

Position	Sequence number	Genus Average identity	SD	Accession (<i>S. pyogenes</i> str. Manfredo)	Annotation
1	59	99.56	0.77	YP_001127646.1	30S ribosomal protein S19
2	72	98.58	1.32	YP_001127667.1	30S ribosomal protein S11
3	304	98.08	1.37	YP_001128728.1	50S ribosomal protein L20
4	54	97.93	1.81	YP_001127641.1	30S ribosomal protein S10
5	62	97.89	1.83	YP_001127649.1	50S ribosomal protein L16
6	103	97.49	2.18	YP_001129139.1	50S ribosomal protein L13
7	63	97.37	2.47	YP_001127652.1	50S ribosomal protein L14
8	61	97.11	2.41	YP_001127648.1	30S ribosomal protein S3
9	396	97.1	1.80	YP_001129319.1	30S ribosomal protein S4
10	298	96.6	2.57	YP_001128714.1	50S ribosomal protein L27
11	65	96.43	2.64	YP_001127654.1	50S ribosomal protein L5
12	60	96.23	4.74	YP_001127647.1	50S ribosomal protein L22
13	368	96.13	2.31	YP_001127805.1	elongation factor G
14	58	96.11	3.71	YP_001127645.1	50S ribosomal protein L2
15	55	96.01	2.75	YP_001127642.1	50S ribosomal protein L3
16	147	95.77	2.11	YP_001128896.1	elongation factor Tu
17	76	95.77	2.14	YP_001127937.1	molecular chaperone DnaK
18	68	95.73	2.57	YP_001127659.1	30S ribosomal protein S5
19	366	95.45	2.79	YP_001127843.1	phosphoglycerate kinase
20	106	95.45	2.89	YP_001128168.1	BipA family GTPase
21	2	95.24	1.96	YP_001127607.1	GTP-dependent nucleic acid-binding protein EngD
22	370	95.19	3.29	YP_001127803.1	30S ribosomal protein S12
23	369	95.19	3.65	YP_001127804.1	30S ribosomal protein S7
24	57	95.11	4.89	YP_001127644.1	50S ribosomal protein L23
25	167	94.98	2.97	YP_001128766.1	F0F1 ATP synthase subunit beta
26	126	94.95	3.93	YP_001128787.1	phosphopyruvate hydratase
27	73	94.89	4.30	YP_001127668.1	DNA-directed RNA polymerase subunit alpha
28	97	94.82	3.29	YP_001127676.1	DNA-directed RNA polymerase subunit beta
29	66	94.31	3.60	YP_001127656.1	30S ribosomal protein S8
30	56	94.21	4.97	YP_001127643.1	50S ribosomal protein L4
31	358	94.07	4.02	YP_001127886.1	30S ribosomal protein S6
32	372	93.96	3.13	YP_001127727.1	adenylosuccinate synthetase
33	166	93.88	4.30	YP_001128768.1	F0F1 ATP synthase subunit alpha
34	98	93.88	3.84	YP_001127677.1	DNA-directed RNA polymerase subunit beta'
35	404	93.78	3.61	YP_001129342.1	inosine 5'-monophosphate dehydrogenase
36	43	93.72	3.59	YP_001127754.1	queuine tRNA-ribosyltransferase
37	211	93.66	3.68	YP_001129345.1	ABC transporter ATP-binding protein
38	253	93.58	3.44	YP_001128484.1	peptide chain release factor 1
39	319	93.44	4.72	YP_001129003.1	GTP-binding protein Era
40	64	93.37	3.73	YP_001127653.1	50S ribosomal protein L24
41	325	93.11	4.58	YP_001129053.1	ATP-dependent Clp protease proteolytic subunit
42	305	92.89	6.45	YP_001128730.1	translation initiation factor IF-3
43	90	92.49	4.69	YP_001127818.1	hypothetical protein SpyM50224
44	399	92.14	3.32	YP_001129325.1	tRNA-specific 2-thiouridylase MnmA
45	69	91.98	4.40	YP_001127661.1	50S ribosomal protein L15
46	383	91.94	3.87	YP_001129237.1	chaperonin GroEL
47	336	91.92	4.02	YP_001129091.1	GTP-binding protein EngA
48	262	91.58	5.19	YP_001128642.1	30S ribosomal protein S1
49	237	91.17	5.33	YP_001128438.1	GMP synthase
50	149	91.17	3.94	YP_001128270.1	recombination protein RecR
51	28	91.01	3.84	YP_001127948.1	(3R)-hydroxymyristoyl-ACP dehydratase
52	367	90.81	5.90	YP_001127806.1	glyceraldehyde-3-phosphate dehydrogenase
53	388	90.8	5.38	YP_001129272.1	recombinase A
54	387	90.61	6.50	YP_001129271.1	Spx family transcriptional regulator
55	373	90.48	5.83	YP_001129255.1	elongation factor Ts
56	265	90.01	5.04	YP_001128647.1	DNA topoisomerase IV subunit B
57	174	89.91	5.53	YP_001128551.1	phosphoglucosamine mutase
58	230	89.86	5.47	YP_001128909.1	lysyl-tRNA synthetase
59	14	89.83	6.38	YP_001128037.1	DNA-directed RNA polymerase subunit omega
60	242	89.77	6.21	YP_001128404.1	phosphate ABC transporter permease
61	133	89.58	6.78	YP_001128956.1	response regulator protein
62	320	89.4	6.33	YP_001129013.1	ribosome recycling factor
63	13	89.36	5.56	YP_001128036.1	guanylate kinase
64	67	89.33	5.52	YP_001127657.1	50S ribosomal protein L6
65	159	89.29	5.70	YP_001128320.1	methionine aminopeptidase
66	86	89.09	5.60	YP_001127814.1	ABC transporter ATP-binding protein
67	238	89.08	5.95	YP_001128442.1	signal recognition particle protein
68	84	88.96	6.15	YP_001127837.1	fructose-bisphosphate aldolase
69	179	88.88	7.07	YP_001128372.1	pyruvate kinase
70	364	88.82	5.25	YP_001127846.1	glutamine synthetase
71	234	88.82	5.67	YP_001128532.1	tRNA modification GTPase TrmE
72	130	88.69	8.96	YP_001128973.1	catabolite control protein A
73	346	88.65	6.60	YP_001127928.1	aspartyl/glutamyl-tRNA amidotransferase subunit A
74	169	88.64	7.74	YP_001128761.2	phenylalanyl-tRNA synthetase subunit alpha
75	144	88.6	7.06	YP_001128912.1	peptidase
76	220	88.53	5.92	YP_001127956.1	mannose-specific phosphotransferase system (PTS), IIB component
77	333	88.42	6.75	YP_001129085.1	transcription elongation factor GreA
78	236	88.18	7.96	YP_001128474.1	L-lactate dehydrogenase
79	226	87.74	7.10	YP_001127674.1	tyrosyl-tRNA synthetase
80	280	87.55	6.58	YP_001128530.1	50S ribosomal protein L10
81	386	87.48	6.44	YP_001129266.1	anaerobic ribonucleoside triphosphate reductase
82	239	87.36	5.18	YP_001128441.1	DNA-binding protein

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83	36	87.33	6.66	YP_001127969.1	transcription elongation factor NusA
84	394	87.09	6.98	YP_001129303.1	aspartyl-tRNA synthetase
85	206	87.04	8.60	YP_001127697.1	tRNA-dihydrouridine synthase
86	326	86.96	6.55	YP_001129071.1	ribosomal large subunit pseudouridine synthase B
87	223	86.96	6.31	YP_001127769.1	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
88	148	86.89	9.57	YP_001128895.1	triosephosphate isomerase
89	345	86.61	7.38	YP_001129116.1	GTP-binding protein YqeH
90	263	86.41	7.35	YP_001128644.1	branched-chain amino acid aminotransferase
91	274	86.31	6.12	YP_001128629.1	adenine phosphoribosyltransferase
92	77	86.31	7.01	YP_001127938.1	chaperone protein DnaJ
93	156	86.18	7.91	YP_001128308.1	uridine kinase
94	375	86.14	6.81	YP_001129164.1	prolyl-tRNA synthetase
95	241	86.02	7.76	YP_001128406.1	phosphate transporter ATP-binding protein
96	222	85.91	5.75	YP_001127768.1	UTP--glucose-1-phosphate uridylyltransferase 2
97	50	85.87	5.59	YP_001127634.1	Holliday junction DNA helicase RuvB
98	381	85.81	7.71	YP_001129175.1	GTP pyrophosphokinase
99	40	85.79	8.24	YP_001127973.1	ribosome-binding factor A
100	35	85.78	6.75	YP_001127967.1	tRNA (guanine-N(7)-)-methyltransferase
101	183	85.64	6.49	YP_001128473.1	DNA gyrase subunit A
102	356	85.54	11.11	YP_001127890.1	CorA-like Mg2+ transporter protein
103	196	85.47	7.13	YP_001129044.1	exodeoxyribonuclease
104	371	85.45	8.27	YP_001127801.1	pur operon repressor
105	158	85.34	6.55	YP_001128316.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
106	349	85.33	7.43	YP_001127903.1	preprotein translocase subunit SecA
107	281	85.32	6.41	YP_001128665.1	ribosome biogenesis GTP-binding protein YsxC
108	154	85.27	8.49	YP_001128283.1	superoxide dismutase
109	397	85.16	9.08	YP_001129321.1	replicative DNA helicase
110	113	85.13	8.05	YP_001128180.1	isoleucyl-tRNA synthetase
111	180	85.09	7.66	YP_001128374.1	glucosamine--fructose-6-phosphate aminotransferase
112	37	85.03	8.04	YP_001127970.1	hypothetical protein SpyM50380
113	120	84.99	7.53	YP_001128873.1	cell division ATP-binding protein
114	18	84.85	9.33	YP_001128045.1	response regulator protein
115	357	84.81	9.25	YP_001127887.1	single-stranded DNA-binding protein
116	23	84.79	6.94	YP_001127943.1	enoyl-ACP reductase
117	70	84.71	10.34	YP_001127662.1	preprotein translocase subunit SecY
118	250	84.69	6.78	YP_001128430.1	formate--tetrahydrofolate ligase
119	315	84.64	7.25	YP_001128982.1	SsrA-binding protein
120	182	84.63	9.81	YP_001128475.1	NADH oxidase
121	292	84.61	7.25	YP_001128694.1	tRNA (guanine-N(1)-)-methyltransferase
122	258	84.59	8.50	YP_001128518.1	spermidine/putrescine ABC transporter permease
123	395	84.44	7.91	YP_001129304.1	histidyl-tRNA synthetase
124	219	84.43	10.16	YP_001127954.1	PTS system mannose-specific transporter subunit IID
125	71	84.4	7.98	YP_001127663.1	adenylate kinase
126	151	84.38	8.72	YP_001128275.1	DEAD/DEAH box helicase
127	334	84.29	6.74	YP_001129088.1	UDP-N-acetylmuramate--L-alanine ligase
128	30	84.27	9.13	YP_001127951.1	acetyl-CoA carboxylase subunit alpha
129	12	84.25	7.67	YP_001128027.1	RNA methylase family protein
130	363	84.22	6.77	YP_001127851.1	DNA-binding/iron metalloprotein/AP endonuclease
131	139	84.22	9.37	YP_001128918.1	HPr kinase/phosphorylase
132	254	84.19	9.69	YP_001128485.1	thymidine kinase
133	29	84.11	8.91	YP_001127950.1	acetyl-CoA carboxylase subunit beta
134	374	84.1	9.20	YP_001129163.1	DNA polymerase III PolC
135	276	84.09	8.53	YP_001128632.1	ribonuclease Z
136	283	84.08	6.55	YP_001128669.1	thymidylate synthase
137	344	84.01	8.42	YP_001129114.1	nicotinic acid mononucleotide adenyllyltransferase
138	191	84.01	7.72	YP_001128657.1	LysR family transcriptional regulator
139	309	83.94	8.28	YP_001129062.1	manganese-dependent inorganic pyrophosphatase
140	359	83.74	8.43	YP_001127882.1	thioredoxin
141	205	83.73	9.25	YP_001127698.1	Hsp33-like chaperonin
142	248	83.62	6.67	YP_001128654.1	orotate phosphoribosyltransferase
143	270	83.6	9.63	YP_001128572.1	7,8-dihydro-8-oxoguanine-triphosphatase
144	102	83.5	6.85	YP_001129144.1	SpoU rRNA methylase family protein
145	260	83.4	8.46	YP_001128382.1	DNA helicase II
146	95	83.31	8.26	YP_001127672.1	ABC transporter ATP-binding protein
147	257	83.28	9.00	YP_001128517.1	spermidine/putrescine ABC transporter permease
148	82	83.27	7.60	YP_001127833.1	trigger factor
149	294	83.26	10.18	YP_001128710.1	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase
150	244	83.08	11.60	YP_001128398.1	Spx family transcriptional regulator
151	264	82.84	8.90	YP_001128645.1	DNA topoisomerase IV subunit A
152	83	82.84	8.10	YP_001127774.1	deoxyuridine 5'-triphosphate nucleotidohydrolase
153	123	82.79	8.96	YP_001128865.1	hypothetical protein SpyM51324
154	266	82.74	9.40	YP_001128564.1	Zn-dependent hydrolase
155	398	82.59	9.32	YP_001129322.1	50S ribosomal protein L9
156	25	82.46	8.84	YP_001127945.1	3-ketoacyl-ACP reductase
157	311	82.33	9.47	YP_001129064.1	transporter
158	347	82.3	10.64	YP_001127927.1	aspartyl/glutamyl-tRNA amidotransferase subunit C
159	122	82.26	7.82	YP_001128866.1	hypothetical protein SpyM51325
160	240	82.24	11.62	YP_001128407.1	phosphate transport system protein
161	175	82.01	9.33	YP_001128549.1	coproporphyrinogen III oxidase
162	299	81.94	7.73	YP_001128718.1	thiamine biosynthesis protein Thil
163	177	81.69	10.26	YP_001128547.1	haloacid dehalogenase-like hydrolase
164	26	81.63	10.15	YP_001127946.1	3-oxoacyl-(acyl carrier protein) synthase II

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165	293	81.47	9.41	YP_001128695.1	16S rRNA-processing protein RimM
166	295	81.29	8.36	YP_001128711.1	RNA pseudouridylylase synthase
167	390	81.15	10.37	YP_001129275.1	Holliday junction DNA helicase RuvA
168	354	81.13	18.45	YP_001127893.1	cytidine and deoxycytidylate deaminase
169	227	80.87	9.67	YP_001128264.1	dihydroorotate dehydrogenase 1A
170	42	80.84	8.48	YP_001127749.1	DNA polymerase I
171	171	80.79	8.66	YP_001128561.1	ABC transporter ATP-binding protein
172	109	80.67	11.18	YP_001128173.1	cell division protein
173	310	80.57	10.34	YP_001129063.1	pyruvate formate-lyase activating enzyme
174	255	80.51	11.97	YP_001128497.1	inorganic polyphosphate/ATP-NAD kinase
175	7	80.45	9.29	YP_001127995.1	glycyl-tRNA synthetase subunit beta
176	259	80.4	10.28	YP_001128520.1	UDP-N-acetylenolpyruvoylglucosamine reductase
177	313	80.38	8.44	YP_001128747.1	hypothetical protein SpyM51206
178	279	80.34	10.98	YP_001128533.1	dipeptidase PepV
179	378	80.25	10.06	YP_001129167.1	undecaprenyl pyrophosphate synthase
180	87	80.18	9.17	YP_001127815.1	hypothetical protein SpyM50221
181	1	80.1	13.94	YP_001127604.1	chromosomal replication initiation protein
182	342	80.07	11.75	YP_001129111.1	hypothetical protein SpyM51588
183	306	80.02	11.43	YP_001128731.1	cytidylate kinase
184	380	79.95	10.26	YP_001129174.1	D-tyrosyl-tRNA(Tyr) deacylase
185	207	79.88	9.33	YP_001129160.1	peptide deformylase
186	96	79.79	10.32	YP_001127673.1	ABC transporter permease
187	391	79.74	10.11	YP_001129277.1	DNA mismatch repair protein
188	150	79.59	8.58	YP_001128271.1	D-alanyl-alanine synthetase A
189	190	79.57	11.63	YP_001128503.1	redox-sensing transcriptional repressor Rex
190	33	79.55	9.49	YP_001127964.1	ABC transporter ATP-binding protein
191	247	79.46	10.79	YP_001128649.1	dihydroorotate
192	290	79.4	8.24	YP_001128689.1	1-phosphofructokinase
193	307	79.31	10.88	YP_001128735.1	peptidase T
194	198	79.2	8.71	YP_001129100.1	16S rRNA methyltransferase GidB
195	215	79.18	9.68	YP_001128024.1	Holliday junction-specific endonuclease
196	101	79.1	9.52	YP_001129146.1	hypothetical protein SpyM51627
197	193	79.09	10.84	YP_001128469.1	hypothetical protein SpyM50910
198	143	79.03	12.44	YP_001128913.1	peptidase
199	353	79.01	13.70	YP_001127895.1	hypothetical protein SpyM50304
200	400	78.91	11.59	YP_001129329.1	cobalt transport protein
201	243	78.73	11.61	YP_001128402.1	phosphate ABC transporter,extracellular phosphate-binding lipoprotein
202	79	78.61	8.27	YP_001127828.1	tRNA pseudouridine synthase A
203	125	78.59	12.79	YP_001128795.1	flavodoxin
204	267	78.48	9.61	YP_001128566.1	ABC transporter permease
205	331	78.38	8.98	YP_001129078.1	glutamate racemase
206	200	78.2	9.18	YP_001127921.1	L-asparaginase
207	155	78.2	9.54	YP_001128291.1	O-methyltransferase
208	117	78.14	11.59	YP_001128196.1	DNA repair protein
209	88	78.13	8.31	YP_001127816.1	cysteine desulfurase
210	38	78.08	12.10	YP_001127971.1	hypothetical protein SpyM50381
211	256	78.05	13.32	YP_001128516.1	spermidine/putrescine extracellular binding protein
212	360	77.98	11.68	YP_001127880.1	DNA mismatch repair protein
213	75	77.9	11.78	YP_001127936.1	heat shock protein GrpE
214	362	77.88	12.19	YP_001127858.1	DNA-binding protein
215	114	77.87	11.70	YP_001128191.1	exodeoxyribonuclease VII large subunit
216	134	77.83	13.26	YP_001128955.1	sensor histidine kinase
217	351	77.78	9.51	YP_001127901.1	fructokinase
218	194	77.73	9.85	YP_001128349.1	glutamine ABC transporter,glutamine-binding protein/permease protein
219	393	77.72	12.78	YP_001129302.1	hypothetical protein SpyM51787
220	168	77.65	14.79	YP_001128765.1	F0F1 ATP synthase subunit epsilon
221	39	77.63	9.26	YP_001127972.1	translation initiation factor IF-2
222	74	77.49	13.08	YP_001127935.1	heat-inducible transcription repressor
223	189	77.4	10.21	YP_001128502.1	hypothetical protein SpyM50945
224	9	77.33	10.96	YP_001128013.1	phospho-N-acetylmuramoyl-pentapeptide-transferase
225	152	77.29	12.41	YP_001128279.1	1-acyl-sn-glycerol-3-phosphate acyltransferase
226	316	77.22	11.95	YP_001128983.1	exoribonuclease R
227	340	77.19	12.78	YP_001129105.1	ABC transporter permease
228	135	76.99	11.03	YP_001128953.1	ribonuclease III
229	202	76.94	14.08	YP_001127897.1	sucrose operon repressor
230	350	76.82	11.08	YP_001127902.1	mannose-6-phosphate isomerase
231	121	76.67	9.55	YP_001128868.1	aspartate aminotransferase
232	10	76.67	13.06	YP_001128015.1	ABC transporter permease
233	21	76.53	14.43	YP_001127940.1	MarR family transcriptional regulator
234	229	76.52	13.74	YP_001128923.1	hypothetical protein SpyM51383
235	161	76.49	9.14	YP_001128774.1	NAD-dependent DNA ligase LigA
236	162	76.24	20.85	YP_001128773.1	lipid kinase
237	301	76.1	9.31	YP_001128724.1	chorismate synthase
238	107	75.98	9.61	YP_001128170.1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
239	321	75.97	10.18	YP_001129017.1	DNA translocase FtsK
240	249	75.93	10.13	YP_001128655.1	orotidine 5'-phosphate decarboxylase
241	377	75.62	13.17	YP_001129166.1	phosphatidate cytidylyltransferase
242	297	75.31	12.69	YP_001128713.1	LysR family transcriptional regulator
243	146	75.01	13.22	YP_001128898.1	cell division protein
244	157	74.88	12.56	YP_001128311.1	hypothetical protein SpyM50747
245	291	74.68	13.86	YP_001128693.1	pyridine nucleotide-disulfide oxidoreductase family protein
246	15	74.62	12.67	YP_001128040.1	16S rRNA m(5)C 967 methyltransferase

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247	382	74.61	12.42	YP_001129180.1	16S ribosomal RNA methyltransferase RsmE
248	16	74.56	14.93	YP_001128041.1	protein phosphatase
249	401	74.41	11.01	YP_001129331.1	cobalt transporter ATP-binding subunit
250	376	74.38	11.70	YP_001129165.1	pheromone-processing membrane metalloprotease
251	145	74.36	10.86	YP_001128899.1	phosphoenolpyruvate carboxylase
252	118	74.28	11.77	YP_001128198.1	hypothetical protein SpyM50627
253	235	74.18	11.92	YP_001128412.1	pantothenate kinase
254	322	74.12	11.89	YP_001129026.1	ADP-ribose pyrophosphatase
255	3	74.08	11.86	YP_001127608.1	peptidyl-tRNA hydrolase
256	216	74.06	9.95	YP_001128029.2	S-ribosylhomocysteinase
257	343	73.79	13.71	YP_001129113.1	hypothetical protein SpyM51590
258	100	73.64	13.95	YP_001127686.1	hypothetical protein SpyM50091
259	6	73.57	14.68	YP_001127991.1	N-acetylglucosamine-6-phosphate deacetylase
260	221	73.45	13.04	YP_001127963.1	HIT-family protein
261	108	73.45	10.62	YP_001128171.1	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase
262	302	73.43	12.69	YP_001128725.1	3-dehydroquinate dehydratase
263	323	73.4	17.67	YP_001129049.1	DNA replication initiation control protein YabA
264	172	73.38	14.49	YP_001128553.1	hypothetical protein SpyM50998
265	210	73.36	13.96	YP_001129340.1	recombination protein F
266	185	73.36	12.58	YP_001128440.1	GntR family transcriptional regulator
267	330	73.33	11.08	YP_001129076.1	phosphoesterase
268	246	73.21	12.79	YP_001128466.1	ribonuclease HII
269	332	73.1	15.29	YP_001129080.1	hypothetical protein SpyM51557
270	89	73	11.83	YP_001127817.1	NifU-like protein
271	140	72.81	12.38	YP_001128917.1	prolipoprotein diacylglycerol transferase
272	337	72.52	16.04	YP_001129092.1	primosomal protein DnaI
273	339	72.33	18.12	YP_001129099.1	LemA family protein
274	132	72.3	14.58	YP_001128971.1	1,2-diacylglycerol 3-glucosyltransferase
275	218	72.18	12.45	YP_001127953.1	hypothetical protein SpyM50363
276	318	72.17	11.97	YP_001128989.1	formamidopyrimidine-DNA glycosylase
277	181	72.08	11.12	YP_001128413.1	16S rRNA m(2)G 1207 methyltransferase
278	261	71.96	21.45	YP_001128709.1	uracil permease
279	81	71.87	10.74	YP_001127831.1	hypothetical protein SpyM50240
280	160	71.85	13.70	YP_001128775.1	hypothetical protein SpyM51236
281	327	71.81	11.39	YP_001129072.1	segregation and condensation protein B
282	24	71.74	11.96	YP_001127944.1	acyl-carrier-protein S-malonyltransferase
283	153	71.56	13.73	YP_001128282.1	DNA polymerase III subunit delta
284	286	71.47	15.87	YP_001128674.1	mevalonate diphosphate decarboxylase
285	115	71.47	15.12	YP_001128193.1	geranyltranstransferase
286	303	71.41	12.47	YP_001128726.1	hypothetical protein SpyM51184
287	22	71.37	11.60	YP_001127941.1	3-oxoacyl-ACP synthase
288	284	71.25	16.18	YP_001128672.1	isopentenyl pyrophosphate isomerase
289	271	71.14	12.14	YP_001128625.1	NIF3 (NGG1p interacting factor 3) family protein
290	199	71.02	12.52	YP_001127923.1	universal stress protein
291	124	70.91	16.90	YP_001128800.1	zinc-binding protein AdcA precursor
292	289	70.83	12.19	YP_001128683.1	tRNA CCA-pyrophosphorylase
293	392	70.71	19.25	YP_001129297.1	arginine repressor
294	192	70.65	11.74	YP_001128670.1	3-hydroxy-3-methylglutaryl coenzyme A synthase
295	20	70.53	14.92	YP_001127939.1	enoyl-CoA hydratase
296	314	70.49	14.67	YP_001128363.1	4-alpha-glucanotransferase
297	275	70.41	15.27	YP_001128631.1	short chain dehydrogenase
298	178	70.34	13.85	YP_001128370.1	DNA polymerase III DnaE
299	94	70.22	16.73	YP_001127671.1	MarR family transcriptional regulator
300	195	70.17	14.78	YP_001128977.1	glucosyl transferase
301	348	69.97	12.08	YP_001127905.1	alanine racemase
302	209	69.78	17.06	YP_001129318.1	TetR family transcriptional regulator
303	365	69.71	13.49	YP_001127844.1	hypothetical protein SpyM50253
304	44	69.64	13.99	YP_001128415.1	lipoprotein
305	214	69.58	16.27	YP_001128023.1	penicillin-binding protein 1A
306	251	69.56	15.51	YP_001128478.1	hypothetical protein SpyM50921
307	328	69.54	12.55	YP_001129073.1	segregation and condensation protein A
308	232	69.49	15.93	YP_001128904.1	N-acetylmuramoyl-L-alanine amidase
309	213	69.4	17.17	YP_001129348.1	serine protease
310	46	69.33	16.73	YP_001127782.1	membrane protein OxaA 1 precursor
311	278	69.31	14.91	YP_001129006.1	uracil DNA glycosylase superfamily protein
312	131	69.16	21.67	YP_001128972.1	glycosyltransferase
313	45	69.05	14.79	YP_001127781.1	ribonuclease P
314	127	68.75	12.45	YP_001128322.1	3-phosphoshikimate 1-carboxyvinyltransferase
315	197	68.73	17.62	YP_001129084.1	OxaA-like protein precursor
316	272	68.71	12.74	YP_001128626.1	hypothetical protein SpyM51076
317	19	68.43	12.55	YP_001128047.1	hypothetical protein SpyM50461
318	233	68.41	16.57	YP_001128313.1	biotin-protein ligase
319	201	68.13	14.53	YP_001127898.1	sucrose-6-phosphate hydrolase
320	308	68.12	18.26	YP_001129055.1	polysaccharide biosynthesis protein
321	204	67.88	16.53	YP_001127876.1	signal peptidase I
322	296	67.65	14.64	YP_001128712.1	lipoprotein signal peptidase
323	85	67.65	17.62	YP_001127812.1	adaptor protein
324	273	67.61	16.28	YP_001128628.1	DNA replication protein DnaD
325	188	67.32	12.42	YP_001128501.1	cysteine desulfurase
326	110	67.17	13.24	YP_001128175.1	hypothetical protein SpyM50604
327	184	67.13	19.77	YP_001128472.1	sortase A
328	31	67.07	18.87	YP_001127958.1	permease

Position	Sequence number	Genus Average identity	SD	Accession (S. pyogenes str. Manfred)	Annotation
329	27	67.06	13.06	YP_001127947.1	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
330	8	67.06	19.49	YP_001128011.1	cell division protein
331	245	66.92	14.07	YP_001128397.1	bifunctional riboflavin kinase/FMN adenylyltransferase
332	17	66.74	19.07	YP_001128044.1	sensor histidine kinase
333	138	66.5	12.69	YP_001128928.1	cell division protein FtsY
334	389	66.02	16.91	YP_001129274.1	DNA-3-methyladenine glycosylase
335	186	65.89	14.38	YP_001128420.1	hypothetical protein SpyM50861
336	51	65.85	13.36	YP_001127635.1	phosphotyrosine protein phosphatase
337	141	65.71	18.02	YP_001128916.1	hypothetical protein SpyM51375
338	136	65.68	14.27	YP_001128952.1	chromosome partition protein
339	163	65.14	21.90	YP_001128771.1	F0F1 ATP synthase subunit A
340	252	65.04	14.62	YP_001128483.1	methyltransferase
341	203	64.95	12.80	YP_001127877.1	ribonuclease HIII
342	352	64.92	21.60	YP_001127899.1	PTS system sucrose-specific transporter subunit IIABC
343	32	64.84	17.48	YP_001127961.1	LytR family transcriptional regulator
344	300	64.78	19.20	YP_001128723.1	hypothetical protein SpyM51181
345	92	64.68	17.43	YP_001127824.1	oligopeptide transporter ATP-binding protein
346	384	64.57	16.66	YP_001129238.1	co-chaperonin GroES
347	355	64.46	21.04	YP_001127889.1	hypothetical protein SpyM50298
348	231	64.3	15.41	YP_001128907.1	phosphoglycerate mutase family protein
349	228	64.24	17.53	YP_001128871.1	metallo-beta-lactamase superfamily protein
350	277	63.91	16.90	YP_001128633.1	hypothetical protein SpyM51083
351	11	63.81	14.12	YP_001128025.1	hypothetical protein SpyM50438
352	187	63.51	15.85	YP_001128499.1	adenylate cyclase family protein
353	341	63.39	18.90	YP_001128504.1	peptidase
354	47	63.24	19.31	YP_001127783.1	ssDNA-binding protein
355	41	63.09	19.81	YP_001127976.1	copper-transporting ATPase
356	317	63.06	14.79	YP_001128988.1	dephospho-CoA kinase
357	224	63.03	18.73	YP_001127832.1	mechanosensitive ion channel protein
358	164	62.92	21.52	YP_001128770.1	F0F1 ATP synthase subunit B
359	93	62.58	18.95	YP_001127825.1	oligopeptide transporter ATP-binding protein
360	385	62.55	16.84	YP_001129263.1	acetyltransferase (GNAT) family protein
361	208	62.52	13.27	YP_001129234.1	RNA pseudouridylylase
362	217	62.46	13.93	YP_001128049.1	hypothetical protein SpyM50463
363	170	62.46	15.61	YP_001128753.1	ATP-dependent exonuclease subunit A
364	173	61.69	24.17	YP_001128552.1	hypothetical protein SpyM50997
365	53	61.31	16.50	YP_001127640.1	MATE family transporter
366	324	61.06	19.23	YP_001129050.1	DNA polymerase III subunit delta'
367	129	60.98	16.33	YP_001128324.1	cell envelope-related function transcriptional attenuator
368	80	60.85	14.50	YP_001127829.1	phosphomethylpyrimidine kinase
369	268	60.64	15.87	YP_001128568.1	hypothetical protein SpyM51016
370	116	60.48	22.35	YP_001128195.1	repressor protein
371	104	59.68	15.88	YP_001128158.1	phosphopantetheine adenylyltransferase
372	176	59.34	20.24	YP_001128548.1	acyl-ACP thioesterase
373	137	59.13	21.10	YP_001128930.1	haloacid dehalogenase-like hydrolase
374	282	59.09	17.93	YP_001128668.1	dihydrofolate reductase
375	165	59	22.86	YP_001128769.1	F0F1 ATP synthase subunit delta
376	379	58.98	21.46	YP_001129168.1	preprotein translocase subunit YajC
377	403	58.88	20.05	YP_001129335.1	hypothetical protein SpyM51822
378	52	58.52	17.99	YP_001127636.1	hypothetical protein SpyM50037
379	5	58.52	16.54	YP_001127614.1	PP-loop family protein
380	128	58.22	16.04	YP_001128323.1	shikimate kinase
381	338	57.91	17.47	YP_001129097.1	hypothetical protein SpyM51574
382	285	57.88	18.47	YP_001128673.1	phosphomevalonate kinase
383	4	57.83	18.77	YP_001127613.1	hypothetical protein SpyM50010
384	119	57.11	18.07	YP_001128889.1	hypothetical protein SpyM51348
385	212	56.87	16.88	YP_001129346.1	ABC transporter permease
386	111	56.57	18.19	YP_001128176.1	hypothetical protein SpyM50605
387	34	56.39	17.84	YP_001127965.1	ABC transporter
388	105	56.23	18.46	YP_001128161.1	hypothetical protein SpyM50590
389	312	56.13	17.98	YP_001129067.1	PAP2 superfamily protein
390	225	56.05	17.57	YP_001127820.1	D-alanyl-D-alanine carboxypeptidase
391	48	55.77	34.57	YP_001127790.1	N-acetylneuraminate lyase
392	361	54.69	17.98	YP_001127879.1	hypothetical protein SpyM50288
393	402	54.41	19.22	YP_001129334.1	protease
394	78	54.34	19.62	YP_001128433.1	GntR family transcriptional regulator
395	112	54.23	19.20	YP_001128178.1	RNA binding protein
396	99	54.16	20.99	YP_001127678.1	DNA binding protein
397	329	53.06	19.26	YP_001129074.1	site-specific tyrosine recombinase XerD
398	49	52.36	28.03	YP_001127791.1	ROK family protein
399	335	50.54	20.45	YP_001129089.1	hypothetical protein SpyM51566
400	287	50.5	23.81	YP_001127772.1	ABC transporter ATP-binding protein
401	142	48.99	24.37	YP_001128915.1	hypothetical protein SpyM51374
402	269	46.95	28.77	YP_001128182.1	Mut/NUDIX family protein
403	91	43.95	27.79	YP_001127823.1	oligopeptide transporter permease
404	288	42.63	22.63	YP_001127771.1	ABC transporter ATP-binding protein