid dehalogenase-like hydrolase family	127.2	123.1	140.5	195.6	204.5
SPy0598 phosphoglycerate mutase, putative	169.9	196.4	214.2	227.4	256.2
SPy0600 conserved hypothetical protein	162.8	243.9	212.9	206.4	191.5
SPy0601 endolysin, putative	160.4	249.6	234.8	205.3	232.1
Hypothetical protein	63.5	77.4	64.7	92.7	86.8
SPy0603 hypothetical protein	199.9	167.8	210.6	305.3	319.4
SPy0604 hypothetical protein	143.7	110.1	103.1	165.8	151.3
SPy0606 oligoendopeptidase F	234.8	205.0	224.8	228.7	228.0
Hypothetical protein	57.4	66.8	58.8	53.8	64.7
SPy0608 phosphoenolpyruvate carboxylase, putative	136.0	138.8	123.5	151.1	149.0
SPy0609 cell division protein FtsW, putative	166.2	213.5	153.6	229.0	233.8
Hypothetical protein	252.5	260.4	231.9	287.5	272.3

SPy0611 translation elongation factor Tu	135.3	275.2	244.8	240.4	284.1
SPy0613 triosephosphate isomerase	166.0	170.3	183.0	168.5	183.4
SPy0615 MurN protein	84.9	114.1	89.6	65.1	118.2
SPy0616 beta-lactam resistance factor	173.2	151.4	184.4	194.2	201.7
SPy0617 f270	122.9	104.8	127.3	159.5	158.9
Hypothetical protein	94.5	95.1	101.6	119.6	131.7
SPy0621 unknown conserved protein	79.0	82.1	84.0	83.6	99.0
SPy0622 hypothetical protein	121.9	133.7	117.8	130.6	139.0
SPy0623 H(+)-transporting ATPase	134.7	114.6	136.9	138.2	158.9
SPy0627 transcriptional regulator, LacI family, putative	83.7	93.6	75.2	97.5	93.9
SPy0628 hypothetical protein	77.5	77.4	87.0	102.2	153.7
SPy0630 PTS permease for mannose subunit IIPMan, putative	151.9	57.3	52.7	88.2	86.9
SPy0631 mannose-specific phosphotransferase system component IIAB, putative	104.4	108.5	91.9	94.8	98.7
SPy0632 unsaturated glucuronyl hydrolase	109.1	93.4	114.5	92.4	100.4
SPy0634 mannose-specific phosphotransferase system component IIAB, putative	97.3	110.8	121.0	150.8	104.5
SPy0636 3-oxoacyl-(acyl-carrier-protein) reductase	228.0	230.5	218.8	299.9	349.8
SPy0638 2-keto-3-deoxygluconate kinase, putative	121.2	84.9	117.7	103.5	135.1
SPy0639 2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	157.4	123.4	173.4	163.4	173.4
SPy0640 CbbY family protein	65.6	53.4	57.7	53.2	60.5
Hypothetical protein	86.0	91.1	99.8	122.6	156.5
Hypothetical protein	90.4	90.5	88.0	94.5	114.7
SPy0643 peptide chain release factor 2	84.9	77.0	80.7	105.6	118.3
SPY0644 cell division ATP-binding protein FtsE	100.1	91.3	119.2	125.2	153.9
SPy0645 cell division protein FtsX, putative	166.0	145.5	166.8	189.5	214.2
SPy0646 metallo-beta-lactamase superfamily protein	72.6	86.8	80.4	115.0	132.2
3-ketoacyl-acyl carrier protein reductase	143.2	131.0	133.0	189.2	192.1
SPy0649 ATP-dependent helicase, putative	119.4	127.3	166.7	124.0	152.5
SPy0650 aspartate aminotransferase	94.8	103.3	135.8	111.2	123.7
SPy0651 asparaginyl-tRNA synthetase	89.3	97.6	114.6	101.6	130.1

SPy0652 conserved hypothetical protein	132.6	124.5	164.4	118.0	129.2
SPy0653 Uncharacterised protein family superfamily	114.0	121.8	108.7	129.1	143.9
SPy0654 conserved hypothetical protein superfamily	107.8	110.8	119.0	170.4	183.3
SPy0713 dipeptidase	153.8	131.4	147.5	171.6	181.0
SPy0714 AdcA protein	130.7	136.6	125.1	149.4	171.1
SPy0715 repressor protein PhnR, putative	120.7	167.4	119.7	261.4	239.7
SPy0716 agas protein	140.5	119.7	141.7	119.8	148.1
SPy0717 ribosomal protein L31	151.9	130.7	153.4	127.9	125.2
Hypothetical protein	61.9	79.4	58.1	77.5	79.1
SPy0720 DHH family protein, putative	110.9	121.2	86.2	109.4	104.1
SPy0721 flavodoxin	92.2	124.2	104.7	125.1	126.9
SPy0722 chorismate mutase/prephenate dehydratase, putative	166.4	206.1	194.8	306.9	278.0
SPy0723 chloride channel, putative, putative	269.7	301.4	412.8	364.8	342.6
SPy0724 ribosomal protein L19	159.3	156.1	176.1	127.7	113.0
SPy0726 CbbY family protein, putative	115.4	126.0	120.4	178.0	158.2
SPy0727 DNA gyrase, subunit B	204.2	141.8	156.1	239.2	244.6
SPy0728 unknown conserved protein, putative	134.9	121.8	116.8	168.2	160.6
Hypothetical protein	42.5	51.6	47.3	59.8	57.6
SPy0731 enolase	170.4	128.9	172.4	218.3	185.4
SPy0732 Transposase IS116/IS110/IS902 family domain protein	91.6	9.9	100.8	99.7	15.9
SPy0733 mitogen-activated protein kinase kinase kinase	148.3	70.7	165.7	213.8	109.2
RofA, putative, RALP-3	204.3	41.2	233.4	315.1	81.1
SPy0737 extracellular matrix binding protein, putative	139.8	38.5	151.6	148.2	55.1
Hypothetical protein	38.0	2.2	43.2	47.0	7.5
SPy0738 streptolysin S associated protein SAGA-related protein	86.0	88.7	86.4	87.8	106.4
SPy0739 SagB	76.6	76.7	73.0	116.2	83.9
SPy0740 SagC	104.9	118.5	138.4	153.4	177.9
SPy0742 hypothetical protein	133.0	133.6	140.7	163.8	165.3
SPy0743 hypothetical protein	76.0	77.9	83.3	99.0	120.0
SPy0744 ABC transporter, ATP-binding protein, putative	111.5	100.3	97.2	110.1	130.3
SPy0745 SagH	84.8	93.7	92.1	133.3	135.7
SPy0746 conserved hypothetical protein	101.9	99.4	101.5	135.3	152.2

Hypothetical protein	75.4	80.2	73.3	79.6	86.5
SPy0749 conserved hypothetical protein	37.8	36.8	37.1	56.3	59.1
SPy0751 DNA ligase	151.4	150.6	174.2	211.9	250.8
SPy0752 conserved hypothetical protein TIGR00147	120.9	118.6	138.0	222.0	189.3
SPy0754 ATP synthase c subunit	89.3	100.1	111.6	162.7	176.1
SPy0756 ATP synthase B chain, putative	77.4	76.6	76.4	76.8	86.6
SPy0757 ATP synthase delta (OSCP) subunit	139.1	116.8	109.9	124.2	140.3
SPy0758 ATP synthase F1, alpha subunit	190.7	177.3	237.3	182.5	263.9
SPy0759 ATP synthase	99.8	94.8	100.8	110.3	111.8
SPy0760 ATP synthase F1, beta subunit	209.2	182.7	151.1	204.1	291.5
SPy0761 ATP synthase, Delta/Epsilon chain	165.2	198.6	198.4	312.4	327.1
SPy0763 UDP-N-acetylglucosamine 1-carboxyvinyltransferase	93.3	82.0	100.1	94.9	91.1
SPy0764 epua protein-related protein	106.4	101.2	115.3	100.4	145.4
SPy0766 DNA-entry nuclease	167.4	172.4	211.7	196.0	250.5
SPy0768 phenylalanyl-tRNA synthetase, alpha subunit	109.1	145.0	151.6	162.0	207.9
SPy0769 phenylalanyl-tRNA synthetase, beta subunit	166.0	164.6	155.4	144.3	151.3
SPy0770 hypothetical protein	149.2	186.6	188.6	207.7	290.5
SPy0771 hypothetical protein	141.1	119.2	148.6	195.3	223.3
SPy0772 Predicted permease family	157.7	165.0	186.6	52.7	262.9
SPy0773 ABC transporter, ATP-binding protein	105.5	91.2	96.7	96.8	109.2
SPy0775 conserved hypothetical protein	88.8	85.5	78.9	62.7	66.9
SPy0776 exonuclease RexB, putative	198.5	173.5	184.2	187.0	215.7
SPy0777 exonuclease RexA	217.5	217.1	191.1	299.8	375.2
Hypothetical protein	80.2	85.3	93.7	113.3	136.7
SPy0778 probable binding protein component of ABC transporter, putative	105.2	107.0	121.7	104.5	133.5
SPy0779 ribosomal protein S21	51.5	51.5	44.7	39.4	44.2
SPy0780 large conductance mechanosensitive channel protein	89.4	101.6	94.9	115.1	131.8
SPy0781 DNA primase, putative	115.6	97.6	77.4	125.5	141.8
SPy0782 RNA polymerase sigma factor RpoD	118.0	160.2	182.5	121.7	119.6
SPy0783 unnamed protein product	231.7	183.1	289.7	303.9	216.6
SPy0784 dTDP-4-dehydrorhamnose reductase	167.0	136.3	150.7	163.5	150.8

hypothetical protein	120.8	103.0	153.1	172.0	96.0
SPy0786 alpha-(1,2)-rhamnosyltransferase	156.6	162.6	180.6	211.1	177.2
SPy0787 alpha-L-Rha alpha-1,3-L-rhamnosyltransferase	117.9	182.6	172.7	204.8	194.6
Hypothetical protein	39.0	40.3	40.4	30.6	24.2
SPy0789 polysaccharide export ABC transporter permease protein	116.0	174.7	124.0	113.0	117.4
SPy0790 polysaccharide export ATP-binding protein	92.1	102.8	97.6	98.9	100.3
SPy0791 glycosyltransferase	105.8	93.5	112.9	103.6	145.7
SPy0792 alpha-L-Rha alpha-1,2-L-rhamnosyltransferase	97.8	165.9	106.4	153.4	140.4
SPy0793 conserved hypothetical protein	190.9	232.4	235.5	289.5	133.9
SPy0794 glycosyl transferase, putative	115.4	141.9	127.0	133.8	136.0
SPy0796 hypothetical protein	96.3	117.8	103.7	139.1	130.0
SPy0797 wzx sugar exporter required for full mga expression	119.8	155.4	154.5	173.7	197.4
SPy0798 conserved hypothetical protein	96.0	122.3	106.6	120.5	125.7
SPy0799 peptidase T	163.1	201.7	182.6	213.1	210.1
SPy0800 pore forming protein ebsa, putative	126.9	158.0	125.7	174.9	174.7
SPy0801 ferredoxin	61.3	80.9	71.3	56.2	52.4
SPy0802 hypothetical protein	59.6	74.5	76.8	59.4	53.9
SPy0803 cytidylate kinase	139.6	169.4	139.2	176.8	188.9
SPy0804 translation initiation factor IF-3	143.5	142.7	156.2	140.9	144.5
SPy0805 ribosomal protein L35	91.1	104.0	101.9	112.8	104.2
SPy0806 ribosomal protein L20	93.6	142.3	103.1	225.2	162.7
SPy0807 minimal change nephritis transmembrane glycoprotein	125.4	139.5	157.7	135.9	134.4
SPy0808 conserved hypothetical protein	148.8	164.4	167.9	115.9	120.6
SPy0809 3-dehydroquinate dehydratase, type I	73.0	82.8	71.2	92.2	90.3
SPy0810 chorismate synthase	103.8	99.8	104.1	151.2	140.7
SPy0811 conserved hypothetical protein	117.7	135.8	145.1	161.8	134.3
SPy0813 glutathione reductase	134.0	156.0	128.0	142.2	171.0
SPy0814 folylpolyglutamate synthase/dihydrofolate synthase, putative	134.2	181.1	168.1	158.4	171.3
SPy0815 hypothetical protein	131.9	154.6	157.2	158.7	158.0
SPy0816 nifs protein homolog , fragment	121.0	104.6	115.4	138.1	134.3
SPY0817 thiazole biosynthesis protein ThiI	137.6	153.9	147.4	202.1	200.4

SPy0818 capa protein, putative	126.2	159.0	154.6	222.0	216.8
SPy0819 ribosomal protein L21	103.1	97.2	106.4	103.0	87.9
SPy0821 unknown conserved protein in B. subtilis, putative	116.9	164.9	121.0	123.9	119.2
SPy0822 ribosomal protein L27	153.2	118.6	143.3	176.2	197.3
SPy0824 transcriptional regulator, LysR family, putative	68.4	67.5	61.6	104.4	81.5
SPy0826 lipoprotein signal peptidase	99.7	113.9	87.9	150.2	175.0
Hypothetical protein	68.9	110.2	90.1	96.6	97.3
SPy0831 uracil permease	127.7	122.6	135.4	173.5	179.8
SPy0832 aspartate carbamoyltransferase	114.4	110.4	125.9	144.8	150.1
SPy0833 carbamoyl-phosphate synthase, small subunit	93.2	114.0	123.4	132.3	96.5
SPy0835 carbamoyl-phosphate synthase, large subunit	94.7	97.9	112.3	111.8	121.1
SPy0836 ATP-binding cassette transporter-like protein, putative	60.8	64.3	55.4	50.7	50.8
SPy0837 ABC transporter, ATP-binding protein	102.1	104.7	112.1	103.2	113.8
SPy0838 ABC transporter, ATP-binding protein	134.2	153.6	136.3	179.2	201.0
SPy0839 hypothetical protein	103.9	79.7	107.8	159.5	171.6
SPy0841 KH domain protein	45.9	49.9	46.9	49.9	50.2
Hypothetical protein	36.2	38.9	29.2	39.7	34.6
Hypothetical protein	46.4	68.9	51.6	45.6	48.1
SPy0843 Leucine Rich Repeat domain protein	165.6	137.2	97.9	133.0	161.4
SPy0844 conserved hypothetical protein	188.8	153.7	168.1	223.9	247.3
SPy0846 Bacterial regulatory proteins, tetR family domain protein	73.5	59.6	59.2	65.5	69.8
SPy0847 16S rRNA processing protein RimM, putative	125.4	147.9	127.2	168.0	179.3
SPy0849 tRNA (guanine-N1)-methyltransferase	139.8	123.5	123.6	179.5	194.1
SPy0850 thioredoxin reductase, putative	104.0	106.3	108.5	138.3	149.9
SPy0851 regulatory protein	147.1	155.2	130.3	257.5	217.7
SPy0853 glycerol-3-phosphate regulon repressor, putative	114.3	83.2	117.6	110.8	138.4
SPy0854 1-phosphofructokinase, putative	142.2	104.3	121.6	162.5	163.6
SPy0855 PTS system, fructose-specific IIABC component	219.8	156.5	187.5	266.0	293.2
SPy0856 N-acetylmuramidase, putative	63.8	63.4	50.3	69.1	61.3
SPy0857 N-acetylmuramidase, putative	98.4	87.4	73.8	121.6	129.4
Hypothetical protein	86.1	54.2	54.9	113.7	110.6
Exotoxin type c precursor	46.9	62.5	50.9	48.6	46.1

SPy0861 secreted IgG-degrading protease	129.5	119.0	142.4	148.2	182.9
Hypothetical protein	110.3	164.7	99.2	126.0	153.6
Nucleoside diphosphate kinase	183.6	204.9	185.9	314.7	186.7
SPy0864 hypothetical protein	154.5	136.1	115.9	183.8	202.6
SPy0865 unknown conserved protein	82.9	92.6	102.0	172.5	195.3
SPy0866 poly(A) polymerase family protein	161.4	160.5	205.8	186.6	224.0
SPy0867 ABC transporter, ATP-binding protein, putative	160.2	175.7	246.4	234.3	296.7
Hypothetical protein	70.8	86.0	59.8	65.4	79.9
SPy0870 polypeptide deformylase	115.4	125.3	99.4	147.9	140.6
SPy0872 5`-nucleotidase family protein, putative	131.7	170.1	140.4	188.7	207.7
SPy0873 permease	90.9	85.4	99.9	129.9	138.1
SPy0874 response regulator saliva persistence (Spt); our spt4R designation	90.1	92.3	87.8	95.0	110.6
SPy0875 histidine kinase saliva persistence; our spt4S designation	101.3	97.4	103.2	93.1	102.5
SPy0876 mevalonate kinase	158.4	155.8	188.2	140.3	137.1
SPy0877 mevalonate diphosphate decarboxylase, putative	147.5	145.2	127.0	163.1	210.5
SPy0878 phosphomevalonate kinase	167.9	167.0	162.7	248.9	274.8
SPy0879 FMN-dependent dehydrogenase superfamily	201.7	166.3	250.3	223.3	224.9
SPy0880 hydroxymethylglutaryl-CoA reductase, degradative	206.8	332.9	348.2	257.3	290.0
SPy0881 condensing enzyme, putative, FabH-related	106.3	109.8	128.8	111.5	147.9
SPy0882 Thymidylate synthase	120.7	135.5	133.9	137.9	162.9
SPy0884 hypothetical protein	113.3	114.5	88.0	155.3	189.3
SPy0885 ATP-dependent Clp protease, ATP-binding subunit ClpX	110.4	137.1	122.5	115.3	81.6
SPy0886 hypothetical gtp-binding protein in pola-hemn intergenic region	142.9	111.8	132.3	110.7	118.6
SPy0887 hypothetical protein	99.0	109.6	97.2	118.8	119.8
SPy0888 ClpE	139.6	162.1	174.9	194.3	169.6
SPy0889 ribose 5-phosphate isomerase	138.4	165.6	127.4	195.7	200.6
SPy0890 phosphopentomutase	185.3	244.8	290.3	420.6	433.2
SPy0891 arsenate reductase	138.6	183.9	190.9	171.0	172.9

SPy0892 purine nucleoside phosphorylase	130.4	132.6	175.9	174.4	169.4
Hypothetical protein	98.3	115.5	75.0	104.2	94.0
SPy0894 purine nucleoside phosphorylase	168.8	208.1	221.6	233.5	203.9
SPy0895 hypothetical protein	124.6	151.2	162.9	649.0	177.5
SPy0898 transcriptional regulator, LysR family, putative	168.5	191.7	199.1	240.3	207.3
SPy0899 conserved hypothetical protein	87.5	110.1	97.3	88.1	73.5
SPy0900 orotidine 5`-phosphate decarboxylase	230.1	236.2	250.9	276.8	292.8
SPy0901 orotate phosphoribosyltransferase	270.7	229.0	248.5	338.7	332.2
SPy0902 amidase family protein, putative	145.6	179.2	134.2	207.7	207.8
SPy0903 amino acid ABC transporter, periplasmic amino acid-binding portion	138.6	161.3	172.5	213.2	211.8
SPy0904 amino acid ABC transporter, permease protein	116.3	200.4	169.1	383.8	362.1
SPy0905 uracil-DNA glycosylase	200.4	277.3	268.1	245.0	211.7
SPy0907 dihydroorotase	114.6	101.2	132.7	127.8	133.8
SPy0908 conserved hypothetical protein TIGR00023	131.3	173.3	128.4	209.7	192.6
SPy0909 DNA topoisomerase IV, subunit B	258.4	144.1	87.4	211.0	179.9
SPy0910 DNA topoisomerase IV, subunit A	113.4	129.9	115.6	155.1	127.2
SPy0911 branched-chain amino acid aminotransferase	170.3	190.4	158.1	250.6	221.7
SPy0912 hypothetical protein	58.8	89.9	72.9	84.6	77.9
Hypothetical protein	111.5	147.1	106.9	170.0	159.3
SPy0914 hypothetical protein	59.2	50.2	48.8	74.6	75.7
Hypothetical protein	160.3	129.1	139.2	163.2	114.6
SPy0919 hypothetical protein	123.8	90.7	105.8	85.0	89.5
SPy0921 tRNA delta(2)-isopentenylpyrophosphate transferase	93.6	113.1	93.9	108.1	101.8
SPy0922 GTP-binding protein	85.3	100.9	90.7	103.8	94.6
SPy0924 AtsA/ElaC family protein, putative	170.9	155.8	212.1	169.9	122.7
SPy0926 single-stranded-DNA-specific exonuclease RecJ	96.7	98.0	77.9	84.6	93.0
SPy0927 adenine phosphoribosyltransferase	130.5	111.1	116.9	175.8	202.1
SPy0928 conserved hypothetical protein	94.3	107.7	92.8	140.7	126.6
SPy0930 conserved hypothetical protein	145.5	172.1	208.9	198.5	169.8
SPy0931 conserved hypothetical protein TIGR00486	150.7	146.8	190.9	168.2	162.6
SPy0932 conserved hypothetical protein	232.5	239.3	178.3	337.5	307.9

SPy0933 glucose-1-phosphate thymidylyltransferase	102.2	77.9	87.1	92.9	89.9
SPy0935 dTDP-4-dehydrorhamnose 3,5-epimerase	114.8	149.1	128.7	183.3	182.7
SPy1010 7,8-dihydro-8-oxoguanine-triphosphatase	102.4	117.6	137.4	142.4	109.8
SPy1011 permease PerM, putative	175.2	177.3	316.9	403.1	339.1
SPy1012 alpha-acetolactate synthase, putative	94.9	125.4	111.8	99.8	93.8
SPy1013 fibronectin/fibrinogen-binding protein	152.6	138.4	169.1	140.1	112.3
Hypothetical protein	71.9	67.4	69.3	63.7	52.1
SPy1016 conserved hypothetical protein	126.8	127.0	131.0	132.3	90.1
SPy1017 hypothetical protein	72.7	67.3	47.9	81.4	52.4
SPy1018 ABC transporter, permease protein, putative	102.7	133.5	135.3	171.3	127.5
SPy1019 ABC transporter, ATP-binding protein	69.8	76.2	98.4	78.2	76.0
SPy1020 unknown conserved protein	109.0	75.4	79.4	105.8	105.2
SPy1022 esterase, putative, antigen 85-B	171.9	172.9	166.5	261.6	223.4
SPy1025 ABC transporter, ATP-binding protein, putative	252.1	139.4	180.8	332.6	299.0
SPy1026 probable dehydrogenase E1 component	116.0	112.2	112.7	168.6	138.3
SPy1029 2-oxoglutarate dehydrogenase, E2 comp.t, dihydrolipoamide succinyltransferase	147.2	127.0	150.6	134.7	75.1
SPy1031 lipoamide dehydrogenase-glc	169.9	179.4	126.3	141.7	124.5
SPy1032 extracellular hyaluronate lyase	114.4	119.6	130.8	129.5	103.7
SPy1033 lipoate-protein ligase A, putative	122.4	158.5	114.2	135.6	106.0
SPy1035 UDP-N-acetylmuramyl tripeptide synthetase MurC, putative	126.3	139.2	178.0	169.9	123.9
SPy1037 conserved hypothetical protein	83.2	80.8	68.1	111.2	95.6
SPy1038 phosphoglucomutase/phosphomannomutase family protein	90.1	92.3	92.9	126.1	101.1
SPy1039 hypothetical protein	88.9	107.9	86.2	139.9	100.4
Hypothetical protein	107.7	136.9	131.0	129.1	107.8
SPy1042 acyl-ACP thioesterase, putative	115.0	123.6	121.4	110.8	82.9
SPy1043 p-nitrophenyl phosphatase	194.6	152.2	172.0	275.3	213.0
SPy1044 hypothetical protein	88.1	81.5	73.1	116.0	103.9
Hypothetical protein	39.5	5.4	9.9	19.2	12.0
SPy1046 hypothetical protein	102.8	10.5	13.7	26.8	21.8

SPy1047 Protein of unknown function superfamily	74.2	11.0	16.5	27.5	20.4
Hypothetical protein	54.3	8.0	21.8	13.6	8.0
SPy1052 nucleoside diphosphate kinase	124.4	133.1	73.4	126.5	119.0
SPy1053 GTP-binding protein LepA	95.8	112.1	74.5	175.7	148.2
SPy1055 PilB-related protein	150.8	92.6	117.2	116.4	125.8
SPy1056 conserved hypothetical integral membrane protein, putative	88.7	113.1	74.5	139.3	117.3
SPy1057 PTS system, mannose/fructose family IIA component	69.2	62.7	59.9	101.2	105.1
SPy1058 PTS system, mannose/fructose family IIB component	115.5	84.8	121.9	124.9	101.8
SPy1059 PTS system, mannose/fructose family IIC component	96.3	98.0	90.9	123.1	100.4
SPy1061 two-component sensor histidine kinase, putative spt5S; hk09	84.6	78.4	94.6	82.6	70.2
SPy1062 response regulator, yesNM, rr09	86.3	78.9	87.8	101.5	106.0
SPy1063 iron(III) ABC transporter, periplasmic iron-compound-binding prot.	112.0	104.5	116.8	122.7	116.5
SPy1064 hypothetical protein	62.4	8.4	8.9	20.2	5.8
SPy1065 hexapeptide-repeat containing-acetyltransferase	162.6	35.6	28.8	57.2	57.2
SPy1067 succinate-semialdehyde dehydrogenase	115.2	93.8	82.4	124.7	134.3
SPy1068 excinuclease ABC, subunit C	165.4	170.7	189.5	241.8	228.9
SPy1069 NAD(P)H-flavin oxidoreductase, putative	127.9	113.7	150.2	161.9	169.6
SPy1070 dipeptidase	138.8	94.1	136.8	135.9	126.6
SPy1071 thiophene and furan oxidation (thdF)	128.6	104.0	104.4	157.7	169.7
SPy1073 ribosomal protein L7/L12	173.5	126.2	161.9	189.9	188.8
Conserved hypothetical protein	214.4	189.9	191.7	240.1	257.5
SPy1075 conserved hypothetical protein	73.5	5.5	36.6	18.7	13.3
Hypothetical protein	128.3	21.2	181.3	45.0	35.4
Relaxase	101.0	5.8	144.5	16.3	14.6
Relaxase	63.3	5.9	75.0	34.8	27.3
SPy1080 SrtI	81.5	2.1	113.6	16.6	9.2
SPy1081 DNA-binding response regulator TrcR, spt6R, srtR	59.5	4.3	66.5	21.4	18.1
SPy1082 SrtK histidine kinase, spt6S	81.9	5.5	103.4	18.1	14.7
SPy1084 ABC transporter, ATP-binding protein, MsbA family	80.2	11.9	104.8	22.0	17.6
SPy1085 MrsF protein	92.8	13.5	109.1	50.5	57.8

SPy1086 SrtE	82.4	15.0	111.0	41.9	35.6
SPy1087 SrtG	67.9	10.5	71.7	25.7	22.4
SPy1088 repressor protein, putative	56.5	6.0	60.7	21.2	16.1
Hypothetical protein	72.7	9.6	77.2	30.6	3.3
Hypothetical protein	90.3	6.6	93.6	23.2	15.1
Integrase/recombinase XerD, putative	83.4	28.5	86.8	60.6	54.1
SPy1093 D-alanyl-D-alanine carboxypeptidase, putative	96.6	86.7	126.8	117.4	121.8
SPy1094 conserved hypothetical protein	48.5	62.3	67.5	47.5	51.8
SPy1094 folylpolyglutamate synthase/dihydrofolate synthase, putative	85.1	95.0	94.6	89.8	88.1
SPy1097 GTP cyclohydrolase I	105.5	115.4	108.8	123.0	87.8
SPy1098 dihydropteroate synthase	159.6	175.1	147.0	241.6	228.8
SPy1099 dihydroneopterin aldolase	160.1	138.7	221.7	157.4	133.2
SPy1100 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinas	132.9	145.0	165.9	174.3	148.8
SPy1101 UDP-N-acetylenolpyruvoylglucosamine reductase	154.8	187.8	171.1	206.0	181.7
SPy1102 spermidine/putrescine ABC transporter, ATP-binding protein	106.7	140.7	119.2	129.7	94.9
SPy1103 spermidine/putrescine ABC transporter, permease protein, putative	115.9	172.9	102.6	149.4	103.6
SPy1104 spermidine/putrescine ABC transporter, permease protein, putative	152.6	199.3	212.6	421.5	312.5
SPy1105 spermidine/putrescine ABC transporter, periplasmic	128.8	111.2	138.4	115.4	114.3
SPy1106 transcriptional regulator CitB, putative/ dpiA	93.3	119.7	90.9	88.7	91.1
SPy1107 sensor kinase citA, putative/ dpiB	127.4	124.0	140.2	147.4	131.9
SPy1109 citrate/sodium symporter, putative	174.9	173.7	218.9	237.1	230.5
SPy1110 malate oxidoreductase, putative	129.9	173.6	191.1	192.3	152.1
SPy1111 zinc-binding dehydrogenase, putative	175.2	216.5	218.8	366.1	345.9
SPy1113 acid phosphatase	74.6	108.3	100.2	86.8	68.4
SPy1114 Voltage gated chloride channels family	126.7	173.2	170.5	185.8	158.7
SPy1115 acylneuraminate cytidylyltransferase, putative	70.7	90.6	68.9	90.7	66.9
SPy1117 putative permease, putative	99.6	137.7	103.9	135.6	126.0

SPy1118 DNA repair protein RadC, putative	64.0	85.0	80.7	86.5	69.3
SPy1119 glutamine amidotransferase, putative	128.4	199.4	186.8	326.4	230.9
SPy1120 AT-rich DNA-binding protein p25	118.2	168.3	142.9	119.2	99.8
SPy1121 hypothetical protein	77.2	100.7	84.2	74.2	63.6
SPy1122 aminotransferase NifS, class V	174.1	240.3	212.6	216.5	177.8
SPy1123 ribose-phosphate pyrophosphokinase	142.5	161.8	175.3	180.5	135.5
SPy1124 conserved hypothetical protein	66.3	94.9	85.7	79.7	69.7
SPy1125 GTP pyrophosphokinase	156.0	213.7	245.3	308.6	237.8
SPy1126 BC541A protein	133.7	127.4	135.1	140.1	104.4
SPy1128 phosphotransacetylase	99.9	80.0	67.5	98.0	80.4
3-oxoacyl-(acyl-carrier-protein) reductase, putative	144.6	136.3	169.9	248.2	218.0
Short chain dehydrogenase/reductase	208.0	184.9	126.3	269.4	251.8
SPy1133 amino acid ABC transporter, ATP-binding protein	193.2	189.1	175.7	178.8	159.4
SPy1135 GMP reductase	111.7	101.8	96.0	96.6	104.7
SPy1136 xanthine phosphoribosyltransferase	133.7	148.7	150.3	187.1	176.4
SPy1137 xanthine/uracil permease family protein, putative	148.7	163.9	164.5	223.0	209.2
SPy1139 4-oxalocrotonate tautomerase	71.5	97.9	83.6	78.9	72.2
SPy1140 Thymidine kinases	291.2	218.2	246.8	215.6	258.2
SPy1141 peptide chain release factor 1	110.0	106.6	95.5	133.2	118.8
SPy1142 hemK protein	56.3	47.9	44.5	59.1	52.7
SPy1143 Sua5/YciO/YrdC/YwlC family protein	133.8	147.6	117.9	180.7	179.7
SPy1145 Serine hydroxymethyltransferase	131.7	153.5	179.7	206.8	159.4
SPy1146 hypothetical protein	104.9	109.7	120.9	89.4	84.8
SPy1147 conserved hypothetical protein	109.5	101.3	97.1	139.5	104.9
SPy1148 ABC transporter, ATP-binding protein, putative	118.4	118.1	154.9	190.1	199.5
SPy1149 transport ATP-binding protein MsbA, putative	151.1	192.2	125.9	218.7	197.4
SPy1150 NADH oxidase, putative	161.6	186.2	161.8	271.6	259.3
Hypothetical protein	45.1	47.4	40.0	50.3	40.1
SPy1151 l-lactate dehydrogenas	131.8	114.8	145.6	175.9	175.8
SPy1152 DNA gyrase, subunit A	151.0	134.7	142.8	173.8	164.8
Hypothetical protein	64.6	60.5	47.1	71.7	65.2
SPy1154 sortase, putative	67.0	62.3	61.1	86.8	79.5

SPy1156 hypothetical protein	59.1	55.7	43.3	69.4	61.9
SPy1157 chromosome assembly protein homolog, putative	62.6	59.9	61.6	45.2	50.7
SPy1158 conserved hypothetical protein TIGR00147	72.9	73.6	68.4	90.9	79.7
Hypothetical protein	54.2	46.4	51.2	91.0	93.7
SPy1159 hemolysin, putative	129.0	165.9	166.4	193.6	227.0
SPy1161 GTPase of unknown function subfamily	114.4	100.3	119.6	122.0	132.3
SPy1162 ribonuclease HII	101.6	89.8	101.8	85.8	86.8
SPy1163 smf protein	108.3	93.1	105.3	125.0	106.8
Hypothetical protein	79.4	64.3	69.8	111.3	92.7
SPy1164 DNA topoisomerase I	80.3	80.0	79.2	137.9	82.0
SPy1168 cyn operon transcriptional activator, putative	96.5	11.9	105.3	35.0	24.7
Hypothetical protein	73.5	8.2	76.8	20.2	13.7
Transcriptional regulator, LysR family	82.1	16.8	80.1	35.7	21.5
SPy1169 hypothetical protein	106.2	17.7	97.8	28.1	24.8
SPy1170 D-lactate dehydrogenase, putative	115.0	40.6	111.3	51.5	36.0
SPy1172 hypothetical protein	103.1	7.9	119.9	48.0	47.2
SPy1173 Gid protein	140.8	158.0	228.2	202.2	192.5
SPy1174 oxaloacetate decarboxylase, alpha subunit	193.0	182.7	246.8	290.7	296.9
SPy1175 hypothetical protein	78.2	77.1	74.1	59.3	56.5
SPy1177 oxaloacetate decarboxylase, beta subunit	150.3	150.9	129.1	146.8	147.2
SPy1178 CitG family	153.3	175.6	179.2	178.8	182.5
SPy1179 transcriptional regulator, GntR family, putative	86.6	91.2	93.5	90.9	85.5
SPy1180 citrate transport	130.6	144.7	169.0	150.4	171.2
SPy1181 hypothetical protein	68.8	55.7	59.5	72.8	62.1
SPy1183 oxaloacetate decarboxylase, alpha subunit	138.9	138.1	125.2	204.3	174.8
SPy1184 oxaloacetate decarboxylase, beta subunit	136.8	126.3	144.4	159.6	161.7
Hypothetical protein	241.2	214.9	283.6	244.9	304.0
SPy1186 citrate lyase, gamma subunit	145.8	124.6	152.9	124.0	129.9
SPy1188 citrate lyase, beta subunit	120.5	97.4	95.5	109.2	114.5
SPy1189 citrate lyase, alpha subunit	125.2	124.5	145.0	130.6	121.8
SPy1190 citX protein, putative	174.7	178.0	139.4	201.1	181.9
SPy1191 oxaloacetate decarboxylase, alpha subunit	113.1	94.9	148.4	171.9	170.0

SPy1192 citrate lyase ligase	98.1	109.2	161.3	127.6	136.5
SPy1193 hypothetical protein	71.8	86.0	95.6	84.7	96.4
SPy1196 integrase/recombinase XerC, putative	55.3	72.1	86.0	81.8	76.3
SPy1198 Helix-turn-helix domain protein	117.4	114.0	106.8	146.9	151.0
SPy1200 signal recognition particle protein	129.2	153.8	70.2	193.2	220.8
SPy1201 Helix-turn-helix domain, fis-type protein	89.8	103.2	100.8	91.5	78.1
SPy1202 mercuric reductase/transcriptional regulator, fusion	114.1	110.6	144.3	105.0	88.4
SPy1203 hypothetical protein	100.2	131.1	102.8	126.0	106.1
SPy1204 GMP synthase	115.6	115.4	119.0	109.6	86.8
SPy1205 beta-lactam resistance factor	131.6	117.5	144.1	117.6	116.1
SPy1206 ABC transporter, ATP-binding protein, putative	102.1	144.3	112.5	170.5	162.3
SPy1208 hypothetical protein	70.6	97.4	77.6	81.2	69.6
SPy1209 pyridoxal kinase, putative	87.3	106.1	111.8	109.1	95.9
SPy1210 transcriptional regulator, GntR family, putative	107.5	142.3	106.9	121.7	111.8
SPy1211 ribonucleoside-diphosphate reductase, alpha subunit	138.4	147.5	164.8	237.7	240.7
SPy1212 cardiolipin synthase, putative	99.0	129.8	134.9	168.9	150.3
SPy1213 formate--tetrahydrofolate ligase	137.9	193.2	177.4	308.7	242.5
SPy1214 lipoate-protein ligase A, putative	107.2	104.2	129.4	93.5	78.5
SPy1215 hypothetical protein	120.9	160.7	156.9	140.6	125.2
SPy1216 Domain of unknown function, putative	170.0	167.2	173.0	232.9	231.7
SPy1217 glycine cleavage system H protein, putative	262.6	253.5	264.0	287.8	242.5
SPy1218 unknown conserved protein	126.7	158.6	165.3	192.5	163.6
SPy1219 NADH-dependent flavin oxidoreductase, Oye family, putative	135.7	174.6	165.1	251.6	201.7
SPy1220 unknown conserved protein in B. subtilis	206.6	190.0	253.7	214.4	196.6
SPy1221 pantothenate metabolism flavoprotein homolog	86.7	89.2	99.0	85.1	71.4
SPy1222 DNA/pantothenate metabolism flavoprotein	159.1	191.0	146.9	175.2	160.6
SPy1223 hypothetical protein	73.6	115.3	88.3	84.1	76.3
SPy1224 phosphoglucomutase/phosphomannomutase, putative	90.8	120.6	87.9	126.3	113.3
Hypothetical protein	77.9	105.8	80.9	97.9	85.6
SPy1225 ribose/galactose ABC transporter, permease protein	115.5	150.5	148.1	174.0	150.6

SPy1227 galactoside ABC transporter, ATP-binding protein, putative	119.8	110.0	105.9	139.2	136.3
SPy1228 basic membrane protein D, putative	180.6	162.4	158.0	199.0	172.9
SPy1230 cytidine deaminase	147.7	149.4	154.2	264.8	49.8
SPy1233 pantothenate kinase	87.3	79.7	73.4	68.9	45.0
Hypothetical protein	37.3	46.8	36.1	39.3	29.3
SPy1236 histidine kinase PnpS, ciaH, spt8S	99.1	98.7	93.3	115.8	96.2
SPy1237 DNA-binding response regulator ciaR	85.7	105.8	109.8	126.0	121.5
SPy1240 phosphate transport system regulatory protein PhoU, putative	98.7	116.3	101.4	122.0	119.7
SPy1241 phosphate ABC transporter, ATP-binding protein	185.5	146.7	183.1	158.0	192.4
SPy1242 phosphate ABC transporter, ATP-binding protein	89.8	87.3	86.6	110.9	114.5
SPy1243 phosphate ABC transporter, permease protein, putative	97.2	91.4	91.0	156.2	147.7
SPy1244 phosphate ABC transporter, permease protein	200.2	236.7	289.4	379.6	349.6
SPy1246 Sun/nucleolar protein family protein, putative	120.9	183.1	167.7	164.9	156.0
SPy1247 inositol monophosphate family protein, putative	125.6	115.7	126.5	103.0	111.5
SPy1248 conserved hypothetical protein	67.0	60.6	51.0	77.7	65.0
SPy1249 conserved hypothetical protein	82.5	96.2	64.9	100.1	73.8
SPy1250 riboflavin biosynthesis protein RibF	162.3	153.7	163.3	260.7	216.2
SPy1251 tRNA pseudouridine 55 synthase	186.2	218.9	198.1	383.5	355.0
SPy1252 conserved hypothetical, putative	130.7	94.4	129.4	161.7	159.8
SPy1253 conserved hypothetical protein	69.9	74.6	75.5	85.4	75.1
SPy1254 hypothetical protein	105.7	105.2	95.2	123.2	119.3
SPy1255 Predicted permease family	105.1	105.0	116.9	112.8	123.9
SPy1257 ABC transporter, ATP-binding protein	81.6	69.3	77.8	96.8	88.4
SPy1259 TrkA potassium uptake protein family	123.4	119.7	100.5	155.4	152.2
SPy1260 gls24	67.0	61.7	54.7	59.8	72.0
SPy1261 conserved hypothetical protein	64.0	58.1	49.6	68.1	66.8
SPy1262 gls24	114.8	98.9	82.4	103.1	118.4
SPy1263 putative 6-kDa protein	81.1	70.0	67.4	122.8	117.6
SPy1265 conserved hypothetical protein	133.9	97.3	119.8	180.3	177.8
SPy1267 ATP-dependent DNA helicase PcrA	80.2	78.0	76.6	82.9	82.6

Hypothetical protein		31.9	33.6	36.5	43.2	39.3
Hypothetical protein		77.3	58.1	60.8	76.9	71.6
SPy1270 sodium/alanine symporter		131.9	112.5	131.4	188.6	222.5
Hypothetical protein		38.5	29.5	31.1	48.0	40.7
SPy1273 CAMP factor		60.1	55.9	55.4	54.8	55.3
SPy1274 amino acid ABC transporter, periplasmic-binding protein, putative		60.5	53.2	43.6	52.5	53.7
SPy1275 amino acid ABC transporter, ATP-binding protein		90.3	116.3	106.4	124.7	122.1
SPy1276 amino acid ABC transporter, permease protein		101.9	78.6	85.0	128.7	124.4
SPy1280 glucosamine--fructose-6-phosphate aminotransferase (isomerizing)		143.9	170.7	196.7	213.2	60.2
SPy1281 signal peptidase , putative		103.4	125.4	121.9	135.2	24.3
SPy1282 pyruvate kinase		147.2	155.3	186.9	182.4	210.5
SPy1283 Phosphofructokinase		134.3	120.8	134.9	126.3	135.3
SPy1285 Bacterial regulatory proteins, gntR family, putative		100.2	113.5	94.0	140.5	110.1
SPy1286 ABC transporter, ATP-binding protein, putative		130.8	106.8	136.6	223.4	223.4
SPy1287 hypothetical protein		87.1	83.8	80.9	110.4	117.4
Hypothetical protein		139.2	127.1	108.7	141.8	140.7
SPy1291 maltodextrin phosphorylase		180.0	138.1	121.6	192.7	206.7
SPy1292 4-alpha-glucanotransferase/amylomaltase/Disproportionating enzyme		97.6	91.6	124.0	119.2	98.1
SPy1293 transcriptional regulator, LacI family, putative		61.7	67.2	71.9	90.5	107.1
Hypothetical protein		82.2	72.8	73.2	68.7	76.1
SPy1294 maltose ABC transporter, periplasmic maltose-binding protein, putative	Maltose locus	119.5	96.6	102.9	119.4	137.8
SPy1295 maltose ABC transporter, permease protein	Maltose locus	199.4	123.9	103.8	151.1	201.0
SPy1296 maltose ABC transporter, permease protein, putative	Maltose locus	105.9	137.7	95.1	147.9	143.6
SPy1297 regulator protein	Maltose locus	60.4	6.8	9.8	63.2	67.8
SPy1298 mala protein	Maltose locus	137.6	13.1	15.6	25.5	20.5
SPy1299 maltose ABC transporter, permease protein	Maltose locus	81.7	8.1	8.7	15.7	12.8
SPy1301 maltose ABC transporter, permease protein	Maltose locus	133.4	19.8	21.0	41.0	35.7
SPy1302 alpha-cyclodextrin glycosyltransferase (amyA)	Maltose locus	210.0	20.8	18.0	38.4	30.9
SPy1304 glycosyl hydrolase, family 13	Maltose locus	96.1	9.2	8.1	17.8	17.0

SPy1306 maltose ABC transporter, periplasmic maltose-binding protein, putative	Maltose locus	190.9	17.4	25.6	43.4	32.3
SPy1308 PE family protein, putative		211.2	221.0	251.5	391.4	389.1
SPy1309 extramembranal protein		136.7	106.0	88.2	125.6	113.3
SPy1310 acyl carrier protein		123.0	133.7	144.4	186.0	193.0
SPy1311 alginate o-acetyltransferase AlgI		93.1	163.3	149.2	210.8	177.6
SPy1312 CDA peptide synthetase I-related		132.3	160.4	160.3	140.6	118.2
Hypothetical protein		87.8	106.6	85.0	110.6	105.9
SPy1314 excinuclease ABC, subunit B		172.0	176.5	225.4	204.2	187.3
SPy1315 amino acid ABC transporter, permease protein, putative		318.2	288.6	293.3	472.9	438.1
SPy1316 amino acid ABC transporter, ATP-binding protein		175.7	172.3	189.6	243.2	195.0
Hypothetical protein		98.1	127.3	134.4	141.8	131.9
PTS system, cellobiose-specific IIC component, putative		141.9	199.0	194.3	331.2	243.8
PTS system, cellobiose-specific IIC component, putative		143.0	233.0	178.3	169.0	153.6
SPy1322 hypothetical protein		118.5	167.4	148.7	186.9	186.6
SPy1323 PTS system, cellobiose-specific IIA component		224.2	231.0	201.0	308.8	289.9
SPy1324 PTS system, cellobiose-specific IIB component		74.6	97.3	82.2	89.5	69.1
SPy1325 putative cel operon regulator		147.1	157.0	163.9	192.7	174.8
SPy1326 outer surface protein, putative		173.4	226.8	209.0	317.7	273.0
SPy1328 6-phospho-beta-galactosidase		116.1	104.6	155.0	149.7	127.3
SPy1329 nicotinamide mononucleotide transporter, putative		88.6	122.7	98.3	141.1	113.9
Hypothetical protein		172.7	186.0	148.6	180.4	174.7
SPy1332 hypothetical protein		91.9	89.2	82.2	104.4	100.2
SPy1333 GTP-binding protein		167.0	168.0	206.1	247.1	209.1
Hypothetical protein		177.2	161.4	137.2	178.2	140.4
SPy1336 probable transposase (insertion sequence IS861)		89.5	139.5	335.5	70.2	106.8
SPy1337 ribosomal small subunit pseudouridine synthase A		165.9	164.7	183.8	222.1	150.2
SPy1339 hypothetical protein		155.0	141.2	195.1	191.2	174.9
SPy1340 sugar transporter family protein, putative		196.8	251.1	224.4	309.9	301.9
Hypothetical protein		96.6	142.4	103.6	145.7	123.4
Hypothetical protein		88.3	153.0	108.9	157.5	146.7
SPy1343 hypothetical protein		185.4	269.2	222.6	205.3	186.8
SPy1344 uncharacterized domain 1, putative		116.9	120.7	150.2	88.7	86.0

SPy1345 uridine phosphorylase, putative	141.2	152.8	148.2	195.7	177.3
Hypothetical protein	100.7	73.0	95.6	169.6	170.2
SPy1346 RNA methyltransferase, TrmA family	183.6	149.9	225.9	187.9	158.2
SPy1350 PSR protein	131.4	145.9	143.7	225.1	186.4
SPy1351 Shikimate kinase	81.2	119.3	111.2	104.6	78.7
SPy1352 3-phosphoshikimate 1-carboxyvinyltransferase, putative	134.5	134.4	150.3	136.4	145.0
SPy1353 ribonuclease BN, putative	112.7	102.5	106.2	147.4	119.2
SPy1354 methionine aminopeptidase, type I	138.1	117.3	146.9	183.8	162.6
SPy1355 unknown conserved protein	105.6	122.6	113.0	156.4	121.5
SPy1356 acetyltransferase, putative	55.2	72.0	51.5	79.5	69.1
SPy1357 GRAB precursor	297.2	271.9	28.5	474.0	166.5
SPy1358 UDP-N-acetylglucosamine 1-carboxyvinyltransferase	105.3	98.4	103.1	107.7	93.4
SPy1359 S-adenosylmethionine synthetase	382.2	355.1	369.7	522.9	512.4
SPy1361 Leucine Rich Repeat domain protein; internalin homolog	125.5	131.9	134.1	151.6	130.1
SPy1362 birA bifunctional protein, putative	178.8	230.1	219.4	249.0	239.0
SPy1363 hypothetical protein	143.1	230.7	188.9	325.0	302.4
SPy1364 DNA polymerase III, subunits gamma and tau	200.6	113.9	137.0	172.4	144.5
SPy1365 conserved hypothetical protein	163.2	144.9	174.0	181.2	216.4
Hypothetical protein	55.5	57.7	48.0	68.6	68.2
SPy1366 hypothetical protein	56.2	71.8	62.5	84.2	80.4
SPy1368 uridine kinase	93.9	100.3	61.0	123.1	120.4
SPy1370 peptidoglycan GlcNAc deacetylase, putative	129.6	102.2	114.1	135.3	112.2
SPy1371 succinate semialdehyde dehydrogenase, putative	107.7	120.1	133.8	123.7	145.7
SPy1372 phosphoenolpyruvate-protein phosphotransferase	127.6	116.1	150.2	145.8	177.8
SPy1373 phosphocarrier protein HPr	96.3	73.4	82.8	119.8	103.8
SPy1374 NrdH-redoxin-related protein	96.3	86.7	63.6	100.2	94.6
SPy1378 Ribonucleotide reductases	120.1	109.6	124.0	153.2	138.9
SPy1379 chloride channel, putative	130.1	122.2	133.2	139.0	173.7
SPy1380 transposase for insertion sequence elemen	86.5	112.2	96.1	80.7	49.7
SPy1384 pXO1-85, putative	62.8	56.6	55.3	65.3	65.9
SPy1385 hypothetical protein	87.4	75.0	71.1	116.2	109.2
Hypothetical protein	58.2	63.8	54.5	75.4	72.0
SPy1389 alanyl-tRNA synthetase	89.5	77.1	104.9	93.2	90.0

SPy1390 protease maturation protein, putative	122.5	108.9	115.1	123.9	133.7
SPy1391 O-methyltransferase, putative	90.3	100.4	117.3	131.1	133.0
SPy1392 oxalate/formate antiporter, putative	123.4	108.1	103.6	175.5	194.4
SPy1393 oligoendopeptidase F	115.0	105.5	129.5	185.6	118.5
SPy1395 competence protein	81.1	88.0	85.5	85.4	90.2
Conserved hypothetical protein	128.2	104.8	157.1	130.4	136.6
SPy1398 ribosomal small subunit pseudouridine synthase A	101.6	107.9	127.2	152.8	143.9
SPy1399 glucosamine-6-phosphate isomerase	88.1	70.0	57.8	97.1	77.9
SPy1400 S-adenosylmethionine:tRNA ribosyltransferase-isomerase	100.6	123.7	113.9	217.7	189.9
SPy1401 hypothetical protein	165.0	149.0	147.7	171.0	163.3
Hypothetical protein	62.5	59.8	72.3	76.3	95.3
SPy1402 hypothetical protein	177.4	151.5	213.3	156.8	191.5
SPy1404 hypothetical protein	113.3	108.3	112.7	90.3	88.1
SPy1405 putative lipoprotein	116.7	120.3	107.2	189.1	151.2
SPy1406 superoxide dismutase (EC 1.15.1.1) (Mn) [validated]	188.6	182.1	158.1	296.4	306.7
SPy1407 DNA polymerase III delta subunit	111.2	97.0	134.8	173.2	175.3
SPy1408 DNA internalization-related competence protein ComEC/Rec2	101.0	140.0	171.4	135.5	149.8
SPy1409 comE operon protein 1, putative	82.6	95.3	97.5	91.3	100.6
SPy1410 Acyltransferase family	136.4	139.5	161.9	171.5	143.6
SPy1411 conserved hypothetical protein	97.3	103.0	90.9	130.3	129.2
SPy1412 conserved hypothetical protein	125.9	185.8	120.5	190.6	234.9
SPy1414 potassium uptake protein, Kup system, putative	168.2	126.4	113.3	239.0	166.0
SPy1415 ATP-dependent RNA helicase DeaD	70.6	86.9	75.8	86.6	68.1
SPy1416 peptide chain release factor 3	163.3	148.5	213.7	220.5	236.7
SPy1419 conserved hypothetical protein	117.4	116.2	122.3	167.1	180.9
SPy1420 UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	102.0	90.2	108.9	116.0	127.4
SPy1421 D-alanine--D-alanine ligase	79.4	142.0	115.1	211.5	229.1
SPy1422 recombination protein RecR	166.5	143.4	176.8	190.4	176.6
SPy1424 formate transporter 1, putative	219.4	238.4	247.9	333.9	297.4

SPy1425 hypothetical protein	205.8	236.5	207.4	302.5	239.6
Hypothetical protein	70.2	81.7	60.3	80.5	80.4
SPy1427 transcriptional regulator, biotin repressor family	104.9	150.3	148.4	175.5	156.3
Hypothetical protein	63.9	91.0	75.6	80.1	76.0
SPy1429 phosphoglycerate mutase	161.4	189.5	205.4	145.4	136.4
Hypothetical protein	63.8	80.6	66.6	73.1	63.3
Hypothetical protein	46.0	47.4	37.9	50.8	41.0
SPy1432 dihydroorotate dehydrogenase, putative	123.7	164.8	122.0	165.2	159.1
Hypothetical protein	79.9	95.4	118.0	79.5	77.6
SPy1434 cation-transporting ATPase, E1-E2 family	109.6	151.6	121.4	183.6	168.3
SPy1489 DNA-binding protein HU	130.0	124.4	134.6	154.5	126.0
SPy1492 conserved hypothetical protein	86.5	83.5	100.7	101.7	81.3
SPy1493 degV protein, putative	76.7	75.2	78.7	85.8	74.8
SPy1494 hypothetical protein	96.8	71.8	82.2	86.2	71.1
SPy1495 DNA repair protein RecN	59.4	55.8	52.4	62.7	51.2
SPy1496 arginine repressor, putative	69.9	59.3	60.5	76.8	60.2
SPy1498 geranyltranstransferase	132.4	103.2	115.2	127.0	102.0
SPy1499 exodeoxyribonuclease, small subunit, putative	69.5	69.4	67.7	64.4	48.2
SPy1500 exodeoxyribonuclease VII, large subunit	122.8	108.3	143.2	150.3	112.4
Hypothetical protein	93.2	107.2	94.9	114.3	87.8
SPy1502 methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	135.8	134.3	112.9	153.2	115.9
Hypothetical protein	69.2	72.8	59.9	90.9	70.6
SPy1505 DNA photolyase	88.5	70.0	66.6	77.3	48.7
SPy1506 arginine transport ATP-binding protein	163.6	115.5	127.3	165.7	153.3
SPy1507 arginine transport system permease protein	147.6	138.1	169.4	217.3	161.5
SPy1508 conserved hypothetical protein	117.9	109.2	97.5	174.4	138.5
SPy1509 ATP-dependent Clp protease, ATP-binding subunit ClpC	133.9	96.3	126.2	153.4	92.3
SPy1510 MutT/nudix family protein, putative	124.6	161.3	160.5	170.1	142.6
SPy1511 hypothetical protein	81.8	75.1	78.9	80.9	68.5
SPy1513 isoleucyl-tRNA synthetase	129.8	119.4	86.7	116.7	147.5

SPy1514 cell division protein DivIVA	98.1	89.9	86.5	150.9	98.2
SPy1515 YlmH	143.2	163.7	147.9	233.5	195.0
SPy1516 YlmG	161.9	132.1	151.5	191.4	182.5
SPy1518 YlmF	144.3	115.9	202.9	198.9	199.5
SPy1519 conserved hypothetical protein TIGR00044	91.8	82.8	84.7	78.5	75.6
SPy1520 cell division protein FtsZ	136.9	140.3	177.5	160.9	105.7
SPy1521 cell division protein FtsA	136.4	118.1	101.0	110.0	118.8
Hypothetical protein	60.7	68.0	55.5	79.9	67.0
SPy1523 DivIB	92.4	92.3	138.6	132.2	110.9
SPy1524 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) transferase	109.0	122.6	153.8	130.2	102.3
SPy1525 UDP-N-acetylmuramoylalanine--D-glutamate ligase	97.2	117.0	118.2	103.8	119.5
SPy1526 hypothetical protein	213.3	170.3	164.3	260.3	240.2
SPy1527 GTP-binding protein TypA	95.8	101.7	101.8	132.4	87.8
SPy1528 unknown conserved protein	102.3	127.2	90.5	144.0	113.9
SPy1529 glucose kinase	154.5	138.5	187.1	185.8	150.6
SPy1530 conserved hypothetical protein	146.0	87.9	97.2	86.1	215.3
SPy1531 DPS family protein, putative	98.5	101.5	113.0	107.8	108.7
SPy1532 hypothetical protein	72.8	95.5	70.5	103.0	143.4
SPy1533 conserved hypothetical protein TIGR00048	127.2	118.8	105.9	187.9	186.3
SPy1534 unnamed protein product	90.0	124.3	126.5	161.4	128.0
Hypothetical protein	97.7	121.3	104.4	128.0	71.6
SPy1535 ribose operon repressor, putative	149.8	145.2	171.6	171.7	140.0
SPy1536 PDZ domain family protein, putative	122.5	119.7	117.2	110.4	83.2
SPy1537 lipopolysaccharide core biosynthesis protein KdtB, putative	96.5	103.8	98.2	121.0	93.7
SPy1538 conserved hypothetical protein TIGR00095	85.3	112.7	103.0	110.1	78.3
SPy1539 aspartate--ammonia ligase	222.7	247.0	252.0	339.1	237.9
SPy1541 carbamate kinase	58.6	64.5	70.6	52.8	44.5
SPy1542 Peptidase family M20/M25/M40 superfamily	114.2	109.9	146.9	107.4	74.0
SPy1543 conserved hypothetical transmembrane protein, putative	183.2	246.0	183.2	210.4	179.6
SPy1544 ornithine carbamoyltransferase	131.5	156.8	160.4	169.5	122.9

SPy1546 Acetyltransferase (GNAT) family family	147.9	194.9	176.2	266.7	153.1
SPy1547 arginine deiminase	206.3	249.6	235.3	365.4	273.6
SPy1548 Bacterial regulatory proteins, crp family domain protein	147.0	181.0	156.2	155.3	127.0
SPy1549 arginine repressor, putative	170.3	197.1	164.8	235.7	169.1
SPy1551 conserved hypothetical protein	174.8	164.7	210.1	205.9	172.8
SPy1552 hypothetical protein	137.1	141.3	154.4	155.5	96.2
SPy1553 two-component sensor histidine kinase, ZmpS; spt9S2	109.1	139.2	141.9	137.4	82.7
Histidine sensor kinase 3'end	132.7	180.1	169.6	132.1	103.2
SPy1556 response regulator, spt9S2, ZmpS, hk09	203.2	189.1	276.2	251.4	191.7
SPy1557 peptide methionine sulfoxide reductase	320.1	316.7	299.9	393.6	377.9
SPy1558 peptide methionine sulfoxide reductase	245.0	205.6	254.2	328.8	284.5
SPy1559 c-type cytochrome biogenesis protein	238.6	266.4	290.5	387.0	320.2
SPy1561 unknown conserved protein in others	180.3	24.2	254.3	58.4	48.8
SPy1562 conserved hypothetical protein TIGR00287	164.2	27.9	226.0	33.4	23.7
SPy1563 conserved hypothetical protein	138.8	17.6	191.2	38.8	23.7
SPy1564 unknown conserved protein in others	247.1	67.1	320.5	90.7	84.6
SPy1565 conserved hypothetical protein	120.2	4.4	136.4	19.5	11.5
SPy1566 conserved hypothetical protein	112.4	9.2	139.8	23.7	18.5
Hypothetical protein	66.9	6.7	69.1	16.0	10.9
SPy1567 unknown conserved protein in others, putative	159.7	18.6	285.9	48.7	42.9
SPy1568 valyl-tRNA synthetase	119.1	123.0	154.4	125.1	91.2
SPy1569 hypothetical protein	103.7	110.8	110.2	98.6	77.2
SPy1570 ribosomal-protein-alanine acetyltransferase, putative	132.7	134.1	151.7	164.9	124.6
SPy1571 hypothetical protein	258.2	189.3	253.6	330.6	265.3
SPy1572 hypothetical 213.7 kda protei, putative	89.6	110.9	102.0	112.2	73.5
SPy1576 phospho-2-dehydro-3-deoxyheptonate aldolase, putative	121.0	150.6	137.3	267.2	180.7
SPy1577 3-dehydroquinate synthase	102.3	104.9	112.1	93.7	75.3
Hypothetical protein	75.8	100.1	72.1	84.9	55.1
SPy1580 acetate kinase	115.4	91.8	68.9	98.8	89.6
SPy1581 conserved hypothetical protein	108.7	97.5	110.2	153.2	116.8
SPy1582 methyltransferase	126.3	134.6	110.1	171.6	125.4
SPy1584 shikimate 5-dehydrogenase	251.0	222.7	225.1	353.9	329.0

SPy1586 beta-galactosidase	284.3	241.3	275.7	298.5	302.7
SPy1587 response regulator, spt10R	91.1	131.5	110.9	129.3	103.5
SPy1588 histidine kinase; spt10S, hk07, YesNM	175.0	126.0	151.6	194.5	135.6
SPy1589 conserved hypothetical protein	138.6	139.7	120.7	210.2	178.1
SPy1591 conserved hypothetical protein	132.0	131.9	159.4	170.2	128.0
SPy1592 conserved hypothetical protein	147.8	166.0	176.7	263.0	190.3
SPy1593 integral membrane protein	117.7	85.5	97.9	109.3	90.7
SPy1595 pot. starch degradation products transport system permease protein amyd	154.1	158.8	164.4	192.9	159.3
SPy1596 ROK family protein, putative	146.7	123.8	142.2	80.7	146.2
Hypothetical protein	158.7	149.6	173.3	257.8	188.6
SPy1599 6-phospho-beta-galactosidas, putative	137.3	122.0	121.0	153.6	118.3
Hypothetical protein	90.3	75.0	83.4	70.4	56.3
SPy1602 transcriptional regulator (LacI family), putative	119.9	105.9	105.7	125.3	110.4
SPy1603 unknown conserved protein in others	136.8	135.0	151.4	151.5	151.2
SPy1604 unknown conserved protein in others	115.3	78.2	115.9	125.4	96.4
SPy1605 orphan histidine kinase; regulator of Cov	76.1	81.4	60.5	92.3	79.0
SPy1607 recX protein, putative, putative	68.3	60.8	69.8	68.0	62.8
SPy1608 unknown conserved protein in B. subtilis	59.1	62.5	51.9	70.7	61.1
Hypothetical protein	209.6	166.4	133.4	171.9	169.3
SPy1610 conserved hypothetical protein	90.6	80.2	91.9	100.5	93.6
Conserved hypothetical protein	410.3	359.7	360.0	425.3	550.7
Hypothetical protein	40.0	34.9	33.5	43.3	37.1
SPy1613 S30AE family protein, putative	71.0	71.6	78.0	68.8	59.1
SPy1615 competence protein F	120.5	162.6	160.2	147.5	119.2
SPy1616 late competence protein	124.3	140.9	123.8	169.8	139.3
SPy1617 conserved hypothetical protein TIGR00257	77.7	72.8	75.5	102.5	90.0
SPy1619 ribosomal protein S1	110.9	80.7	114.3	115.9	103.2
SPy1620 Cof family, putative	155.1	122.2	100.0	133.6	113.1
SPy1621 response regulator, rr03 S.pneumo; yvqC	115.0	86.3	89.5	97.0	90.8
SPy1622 sensor histidine kinase, hk03 S.pneumo; yvqE	78.2	82.5	92.8	93.1	82.1
SPy1623 conserved hypothetical protein	101.5	106.7	86.3	186.0	127.4

SPy1625 serine/threonine protein kinase	139.3	166.3	118.7	184.9	167.2
SPy1626 serine/threonine protein phosphatase, putative	91.3	86.9	114.9	115.2	104.1
SPy1627 sun protein	166.5	203.1	255.9	202.7	197.9
SPy1628 methionyl-tRNA formyltransferase	113.9	105.9	121.3	119.0	113.2
SPy1629 primosomal protein N`	161.6	142.1	176.2	223.1	212.0
SPy1630 hypothetical protein	109.7	133.5	139.8	109.3	80.1
Hypothetical protein	88.7	99.4	78.4	154.5	135.3
SPy1632 guanylate kinase	102.7	100.1	126.5	130.8	120.0
SPy1633 uncharacterized domain HDIG protein	173.7	181.1	192.5	170.4	156.6
SPy1634 transcriptional regulator, LysR family, putative	146.2	134.4	155.9	153.1	159.1
SPy1637 acetyl-CoA acetyltransferase	129.8	156.7	179.9	175.6	159.0
SPy1638 3-oxoadipate CoA-succinyl transferase alpha subunit	129.6	141.9	121.0	187.0	132.4
SPy1639 butyrate-acetoacetate coa-transferase subunit b	164.0	189.7	145.3	246.4	219.8
SPy1640 3-oxoacyl-(acyl-carrier-protein) reductase	113.2	100.7	113.5	127.7	104.5
SPy1641 unknown conserved protein	122.0	145.7	185.8	179.9	148.2
SPy1642 autoinducer-2 production protein LuxS	90.5	83.2	89.4	77.5	71.8
SPy1643 hypothetical protein	144.0	112.9	151.8	140.3	142.2
SPy1644 Uncharacterized protein family UPF0020, putative	252.4	218.4	206.2	439.0	386.2
SPy1646 cell division protein DivIVA	104.7	109.0	66.3	130.7	114.6
SPy1647 conserved hypothetical protein	93.9	101.1	97.9	106.0	74.9
SPy1648 recombination protein U	104.3	132.8	119.0	119.5	79.2
SPy1649 penicillin-binding protein 1a	158.9	193.4	175.1	175.1	133.7
SPy1651 aminopeptidase C	211.2	191.5	206.2	268.1	275.6
SPy1652 NAD+ synthetase	166.5	169.6	152.3	215.4	142.5
SPy1653 nicotinate phosphoribosyltransferase, putative	161.9	206.7	197.4	240.4	157.2
SPy1654 amino acid permease	121.2	153.6	160.7	122.0	89.9
Thioredoxin reductase (ec 1.6.4.5) (general stress protein 35) (gsp35)	127.6	126.7	148.9	117.2	102.0
SPy1656 hypothetical protein	90.1	89.6	100.0	76.3	65.0
SPy1657 amino acid ABC transporter, ATP-binding protein	154.6	186.0	169.8	202.8	151.4
SPy1658 amino acid ABC transproter, permease protein	154.6	207.9	179.6	228.0	157.0
SPy1659 ATP-dependent RNA helicase DeaD, putative	193.9	229.9	246.0	228.5	216.5

Hypothetical protein	105.4	73.6	98.2	73.4	56.2
SPy1662 phospho-N-acetylmuramoyl-pentapeptide-transferase	135.2	152.9	135.0	124.1	104.8
SPy1664 unnamed protein product	109.0	113.0	132.0	121.6	89.4
SPy1665 FtsL	98.1	131.5	98.3	115.5	90.9
SPy1666 conserved hypothetical protein TIGR00006	129.0	177.2	161.9	195.1	154.6
Hypothetical protein	110.6	107.6	167.5	180.9	109.6
Hypothetical protein	87.8	87.9	83.8	105.2	74.3
SPy1670 gamma-glutamyl phosphate reductase	192.9	160.6	202.2	222.0	160.3
SPy1672 glutamate 5-kinase	667.3	553.7	662.5	850.4	711.5
SPy1673 hypothetical protein	306.6	343.2	398.6	507.8	420.2
SPy1674 ABC transporter, ATP-binding protein	223.1	205.8	214.2	309.9	251.0
SPy1675 BacB protein, putative	75.4	114.9	82.2	99.1	62.7
SPy1676 transketolase	131.3	118.0	137.8	109.1	79.3
SPy1678 transaldolase, putative	148.1	163.9	153.9	153.2	130.3
SPy1680 hypothetical protein	185.1	183.3	157.6	215.6	187.6
SPy1681 NADH oxidase, putative	162.0	154.4	162.7	260.1	167.7
SPy1682 glycerol uptake facilitator protein	235.3	192.6	219.1	319.3	247.5
SPy1683 glycerol-3-phosphate dehydrogenase	197.3	189.6	284.4	240.0	211.9
SPy1684 glycerol kinase	204.1	199.4	240.1	243.0	194.3
SPy1686 hypothetical protein	92.9	77.5	99.8	84.1	63.5
SPy1687 conserved hypothetical protein	160.9	135.1	171.6	192.0	114.6
SPy1688 glycyl-tRNA synthetase, tetrameric type, beta subunit	120.5	137.0	112.3	231.0	140.3
SPy1689 glycyl-tRNA synthetase, tetrameric type, alpha subunit	184.9	218.1	216.3	313.0	235.6
Hypothetical protein	82.3	114.8	82.6	147.9	112.1
SPy1691 conserved hypothetical protein	159.4	168.2	156.9	154.0	131.8
Hypothetical protein	70.3	106.7	79.4	93.8	76.0
SPy1693 probable aldehyde reductase (EC 1.1.1.-) - Leishmania major	103.6	88.6	112.4	122.0	105.2
SPy1694 N-acetylglucosamine-6-phosphate deacetylase	156.0	139.6	150.7	177.9	179.7
SPy1695 sodium dependent phosphate pump-related	121.8	115.4	111.5	152.8	128.1
Hypothetical protein	83.4	109.4	88.0	110.5	99.1
SPy1697 hypothetical protein	152.5	170.7	188.7	138.6	120.9

SPy1698 degV family protein superfamily	678.2	731.4	637.1	784.9	683.5
SPy1699 Bacterial regulatory proteins, tetR family domain protein	727.4	666.7	639.1	1112.7	925.2
SPy1700 haloacid dehalogenase-like hydrolase superfamily	177.7	175.5	215.5	257.4	203.1
SPy1701 unknown conserved protein	129.0	126.5	170.6	188.4	123.3
Hypothetical protein	72.3	108.6	91.3	142.8	107.9
SPy1704 tagatose 1,6-diphosphate aldolase	149.2	110.5	142.9	153.4	130.3
Tagatose-6-phosphate kinase	91.2	65.7	70.3	108.3	102.0
SPy1707 galactose-6-phosphate isomerase, LacB subunit	180.1	137.1	131.5	220.3	207.9
SPy1708 galactose-6-phosphate isomerase, LacA subunit	239.6	165.3	182.0	309.8	213.7
SPy1709 putative phosphotransferase enzyme ii, c component sgcc	184.8	120.2	135.8	192.7	131.4
SPy1711 GatA, putative	95.6	81.7	86.6	117.4	74.0
SPy1712 transcriptional regulator, DeoR family, putative	78.4	83.0	80.1	86.4	58.4
SPy1714 copper-transporting atpas	113.1	97.0	106.3	113.3	98.9
SPy1715 cation transport ATPase, E1-E2 family	95.5	77.3	80.4	104.0	85.9
SPy1717 CopY	145.4	135.3	159.7	193.9	178.3
Hypothetical protein	75.3	86.8	14.9	73.9	56.7
SPy1719 ribosome-binding factor A, putative	97.3	83.7	87.2	100.5	63.5
SPy1721 initiation factor IF-2	105.1	117.0	79.5	106.9	108.6
SPy1722 LSU ribosomal protein L30E	89.5	94.7	85.7	85.9	65.6
SPy1723 conserved hypothetical protein	66.8	63.0	58.5	67.8	70.1
SPy1725 unknown conserved protein	548.5	431.8	457.7	665.1	586.7
SPy1726 conserved hypothetical protein TIGR00091	490.3	468.9	460.3	599.8	568.1
SPy1727 conserved hypothetical protein	126.6	105.4	126.6	147.4	131.4
SPy1728 conserved hypothetical protein	89.9	89.3	87.7	114.6	91.4
SPy1729 ABC transporter, ATP-binding protein	129.8	108.1	99.9	178.5	165.8
SPy1731 hypothetical protein	187.5	161.0	183.0	327.1	317.3
SPy1733 EpsA, putative	324.6	324.7	295.2	420.6	404.1
SPy1734 acetyltransferase, putative	265.3	231.0	214.3	383.4	302.9
SPy1735 conserved hypothetical protein TIGR00150	244.6	194.4	266.3	341.7	229.8
SPy1736 unknown conserved protein	140.2	156.4	133.8	288.1	199.3
SPy1737 YcsE protein, putative	144.9	134.0	123.3	180.8	140.7

Hypothetical protein	69.8	57.5	73.6	63.8	53.0
SPy1738 mannose-specific phosphotransferase system component IIAB	79.7	68.5	72.2	75.6	74.6
SPy1739 mannose-specific phosphotransferase system component IIC	162.4	151.8	174.5	167.7	146.4
SPy1740 pts system, sorbose-specific iid component	123.3	146.8	161.4	144.4	115.2
SPy1741 conserved hypothetical protein	69.4	68.0	52.8	62.4	46.7
SPy1742 seryl-tRNA synthetase	127.6	151.2	116.5	171.9	159.1
SPy1743 acetyl-CoA carboxylase, carboxyl transferase subunit alpha	228.7	199.1	353.2	344.2	312.9
SPy1744 acetyl-CoA carboxylase, carboxyl transferase subunit beta	208.1	215.0	380.7	256.1	261.8
SPy1745 acetyl-CoA carboxylase, biotin carboxylase	98.6	93.8	129.7	102.6	101.3
Spy1746 (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase	144.2	145.3	150.2	132.6	132.6
SPy1747 acetyl-CoA carboxylase, biotin carboxyl carrier protein	99.2	103.8	106.4	93.7	63.1
SPy1748 3-oxoacyl-(acyl-carrier-protein) synthase II	355.2	354.0	303.2	537.9	484.6
SPy1749 3-oxoacyl-(acyl-carrier-protein) reductase	526.7	401.3	433.1	591.0	520.0
SPy1750 malonyl CoA-acyl carrier protein transacylase	122.1	101.7	110.9	116.3	109.7
SPy1751 trans-2-enoyl-ACP reductase II	109.8	114.6	106.6	122.0	110.1
SPy1753 acyl carrier protein	70.2	52.3	52.8	80.5	66.5
SPy1754 3-oxoacyl-(acyl-carrier-protein) synthase III	94.8	74.4	73.1	108.1	98.5
SPy1755 hypothetical 16.1 kDa transcriptional regulator, putative	111.7	122.2	123.7	182.7	165.7
SPy1758 enoyl-CoA isomerase, putative	112.3	128.0	129.4	127.9	85.7
SPy1759 dnaJ protein	158.5	145.5	155.7	124.8	122.9
SPy1760 dnaK protein	193.6	213.5	166.7	232.5	187.7
SPy1761 heat shock protein GrpE	108.0	123.6	130.1	119.0	91.1
SPy1763 heat-inducible transcription repressor HrcA	147.5	193.9	153.4	211.1	157.1
SPy1764 N-acetylmuramidase, putative	142.8	157.7	147.7	197.9	155.8
SPy1765 putative D,D-carboxypeptidase	153.5	138.1	236.3	171.0	99.8
SPy1766 phosphoglycerate mutase family domain protein	189.1	150.9	243.3	243.1	173.4
SPy1768 conserved hypothetical protein	256.7	306.1	290.8	325.9	230.4

SPy1769 hypothetical protein	89.7	105.3	96.0	99.7	86.6
SPy1770 glutamyl-tRNA(Gln) amidotransferase, B subunit	121.9	130.8	145.9	156.8	169.9
SPy1771 glutamyl-tRNA(Gln) amidotransferase, A subunit	158.8	205.9	203.9	197.2	164.4
SPy1772 glutamyl-tRNA(Gln) amidotransferase, C subunit	180.0	109.7	214.3	181.5	118.1
Pyruvate,phosphate dikinas	228.9	257.8	248.1	293.6	209.4
Pyruvate phosphate dikinase 1	206.4	170.8	189.9	230.6	151.7
Hypothetical protein	160.9	158.5	179.1	269.3	198.0
SPy1776 pyrazinamidase/nicotinamidase [includes: pyrazinamidas, putative	99.8	119.6	134.6	228.3	134.3
SPy1777 cody protei	133.2	136.1	147.6	110.0	85.0
SPy1779 aspartate aminotransferase, putative	166.2	171.1	231.9	174.9	183.2
SPy1780 universal stress protein family, putative	115.3	138.3	134.8	107.1	108.6
SPy1781 haloacid dehalogenase-like hydrolase family	361.1	285.4	286.1	443.8	352.3
SPy1782 L-asparaginase, putative	333.3	324.4	336.7	476.9	425.7
Hypothetical protein	165.0	169.7	115.6	229.4	220.4
SPy1783 hypothetical protein	92.2	129.6	92.9	150.0	111.6
SPy1784 cdd4-like protein	122.1	120.7	137.4	138.0	117.3
SPy1785 ATP-dependent DNA helicase RecG	137.7	158.0	125.4	126.6	129.0
Hypothetical protein	257.9	211.6	154.0	215.3	257.7
SPy1787 ABC transporter, ATP-binding protein, putative	101.2	86.1	108.1	122.6	117.6
SPy1788 Cobalt transport protein superfamily	124.4	124.2	119.2	139.0	91.9
SPy1789 hypothetical protein	207.7	199.9	162.8	340.6	294.4
SPy1790 transport ATP-binding protein hemoprotein receptors locus	106.9	103.0	102.5	112.7	87.0
SPy1791 transport ATP-binding protein, hemoprotein receptors locus	129.3	110.0	124.6	131.2	121.7
SPy1793 ABC transporter, ATP-binding protein, hemoprotein receptors locus	87.1	74.4	71.0	63.4	72.7
SPy1794 iron uptake protein	116.8	112.6	116.7	205.7	176.2
SPy1795 similar to ferrichrome ABC transporter (binding protein), putative	125.3	147.4	202.6	236.0	182.1
SPy1796 hypothetical protein	124.9	144.7	151.8	215.4	152.2
SPy1798 Leucine Rich Repeat domain protein	181.2	183.6	219.1	191.2	142.1

Hypothetical protein	72.0	99.6	74.3	72.3	55.8
SPy1801 immunogenic secreted protein precursor 2	271.6	247.3	252.3	234.2	189.8
SPy1802 alanine racemase	127.6	152.3	155.4	213.6	169.0
SPy1804 holo-(acyl-carrier protein) synthase	103.8	118.4	125.2	153.4	108.0
SPy1805 preprotein translocase, SecA subunit	192.0	240.8	259.7	363.2	259.3
SPy1810 mannose-6-phosphate isomerase, class I	161.9	196.6	178.4	141.6	123.5
SPy1811 fructokinase	250.6	265.2	255.0	239.0	211.1
Hypothetical protein	429.6	397.8	346.4	581.3	492.5
SPy1813 endoglycosidase S; inactivates immunoglobulin; secreted	284.8	247.6	275.0	383.6	343.2
SPy1815 PTS system, sucrose-specific IIBC component	172.1	184.7	156.0	226.4	194.7
SPy1816 sucrose-6-phosphate dehydrogenase	155.4	149.2	164.1	241.9	183.3
SPy1817 transcriptional regulator, LacI family, putative	82.8	75.0	79.9	75.5	62.5
SPy1818 N utilization substance protein B, putative	57.7	50.7	42.5	51.3	45.8
SPy1820 conserved hypothetical protein	83.0	71.5	58.5	26.4	82.7
SPy1821 translation elongation factor P	112.7	88.9	104.5	119.7	95.1
SPy1823 yfhC protein	205.9	203.1	179.0	260.8	229.9
SPy1825 excinuclease ABC, subunit A	253.0	170.5	334.5	271.1	200.8
Hypothetical protein	58.1	49.8	48.5	57.4	53.0
SPy1827 magnesium and cobalt transport protein, putative	146.7	152.6	167.4	164.7	169.3
SPy1828 hypothetical protein	179.3	200.6	241.9	252.2	220.3
SPy1829 ribosomal protein S18	68.7	56.9	68.3	70.6	57.7
SPy1831 ribosomal protein S6	118.5	86.4	119.9	105.7	86.1
SPy1832 hypothetical protein	107.4	113.7	107.9	145.2	134.6
SPy1833 A/G-specific adenine glycosylase	122.7	133.1	97.0	147.1	131.3
SPy1834 sinr protein, putative	76.4	94.7	86.3	112.4	110.4
SPy1835 thioredoxin	71.2	74.8	57.9	96.3	81.3
SPy1837 MutS-like protein	84.4	69.2	89.1	77.6	73.0
SPy1839 unknown conserved protein in B. subtilis, putative	84.4	96.5	97.7	109.5	111.6
SPy1840 conserved hypothetical protein	113.6	105.5	117.7	121.1	96.5
SPy1841 ribonuclease HIII	245.9	244.7	240.8	301.7	261.8
SPy1842 Signal peptidase I	195.8	232.5	200.3	353.7	335.6

SPy1845 hypothetical protein	70.9	72.3	76.5	96.0	104.6
SPy1846 DNA-damage-inducible protein P	160.5	133.6	166.6	193.7	159.9
SPy1849 formate acetyltransferase	111.8	110.9	133.3	114.6	116.1
SPy1850 conserved hypothetical protein	122.8	108.2	100.7	103.3	89.6
SPy1851 C3-degrading proteinase	76.7	81.0	61.6	60.4	53.8
SPy1852 hypothetical protein	158.7	173.9	130.8	208.0	199.6
SPy1854 glycerol uptake facilitator protein	148.1	143.5	181.5	181.3	145.7
SPy1856 quinolene resistance protein NorA, putative	125.3	121.1	168.3	150.2	152.3
SPy1857 PrfA, putative	89.0	102.9	110.7	70.6	77.6
SPy1858 xaa-pro dipeptidyl-peptidas	82.6	93.9	79.8	88.2	72.5
Hypothetical protein	80.5	79.9	57.9	72.8	65.8
Hypothetical protein	61.3	64.6	41.1	101.6	81.7
SPy1861 Helix-turn-helix domain protein	92.4	82.0	101.8	91.7	83.2
SPy1862 conserved hypothetical protein TIGR00103	109.6	94.2	113.9	96.1	90.8
SPy1863 heavy metal dependent transcriptio	154.5	113.3	151.0	138.6	138.3
SPy1864 dna polymerase iii, alpha chain polc-type (ec 2.7.7.7) (poliii)	151.6	129.3	139.2	158.2	144.4
SPy1865 conserved hypothetical protein	103.4	71.9	66.7	108.8	102.7
SPy1866 conserved hypothetical protein TIGR00275	71.3	109.0	95.8	133.4	113.1
SPy1867 deoxyribose-phosphate aldolase	251.0	183.3	225.3	276.3	238.7
SPy1868 NupC family protein	196.0	166.8	238.5	236.7	243.3
SPy1869 purine nucleoside phosphorylase	91.0	83.2	91.4	74.6	78.1
SPy1870 regulator of resistance to cathelicidins; Victor Nizet	226.2	200.6	240.0	298.9	276.3
Spy1871 Ribosomal protein S14p/S29e	275.6	305.4	249.9	495.0	366.1
SPy1872 O-sialoglycoprotein endopeptidase	97.0	121.2	85.0	127.8	116.6
SPy1873 ribosomal-protein-alanine acetyltransferase	73.4	85.9	82.2	69.3	55.8
SPy1874 glycoprotein endopeptidase	176.4	189.3	199.1	232.1	209.1
SPy1875 conserved hypothetical protein	128.2	126.4	115.1	131.6	103.9
SPy1876 unknown conserved protein	163.7	213.7	199.0	229.5	183.2
SPy1877 glutamine synthetase, type I	175.1	247.5	224.6	311.6	219.3
SPy1878 glutamine synthetase repressor	162.5	204.6	199.3	322.2	239.4
SPy1879 hypothetical protein	131.9	154.0	170.5	110.5	104.7

SPy1881 Phosphoglycerate kinases	184.2	174.9	229.8	166.9	137.4
SPy1882 acid phosphatase	88.5	98.4	93.6	97.4	82.0
SPy1884 putative periplasmic protein	188.9	180.2	218.1	203.5	153.3
SPy1885 conserved hypothetical protein	162.8	223.7	198.9	226.6	202.7
SPy1886 conserved hypothetical protein	106.2	149.1	115.5	180.9	119.0
SPy1888 ribosomal protein L28	134.9	133.3	119.1	127.3	106.5
SPy1889 fructose-bisphosphate aldolase (ec 4.1.2.13)	193.8	215.5	275.9	285.1	198.6
SPy1892 hypothetical 2-acetyl-1-alkylglycerophosph ocholine esterase, putative	204.2	212.1	191.5	230.3	207.7
Hypothetical protein	63.8	75.8	64.4	80.4	127.5
SPy1894 CTP synthase	191.9	212.0	301.4	274.9	188.5
SPy1895 DNA-directed RNA polymerase, subunit delta, putative	119.0	148.4	151.5	134.0	109.6
SPy1896 trigger factor	205.6	197.4	246.4	226.3	174.2
SPy1897 unknown conserved protein	177.4	182.1	217.7	190.6	160.2
SPy1898 conserved hypothetical protein	203.8	216.3	214.7	269.3	213.7
SPy1899 conserved hypothetical protein	205.4	235.6	289.6	345.0	313.0
SPy1900 phosphomethylpyrimidine kinase	215.2	278.8	229.9	333.1	279.3
SPy1901 tRNA pseudouridine synthase A	176.0	209.5	238.4	291.8	206.2
SPy1903 Uncharacterized BCR, COG1929 superfamily	107.2	102.7	117.3	108.1	89.3
SPy1904 type I restriction-modification system endonuclease	141.4	99.7	141.2	122.4	134.9
SPy1905 type I restr.-mod. system, S subunit, EcoA family domain protein	79.1	84.1	54.3	129.1	71.0
SPy1906 type I restriction-modification system, M subunit	108.6	95.0	118.0	113.5	123.1
Hypothetical protein	48.4	73.9	46.5	61.6	52.7
Spy1908 response regulator spt12R; salR	72.9	96.9	70.8	108.4	103.0
SPy1909 histidine kinase spt12S; salS	68.7	67.2	71.6	56.9	63.5
Hypothetical protein	68.8	79.3	66.9	75.3	73.4
SPy1911 permease, putative	82.8	4.5	86.4	95.4	97.9
SPy1912 ATP-binding protein	62.9	3.2	56.5	90.3	91.8
SPy1913 RTX toxin transporter, putative	57.2	4.4	67.0	78.9	72.6
SPy1914 cylM protein, putative	78.2	67.6	90.6	95.1	138.7
SPy1915 lantibiotic salivaricin a precursor-related protein	118.2	150.3	110.2	88.1	110.4

SPy1916 6-phospho-beta-galactosidas	157.5	163.9	139.7	126.1	166.1
SPy1917 PTS system, cellobiose-specific IIC component, putative	103.0	96.5	102.4	106.8	74.2
SPy1918 PTS system, cellobiose-specific IIA component	129.6	122.4	140.0	129.5	133.7
SPy1919 tagatose 1,6-diphosphate aldolase	207.0	181.9	224.0	240.4	246.0
SPy1921 1-phosphofructokinase, putative	207.5	168.8	215.0	206.9	271.9
SPy1922 galactose-6-phosphate isomerase, LacB subunit	77.5	76.8	107.6	72.7	82.8
SPy1923 galactose-6-phosphate isomerase, LacA subunit	160.7	193.9	167.4	156.7	153.6
Hypothetical protein	58.2	37.1	39.7	56.8	55.0
SPy1924 transcriptional regulator, DeoR family, putative	72.0	64.6	75.5	82.5	81.0
SPy1926 hypothetical protein (Phage R1930)	142.3	142.4	137.0	209.2	213.2
SPy1927 hypothetical protein (Phage R1930)	171.7	178.6	160.6	221.3	215.4
Phage integrase, putative (Phage R1930)	78.5	66.6	78.7	67.9	59.0
Hypothetical protein (Phage R1930)	84.0	70.7	66.1	119.2	101.9
Integrase-like protein, putative (Phage R1930)	116.3	115.2	98.5	112.9	112.4
SPy1930 integrase, putative (Phage R1930)	97.7	85.9	70.3	85.5	91.0
SPy1931 Ribosomal protein S9/S16	151.7	123.5	120.9	152.9	153.5
SPy1934 repressor protein	138.4	113.0	132.5	154.5	181.2
SPy1935 hypothetical protein	209.5	193.1	466.0	194.8	381.8
SPy1936 degV family protein superfamily	195.8	178.0	220.5	206.8	212.0
SPy1937 conserved hypothetical protein	108.3	114.7	136.6	133.3	138.8
SPy1938 RNA methyltransferase, TrmH family, group 3	132.5	79.6	119.5	150.0	153.6
SPy1940 unknown conserved protein	87.5	72.8	84.7	91.6	81.3
SPy1941 cysteinyl-tRNA synthetase	86.1	55.7	92.3	84.9	79.8
SPy1942 hypothetical protein	91.3	77.0	100.3	90.3	116.9
Hypothetical protein	147.9	170.3	131.0	168.4	186.2
SPy1944 serine O-acetyltransferase	206.0	156.2	201.8	328.3	314.1
SPy1946 polyribonucleotide nucleotidyltransferase	164.4	127.5	184.2	205.9	180.0
SPy1947 transaldolase, putative, TalC family, putative	153.3	113.2	155.6	158.7	172.9
Hypothetical protein	117.1	104.3	127.1	168.1	141.3
SPy1949 SgaT protein, putative	135.4	115.1	102.2	131.0	125.8
SPy1950 unknown conserved protein	210.4	189.9	165.9	292.4	323.8
Hypothetical protein	72.1	73.0	87.4	71.6	86.2

SPy1955 ribosomal protein S15	117.3	124.7	129.8	129.8	136.8
SPy1956 hypothetical protein	130.1	146.4	153.8	159.9	162.1
SPy1957 hypothetical protein	146.9	120.3	67.2	146.7	137.6
SPy1958 polypeptide deformylase	142.8	140.3	179.7	154.9	149.2
SPy1959 SEQ ID N 14P	159.2	141.2	184.9	215.1	158.3
SPy1960 transcriptional regulator, MarR family, putative	116.6	86.3	133.1	136.2	101.3
SPy1961 dna polymerase iii, alpha chain polc-type (ec 2.7.7.7) (poliii)	241.2	209.9	272.8	257.2	271.1
SPy1962 prolyl-tRNA synthetase	140.2	105.8	131.7	138.0	124.0
SPy1963 membrane-associated zinc metalloprotease, putative	107.6	119.1	170.1	132.0	155.9
SPy1964 phosphatidate cytidylyltransferase	176.1	163.2	175.3	177.6	193.9
SPy1965 undecaprenyl diphosphate synthase	171.4	160.2	155.0	214.0	249.6
Hypothetical protein	68.1	78.8	72.4	80.2	76.4
SPy1968 preprotein translocase, YajC subunit, putative	104.8	95.7	87.7	105.4	102.7
SPy1971 Bta, putative	119.8	120.9	152.4	175.7	123.6
SPy1972 alkaline amylopullulanase	196.4	145.1	184.9	201.2	213.5
SPy1973 glucan 1,6-alpha-glucosidase (dexB)	111.2	96.5	105.1	103.1	104.0
SPy1976 multiple sugar transport ATP-binding protein	147.9	184.0	171.0	244.4	227.0
Hypothetical protein	137.6	108.6	112.7	127.8	117.4
SPy1978 ABC transporter	169.1	158.4	187.0	180.0	209.3
SPy1979 streptokinase a precursor	98.9	102.9	125.7	89.6	101.5
Hypothetical protein	173.6	119.4	174.1	215.8	200.4
SPy1980 conserved hypothetical protein TIGR00256	413.2	382.0	373.1	218.1	267.7
SPy1981 stringent response-like protein (rel)	219.5	185.0	187.2	322.0	319.6
SPy1983 collagen-like protein Scl1, sclA	206.1	146.9	266.5	217.3	132.5
SPy1984 nrdI protein	133.1	155.5	175.0	136.9	140.8
Hypothetical protein	202.1	128.3	165.2	172.2	162.8
SPy1985 hypothetical protein	197.6	240.9	249.3	310.3	287.6
SPy1986 PTS system, glucose-specific IIBC component, putative	189.6	249.8	385.1	376.0	264.8
SPy1987 conserved hypothetical protein TIGR00046	152.9	189.8	190.9	161.0	152.6
SPy1988 ribosomal protein L11 methyltransferase	147.5	197.6	199.4	155.3	130.5

SPy1989 hypothetical protein		134.4	168.2	190.5	172.6	144.9
SPy1990 para-aminobenzoate synthase, component I		140.6	150.1	195.1	179.4	162.9
SPy1991 para-aminobenzoate synthase glutamine amidotransferase, component II		241.0	217.8	229.4	257.1	250.6
SPy1992 ATPase, AAA family domain protein		140.0	125.8	191.2	151.4	131.2
SPy1994 pail repressor		116.2	8.2	8.8	14.8	137.4
SPy1995 FlaR		177.9	24.4	29.9	37.9	195.4
SPy1998 smeZ		105.2	100.9	135.0	98.2	122.3
SPy1999 hypothetical protein		82.6	73.5	75.5	58.7	58.9
SPy2000 oligopeptide-binding protein appa precursor, putative		214.0	169.6	215.7	227.1	233.2
SPy2001 peptide ABC transporter, permease protein, putative		207.7	249.5	248.2	302.8	238.6
SPy2002 oligopeptide ABC transporter, permease protein, putative		249.2	327.4	322.7	308.5	319.6
SPy2003 peptide ABC transporter, ATP-binding protein, putative		141.8	149.8	175.0	137.6	113.8
SPy2004 peptide ABC transporter, ATP-binding protein, putative		115.4	103.2	134.8	117.2	120.0
SPy2005 late embryogenesis abundant protein d-29 (lea d-29)		193.3	131.4	183.9	166.0	173.5
SPy2006 putative histidine triad protein; toxin, pathogenesis		287.4	342.7	427.1	492.1	475.3
SPy2007 laminin binding protein		339.1	365.4	376.3	440.9	428.0
Hypothetical protein		108.0	122.4	92.4	151.4	99.8
SPy2009 fibronectin- and factor H-binding protein, Mga-regulated	Mga locus	183.2	139.2	230.0	163.0	28.6
SPy2010 c5a peptidase precursor	Mga locus	194.6	159.6	255.0	174.3	146.8
ScpA 5' probe	Mga locus	147.5	140.7	118.5	140.4	158.3
SPy2013 transposase	Mga locus	135.4	183.1	98.0	172.0	128.4
SPy2016 Sic1.225	Mga locus	114.8	12.3	15.4	18.1	9.7
SPy2018 M1 protein precursor	Mga locus	256.4	295.7	147.8	284.0	148.7
SPy2019 trans-acting positive regulator of M protein	Mga locus	176.5	28.9	39.3	50.8	134.3
Hypothetical protein	Mga locus	126.1	75.4	71.0	76.6	85.5
SPy2023 conserved hypothetical protein	Mga locus	110.2	102.9	103.9	154.9	155.4
SPy2025 immunogenic secreted protein precursor	Mga locus	116.3	92.1	112.7	145.1	116.9
SPy2026 isp1-associated histidine kinase, spt13S	Mga locus	166.1	156.9	153.7	191.7	192.2
SPy2027 isp1-associated response regulator arlSR, spt13R	Mga locus	140.5	138.1	127.8	243.6	190.6
SPy2029 ABC transporter, ATP-binding protein	Mga locus	196.8	180.5	269.0	183.7	183.0
SPy2031 ABC transporter, ATP-binding protein	Mga locus	162.7	97.7	189.2	142.8	126.5

SPy2032 ATP-binding cassette transporter-like protein, putative	Mga locus	148.9	132.6	146.8	164.5	199.9
SPy2033 ATP-binding cassette lipoprotein		156.9	115.4	166.8	175.2	159.7
SPy2034 conserved hypothetical protein		181.6	212.3	234.3	251.0	228.9
Hypothetical protein		109.4	125.8	52.5	167.8	144.7
Spy2036 Gene regulated by Mga - sof inserts in MBS class II GAS		142.0	137.2	153.5	101.4	111.8
SPy2037 protease maturation protein; prtM		256.7	184.5	293.5	194.2	189.7
SPy2038 inhibitor of SpeB; co-transcribed		188.0	166.5	148.2	213.5	204.7
SPy2039 pyrogenic exotoxin B; streptopain precurso		202.8	175.0	203.6	285.7	271.1
SPy2040 hypothetical protein		188.5	235.8	192.3	269.9	281.9
SPy2041 hypothetical protein		78.0	92.8	67.8	124.0	120.8
SPy2042 positive regulator of speB; rgg, ropB		161.8	139.6	152.7	145.1	165.5
SPy2043 phage-associated deoxyribonuclease; originally mitogenic factor		142.8	127.9	146.1	126.3	142.7
Hypothetical protein		92.7	80.5	85.1	103.4	99.0
SPy2045 low temperature requirement C protein		167.8	153.4	182.4	211.0	204.2
SPy2047 glycerol dehydrogenase		173.0	146.0	191.0	216.8	210.4
SPy2049 formate acetyltransferase, putative		136.2	102.1	139.9	103.7	115.2
SPy2050 PTS system, cellobiose-specific IIC component		251.1	194.0	234.2	300.9	317.9
SPy2051 PTS system, cellobiose-specific IIB component		139.6	121.6	167.9	142.3	112.5
SPy2052 PTS system, cellobiose-specific IIA component		103.6	89.4	107.9	109.0	116.8
Hypothetical protein		91.2	79.7	80.2	99.0	121.0
SPy2054 transcriptional regulator, DeoR family, putative		141.6	111.3	143.2	137.2	151.1
SPy2055 pyruvate formate-lyase 1 activating enzyme, putative		130.1	125.4	155.6	155.2	174.2
Hypothetical protein		73.1	66.0	65.5	59.7	60.8
SPy2058 preprotein translocase, SecE subunit, putative		84.2	91.6	85.9	98.6	107.1
SPy2059 penicillin-binding protein 1B		159.5	154.3	161.9	207.0	190.4
Hypothetical protein		157.9	153.4	175.7	154.6	167.4
SPy2063 ribosomal large subunit pseudouridine synthase D		114.5	92.3	122.3	108.9	121.1
SPy2065 hypothetical protein		154.6	115.5	143.8	143.0	172.0
SPy2066 conserved hypothetical protein		178.7	156.5	176.5	159.0	228.4
Hypothetical protein		187.8	146.0	146.0	240.2	262.2

SPy2072 10 kDa chaperonin	115.3	96.3	106.2	137.2	144.6
SPy2073 clpB protein	117.1	120.0	153.4	139.9	143.5
SPy2074 CtsR protein	103.0	96.4	114.3	87.7	97.9
Hypothetical protein	103.9	91.3	86.9	116.8	123.3
SPy2077 cold shock DNA-binding domain protein-related protein	65.9	68.1	72.4	52.3	56.4
SPy2079 alkyl hydroperoxide reductase C	185.9	205.2	218.9	231.1	303.7
SPy2080 NADH dehydrogenase	148.2	135.1	131.4	159.7	209.0
SPy2081 imidazolonepropionase	138.2	131.3	183.4	128.3	147.4
SPy2082 urocanate hydratase	160.1	134.1	131.6	190.3	198.6
SPy2083 formiminotransferase-cyclodeaminase	97.5	92.5	148.8	126.8	144.1
SPy2084 putative serine cycle enzyme	109.2	114.7	108.5	97.7	125.2
SPy2085 formate--tetrahydrofolate ligase	313.5	306.1	355.5	410.4	516.9
SPy2087 hypothetical protein	136.4	90.2	148.9	120.0	148.1
SPy2088 amino acid permease, putative	137.6	119.5	158.8	134.1	174.2
SPy2089 histidine ammonia-lyase	98.8	77.1	104.3	86.7	90.6
SPy2090 formiminoglutamase, putative	234.0	194.3	226.1	263.2	321.0
SPy2091 hypothetical protein	142.6	135.7	170.9	184.0	208.4
SPy2092 ribosomal protein S2	154.7	170.1	125.9	199.4	220.9
SPy2093 translation elongation factor Ts	87.7	88.3	100.4	80.6	81.1
SPy2095 endopeptidase O	170.2	153.6	168.0	139.7	207.0
SPy2096 trehalose-6-phosphate hydrolase	118.2	121.3	130.3	112.0	124.7
SPy2097 PTS system, trehalose-specific IIBC component	178.4	102.1	148.6	237.0	308.0
SPy2099 similar to transcriptional regulator (GntR family), putative	202.6	179.3	211.7	268.8	320.4
Hypothetical protein	101.2	93.4	80.8	100.2	118.8
SPy2102 ydzf protein	164.1	194.2	284.1	178.7	182.8
SPy2103 Glyoxalase family	164.8	183.6	153.0	128.6	136.1
SPy2104 conserved hypothetical protein	212.9	205.7	217.5	220.2	230.3
SPy2105 anaerobic ribonucleoside-triphosphate reductase activating protein	181.8	183.1	229.9	237.5	218.6
SPy2106 unknown conserved protein in others	219.0	232.0	251.3	257.8	305.0
SPy2107 oxidoreductase, Gfo/Idh/MocA family, putative	176.4	196.4	269.0	236.4	279.1

Hypothetical protein	111.8	87.7	95.7	68.2	57.3
SPy2110 anaerobic ribonucleoside-triphosphate reductase	126.6	135.8	147.8	108.4	117.0
SPy2111 hypothetical protein	210.1	239.7	269.8	267.5	323.7
SPy2112 conserved hypothetical protein	107.2	106.3	110.7	93.3	97.9
SPy2113 conserved hypothetical protein TIGR00250	156.9	169.5	214.6	179.3	185.6
SPy2114 conserved hypothetical protein	126.7	156.0	160.6	140.8	138.9
SPy2115 arsenate reductase, putative	99.9	100.6	110.4	89.4	94.8
SPy2116 recA bacterial DNA recombination proteins	143.6	114.0	164.7	146.3	151.2
SPy2117 competence/damage-inducible protein CinA, putative	275.2	219.4	242.8	337.2	314.3
SPy2118 DNA-3-methyladenine glycosidase I	128.3	151.7	128.4	149.7	142.6
SPy2119 Holliday junction DNA helicase RuvA	195.0	203.8	265.8	217.5	216.9
SPy2120 integral membrane protein LmrP, putative	204.1	267.9	302.1	243.4	232.7
SPy2121 DNA mismatch repair protein MutL, putative	118.1	127.5	154.1	112.7	101.2
SPy2148 DNA mismatch repair protein MutS	132.0	115.2	125.7	129.7	121.1
SPy2149 conserved hypothetical protein	99.5	118.7	89.5	159.6	99.3
SPy2150 arginine repressor	128.3	230.2	169.7	347.7	250.5
SPy2151 arginyl-tRNA synthetase	169.4	166.6	139.9	189.1	175.4
Hypothetical protein	69.2	60.3	58.8	62.8	72.4
SPy2152 BacB protein, putative	98.6	90.6	115.3	87.1	119.3
SPy2153 Uncharacterized BCR, YitT family COG1284 family	119.1	95.0	113.7	111.8	131.6
SPy2154 unknown conserved protein	149.0	120.9	162.8	190.8	215.4
SPy2155 Uncharacterized BCR, YitT family COG1284 family	248.9	179.5	244.7	353.9	388.6
SPy2157 histidyl-tRNA synthetase	159.1	104.8	180.8	159.6	187.5
SPy2159 ribosomal protein L32-related protein	80.3	67.0	75.7	64.1	81.4
SPy2160 ribosomal protein L33	43.8	37.7	42.1	33.2	43.7
SPy2162 cadmium resistance protein	98.3	94.1	89.1	115.9	114.8
SPy2163 accessory protein	94.3	93.4	85.1	95.8	105.5
SPy2165 FtsK/SpoIIIE family family	101.2	111.0	159.9	126.9	147.0
SPy2166 hypothetical protein	107.3	80.5	97.6	98.6	106.2
Hypothetical protein	169.3	158.6	203.6	252.0	305.2
Hypothetical protein	76.1	73.3	85.4	71.7	82.5
SPy2169 unknown conserved protein in others, putative	121.1	117.4	119.9	156.1	171.0

Hypothetical protein	85.5	70.3	88.3	81.2	82.8
SPy2172 30S ribosomal protein S14 homolog	74.8	67.4	73.6	72.7	83.6
SPy2173 hypothetical protein	390.3	350.4	369.3	485.6	447.6
SPy2174 hypothetical protein	328.8	260.5	278.8	495.9	513.8
Hypothetical protein	256.2	220.8	215.4	411.2	532.3
SPy2177 transcriptional regulator, putative	67.0	65.0	87.9	89.4	102.4
SPy2178 ribosomal protein S4	119.1	114.2	135.3	95.2	108.5
SPy2181 conserved hypothetical protein	75.8	75.5	75.4	75.9	92.1
SPy2182 replicative DNA helicase	110.8	97.5	108.7	92.9	98.3
SPy2183 ribosomal protein L9	100.7	100.8	93.1	97.8	112.6
SPy2184 unknown conserved protein in B. subtilis, putative	101.9	103.2	74.0	106.0	130.5
SPy2185 Glucose inhibited division protein A	128.7	103.8	135.2	120.2	147.9
SPy2186 unknown conserved protein in others, putative	107.3	119.6	145.7	115.4	137.2
SPy2188 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	161.7	149.3	265.8	207.9	233.4
SPy2189 L-serine dehydratase, iron-sulfur-dependent, beta subunit	95.1	123.5	158.4	105.1	101.4
SPy2190 L-serine dehydratase, iron-sulfur-dependent, alpha subunit	210.9	167.4	159.7	184.2	188.7
SPy2191 unnamed protein product	190.5	150.9	148.2	211.3	244.4
SPy2193 Cobalt transport protein superfamily	95.2	81.9	118.8	88.3	83.3
SPy2194 similar to ABC transporter (ATP-binding protein)	83.4	66.4	84.7	68.9	85.3
SPy2195 ABC transporter, ATP-binding protein	131.5	131.8	148.2	122.1	160.4
SPy2196 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	140.4	134.4	163.1	229.8	188.1
SPy2197 conserved hypothetical protein	107.8	108.1	119.7	157.7	149.6
SPy2198 unknown conserved protein	188.7	187.0	175.6	283.7	334.5
SPy2199 conserved hypothetical protein	100.7	94.2	122.7	123.9	128.0
SPy2200 hyaluronate synthase	149.5	225.1	230.8	167.9	188.3
SPy2201 udp-glucose 6-dehydrogenase	217.8	190.1	162.9	275.0	299.7
SPy2202 UTP-glucose-1-phosphate uridylyltransferase	397.0	353.0	339.2	649.8	659.0
SPy2203 conserved hypothetical protein	193.1	209.4	270.6	182.7	209.5

SPy2204 RecF protein		165.0	163.8	193.9	234.9	241.2
SPy2205 putative multiple membrane domain protein		147.4	125.4	210.5	130.0	125.2
SPy2206 inosine-5-monophosphate dehydrogenase		263.0	213.6	286.5	314.0	312.6
SPy2207 tryptophanyl-tRNA synthetase		176.3	161.8	182.1	202.3	227.0
Hypothetical protein		122.8	130.7	116.1	123.6	121.9
SPy2209 Uncharacterized BCR, YitT family COG1284 family		150.6	170.4	210.9	224.7	241.9
SPy2210 ABC transporter, ATP-binding protein		154.0	185.1	190.2	300.7	254.0
SPy2211 hypothetical protein		80.9	97.7	92.5	78.5	74.4
Hypothetical protein		51.5	61.4	48.3	44.7	34.3
Transposase, IS30 family		239.4	285.3	410.0	328.6	159.1
Transposase, IS30 family		102.1	211.0	299.5	252.7	82.6
SPy2215 conserved hypothetical protein TIGR00246		122.4	109.3	124.3	147.6	164.5
SPy2216 serine protease, HtrA/DegQ/DegS family		119.6	169.5	175.5	102.2	109.3
M5005_Spy_0138_transcription antitermination protein NusG	SLO/Nga locus in M1T1	91.7	108.6	124.5	97.1	80.8
M5005_Spy_0139_NAD glycohydrolase	SLO/Nga locus in M1T1	111.0	128.2	121.5	147.1	138.5
M5005_Spy_0140_hypothetical protein	SLO/Nga locus in M1T1	55.0	55.5	68.4	54.8	45.6
M5005_Spy_0141_streptolysin O	SLO/Nga locus in M1T1	79.8	87.9	98.8	110.4	103.9
M5005_Spy_0142_hypothetical protein	SLO/Nga locus in M1T1	106.8	1.6	75.2	7.2	5.4
M5005_Spy_0143_hypothetical protein	SLO/Nga locus in M1T1	229.9	113.0	98.1	151.7	135.1
M5005_Spy_0144_hypothetical protein	SLO/Nga locus in M1T1	126.1	143.1	147.3	117.7	91.9
M5005_Spy_0145_hypothetical protein		87.9	7.6	10.1	19.4	10.4
SpyM18 0168	SLO/Nga Locus in M18	13.4	9.2	9.9	57.6	52.8
SpyM18 0426		28.5	15.9	19.1	95.1	788.7
SpyM18 0480		107.5	175.3	111.3	316.8	105.5
SpyM18 0520		71.1	98.5	71.9	74.5	78.6
SpyM18 0538 silA		10.5	76.4	64.4	100.7	15.3
SpyM18 0539 silB		7.9	69.6	78.8	67.2	5.4
SpyM18 0540		7.2	61.5	37.1	50.6	9.2
SpyM18 0541 silD		11.9	84.4	75.0	79.3	8.9
SpyM18 0542 silD		5.2	58.9	50.3	54.5	6.6
SpyM18 0543 silE		10.2	123.7	119.7	164.8	13.1
SpyM18 0585		56.1	41.9	43.2	57.8	70.8

SpyM18 0586		20.5	17.9	19.0	32.4	26.6
SpyM18 0587		20.5	10.4	10.5	26.3	20.2
SpyM18 0588		15.4	9.7	14.1	20.7	13.4
SpyM18 0589		15.1	8.4	9.4	19.4	14.4
SpyM18 2046		33.6	16.9	24.8	53.6	51.1
SpyM18 2047		68.7	51.3	50.4	63.3	54.7
SpyM18 2048		146.5	232.7	168.7	141.5	113.2
SpyM18 2055		64.3	242.1	33.8	274.4	50.4
SpyM18 2063		55.5	53.4	44.2	59.0	52.9
SpyM18 2077		72.4	109.2	131.3	111.0	107.3
SpyM18 2201		131.8	139.2	136.4	137.3	140.5
SpyM3 0097 nra	FCT locus in MGAS315	12.7	162.6	18.3	127.3	13.9
SpyM3 0098	FCT locus in MGAS315	8.7	104.0	137.7	92.8	7.4
SpyM3 0100	FCT locus in MGAS315	54.7	230.8	204.2	228.1	34.6
SpyM3 0101	FCT locus in MGAS315	6.0	102.2	74.4	87.5	6.6
SpyM3 0102	FCT locus in MGAS315	22.3	204.6	266.5	328.8	29.4
SpyM3 0103	FCT locus in MGAS315	10.2	128.0	115.1	169.3	14.9
SpyM3 0104	FCT locus in MGAS315	11.0	144.0	148.9	125.8	11.1
SpyM3 0221		397.6	530.7	17.6	203.0	91.9
SpyM3 0757		71.8	69.9	75.0	81.3	92.2
SpyM3 0788		120.0	125.2	158.6	190.4	171.6
SpyM3 0986		62.5	58.0	62.7	64.1	56.3
SpyM3 0989		99.6	127.2	184.5	206.4	144.9
SpyM3 1015		96.8	170.8	118.0	137.0	120.0
SpyM3 1086		75.6	69.7	73.1	72.7	72.9
SpyM3 1650		5.2	61.9	4.9	10.5	11.3
SpyM3 1703		38.9	13.5	53.0	95.2	71.5
SpyM3 1716		28.0	14.6	47.7	27.9	28.8
SpyM3 1729		89.9	80.0	77.6	85.5	117.9
SpyM3 1865		57.4	46.4	46.5	38.3	43.4
SPyM18_0036		8.6	67.5	10.1	64.8	12.2
Unknown		108.7	98.2	81.4	85.8	119.7

Unknown	73.1	112.2	86.0	116.6	107.7
Unknown	56.4	56.3	60.9	77.2	68.0
Unknown	51.6	51.6	53.6	39.6	36.8
Unknown	73.9	43.1	48.6	46.5	42.6
Unknown	42.6	29.1	89.6	60.7	49.8
SpyM18_0238_Protein yjgK	24.1	18.6	199.7	37.4	28.3
SpyM18_0253	14.8	9.3	9.9	33.7	1721.7
Unknown	64.6	74.5	67.7	60.0	59.8
Unknown	171.0	152.8	125.8	176.9	223.3
Unknown	145.6	287.1	189.9	216.8	201.7
Unknown	15.9	11.5	12.0	25.2	20.6
Unknown	6.9	3.7	7.3	8.5	6.2
Unknown	64.5	40.6	57.7	59.6	28.4
Unknown	82.4	16.0	14.7	22.5	17.3
Unknown	103.4	171.3	137.3	102.1	114.0
Unknown	132.7	168.9	206.0	153.0	145.8
Unknown	86.7	110.3	95.1	84.8	67.6
Unknown	109.9	125.0	110.9	102.2	104.7
Unknown	116.7	101.8	102.9	88.0	70.2
Unknown	88.0	119.6	123.2	97.1	101.0
Unknown	153.2	201.8	161.2	182.2	144.7
Unknown	84.4	70.6	95.3	66.2	60.4
Unknown	8.0	86.6	74.8	88.5	7.4
Unknown	11.4	92.2	77.0	81.9	10.7
Unknown	18.2	136.2	115.8	197.1	15.3
Unknown	13.4	114.2	114.2	156.9	16.5
Unknown	13.1	107.2	163.3	178.4	13.2
Unknown	14.3	81.1	91.1	107.0	6.8
Unknown	16.2	68.7	73.3	99.0	22.2
Unknown	9.9	84.0	87.8	112.2	14.0
Unknown	24.2	155.7	152.5	275.3	25.5
Unknown	18.6	113.7	75.6	233.4	19.0

Unknown	56.5	154.3	92.8	75.8	30.5
Unknown	91.2	108.7	56.2	33.7	37.6
SilC	8.1	90.6	52.6	78.8	7.7
Unknown	48.7	44.3	9.8	61.4	55.1
SpyM18_0551	156.0	172.7	174.0	276.6	271.7
SpyM18_0583	45.6	41.4	50.4	56.7	56.4
SpyM18_0584	9.6	5.8	7.1	11.8	8.4
Unknown	8.3	9.0	10.5	18.5	10.0
Unknown	36.4	46.1	37.4	40.1	33.8
Unknown	41.1	4.1	35.2	9.8	40.4
Unknown	83.9	1.8	73.0	10.5	127.1
Unknown	56.8	57.4	52.4	58.4	63.9
SpyM18_0717	35.9	12.5	36.1	53.8	117.8
Unknown	6.6	6.0	5.5	11.3	44.0
SpyM18_0719	92.0	103.0	24.5	44.6	373.5
SpyM18_0721	7.1	3.9	9.7	9.0	166.6
Unknown	7.0	55.4	6.5	10.2	52.6
Unknown	67.3	12.4	34.0	90.4	111.8
Unknown	28.0	92.3	22.5	31.9	195.9
Unknown	9.3	7.5	3.0	16.3	122.4
Unknown	58.2	61.3	55.9	50.4	64.3
Unknown	53.9	50.8	44.4	45.6	50.6
Unknown	66.4	67.5	61.9	77.4	52.8
Unknown	50.0	53.0	31.5	49.1	45.8
Unknown	38.2	37.2	38.3	43.5	69.7
Unknown	44.3	53.4	53.2	38.1	54.8
Unknown	60.3	143.7	45.5	199.3	211.6
Unknown	69.2	73.9	75.6	82.4	85.2
Unknown	57.4	8.8	50.5	67.2	48.9
Unknown	61.5	76.1	55.0	98.6	82.0
Unknown	36.5	81.0	53.0	73.2	53.5
Unknown	30.1	45.6	43.2	33.7	29.7

Unknown	58.2	58.5	62.8	49.0	59.3
SpyM18_1057	16.7	9.3	11.2	37.3	1441.7
Unknown	70.9	72.9	65.6	80.0	65.6
SpyM18_1077	64.5	87.4	56.7	90.4	94.4
Unknown	43.2	43.5	44.0	48.2	34.6
Unknown	34.8	62.6	58.2	49.0	53.6
SpyM18_1162	57.0	66.7	52.9	64.0	51.2
Unknown	69.7	119.5	79.1	86.7	84.7
Unknown	32.7	57.5	36.4	43.9	34.8
SpyM18_1209	127.4	160.5	97.3	153.5	137.4
Unknown	142.7	13.2	20.7	27.6	119.3
Unknown	5.9	66.4	6.1	15.6	10.8
Unknown	8.6	6.7	8.9	14.3	10.0
Unknown	81.6	63.8	8.8	7.8	7.4
Unknown	44.7	55.5	47.0	63.4	58.0
SpyM18_1359	80.6	94.4	66.1	130.5	154.9
Unknown	42.1	65.2	42.8	55.9	49.8
Unknown	49.6	69.6	38.4	66.9	67.7
Unknown	59.5	53.6	60.4	79.6	79.3
Unknown	20.7	238.4	24.8	268.8	27.3
SpyM18_1508	164.0	125.8	152.6	158.7	174.2
Unknown	68.3	61.5	63.0	64.9	57.9
Unknown	64.4	77.9	68.8	81.2	95.9
Unknown	165.8	145.3	175.7	235.1	197.6
Unknown	33.3	28.9	23.7	41.2	37.9
Unknown	84.3	80.7	82.7	82.8	71.3
Unknown	68.9	65.7	67.6	71.1	65.4
Unknown	133.1	113.2	135.2	113.1	103.1
Unknown	168.3	136.5	194.8	46.6	242.7
Unknown	16.5	66.2	67.4	17.4	13.3
Unknown	31.1	17.2	148.8	25.8	32.6
Unknown	15.9	52.8	35.7	20.5	19.2

Unknown		29.3	167.3	68.7	41.3	80.0
Unknown		11.5	85.3	86.5	21.9	13.8
Unknown		85.0	113.7	107.6	88.5	87.9
Unknown		68.3	70.7	69.7	72.4	75.3
Unknown		79.2	96.0	68.9	95.9	93.5
Unknown		59.7	54.6	58.5	65.6	64.3
Unknown		83.8	93.1	92.0	88.5	85.2
Unknown		106.0	90.9	111.9	123.6	106.9
Unknown		88.5	85.2	128.9	83.9	93.6
Unknown		83.5	91.6	84.5	71.5	94.6
Unknown		55.4	84.6	64.9	89.7	71.3
Unknown		22.5	232.7	172.2	221.7	39.8
Unknown		10.2	68.5	115.4	62.0	11.5
Unknown		173.3	196.4	180.4	262.7	244.1
Unknown		97.1	114.2	104.4	102.3	91.7
Unknown		200.6	272.1	246.3	273.7	265.7
Unknown		103.3	120.9	132.3	136.3	128.0
Unknown		61.8	62.8	73.3	67.8	72.4
Unknown		19.8	20.4	128.9	32.6	109.2
Unknown		186.2	215.9	192.5	230.2	204.4
Unknown		101.5	117.7	93.9	100.9	89.2
Unknown		29.9	64.2	41.1	40.9	57.6
Unknown		279.8	251.7	247.8	200.7	223.1
SPy0655 integrase 1, putative (Prophage 370.1)	Φ370.1 (SpeC/MF2)	29.9	19.3	23.9	61.0	246.1
SPy0656 conserved hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	17.3	8.0	11.8	22.9	22.1
SPy0657 repressor (Prophage 370.1)	Φ370.1 (SpeC/MF2)	5.2	4.1	6.0	13.6	16.7
SPy0658 Helix-turn-helix domain protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	12.5	11.5	12.2	15.5	14.9
SPy0659 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	6.8	6.6	8.9	21.3	118.6
SPy0660 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	18.4	48.7	12.0	14.9	13.3
SPy0661 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	23.8	10.1	17.2	25.7	22.3
SPy0663 chromosome segretation protein, putative (Prophage 370.1)	Φ370.1 (SpeC/MF2)	17.5	9.0	15.8	27.4	22.2

SPy0664 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	5.7	7.4	11.6	7.7	9.2
SPy0665 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	64.2	25.0	37.9	46.3	50.3
SPy0666 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	56.1	51.2	47.1	81.1	86.2
SPy0667 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	25.3	11.9	19.0	34.4	35.0
SPy0669 helicase-related protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	21.3	11.3	9.7	32.5	29.3
SPy0670 conserved hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	29.6	19.1	21.7	40.1	46.6
SPy0671 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	12.4	8.4	10.0	21.5	18.7
SPy0672 MADS box protein, putative (Prophage 370.1)	Φ370.1 (SpeC/MF2)	12.3	11.3	11.9	22.2	16.4
Hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	41.5	24.7	15.2	28.0	20.0
SPy0674 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	34.6	14.3	20.8	38.7	34.9
Hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	116.2	9.4	11.1	17.6	12.9
SPy0676 conserved hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	377.3	293.2	350.7	530.3	369.5
SPy0677 gp137 (Prophage 370.1)	Φ370.1 (SpeC/MF2)	140.6	181.5	202.9	45.5	206.7
Hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	11.0	25.5	24.1	23.9	152.3
SPy0679 ParB-like nuclease domain family (Prophage 370.1)	Φ370.1 (SpeC/MF2)	41.6	194.6	164.5	169.6	65.8
SPy0680 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	4.6	151.4	6.8	9.1	5.9
SPy0681 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	30.4	148.8	23.6	41.8	40.2
SPy0682 minor capsid protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	37.7	249.9	42.4	70.6	70.5
SPy0683 gp4, putative (Prophage 370.1)	Φ370.1 (SpeC/MF2)	6.1	151.4	5.7	14.2	10.6
SPy0684 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	6.1	85.2	5.6	11.1	6.6
SPy0685 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	129.6	384.0	30.3	61.6	391.8
SPy0686 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	25.0	195.7	18.3	26.3	20.0
SPy0688 major head protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	24.9	193.1	31.0	56.9	47.1
SPy0689 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	32.9	242.6	27.7	46.9	41.8
SPy0690 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	15.3	143.2	14.5	31.1	18.8
SPy0691 minor capsid protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	12.3	72.2	9.5	16.3	11.3
SPy0693 minor capsid protein, putative (Prophage 370.1)	Φ370.1 (SpeC/MF2)	19.9	145.6	16.1	33.6	18.8
SPy0694 major tail shaft protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	40.1	15.1	32.3	37.1	35.0
SPy0695 conserved hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	9.2	90.4	8.2	17.0	14.4
SPy0696 gp15 (Prophage 370.1)	Φ370.1 (SpeC/MF2)	21.4	167.0	14.8	29.1	24.7
SPy0697 putative tape-measure protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	31.4	209.0	20.7	39.3	31.9
SPy0698 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	42.3	285.1	30.4	52.0	465.1
SPy0700 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	15.8	191.1	14.0	29.0	636.1

SPy0701 hyaluronidase (Prophage 370.1)	Φ370.1 (SpeC/MF2)	20.0	268.3	36.8	154.9	179.4
SPy0702 conserved hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	49.9	328.9	41.6	175.0	322.3
SPy0703 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	58.6	219.9	11.7	152.7	165.5
SPy0705 hypothetical protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	120.8	91.3	136.7	190.2	454.0
SPy0710 N-acetylmuramoyl-L-alanine amidase domain protein (Prophage 370.1)	Φ370.1 (SpeC/MF2)	68.1	141.6	112.3	111.2	103.3
SPy0711 exotoxin type c precurso (Prophage 370.1)	Φ370.1 (SpeC/MF2)	9.1	101.5	10.6	18.8	100.4
SPy0712 mitogenic factor 2 precursor (Prophage 370.1)	Φ370.1 (SpeC/MF2)	24.3	100.6	18.4	39.1	224.2
SPy0937 integrase 3 (Prophage 370.2)	Φ370.2 (SpeI/H)	27.5	22.6	27.4	93.6	101.5
SPy0938 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	23.3	52.6	21.9	40.4	58.1
SPy0939 repressor protein (Prophage 370.2)	Φ370.2 (SpeI/H)	66.1	105.6	9.2	137.5	79.7
SPy0940 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	85.2	67.5	7.7	48.8	122.8
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	6.6	35.1	6.1	36.4	30.6
SPy0944 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	6.5	4.7	7.7	15.5	7.7
SPy0945 tec protein (Prophage 370.2)	Φ370.2 (SpeI/H)	17.5	8.1	10.1	17.1	13.5
SPy0946 putative phage anti-repressor protein (Prophage 370.2)	Φ370.2 (SpeI/H)	41.4	18.4	17.5	165.3	294.3
SPy0947 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	148.9	14.1	16.7	118.4	141.1
SPy0948 ymh (Prophage 370.2)	Φ370.2 (SpeI/H)	107.4	23.6	28.5	126.3	115.8
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	111.2	128.5	29.0	130.4	152.2
SPy0952 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	149.5	69.3	36.5	148.6	194.6
SPy0953 conserved hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	86.0	72.1	15.0	79.0	124.8
SPy0954 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	67.7	109.2	12.0	85.5	145.5
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	111.9	92.0	10.5	155.2	184.6
SPy0957 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	93.6	87.2	9.8	100.7	138.7
SPy0958 conserved hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	21.4	13.4	21.7	93.3	24.0
SPy0959 chromosome assembly protein homolog, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	26.5	17.7	16.4	126.4	28.4
SPy0960 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	85.0	56.2	81.0	197.4	133.7
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	96.1	6.3	10.6	101.2	161.7
SPy0962 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	14.7	4.6	5.0	64.7	82.7
SPy0963 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	14.4	5.9	7.5	15.2	120.1
SPy0965 gp51 (Prophage 370.2)	Φ370.2 (SpeI/H)	12.0	8.9	11.4	21.5	134.2
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	152.9	173.1	81.2	99.3	291.0

SPy0968 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	16.7	10.5	12.1	151.4	17.3
Probable oligomycin sensitivity conferring protein, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	5.7	5.8	7.3	73.8	21.4
SPy0971 Rorf172 (Prophage 370.2)	Φ370.2 (SpeI/H)	6.6	9.1	13.4	6.7	5.7
SPy0972 terminase large subunit, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	37.5	105.2	22.3	49.5	47.3
Gp502 (Prophage 370.2)	Φ370.2 (SpeI/H)	13.1	129.0	48.3	71.7	30.9
SPy0975 gp284 (Prophage 370.2)	Φ370.2 (SpeI/H)	33.2	184.6	20.1	35.4	32.3
SPy0976 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	12.0	98.2	13.6	39.5	42.2
SPy0977 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	72.1	19.2	12.4	31.8	26.3
SPy0978 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	6.1	51.0	6.4	14.1	10.6
SPy0979 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	37.5	125.1	29.0	55.4	48.9
SPy0981 conserved hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	1.8	155.0	184.9	242.8	2.3
SPy0982 gp119 (Prophage 370.2)	Φ370.2 (SpeI/H)	13.7	27.6	49.5	39.8	42.9
SPy0984 gp348 (Prophage 370.2)	Φ370.2 (SpeI/H)	15.6	25.1	35.3	99.5	31.6
SPy0985 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	7.2	5.0	7.8	17.0	13.9
SPy0986 gp113 (Prophage 370.2)	Φ370.2 (SpeI/H)	34.7	20.3	24.9	104.9	28.1
SPy0987 b3, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	15.3	75.4	84.2	22.6	9.0
SPy0988 a1 (Prophage 370.2)	Φ370.2 (SpeI/H)	12.6	129.1	104.7	19.7	10.0
SPy0989 x (Prophage 370.2)	Φ370.2 (SpeI/H)	6.1	56.6	59.9	22.4	13.9
SPy0991 structural protein (Prophage 370.2)	Φ370.2 (SpeI/H)	34.1	146.2	192.7	52.1	45.7
SPy0992 a2 (Prophage 370.2)	Φ370.2 (SpeI/H)	27.0	226.6	29.8	37.1	27.8
SPy0993 c2 (Prophage 370.2)	Φ370.2 (SpeI/H)	13.7	148.0	140.3	21.8	14.3
SPy0994 putative minor tail protein (Prophage 370.2)	Φ370.2 (SpeI/H)	20.1	113.9	311.9	23.0	20.5
SPy0995 gene 19.1, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	104.1	215.0	130.2	157.5	213.1
SPy0996 unknown conserved protein in others, putative (Prophage 370.2)	Φ370.2 (SpeI/H)	23.4	139.3	134.5	27.7	27.2
SPy0997 hyaluronoglucosaminidase (Prophage 370.2)	Φ370.2 (SpeI/H)	42.3	112.3	35.1	29.9	101.5
SPy0998 conserved hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	214.3	29.3	273.5	26.6	323.7
SPy0999 M protein (Prophage 370.2)	Φ370.2 (SpeI/H)	89.5	9.7	174.3	9.1	198.2
SPy1001 hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	78.5	88.1	16.6	168.3	186.6
SPy1002 DksA homolog (Prophage 370.2)	Φ370.2 (SpeI/H)	117.1	3.2	6.4	153.9	13.0
Hypothetical protein (Prophage 370.2)	Φ370.2 (SpeI/H)	114.7	16.0	20.7	95.8	18.4

SPy1006 49.7 kDa protein (Prophage 370.2)	Φ370.2 (SpeI/H)	12.2	10.4	11.8	14.1	66.8
SPy1007 exitoxin I precursor 25.7 kDa protein (Prophage 370.2)	Φ370.2 (SpeI/H)	16.6	11.7	11.9	18.7	70.0
SPy1008 exotoxin H precursor (Prophage 370.2)	Φ370.2 (SpeI/H)	37.0	29.5	27.5	135.0	98.1
Mitogenic factor 3 precursor (Prophage 370.3)	Φ370.3 (MF3)	142.1	116.5	71.6	69.8	113.2
SPy1436 DNA-entry nuclease, putative (Prophage 370.3)	Φ370.3 (MF3)	168.7	193.0	32.1	45.9	153.4
SPy1437 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	75.0	110.9	8.8	17.5	70.6
SPy1438 N-acetylmuramoyl-L-alanine amidase domain protein (Prophage 370.3)	Φ370.3 (MF3)	260.7	171.9	112.4	62.5	110.4
SPy1443 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	87.4	147.5	11.0	38.6	15.9
SPy1444 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	158.4	6.5	11.4	20.8	17.1
SPy1445 hyaluronoglucosaminidase (Prophage 370.3)	Φ370.3 (MF3)	31.7	59.5	82.8	204.3	163.0
SPy1446 PblB (Prophage 370.3)	Φ370.3 (MF3)	43.7	132.9	31.1	137.8	41.3
SPy1447 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	178.4	161.4	10.9	179.1	132.7
SPy1448 PblA (Prophage 370.3)	Φ370.3 (MF3)	197.0	127.0	12.0	198.9	133.0
SPy1449 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	152.5	172.5	27.4	282.9	192.2
SPy1450 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	142.6	114.6	7.8	128.4	86.7
SPy1451 Structural protein (Prophage 370.3)	Φ370.3 (MF3)	149.4	48.2	13.6	70.6	58.5
SPy1452 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	87.3	133.3	10.6	48.8	45.2
SPy1453 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	108.8	83.3	33.1	130.0	91.5
SPy1454 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	103.6	16.6	22.9	89.6	104.6
SPy1455 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	128.5	17.1	14.7	113.1	91.4
SPy1456 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	137.0	25.5	25.8	36.3	34.2
SPy1457 Structural protein (Prophage 370.3)	Φ370.3 (MF3)	244.4	32.3	42.2	74.7	69.9
SPy1459 cell division protein MukB, putative (Prophage 370.3)	Φ370.3 (MF3)	100.0	2.5	5.0	5.9	6.1
SPy1460 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	146.2	31.9	31.4	153.4	119.8
SPy1461 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	166.7	121.2	29.3	102.5	152.7
SPy1462 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	156.6	62.7	32.7	194.6	117.3
SPy1463 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	164.3	6.9	8.2	216.4	174.3
SPy1464 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	111.7	6.7	13.0	98.8	76.4
SPy1465 Structural protein (Prophage 370.3)	Φ370.3 (MF3)	174.9	12.0	13.2	185.8	59.2
SPy1466 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	55.5	2.6	7.3	44.7	35.3
Hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	127.3	33.9	39.8	135.8	104.4
SPy1469 conserved hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	126.2	13.4	12.9	16.3	105.7

SPy1471 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	168.9	6.9	9.0	40.8	430.0
SPy1473 unique hypothetical, putative (Prophage 370.3)	Φ370.3 (MF3)	177.9	22.4	27.4	73.3	158.4
SPy1474 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	122.9	18.6	21.6	32.0	238.6
SPy1475 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	161.7	112.4	29.2	48.6	204.2
SPy1476 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	27.0	120.7	13.2	21.1	184.2
SPy1477 35 protein, putative (Prophage 370.3)	Φ370.3 (MF3)	118.0	105.1	20.0	32.0	250.0
SPy1484 excisionase-related protein (Prophage 370.3)	Φ370.3 (MF3)	85.3	115.2	15.9	146.7	217.1
SPy1485 repressor protein, putative (Prophage 370.3)	Φ370.3 (MF3)	8.6	97.3	8.5	16.9	11.2
SPy1486 repressor protein (Prophage 370.3)	Φ370.3 (MF3)	20.3	75.6	17.8	29.2	28.7
SPy1487 hypothetical protein (Prophage 370.3)	Φ370.3 (MF3)	22.0	66.5	18.3	29.5	27.4
SPy1488 integrase 2 (Prophage 370.3)	Φ370.3 (MF3)	110.2	103.8	14.4	29.4	98.9
SPy2122 integrase-like protein 4, putative (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	81.5	273.2	100.6	371.2	146.1
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	29.8	182.3	20.4	184.8	30.4
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	166.3	261.5	173.1	423.7	348.5
SPy2125 repressor protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	167.7	274.8	139.1	382.2	254.6
SPy2126 DNA-binding protein, putative (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	27.3	159.7	22.5	186.4	28.9
SPy2127 antirepressor (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	18.3	119.4	5.2	6.8	18.5
SPy2128 conserved hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	23.4	117.3	13.7	21.9	15.8
SPy2129 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	12.7	121.7	10.1	16.7	12.9
SPy2130 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	31.9	96.5	27.2	158.4	62.6
SPy2131 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	15.0	196.8	11.3	21.4	14.4
SPy2132 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	21.3	245.4	17.0	258.9	17.7

SPy2133 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	13.2	134.7	10.7	161.9	14.9
SPy2134 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	19.3	130.0	20.0	143.6	15.7
SPy2135 putative replication protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	59.1	153.9	47.8	249.7	77.2
SPy2136 putative DNA primase (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	11.1	86.2	8.7	103.3	8.8
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	15.6	125.7	17.7	122.8	20.3
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	26.6	173.5	15.9	170.1	24.5
SPy2140 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	23.8	114.1	16.9	92.7	18.4
SPy2142 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	38.3	223.0	29.5	245.5	30.5
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	25.2	106.2	23.4	112.4	27.7
SPy2144 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	43.7	126.4	27.3	163.6	36.9
SPy2145 gp137, putative (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	29.1	154.8	33.5	213.4	21.1
Hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	23.2	106.5	14.2	31.1	22.3
SPy2147 hypothetical protein (Prophage 370.4)	Φ370.4 (truncated phage - no toxin)	14.3	99.6	10.2	27.3	13.7
Hypothetical protein	Φ370.4 (truncated phage - no toxin)	60.4	258.3	33.2	60.8	16.5
M5005_SPy_0995_paratox	Φ5005.1 (SpeA2)	119.3	63.0	42.9	94.3	83.8
M5005_SPy_0996_pyrogenic Exotoxin A2	Φ5005.1 (SpeA2)	80.2	10.6	10.4	29.8	8.6
M5005_SPy_0997_phage protein	Φ5005.1 (SpeA2)	113.5	6.5	10.4	18.0	11.6
M5005_SPy_0998_phage protein	Φ5005.1 (SpeA2)	65.3	2.3	5.7	14.4	4.8
M5005_SPy_0999_phage protein	Φ5005.1 (SpeA2)	115.7	7.5	8.2	14.0	10.6

M5005_SPy_1000_phage protein	Φ5005.1 (SpeA2)	74.9	8.0	11.1	16.3	9.5
M5005_SPy_1001_phage-associated cell wall hydrolase	Φ5005.1 (SpeA2)	142.9	16.5	21.4	29.5	16.1
M5005_SPy_1002_N-acetylmuramoyl-L-alanine amidase	Φ5005.1 (SpeA2)	109.0	4.3	9.2	11.7	68.2
M5005_SPy_1003_phage protein	Φ5005.1 (SpeA2)	76.5	7.2	7.4	14.8	4.0
M5005_SPy_1004_phage protein	Φ5005.1 (SpeA2)	63.4	4.8	8.7	7.5	4.9
M5005_SPy_1005_phage protein	Φ5005.1 (SpeA2)	109.2	4.7	7.6	18.0	10.4
M5005_SPy_1006_phage structural protein	Φ5005.1 (SpeA2)	164.7	5.4	9.3	17.0	8.4
M5005_SPy_1007_phage protein	Φ5005.1 (SpeA2)	89.8	4.2	8.0	13.2	8.0
M5005_SPy_1008_hypothetical protein	Φ5005.1 (SpeA2)	95.6	5.2	7.2	14.8	7.3
M5005_SPy_1009_phage protein	Φ5005.1 (SpeA2)	70.6	4.8	7.7	11.8	8.0
M5005_SPy_1010_phage protein	Φ5005.1 (SpeA2)	121.8	2.7	9.5	7.9	4.8
M5005_SPy_1011_phage protein	Φ5005.1 (SpeA2)	87.3	6.0	8.0	15.0	7.4
M5005_SPy_1012_antigen A	Φ5005.1 (SpeA2)	82.0	5.3	8.5	14.9	8.3
M5005_SPy_1013_antigen B	Φ5005.1 (SpeA2)	139.5	7.2	10.8	14.2	11.2
M5005_SPy_1014_antigen C	Φ5005.1 (SpeA2)	117.1	15.1	17.3	21.6	14.2
M5005_SPy_1015_phage protein	Φ5005.1 (SpeA2)	130.1	5.0	7.6	12.9	7.4
M5005_SPy_1016_phage protein	Φ5005.1 (SpeA2)	113.3	11.0	17.7	28.7	19.1
M5005_SPy_1017_phage protein	Φ5005.1 (SpeA2)	113.6	17.8	15.0	27.5	17.9
M5005_SPy_1018_phage protein	Φ5005.1 (SpeA2)	92.5	12.7	20.0	45.2	42.4
M5005_SPy_1019_phage scaffold protein	Φ5005.1 (SpeA2)	98.1	18.6	20.9	25.9	16.3
M5005_SPy_1020_phage protein	Φ5005.1 (SpeA2)	154.2	111.8	53.8	140.4	167.2
M5005_SPy_1021_phage protein	Φ5005.1 (SpeA2)	187.2	9.4	9.5	16.2	9.3
M5005_SPy_1022_portal protein	Φ5005.1 (SpeA2)	160.7	13.7	16.0	21.8	13.1
M5005_SPy_1023_terminase large subunit	Φ5005.1 (SpeA2)	90.4	16.8	16.6	20.7	14.2
M5005_SPy_1024_phage protein	Φ5005.1 (SpeA2)	76.7	4.9	6.6	8.9	6.6
M5005_SPy_1025_phage encoded transcriptional regulator, ArpU family	Φ5005.1 (SpeA2)	49.8	74.3	61.1	16.9	53.4
M5005_SPy_1026_phage protein	Φ5005.1 (SpeA2)	68.7	8.4	85.1	19.0	12.3
M5005_SPy_1027_phage protein	Φ5005.1 (SpeA2)	65.4	9.6	73.5	17.5	8.3
M5005_SPy_1028_phage protein	Φ5005.1 (SpeA2)	206.5	190.7	179.2	160.2	41.6
M5005_SPy_1029_phage protein	Φ5005.1 (SpeA2)	82.0	84.3	84.7	81.1	162.1
M5005_SPy_1030_phage protein	Φ5005.1 (SpeA2)	104.5	133.5	157.4	139.4	31.2

M5005_SPy_1031_phage protein	Φ5005.1 (SpeA2)	140.9	121.9	176.2	190.7	9.6
M5005_SPy_1032_phage protein	Φ5005.1 (SpeA2)	104.1	131.0	128.5	117.1	111.6
M5005_SPy_1033_phage protein	Φ5005.1 (SpeA2)	61.7	74.7	74.1	105.7	85.1
M5005_SPy_1034_phage protein	Φ5005.1 (SpeA2)	105.2	122.3	123.3	25.9	70.7
M5005_SPy_1035_phage protein	Φ5005.1 (SpeA2)	189.4	210.9	170.9	77.7	211.8
M5005_SPy_1036_phage single-strand DNA binding protein	Φ5005.1 (SpeA2)	79.6	94.3	114.8	100.3	97.2
M5005_SPy_1037_phage single-strand DNA binding protein	Φ5005.1 (SpeA2)	132.8	151.2	209.6	18.6	187.3
M5005_SPy_1038_phage protein	Φ5005.1 (SpeA2)	63.0	70.1	69.0	46.9	71.4
M5005_SPy_1039_phage protein	Φ5005.1 (SpeA2)	195.2	243.7	322.2	21.3	404.3
M5005_SPy_1040_phage protein	Φ5005.1 (SpeA2)	87.3	92.6	11.7	12.9	84.8
M5005_SPy_1041_phage protein	Φ5005.1 (SpeA2)	115.7	98.6	114.3	15.2	118.8
M5005_SPy_1042_phage replication protein	Φ5005.1 (SpeA2)	96.5	126.2	5.0	12.2	139.6
M5005_SPy_1043_phage protein	Φ5005.1 (SpeA2)	37.8	1.7	12.2	5.9	32.7
M5005_SPy_1044_phage protein	Φ5005.1 (SpeA2)	43.9	32.4	5.6	12.2	6.2
M5005_SPy_1045_transcriptional regulator	Φ5005.1 (SpeA2)	56.0	57.4	7.4	71.7	64.7
M5005_SPy_1046_phage protein	Φ5005.1 (SpeA2)	55.9	10.6	21.7	22.1	12.0
M5005_SPy_1047_phage protein	Φ5005.1 (SpeA2)	62.6	13.1	16.2	30.8	27.3
M5005_SPy_1048_phage protein	Φ5005.1 (SpeA2)	66.5	6.6	7.8	12.9	7.0
M5005_SPy_1049_phage protein	Φ5005.1 (SpeA2)	84.0	52.4	13.0	43.6	104.3
M5005_SPy_1050_phage transcriptional repressor	Φ5005.1 (SpeA2)	35.3	39.1	6.4	42.5	44.2
M5005_SPy_1051_phage protein	Φ5005.1 (SpeA2)	49.5	10.3	8.6	17.2	14.7
M5005_SPy_1052_phi5005.1 integrase	Φ5005.1 (SpeA2)	89.5	61.0	8.1	87.0	72.6
M5005_SPy_1414_phage protein	Φ5005.3 (Sda1)	126.6	64.1	12.3	37.8	98.4
M5005_SPy_1415_Phage-encoded streptodornase Sda1	Φ5005.3 (Sda1)	67.7	4.5	7.1	14.2	7.9
M5005_SPy_1416_phage-associated cell wall hydrolase	Φ5005.3 (Sda1)	114.9	66.1	52.7	100.4	10.7
M5005_SPy_1417_phage protein	Φ5005.3 (Sda1)	84.4	18.8	17.1	77.8	21.0
M5005_SPy_1419_phage protein	Φ5005.3 (Sda1)	76.3	6.3	10.4	14.1	10.3
M5005_SPy_1420_phage protein	Φ5005.3 (Sda1)	64.6	6.9	78.7	15.1	112.2
M5005_SPy_1422_phage protein	Φ5005.3 (Sda1)	113.3	3.9	7.5	14.0	6.8
M5005_SPy_1423_hyaluronoglucosaminidase	Φ5005.3 (Sda1)	98.3	3.5	6.8	13.0	8.9
M5005_SPy_1425_phage protein	Φ5005.3 (Sda1)	96.4	8.5	12.3	16.6	106.5
M5005_SPy_1426_phage protein	Φ5005.3 (Sda1)	94.6	8.2	8.3	13.6	87.1

M5005_SPy_1428_phage protein	Φ5005.3 (Sda1)	48.9	7.1	11.1	19.7	57.2
M5005_SPy_1429_phage protein	Φ5005.3 (Sda1)	104.0	9.7	12.7	17.2	85.4
M5005_SPy_1430_phage protein	Φ5005.3 (Sda1)	83.7	3.6	6.1	10.4	113.4
M5005_SPy_1431_phage protein	Φ5005.3 (Sda1)	135.8	4.7	10.4	29.2	194.6
M5005_SPy_1432_phage protein	Φ5005.3 (Sda1)	93.7	4.6	10.1	10.9	88.1
M5005_SPy_1433_phage protein	Φ5005.3 (Sda1)	66.7	10.8	14.5	10.0	77.9
M5005_SPy_1435_phage scaffold protein	Φ5005.3 (Sda1)	119.4	8.1	16.4	30.3	196.8
M5005_SPy_1436_phage protein	Φ5005.3 (Sda1)	151.4	92.9	8.7	76.9	133.8
M5005_SPy_1437_hypothetical protein	Φ5005.3 (Sda1)	98.4	5.6	10.4	19.9	74.4
M5005_SPy_1438_phage protein	Φ5005.3 (Sda1)	61.5	6.3	9.1	9.5	58.0
M5005_SPy_1439_portal protein	Φ5005.3 (Sda1)	79.8	13.1	9.8	7.7	66.0
M5005_SPy_1440_terminase large subunit	Φ5005.3 (Sda1)	89.0	3.7	5.9	13.5	96.3
M5005_SPy_1441_phage terminase small subunit	Φ5005.3 (Sda1)	115.9	9.0	6.2	10.8	132.6
M5005_SPy_1442_phage transcriptional activator	Φ5005.3 (Sda1)	74.3	111.9	5.6	11.5	148.0
M5005_SPy_1443_phage protein	Φ5005.3 (Sda1)	79.1	5.9	17.4	33.0	13.9
M5005_SPy_1444_adenine-specific methyltransferase	Φ5005.3 (Sda1)	75.5	3.4	4.5	7.5	6.8
M5005_SPy_1445_phage protein	Φ5005.3 (Sda1)	120.5	4.2	6.5	13.3	6.3
M5005_SPy_1447_phage-related DNA helicase	Φ5005.3 (Sda1)	146.1	59.1	55.9	101.8	177.1
M5005_SPy_1448_hypothetical protein	Φ5005.3 (Sda1)	141.7	10.2	13.1	17.0	251.5
M5005_SPy_1449_DNA primase	Φ5005.3 (Sda1)	63.4	3.3	4.4	9.7	73.6
M5005_SPy_1451_phage protein	Φ5005.3 (Sda1)	103.8	6.3	8.4	9.5	146.3
M5005_SPy_1452_phage protein	Φ5005.3 (Sda1)	136.6	15.8	22.2	26.0	17.4
M5005_SPy_1453_phage protein	Φ5005.3 (Sda1)	157.1	3.4	7.3	13.1	153.7
M5005_SPy_1454_phage protein	Φ5005.3 (Sda1)	147.2	10.3	16.0	16.6	179.2
M5005_SPy_1455_phage protein	Φ5005.3 (Sda1)	141.2	18.9	23.0	24.0	108.4
M5005_SPy_1456_phage protein	Φ5005.3 (Sda1)	193.7	23.7	26.0	31.0	213.0
M5005_SPy_1457_phage protein	Φ5005.3 (Sda1)	84.9	8.1	12.3	13.8	124.2
M5005_SPy_1459_phage protein	Φ5005.3 (Sda1)	160.4	29.4	10.1	85.6	192.2
M5005_SPy_1460_phage protein	Φ5005.3 (Sda1)	69.1	2.0	6.4	5.6	6.7
M5005_SPy_1461_phage protein	Φ5005.3 (Sda1)	95.2	10.9	15.8	22.1	13.1
M5005_SPy_1462_phage protein	Φ5005.3 (Sda1)	61.7	0.3	9.1	12.2	5.6
M5005_SPy_1463_phage protein	Φ5005.3 (Sda1)	74.2	4.5	7.2	12.8	7.0

M5005_SPy_1464_phage transcriptional regulator, Cro/CI family	Φ5005.3 (Sda1)	109.6	14.6	17.8	51.9	42.5
M5005_SPy_1465_phage protein	Φ5005.3 (Sda1)	108.2	4.0	7.1	32.0	6.4
M5005_SPy_1466_phage protein	Φ5005.3 (Sda1)	71.4	14.8	12.3	25.7	21.3
M5005_SPy_1467_phi5005.3 integrase	Φ5005.3 (Sda1)	92.3	4.3	6.4	8.0	10.4
SPyM3_0694_phage protein	Φ315.1 (no toxin)	6.3	4.9	7.3	14.1	7.5
SPyM3_0695_phage protein	Φ315.1 (no toxin)	5.6	2.5	5.5	5.6	5.3
SPyM3_0732_phage protein	Φ315.1 (no toxin)	35.1	27.4	30.4	35.7	37.8
SPyM3_0733_phage protein	Φ315.1 (no toxin)	15.7	14.9	14.6	19.3	18.2
SPyM3_0734_phage protein	Φ315.1 (no toxin)	43.0	20.2	124.9	52.3	39.2
SPyM3_0735_phage protein	Φ315.1 (no toxin)	26.3	9.3	100.5	24.7	28.6
SPyM3_0736_putative repressor C1	Φ315.1 (no toxin)	7.3	2.0	55.3	15.7	8.2
SPyM3_0920_streptococcal superantigen A (SSA)	Φ315.2 (SSA)	68.6	65.2	54.0	110.0	332.7
SPyM3_0921_phage protein	Φ315.2 (SSA)	24.0	26.7	18.8	34.2	178.0
SPyM3_0922_phage-associated cell wall hydrolase	Φ315.2 (SSA)	155.4	139.0	124.3	97.3	99.8
SPyM3_0928	Φ315.2 (SSA)	60.5	194.4	63.1	89.7	152.1
SPyM3_0931	Φ315.2 (SSA)	4.8	3.6	7.7	9.8	128.5
SPyM3_0938	Φ315.2 (SSA)	16.0	12.6	13.0	23.0	150.5
SPyM3_0939	Φ315.2 (SSA)	72.8	37.4	35.1	79.0	534.8
SPyM3_0941	Φ315.2 (SSA)	34.8	27.6	32.0	34.1	87.6
SPyM3_0942	Φ315.2 (SSA)	59.3	25.8	34.3	50.0	159.4
SPyM3_0943	Φ315.2 (SSA)	15.9	9.9	13.6	21.4	110.2
SPyM3_0944	Φ315.2 (SSA)	78.3	61.1	23.8	66.6	247.6
SPyM3_0952	Φ315.2 (SSA)	10.7	15.9	16.4	21.3	14.4
SPyM3_0954	Φ315.2 (SSA)	141.5	183.3	145.6	246.3	113.7
SPyM3_0955	Φ315.2 (SSA)	37.6	33.8	21.7	27.9	33.6
SPyM3_0956	Φ315.2 (SSA)	26.0	22.1	19.9	30.9	26.3
SPyM3_0957	Φ315.2 (SSA)	75.3	61.4	49.1	65.8	57.5
SPyM3_0971	Φ315.2 (SSA)	9.9	5.0	6.4	15.5	17.3
SPyM3_0972	Φ315.2 (SSA)	99.1	22.3	20.3	46.0	39.4
SPyM3_0973_phage protein	Φ315.2 (SSA)	73.8	12.7	12.3	24.9	18.6
SPyM3_0974_phage protein	Φ315.2 (SSA)	17.9	8.3	12.6	21.8	17.5
SPyM3_0975	Φ315.2 (SSA)	7.5	5.8	6.9	11.2	7.6

SPyM3_1094_paratox	Φ315.3 (MF4)	120.9	92.7	46.5	55.5	107.4
SPyM3_1095_mitogenic factor 4 or spd4	Φ315.3 (MF4)	17.6	15.6	21.2	28.1	23.2
SPyM3_1097_phage holin	Φ315.3 (MF4)	21.9	90.5	22.8	30.5	27.8
SPyM3_1098	Φ315.3 (MF4)	51.1	37.6	17.8	21.8	58.2
SPyM3_1101	Φ315.3 (MF4)	9.4	48.2	12.0	22.8	6.0
SPyM3_1110	Φ315.3 (MF4)	54.3	14.7	20.3	97.0	75.7
SPyM3_1116	Φ315.3 (MF4)	81.9	59.8	50.0	86.4	155.4
SPyM3_1126	Φ315.3 (MF4)	29.1	104.2	18.3	25.9	30.1
SPyM3_1127	Φ315.3 (MF4)	8.9	120.1	11.5	21.9	19.3
SPyM3_1129	Φ315.3 (MF4)	10.9	75.7	6.8	12.2	10.6
SPyM3_1130	Φ315.3 (MF4)	32.9	110.3	27.5	41.2	36.1
SPyM3_1131	Φ315.3 (MF4)	7.2	85.1	7.3	12.8	9.6
SPyM3_1204_streptococcal phospholipase A2	Φ315.4 (SpeK/Sla)	28.0	19.0	16.4	38.7	33.6
SPyM3_1205_SpeK	Φ315.4 (SpeK/Sla)	6.9	7.5	8.5	17.0	10.3
SPyM3_1228	Φ315.4 (SpeK/Sla)	30.6	15.1	23.9	49.5	44.3
SPyM3_1237	Φ315.4 (SpeK/Sla)	52.9	13.3	198.9	27.5	73.5
SPyM3_1238	Φ315.4 (SpeK/Sla)	67.5	20.9	246.1	37.4	105.7
SPyM3_1239	Φ315.4 (SpeK/Sla)	13.5	129.0	148.5	111.5	23.5
SPyM3_1242	Φ315.4 (SpeK/Sla)	44.2	130.5	4.8	26.6	32.2
SPyM3_1245	Φ315.4 (SpeK/Sla)	28.0	21.9	16.0	35.2	777.1
SPyM3_1247	Φ315.4 (SpeK/Sla)	14.0	9.0	15.6	24.7	35.7
SPyM3_1253	Φ315.4 (SpeK/Sla)	48.9	61.5	12.3	48.7	75.7
SPyM3_1255	Φ315.4 (SpeK/Sla)	39.5	26.7	26.6	48.0	47.1
SPyM3_1256	Φ315.4 (SpeK/Sla)	51.9	46.3	6.5	94.4	232.3
SPyM3_1257	Φ315.4 (SpeK/Sla)	35.8	8.5	8.6	36.6	68.0
SPyM3_1258	Φ315.4 (SpeK/Sla)	12.0	20.0	136.9	17.7	14.8
SPyM3_1259	Φ315.4 (SpeK/Sla)	18.1	14.6	16.9	27.9	21.7
SPyM3_1260	Φ315.4 (SpeK/Sla)	5.2	3.3	7.8	32.7	8.9
SPyM3_1261_phage antirepressor protein	Φ315.4 (SpeK/Sla)	155.2	18.8	23.1	36.7	137.6
SPyM3_1262	Φ315.4 (SpeK/Sla)	73.8	25.1	18.7	64.8	22.1
SPyM3_1263	Φ315.4 (SpeK/Sla)	10.6	5.2	5.6	13.9	9.5
SPyM3_1265	Φ315.4 (SpeK/Sla)	19.6	12.2	10.9	19.3	13.2

SPyM3_1266_phage integrase	Φ315.4 (SpeK/Sla)	19.4	10.5	16.0	34.2	31.3
SPyM3_1302	Φ315.5 (SpeA3)	160.0	5.3	6.9	11.6	12.1
SPyM3_1303	Φ315.5 (SpeA3)	153.9	30.0	29.6	53.3	39.3
SPyM3_1304	Φ315.5 (SpeA3)	112.2	10.9	8.4	15.7	17.3
SPyM3_1305	Φ315.5 (SpeA3)	101.8	20.0	17.3	35.7	31.8
SPyM3_1306	Φ315.5 (SpeA3)	199.8	13.8	11.8	25.1	22.3
SPyM3_1307_phage holin	Φ315.5 (SpeA3)	115.5	27.8	33.9	54.2	74.0
SPyM3_1308	Φ315.5 (SpeA3)	67.3	4.4	5.3	11.9	7.6
SPyM3_1309	Φ315.5 (SpeA3)	80.6	3.7	6.8	10.3	7.7
SPyM3_1310	Φ315.5 (SpeA3)	201.8	6.9	13.3	14.0	11.1
SPyM3_1311	Φ315.5 (SpeA3)	157.1	26.0	24.3	33.5	30.1
SPyM3_1312	Φ315.5 (SpeA3)	93.7	10.2	18.3	25.7	16.6
SPyM3_1313	Φ315.5 (SpeA3)	155.3	13.6	21.5	18.2	11.6
SPyM3_1314	Φ315.5 (SpeA3)	168.3	32.9	53.4	77.1	64.9
SPyM3_1315	Φ315.5 (SpeA3)	131.7	14.7	14.9	24.2	17.0
SPyM3_1316	Φ315.5 (SpeA3)	144.4	19.0	20.6	32.4	27.5
SPyM3_1317	Φ315.5 (SpeA3)	164.2	5.7	8.5	14.0	11.8
SPyM3_1318	Φ315.5 (SpeA3)	145.9	14.7	17.7	22.2	17.2
SPyM3_1319	Φ315.5 (SpeA3)	178.9	11.8	22.9	14.2	9.0
SPyM3_1320	Φ315.5 (SpeA3)	106.7	16.4	10.7	32.5	17.5
SPyM3_1321	Φ315.5 (SpeA3)	133.3	7.3	9.2	19.1	14.6
SPyM3_1322	Φ315.5 (SpeA3)	148.1	14.3	22.2	27.5	21.3
SPyM3_1323	Φ315.5 (SpeA3)	127.6	20.1	18.5	26.9	20.4
SPyM3_1325	Φ315.5 (SpeA3)	258.8	28.4	47.2	75.7	63.1
SPyM3_1326	Φ315.5 (SpeA3)	112.5	10.0	12.5	19.9	11.9
SPyM3_1327	Φ315.5 (SpeA3)	158.0	3.5	5.6	7.0	6.0
SPyM3_1328	Φ315.5 (SpeA3)	105.5	7.8	8.3	11.9	8.2
SPyM3_1329	Φ315.5 (SpeA3)	104.3	4.5	10.3	14.1	9.8
SPyM3_1332	Φ315.5 (SpeA3)	7.9	179.2	7.9	13.8	224.8
SPyM3_1333	Φ315.5 (SpeA3)	11.6	4.1	7.0	13.4	12.3
SPyM3_1338	Φ315.5 (SpeA3)	16.5	15.8	10.6	99.2	13.4
SPyM3_1339	Φ315.5 (SpeA3)	26.4	11.6	13.3	147.0	8.5

SPyM3_1347	Φ315.5 (SpeA3)	19.2	21.2	83.0	70.5	68.7
SPyM3_1348	Φ315.5 (SpeA3)	12.8	51.3	55.2	14.1	10.2
SPyM3_1349_cro-like repressor	Φ315.5 (SpeA3)	16.9	12.8	11.2	25.7	22.3
SPyM3_1350_cI-like repressor	Φ315.5 (SpeA3)	20.0	15.4	18.6	16.5	14.5
SPyM3_1351_cI-like repressor	Φ315.5 (SpeA3)	5.0	55.5	19.7	15.4	8.4
SPyM3_1352	Φ315.5 (SpeA3)	34.9	29.5	39.6	33.8	22.2
SPyM3_1353	Φ315.5 (SpeA3)	18.7	11.0	13.9	14.3	11.2
SPyM3_1408_paratox	Φ315.6 (Sdn)	35.2	37.7	94.5	39.5	24.3
SPyM3_1409_SdaD (Sdn)	Φ315.6 (Sdn)	31.2	21.9	19.5	32.2	22.8
SPyM3_1410_phage protein	Φ315.6 (Sdn)	27.5	20.7	38.8	38.8	38.5
SPyM3_1415_phage protein	Φ315.6 (Sdn)	167.9	262.9	176.6	213.2	468.9
SPyM3_1419_phage endopeptidase	Φ315.6 (Sdn)	141.7	8.1	15.5	20.8	190.3
SPyM3_1420	Φ315.6 (Sdn)	144.5	25.9	18.7	34.9	157.8
SPyM3_1421_phage tail protein	Φ315.6 (Sdn)	131.8	27.8	27.3	18.6	119.2
SPyM3_1422	Φ315.6 (Sdn)	141.2	15.0	21.0	20.6	142.9
SPyM3_1423	Φ315.6 (Sdn)	147.2	5.6	10.8	17.4	263.5
SPyM3_1424	Φ315.6 (Sdn)	204.2	22.0	30.0	48.0	161.4
SPyM3_1425	Φ315.6 (Sdn)	147.9	30.3	33.6	58.4	175.9
SPyM3_1426	Φ315.6 (Sdn)	119.1	38.1	28.5	43.8	134.9
SPyM3_1427	Φ315.6 (Sdn)	112.0	9.9	18.0	20.2	109.9
SPyM3_1428	Φ315.6 (Sdn)	94.2	4.0	7.5	9.9	121.7
SPyM3_1429	Φ315.6 (Sdn)	133.9	12.3	13.3	18.1	267.3
SPyM3_1430	Φ315.6 (Sdn)	128.2	16.3	26.3	45.3	166.7
SPyM3_1432	Φ315.6 (Sdn)	72.3	5.0	8.2	18.6	95.3
SPyM3_1433	Φ315.6 (Sdn)	119.1	6.9	7.6	14.1	170.8
SPyM3_1434	Φ315.6 (Sdn)	123.8	6.3	9.2	7.2	129.8
SPyM3_1435	Φ315.6 (Sdn)	104.0	5.4	9.6	17.9	155.6
SPyM3_1437	Φ315.6 (Sdn)	116.6	105.1	33.3	40.9	126.6
SPyM3_1438	Φ315.6 (Sdn)	92.4	14.5	17.7	31.9	204.4
SPyM3_1439	Φ315.6 (Sdn)	72.1	8.3	15.2	26.2	86.1
SPyM3_1440	Φ315.6 (Sdn)	75.0	4.4	8.5	12.0	168.7
SPyM3_1441	Φ315.6 (Sdn)	137.9	8.0	9.6	18.6	230.7

SPyM3_1443	Φ315.6 (Sdn)	214.8	28.4	46.7	73.3	156.7
SPyM3_1444	Φ315.6 (Sdn)	27.2	12.5	13.5	18.8	126.3
SPyM3_1445	Φ315.6 (Sdn)	15.5	3.0	4.8	4.9	46.9
SPyM3_1446	Φ315.6 (Sdn)	119.8	12.1	16.3	22.6	130.5
SPyM3_1447	Φ315.6 (Sdn)	122.3	6.6	8.5	16.0	105.4
SPyM3_1449	Φ315.6 (Sdn)	78.1	2.7	6.3	9.3	70.9
SPyM3_1450	Φ315.6 (Sdn)	6.5	3.9	6.7	13.3	9.0
SPyM3_1451	Φ315.6 (Sdn)	129.0	19.2	11.5	67.2	144.8
SPyM3_1453	Φ315.6 (Sdn)	11.0	6.7	9.8	13.4	11.9
SPyM3_1454	Φ315.6 (Sdn)	38.3	9.5	12.0	47.4	11.8
SPyM3_1456	Φ315.6 (Sdn)	64.8	5.6	11.9	24.8	289.4
SPyM3_1457	Φ315.6 (Sdn)	100.3	8.5	11.9	14.4	13.2
SPyM3_1458_phage integrase	Φ315.6 (Sdn)	22.8	14.8	19.6	39.8	41.1
SPyM18_0343_Phage protein	Φ8232.1 (SpeA)	24.2	13.7	11.8	24.8	28.4
SPyM18_0352_phage protein	Φ8232.1 (SpeA)	7.1	6.1	7.8	14.2	7.7
SPyM18_0353_phage protein	Φ8232.1 (SpeA)	46.6	44.5	39.6	54.3	55.1
SPyM18_0355_phage protein	Φ8232.1 (SpeA)	47.1	43.3	40.6	231.0	66.4
SPyM18_0358_phage protein	Φ8232.1 (SpeA)	14.8	8.2	13.4	17.1	18.8
SPyM18_0393_SpeA	Φ8232.1 (SpeA)	69.9	23.6	27.9	35.5	21.9
SPyM18_0394_paratox	Φ8232.1 (SpeA)	173.9	55.4	40.3	120.1	123.0
SPyM18_0736	Φ8232.2 (SpeC/MF2)	30.8	3.4	6.7	43.1	186.3
SPyM18_0740	Φ8232.2 (SpeC/MF2)	185.0	32.8	52.7	142.4	404.1
SPyM18_0742	Φ8232.2 (SpeC/MF2)	29.1	20.7	17.7	32.4	191.8
SPyM18_0744_phage protein	Φ8232.2 (SpeC/MF2)	10.3	8.3	9.8	15.2	173.7
SPyM18_0745	Φ8232.2 (SpeC/MF2)	12.6	7.3	10.5	19.0	130.9
SPyM18_0746	Φ8232.2 (SpeC/MF2)	12.7	5.9	9.8	15.8	95.2
SPyM18_0747	Φ8232.2 (SpeC/MF2)	5.5	1.8	5.5	5.7	93.1
SPyM18_0751	Φ8232.2 (SpeC/MF2)	12.8	9.8	15.9	29.7	321.7
SPyM18_0753	Φ8232.2 (SpeC/MF2)	44.8	22.2	43.6	132.5	241.0
SPyM18_0754_phage portal protein	Φ8232.2 (SpeC/MF2)	21.7	17.6	15.2	28.4	215.0
SPyM18_0755_prophage Clp protease-like protein	Φ8232.2 (SpeC/MF2)	6.6	4.0	11.9	9.2	106.9
SPyM18_0756_phage capsid protein	Φ8232.2 (SpeC/MF2)	12.7	12.8	12.5	24.3	353.5

SPyM18_0759	Φ8232.2 (SpeC/MF2)	10.8	7.2	11.7	16.7	133.0
SPyM18_0762_phage major tail protein	Φ8232.2 (SpeC/MF2)	47.7	36.6	46.3	74.5	65.6
SPyM18_1237_Paratox	Φ8232.3 (SpeL/M)	124.9	188.0	63.4	157.5	156.4
SPyM18_1238_SpeL	Φ8232.3 (SpeL/M)	23.5	99.1	29.4	95.0	34.6
SPyM18_1239_SpeM	Φ8232.3 (SpeL/M)	13.9	73.2	9.9	19.5	14.9
SPyM18_1242	Φ8232.3 (SpeL/M)	152.2	282.4	53.0	396.6	49.9
SPyM18_1243	Φ8232.3 (SpeL/M)	12.3	127.3	11.3	123.8	11.7
SPyM18_1244	Φ8232.3 (SpeL/M)	116.1	183.6	14.6	174.0	18.2
SPyM18_1255	Φ8232.3 (SpeL/M)	21.7	46.0	187.8	25.0	20.5
SPyM18_1256	Φ8232.3 (SpeL/M)	19.4	110.0	200.7	22.3	20.5
SPyM18_1258	Φ8232.3 (SpeL/M)	26.3	166.4	204.0	35.9	44.6
SPyM18_1260	Φ8232.3 (SpeL/M)	54.8	109.8	165.9	67.3	50.8
SPyM18_1265	Φ8232.3 (SpeL/M)	18.8	155.0	213.8	119.7	23.0
SPyM18_1266	Φ8232.3 (SpeL/M)	11.7	103.4	94.7	74.9	11.7
SPyM18_1268_phage major capsid protein	Φ8232.3 (SpeL/M)	67.3	134.4	210.1	73.4	74.4
SPyM18_1272	Φ8232.3 (SpeL/M)	5.1	3.3	7.2	10.1	5.4
SPyM18_1280	Φ8232.3 (SpeL/M)	24.0	14.0	20.2	37.1	29.6
SPyM18_1283	Φ8232.3 (SpeL/M)	23.9	15.1	16.3	20.6	15.5
SPyM18_1284	Φ8232.3 (SpeL/M)	8.6	7.3	9.6	16.1	151.5
SPyM18_1285	Φ8232.3 (SpeL/M)	14.3	17.4	19.9	22.8	15.4
SPyM18_1288	Φ8232.3 (SpeL/M)	18.4	131.6	11.6	22.5	17.1
SPyM18_1289	Φ8232.3 (SpeL/M)	11.6	82.6	8.5	15.3	9.8
SPyM18_1290	Φ8232.3 (SpeL/M)	23.0	66.1	16.9	9.5	22.4
SPyM18_1291	Φ8232.3 (SpeL/M)	25.1	202.5	19.8	36.6	30.4
SPyM18_1292	Φ8232.3 (SpeL/M)	25.4	168.5	17.8	21.2	15.9
SPyM18_1293	Φ8232.3 (SpeL/M)	48.5	151.5	36.3	53.6	54.4
SPyM18_1294	Φ8232.3 (SpeL/M)	17.8	95.0	12.5	21.8	22.9
SPyM18_1295	Φ8232.3 (SpeL/M)	9.9	94.8	7.8	32.6	23.7
SPyM18_1296	Φ8232.3 (SpeL/M)	12.2	224.5	11.5	18.5	12.4
SPyM18_1297	Φ8232.3 (SpeL/M)	25.8	218.4	38.0	67.5	70.7
SPyM18_1299	Φ8232.3 (SpeL/M)	84.2	101.8	56.0	121.6	98.4
SPyM18_1301	Φ8232.3 (SpeL/M)	77.7	87.7	13.1	29.1	8.7

SPyM18_1302	Φ8232.3 (SpeL/M)	97.3	106.7	9.5	54.9	40.6
SPyM18_1303	Φ8232.3 (SpeL/M)	89.7	117.5	9.3	134.0	83.7
SPyM18_1304	Φ8232.3 (SpeL/M)	27.5	29.8	26.7	38.1	31.3
SPyM18_1308_phage protein	Φ8232.3 (SpeL/M)	8.8	91.2	6.2	15.9	69.9
SPyM18_1460_phage minor tail protein	Φ8232.4 (MF3)	106.5	120.9	32.7	106.1	91.5
SPyM18_1461_HNH homing endonuclease	Φ8232.4 (MF3)	13.4	11.1	15.8	103.4	29.1
SPyM18_1462_phage minor tail protein	Φ8232.4 (MF3)	93.0	52.8	5.5	115.3	55.1
SPyM18_1487	Φ8232.4 (MF3)	30.9	10.4	14.7	28.4	35.6
SPyM18_1488	Φ8232.4 (MF3)	12.1	7.0	9.4	23.3	17.9
SPyM18_1490	Φ8232.4 (MF3)	106.5	4.1	4.5	39.7	151.1
SPyM18_1493	Φ8232.4 (MF3)	89.7	4.9	6.4	14.0	8.8
SPyM18_1494	Φ8232.4 (MF3)	44.7	35.7	15.3	22.5	254.3
SPyM18_1746_streptodornase D (Sda)	Φ8232.5 (Sda)	21.8	17.2	16.3	33.7	23.9
SPyM18_1747	Φ8232.5 (Sda)	10.9	8.1	10.6	19.5	13.4
SPyM18_1750_phage lysin	Φ8232.5 (Sda)	21.8	129.2	25.4	35.0	29.4
SPyM18_1752	Φ8232.5 (Sda)	104.2	32.4	20.9	119.4	31.3
SPyM18_1754	Φ8232.5 (Sda)	70.7	74.6	48.4	201.0	196.4
SPyM18_1755	Φ8232.5 (Sda)	36.6	120.9	10.9	122.7	109.6
SPyM18_1761	Φ8232.5 (Sda)	29.9	138.7	12.6	46.6	367.9
SPyM18_1766	Φ8232.5 (Sda)	11.7	194.3	10.6	28.7	27.3
SPyM18_1786	Φ8232.5 (Sda)	86.7	7.0	119.9	15.4	8.7
SPyM18_1793_phage protein	Φ8232.5 (Sda)	79.4	53.3	78.2	71.0	127.8
SPyM18_1799_phage protein	Φ8232.5 (Sda)	83.3	47.8	193.8	97.3	105.4
SPyM18_1801_DNA replication protein dnaC	Φ8232.5 (Sda)	56.2	50.9	160.8	98.8	102.9
SPyM18_1802_phage antirepressor protein	Φ8232.5 (Sda)	57.6	197.2	276.3	63.0	55.6
SPyM18_1803_DNA replication protein dnaD	Φ8232.5 (Sda)	29.0	15.2	25.0	49.7	37.1
SPyM18_1805_phage repressor protein	Φ8232.5 (Sda)	32.2	106.7	80.7	39.6	43.1
SPyM18_1806_chromosome segregation ATPase	Φ8232.5 (Sda)	16.5	140.3	232.2	18.6	13.7
Phi3396_01_putative integrase	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	7.8	8.4	11.5	18.1	8.2
Phi3396_02_hypothetical protein phi3396_02	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	25.3	12.0	15.3	30.9	21.4

Phi3396_03_hypothetical protein phi3396_03	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	57.1	21.3	18.7	40.3	19.8
Phi3396_04_putative repressor	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	5.3	3.6	7.3	14.3	7.7
Phi3396_05_hypothetical protein phi3396_05	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	5.2	5.5	8.3	16.7	9.7
Phi3396_06_hypothetical protein phi3396_06	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	1.7	2.5	7.7	12.3	5.4
Phi3396_07_hypothetical protein phi3396_07	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	7.6	5.2	9.0	18.4	10.4
Phi3396_08_putative antirepressor	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	6.1	3.9	8.1	16.3	7.7
Phi3396_09_hypothetical protein phi3396_09	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	5.2	1.8	4.2	5.3	6.1
Phi3396_10_hypothetical protein phi3396_10	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	12.2	11.1	11.6	12.2	8.6
Phi3396_11_hypothetical protein phi3396_11	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	18.8	22.1	23.2	24.5	17.5
Phi3396_12_hypothetical protein phi3396_12	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	13.0	7.3	7.9	20.3	9.4
Phi3396_14_hypothetical protein phi3396_14	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	7.4	5.1	9.4	9.6	10.1
Phi3396_15_putative single-strand binding protein 1	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	4.9	3.2	6.9	7.2	6.5
Phi3396_16_hypothetical protein phi3396_16	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	4.3	4.1	9.6	13.7	6.4
Phi3396_17_hypothetical protein phi3396_17	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	15.9	10.8	9.5	70.9	102.3
Phi3396_18_hypothetical protein phi3396_18	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.2	7.2	8.8	15.0	8.8
Phi3396_19_hypothetical protein phi3396_19	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	60.7	61.3	57.2	79.6	189.6

Phi3396_20_putative N-6 adenine-specific DNA methylase	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	0.4	1.6	8.4	12.4	6.6
Phi3396_21_hypothetical protein phi3396_21	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	18.6	17.8	20.9	37.7	151.8
Phi3396_22_hypothetical protein phi3396_22	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	3.7	6.2	6.3	12.5	7.3
Phi3396_23_hypothetical protein phi3396_23	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	25.0	16.7	24.1	33.6	28.4
Phi3396_24_putative immunity repressor protein	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	9.4	12.0	14.3	20.7	18.6
Phi3396_25_putative prohibitin	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	13.2	4.8	7.7	14.8	11.0
Phi3396_26_putative phage transcriptional activator	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	4.4	6.5	6.0	7.9	8.4
Phi3396_27_probable site-specific tyrosine recombinase xerc_like	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	24.2	20.1	16.4	35.9	33.3
Phi3396_28_hypothetical protein phi3396_28	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	2.6	1.5	5.1	6.8	9.3
Phi3396_29_hypothetical protein phi3396_29	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	14.5	13.4	12.2	13.2	10.0
Phi3396_30_putative endonuclease	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.8	15.3	17.8	17.2	12.5
Phi3396_31_putative terminase small subunit	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	49.0	31.6	34.5	42.2	47.1
Phi3396_32_putative terminase large subunit	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	57.0	29.2	25.0	34.8	32.0
Phi3396_33_hypothetical protein phi3396_33	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	8.6	11.0	10.7	15.5	8.1
Phi3396_34_putative portal protein	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.7	14.4	15.7	16.1	9.7
Phi3396_35_head maturation protease	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	7.1	3.4	6.9	6.9	6.6

Phi3396_36_major coat protein	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	5.4	7.0	8.6	13.8	7.7
Phi3396_37_hypothetical protein phi3396_37	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.0	5.0	7.1	12.5	8.1
Phi3396_38_hypothetical protein phi3396_38	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	24.3	14.3	15.6	26.6	26.0
Phi3396_40_hypothetical protein phi3396_40	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	22.2	7.1	15.3	33.1	25.8
Phi3396_41_hypothetical protein phi3396_41	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	8.3	10.0	10.5	14.9	9.5
Phi3396_43_hypothetical protein phi3396_43	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	9.9	5.3	7.5	14.3	142.4
Phi3396_44_hypothetical protein phi3396_44	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.4	11.8	12.8	19.5	15.8
Phi3396_46_hypothetical protein phi3396_46	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	7.9	3.8	5.6	11.8	8.0
Phi3396_47_phage endopeptidase	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	9.5	2.5	6.6	9.8	8.4
Phi3396_49_hypothetical protein phi3396_49	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	11.1	9.5	13.3	21.9	13.8
Phi3396_50_phage infection protein	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	84.8	49.2	10.8	49.2	95.5
Phi3396_51_hypothetical protein phi3396_51	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	15.7	135.3	12.1	152.4	24.0
Phi3396_52_hypothetical protein phi3396_52	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	14.5	77.8	12.7	1004.6	22.6
Phi3396_53_hypothetical protein phi3396_53	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	84.3	6.9	11.3	13.5	12.4
Phi3396_54_hypothetical protein phi3396_54	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	12.5	7.7	8.8	13.2	163.0
Phi3396_55_N-acetylmuramoyl-L-alanine amidase	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	58.3	15.2	15.4	874.7	208.6

Phi3396_56_phage-associated cell wall hydrolase	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	10.8	5.8	7.9	93.3	106.2
Phi3396_57_hypothetical protein phi3396_57	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	19.4	12.3	49.1	22.2	20.1
Phi3396_58_hypothetical protein phi3396_58	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	18.1	11.8	82.7	23.4	18.0
Phi3396_59_hypothetical protein phi3396_59	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	10.1	4.3	89.9	12.3	8.4
Phi3396_60_hypothetical protein phi3396_60	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	9.9	8.6	10.1	15.9	14.9
Phi3396_61_hypothetical protein phi3396_61	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	4.4	3.4	4.9	11.5	6.0
Phi3396_62_hypothetical protein phi3396_62	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	14.4	10.2	12.5	25.4	17.3
Phi3396_63_hypothetical protein phi3396_63	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	28.0	12.2	36.3	33.1	30.4
Phi3396_64_putative paratox	Φ3396 (*S. dysgalactiae subsp. equisimilis*)	47.0	14.4	13.5	25.7	28.3