Table 4. *S. aureus* bacteriophage annotations

Bacteriophage PT1028

ORF	Start, nt	End, nt	Size, aa	Predicted function	Representative similarity to proteins in database	*E* value	Percent identity	Percent length of match	Accession no.
7	27	680	217		unknown [S. aureus subsp. aureus MRSA252]	1.00E-120	100	100	CAG39402.1
10	733	1260	175		unknown [S. aureus subsp. aureus MRSA252]	3.30E-95	100	100	CAG39403.1
14	1263	1604	113	C-terminal effector domain of the bipartite response regulators	unknown [S. aureus subsp. aureus MRSA252]	1.40E-60	98	100	CAG39404.1
9	1601	2170	189	Small terminase	putative Small terminase [S. aureus subsp. aureus MRSA252]	1.00E-103	98	100	CAG39405.1
26	3025	3207	60		unknown [S. aureus subsp. aureus MRSA252]	4.00E-28	100	100	CAG39407.1
11	3325	3837	170		putative membrane protein [S. aureus subsp. aureus MRSA252]	2.70E-91	100	100	CAG39408.1
5	5396	4599	265	Chromosome segregation	Chromosome segregation ATPases [T. tengcongensis MB4]	1.40E-05	24	67	AAM24687.1
2	6634	5420	404	Integrase	putative integrase [S. aureus subsp. aureus MRSA252]	0	97	100	CAG39389.1
6	7667	6933	244	Transcription regulator	posible transcriptional regulator [B. licheniformis ATCC 14580]	6.10E-05	29	54	AAU25100.1
20	7808	8029	73	DNA-binding	HTH DNA-binding protein [S. pyogenes MGAS10394]	5.20E-09	38	86	AAT87942.1
19	8030	8302	90		putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.80E-08	36	88	CAG42677.1
21	8453	8662	69		unknown [S. aureus]	5.80E-32	94	100	AAL04139.1
16	8665	8991	108		unknown [S. aureus subsp. aureus MRSA252]	3.40E-57	96	100	CAG39396.1
3	9056	9925	289	DNA replication	putative replication protein [S. thermophilus]	5.80E-11	25	85	CAB46557.2
1	9939	11648	569	P-loop containing nucleotide triphosphate hydrolases	unknown [S. aureus subsp. aureus Mu50]	0	93	99	BAB58183.1
18	11017	10721	98						
13	11960	12340	126	Winged helix DNA-binding domain	Orf12 [S. aureus]	2.40E-70	98	100	AAG29609.1
12	12337	12846	169		Orf11 [S. aureus]	3.10E-15	95	23	AAG29608.1
4	13017	13820	267		unknown [S. pyogenes MGAS8232]	6.40E-38	36	100	AAL97894.1
17	13807	14079	90						
8	14081	14722	213		Orf11 [S. aureus]	1.00E-114	95	100	AAG29608.1
15	15258	15599	113		Orf10 [S. aureus]	2.40E-60	99	100	AAG29607.1

Bacteriophage 66

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
15	281	670	129	Biofim-associated; Topoisomerase	biofilm-associated surface protein [S. aureus] DNA topoisomerase IV subunit A [M. penetrans HF-2]	2.50E-06 9.30E-06	28 28	100 94	AAK38834.2 BAC44437.1
29	684	866	60		unknown [S. aureus phage phiP68]	4.00E-28	100	100	AAO83895.1
6	873	2099	408	Major head	major head protein [S. aureus phage phiP68]	0	100	100	AAO83894.1
47	1813	1953	46						
7	2114	3097	327	Upper collar	upper collar protein [S. aureus phage phiP68]	2.00E-140	100	76	AAO83893.1
8	3090	3845	251	Lower collar	lower collar protein [S. aureus phage phiP68]	2.00E-142	100	100	AAO83892.1
60	3418	3537	39						
2	3859	5802	647	Minor structural protein	minor structural protein [S. aureus phage phiP68]	0	99	100	AAO83891.1
9	5814	6566	250	Amidase	amidase [S. aureus phage phiP68]	9.00E-148	94	100	AAO83890.1
10	6629	7306	225	Minor tail	minor tail protein [S. aureus phage phiP68]	4.00E-113	92	100	AAO83888.1
12	7622	8074	150	Minor tail	minor tail protein [S. aureus phage phiP68]	2.30E-81	97	100	AAO83888.1
3	8132	9895	587	Tail	tail protein [S. aureus phage phiP68]	0	99	100	AAO83887.1
13	9897	10319	140	Holin	holin [S. aureus phage phiP68]	1.50E-74	100	100	AAO83886.1
4	10270	11733	487	Peptidoglycan hydrolase	lysin beta subunit [Streptococcus phage C1]	4.70E-07	22	69	AAP42310.1
38	10741	10577	54						
51	11246	11383	45						
46	11635	11525	36						
1	14133	11848	761	DNA polymerase	DNA-polymerase [S. aureus phage phiP68]	0	98	99	AAO83884.1
5	15396	14149	415	Encapsidation	putative encapsidation protein [S. aureus phage phiP68]	0	100	91	AAO83883.1
45	15463	15317	48						
11	15926	15444	160		unknown [S. aureus phage phiP68]	1.50E-90	99	100	AAO83882.1
14	16505	16092	137		unknown [S. aureus phage phiP68]	5.60E-32	53	100	AAO83880.1
31	16684	16508	58		unknown [S. aureus phage phiP68]	1.20E-27	97	100	AAO83879.1
16	17101	16733	122	ssDNA-binding	putative single stranded DNA-binding protein [S. aureus phage phiP68]	4.60E-64	98	100	AAO83878.1
21	17361	17125	78		unknown [S. aureus phage phiP68]	6.20E-31	79	100	AAO83877.1
17	17678	17376	100		unknown [S. aureus phage phiP68]	2.40E-53	98	100	AAO83876.1
25	17868	17671	65		unknown [S. aureus phage phiP68]	1.50E-30	98	100	AAO83875.1

Bacteriophage 44AHJD

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
113	199	600	133	Amidase; Spore germination; Topoisomerase; Biofilm-associated	Spore germination protein IA [B. cereus ATCC 14579]	3.10E-06	25	90	AAP11636.1
					N-acetylmuramoyl-L-alanine amidase, family 4 [E. faecalis V583]	4.10E-06	33	67	AAO80118.1
					DNA topoisomerase IV subunit A [M. penetrans HF-2]	1.20E-05	28	92	BAC44437.1
					biofilm-associated surface protein [S. aureus]	4.00E-28	29	100	AAK38834.2
123	614	796	60		unknown [Staphylococcus phage 44AHJD]	4.00E-28	100	100	AAO83873.1
39	1743	1883	46						
7	2044	3027	327	Upper collar	upper collar protein [Staphylococcus phage 44AHJD]	2.00E-140	100	76	AAO83871.1
53	3348	3467	39						
2	3789	5732	647	Minor structural protein	minor structural protein [Staphylococcus phage 44AHJD]	0	100	100	AAO83869.1
46	4891	5019	42						
9	5744	6496	250	Amidase	amidase [Staphylococcus phage 44AHJD]	2.00E-156	100	100	AAO83868.1
49	5784	5909	41						
23	6494	6315	59						
3	6626	8389	587	Tail	tail protein [Staphylococcus phage 44AHJD]	0	100	100	AAO83866.1
12	8391	8813	140	Holin	holin [Staphylococcus phage 44AHJD]	1.50E-74	100	100	AAO83865.1
4	8764	10227	487	Lysin	lysin beta subunit [Streptococcus phage C1]	8.00E-07	22	69	AAP42310.1
28	9235	9071	54						
40	9740	9877	45						
19	9836	9630	68						
36	10165	10019	48						
1	12627	10342	761	DNA polymerase	DNA-polymerase [Staphylococcus phage 44AHJD]	0	100	99	AAO83863.1
27	12916	13080	54						
44	12917	12783	44						
35	13957	13811	48						
10	14420	13938	160		unknown [Staphylococcus phage 44AHJD]	2.30E-91	99	100	AAO83861.1
13	14996	14586	136		unknown [Staphylococcus phage 44AHJD]	1.20E-74	100	100	AAO83859.1
25	15175	14999	58		unknown [Staphylococcus phage 44AHJD]	1.10E-28	100	100	AAO83858.1
48	15340	15212	42						
11	15593	15225	122	ssDNA-binding	putative single stranded DNA-binding protein [Staphylococcus phage 44AHJD]	1.60E-64	99	100	AAO83857.1
16	15852	15616	78		unknown [Staphylococcus phage 44AHJD]	3.60E-39	100	100	AAO83856.1
114	16172	15870	100		unknown [Staphylococcus phage 44AHJD]	2.10E-54	100	100	AAO83855.1
121	16362	16165	65		unknown [Staphylococcus phage 44AHJD]	2.90E-31	100	100	AAO83854.1

Bacteriophage P68

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
15	278	679	133	Amidase; Topoisomerase; Biofilm-associated	N-acetylmuramoyl-L-alanine amidase, family 4 [E. faecalis V583] DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2] biofilm-associated surface protein [S. aureus]	4.10E-06 4.10E-06 1.20E-05	33 28 29	67 92 100	AAO80118.1 BAC44437.1 AAK38834.2
25	693	875	60		unknown [S. aureus phage phiP68]	4.00E-28	100	100	AAO83895.1
7	882	2108	408	Major capsid	major head protein [S. aureus phage phiP68]	0	100	100	AAO83894.1
46	1822	1962	46						
8	2123	3106	327	Upper collar	upper collar protein [S. aureus phage phiP68]	2.00E-140	100	76	AAO83893.1
9	3099	3854	251	Lower collar	lower collar protein [S. aureus phage phiP68]	2.00E-142	100	100	AAO83892.1
63	3427	3546	39						
2	3868	5811	647	Minor structural protein	minor structural protein [S. aureus phage phiP68]	0	100	100	AAO83891.1
10	5823	6575	250	Amidase	amidase [S. aureus phage phiP68]	2.00E-156	100	100	AAO83890.1
57	5863	5988	41						
5	6638	8083	481	Minor tail	minor tail protein [S. aureus phage phiP68]	0	100	100	AAO83888.1
3	8141	9904	587	Tail	tail protein [S. aureus phage phiP68]	0	100	100	AAO83887.1
13	9906	10328	140	Holin	holin [S. aureus phage phiP68]	1.50E-74	100	100	AAO83886.1
4	10279	11742	487	Lysin	lysin beta subunit [Streptococcus phage C1]	8.00E-07	22	69	AAP42310.1
33	10750	10586	54						
47	11255	11392	45						
22	11351	11145	68						
43	11680	11534	48						
1	14142	11857	761	DNA polymerase	DNA-polymerase [S. aureus phage phiP68]	0	100	99	AAO83884.1
6	15405	14158	415	Encapsidation	putative encapsidation protein [S. aureus phage phiP68]	0	100	91	AAO83883.1
42	15472	15326	48						
11	15935	15453	160		unknown [S. aureus phage phiP68]	2.30E-91	99	100	AAO83882.1
14	16511	16101	136		unknown [S. aureus phage phiP68]	1.20E-74	100	100	AAO83880.1
30	16690	16514	58		unknown [S. aureus phage phiP68]	1.10E-28	100	100	AAO83879.1
56	16855	16727	42						
12	17108	16740	122	ssDNA-binding	putative single stranded DNA-binding protein [S. aureus phage phiP68]	7.00E-65	100	100	AAO83878.1
19	17367	17131	78		unknown [S. aureus phage phiP68]	3.60E-39	100	100	AAO83877.1
16	17687	17385	100		unknown [S. aureus phage phiP68]	2.10E-54	100	100	AAO83876.1
23	17877	17680	65		unknown [S. aureus phage phiP68]	2.90E-31	100	100	AAO83875.1

Bacteriophage 187

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
30	117	557	146	Small terminase	small terminase [S. aureus phage phi 11]	1.10E-77	100	100	AAL82257.1
5	478	1818	446	Large terminase	large terminase [S. aureus phage phi 11]	0	85.39	85	AAL82258.1
3	1830	3275	481	Portal	portal protein [S. pyogenes MGAS10394]	5.50E-93	41.85	42	AAT87695.1
9	3259	4227	322	Minor capsid	putative minor head protein [C. difficile phage phiC2]	1.20E-15	35.66	36	AAS02083.1
21	4329	4952	207	Scaffold	scaffold protein [S. pyogenes MGAS10394]	3.10E-17	33.73	34	AAT86182.1
11	4971	5882	303	Major capsid	putative major head protein [S. pyogenes SSI-1]	2.60E-33	32.24	32	BAC63531.1
31	5972	6421	149	Tail	major tail protein [S. aureus phage phi 12]	3.70E-47	60.14	60	AAL82319.1
42	6378	6764	128		unknown [S. aureus phage phi 11]	4.00E-25	47.27	47	AAL82264.1
107	6761	7075	104		unknown [S. aureus subsp. aureus Mu50]	6.80E-21	43.43	43	BAB57057.1
49	7065	7412	115		unknown [S. aureus phage phi 11]	5.30E-31	58.41	58	AAL82265.1
39	7425	7820	131		unknown [S. aureus subsp. aureus Mu50]	7.80E-21	39.37	39	BAB57059.1
22	7838	8491	217	Major tail	major tail protein [S. pyogenes MGAS10394]	1.10E-15	31.25	31	AAT87691.1
43	8550	8930	126		unknown [S. aureus phage phi 11]	1.20E-11	39.25	39	AAL82268.1
47	8960	9310	116		unknown [S. aureus phage phi 11]	2.30E-34	62.5	63	AAL82269.1
1	9326	12433	1035	Minor tail	tape measure protein [S. aureus phage phi 11]	0	45.54	46	AAL82270.1
36	11311	11715	134						
23	11514	10957	185						
102	11691	11530	53						
10	12446	13378	310		unknown [S. aureus subsp. aureus Mu50]	8.60E-72	41.59	42	BAB57064.1
4	13391	14788	465	Endopeptidase	endopeptidase [S. pyogenes MGAS10394]	1.70E-22	23.89	24	AAT86193.1
153	14241	14092	49						
19	14792	15484	230		unknown [Staphylococcus phage 187]	7.00E-123	99.1	99	AAM54031.1
8	15496	16539	347	Lipolytic enzyme	unknown [Staphylococcus phage 187]	0	99.42	99	AAM54031.1
6	16556	17827	423	Minor capsid	minor capsid protein [Bacteriophage phig1e]	3.20E-17	29.5	30	CAA66748.1
138	17940	18062	40						
2	18348	20234	628	Amidase	cell wall hydrolase Ply187 [Staphylococcus phage 187]	0	99.84	100	CAA69022.1
89	18418	18600	60	Holin	holin protein Hol187 [Staphylococcus phage 187]	1.10E-25	100	100	CAA69023.1
95	19351	19148	67						
63	20384	20638	84	Holin	holin [S. aureus phage phi 13]	1.50E-42	100	100	AAL82376.1
16	20650	21405	251	Amidase	amidase [S. aureus phage phi 13]	4.00E-153	100	100	AAL82377.1
7	22943	21897	348	Integrase	integrase [S. aureus phage phi 11]	0	97.99	98	AAL82229.1
82	23056	23253	65		unknown [S. pyogenes MGAS8232]	6.40E-10	46.05	46	AAL98050.1

Bacteriophage 187 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
35	23657	23250	135						
32	24088	23651	145		unknown [S. pneumoniae TIGR4]	2.20E-09	28.68	29	AAK75994.1
18	24845	24120	241		unknown [C. perfringens str. 13]	2.70E-37	42.16	42	BAB79844.1
26	25547	24873	224	rRNA binding	Ribosomal protein L22 [V. vulnificus CMCP6]	1.40E-05	26.52	27	AAO08916.1
50	25896	25564	110	Transcriptional Regulator	transcriptional regulator, Cro/CI family [E. faecalis V583]	3.40E-17	43.62	44	AAO81775.1
51	26159	26353	64	Repressor	cro [B. □larkia bacteriophage BCJA1c]	3.00E-07	47.37	47	AAU85054.1
15	26353	27120	255	Antirepressor	similar to anti-repressor [S. aureus subsp. Aureus Mu50]	1.10E-89	88.24	88	BAB57017.1
73	27121	27345	74		unknown [S. aureus phage phi 11]	2.00E-37	100	100	AAL82236.1
100	27385	27555	56						
129	27574	27705	43						
74	27753	27544	69						
17	27810	28562	250	Antirepressor	putative anti repressor [S. aureus subsp. Aureus MRSA252]	9.00E-124	90.8	91	CAG41079.1
90	28578	28760	60						
150	28844	28728	38						
76	28953	28738	71		lmo1659 [Listeria monocytogenes]	1.80E-09	39.71	40	CAC99737.1
40	29017	29280	87	DNA-binding	putative DNA-binding protein [S. aureus subsp. Aureus MSSA476]	3.30E-37	84.71	85	CAG42677.1
105	29293	29454	53		putative exported protein [S. aureus subsp. Aureus MSSA476]	5.20E-23	96.23	96	CAG43717.1
162	29423	29313	36						
60	29546	29806	86		unknown [S. aureus subsp. Aureus MSSA476]	1.80E-43	96.51	97	CAG43716.1
28	29821	30300	159		orf 16 [S. aureus prophage phiPV83]	4.60E-84	98.74	99	BAA97823.1
13	30300	31073	257	AAA ATPase	unknown [S. aureus phage phi 11]	1.70E-56	42.8	43	AAL82240.1
24	31104	31655	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.50E-61	63.04	63	AAL82241.1
78	31444	31647	67		ORF19 [bacteriophage phi ETA]	1.10E-30	98.51	99	BAA97605.1
20	31668	32360	230		phi PV83 orf 19-like protein [S. aureus phage phi 11]	8.00E-132	98.7	99	AAL82242.1
12	32332	33135	267	Replisome organizer	putative replisome organizer [Lactococcus bacteriophage 4268]	3.40E-07	22.39	22	AAM83050.1
14	33145	33918	257	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	4.00E-129	87.45	87	AAL82346.1
108	33912	34070	52		unknown [S. aureus subsp. Aureus Mu50]	2.20E-21	90.38	90	BAB57032.1
69	34083	34304	73		unknown [S. aureus temperate phage phiSLT]	3.80E-36	98.63	99	BAB21717.1
37	34315	34719	134		orf 22 [S. aureus prophage phiPV83]	2.50E-72	97.01	97	BAA97829.1
86	34724	34909	61		ORF26 [bacteriophage phi ETA]	7.60E-27	93.44	93	BAA97612.1
61	34910	35167	85	Transcriptional regulator	Transcriptional regulator, Cro/CI family [S. pyogenes MGAS10394]	1.80E-06	38.98	39	AAT87941.1
45	35179	35535	118		unknown [S. aureus phage phi 11]	2.20E-50	84.35	84	AAL82249.1
64	35539	35781	80		unknown [S. aureus phage phi 11]	8.60E-41	96.2	96	AAL82250.1

Bacteriophage 187 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
38	35796	36188	130		unknown [S. aureus subsp. Aureus MRSA252]	1.70E-71	100	100	CAG40534.1
83	36185	36379	64		unknown [S. aureus subsp. aureus MRSA252]	2.10E-29	96.83	97	CAG40533.1
48	36376	36723	115	Sensor	possible sensor protein [S. aureus phage phi 13]	1.70E-58	95.65	96	AAL82351.1
55	36739	37029	96		unknown [S. aureus subsp. aureus MSSA476]	1.20E-47	97.83	98	CAG42692.1
62	37022	37270	82		orf 52 [S. aureus bacteriophage PVL]	6.70E-38	92.68	93	BAA31925.1
25	37263	37796	177	dUTPase	dUTP pyrophosphatase [S. aureus subsp. aureus Mu50]	7.10E-85	91.53	92	BAB58136.1
77	37833	38039	68		unknown [S. aureus subsp. aureus MRSA252]	6.70E-28	93.85	94	CAG41056.1
41	38036	38422	128		orf31 [S. aureus prophage phiPV83]	3.10E-65	95.28	95	BAA97838.1
98	38419	38592	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	1.20E-22	91.23	91	AAL82255.1
44	38593	38955	120						
116	38956	39102	48		unknown [S. aureus subsp. aureus Mu50]	6.30E-08	96.43	96	BAB57045.1
34	39126	39548	140	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	2.60E-74	97.86	98	AAL82256.1

Bacteriophage 69

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
25	25	540	171	Small terminase	small terminase [S. aureus phage phi 11]	5.00E-77	99	85	AAL82257.1
8	461	1804	447	Large terminase	large terminase [S. aureus phage phi 11]	0	100	100	AAL82258.1
6	1815	3350	511	Portal	portal protein [S. pyogenes MGAS10394]	3.50E-93	41	95	AAT87695.1
14	3357	4352	331	Minor head	putative minor head protein [C. difficile phage phiC2]	3.80E-12	32	40	AAS02083.1
94	4425	4595	56		unknown [S. aureus subsp. aureus Mu50]	4.70E-24	98	100	BAB57051.1
22	4704	5324	206	Penicillin binding	penicillin-binding protein [B. cereus ATCC 10987]	2.20E-07	30	66	AAS40607.1
22	4704	5324	206	Minor structural protein	minor structural protein 2 [Bacteriophage Tuc2009]	1.10E-06	24	100	AAK19862.1
11	5338	6312	324	Major capsid	head protein [S. aureus phage phi 11]	0	100	100	AAL82262.1
55	6334	6621	95		unknown [S. aureus subsp. aureus Mu50]	3.70E-46	97	100	BAB57055.1
44	6630	6962	110		unknown [S. aureus subsp. aureus Mu50]	1.30E-56	100	100	BAB57056.1
40	7261	7608	115		unknown [S. aureus subsp. aureus Mu50]	5.80E-62	99	100	BAB57058.1
36	7620	8003	127		unknown [S. aureus subsp. aureus Mu50]	6.40E-71	100	100	BAB57059.1
23	8022	8603	193	Major tail	major tail protein [S. pyogenes MGAS10394]	1.30E-19	34	82	AAT87691.1
130	8161	8265	34						
38	8665	9030	121		unknown [S. aureus phage phi 11]	2.80E-61	100	100	AAL82268.1
1	9421	12888	1155	Tape measure protein	tape measure protein [S. aureus phage phi 11]	0	99	78	AAL82270.1
128	10751	10611	46						
12	12901	13848	315		ORF54 [bacteriophage phi ETA]	1.40E-21	33	60	BAA97640.1
3	13857	15758	633	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	2.20E-15	24	39	AAT86193.1
70	15571	15780	69						
2	15773	17683	636	Minor structural protein	minor structural protein [S. aureus phage phiP68]	4.20E-38	27	76	AAO83891.1
162	16773	16889	38						
5	17683	19506	607		ORF57 [bacteriophage phi ETA]	0	80	100	BAA97643.1
35	19506	19883	125		ORF58 [bacteriophage phi ETA]	2.10E-61	93	100	BAA97644.1
86	19884	20060	58		ORF59 [bacteriophage phi ETA]	5.00E-26	93	98	BAA97645.1
48	20101	20400	99		unknown [S. aureus temperate phage phiSLT]	1.90E-31	64	100	BAB21751.1
4	20537	22435	632	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	100	100	AAL82277.1
103	20918	20769	49						
9	22448	23620	390	Tail fiber	tail fiber [S. aureus phage phi 11]	0	99	100	AAL82278.1
33	23625	24020	131		ORF63 [bacteriophage phi ETA]	2.60E-69	96	100	BAA97649.1
28	24076	24513	145	Holin	holin [S. aureus subsp. aureus Mu50]	8.70E-75	97	100	BAB57074.1
7	24494	25939	481	Amidase	amidase [S. aureus phage phi 11]	0	99	100	AAL82281.1

Bacteriophage 69 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
163	24852	24959	35	Amidase	amidase [bacteriophage 80 alpha]	1.40E-05	79	82	AAB39699.1
10	27875	26829	348	Integrase	integrase [S. aureus phage phi 11]	0	98	100	AAL82229.1
75	27987	28187	66	Excisionase	excisionase [S. aureus phage phi 11]	7.70E-32	100	100	AAL82230.1
13	29029	28124	301		unknown [S. aureus phage phi 11]	1.00E-172	100	100	AAL82231.1
96	29336	29169	55		unknown [S. aureus phage phi 12]	7.30E-25	100	98	AAL82284.1
19	30125	29406	239	Repressor	cI-like repressor [S. aureus phage phi 11]	3.00E-133	99	100	AAL82233.1
69	30267	30485	72	Repressor; DNA-binding	cro-like repressor [S. aureus phage phi 11]	2.30E-36	100	100	AAL82234.1
16	30501	31289	262	Antirepressor	anti-repressor [S. aureus phage phi 11]	6.00E-144	98	99	AAL82235.1
77	31306	31500	64		unknown [S. aureus subsp. aureus MRSA252]	2.70E-08	52	100	CAG41078.1
39	31851	31495	118		unknown [E. faecalis V583]	8.00E-16	38	100	AAO82542.1
37	31901	32092	63						
43	32321	32094	75		unknown [LactoB. bacteriophage phi adh]	5.70E-08	38	94	CAB52488.1
45	32380	32700	106		unknown [S. aureus subsp. aureus MSSA476]	1.80E-58	99	100	CAG43718.1
100	32697	32858	53		putative exported protein [S. aureus subsp. aureus MRSA252]	2.00E-22	94	100	CAG41074.1
50	32950	33210	86		unknown [S. aureus subsp. aureus MSSA476]	9.90E-42	92	100	CAG43716.1
65	33220	33441	73		unknown [S. aureus subsp. aureus Mu50]	9.20E-22	63	100	BAB57024.1
15	33434	34222	262		ORF17 [bacteriophage phi ETA]	1.70E-99	67	98	BAA97603.1
24	34251	34802	183	ssDNA-binding	ssb [S. aureus phage phi 11]	5.80E-61	63	100	AAL82241.1
160	34433	34314	39						
76	34597	34794	65		ORF19 [bacteriophage phi ETA]	1.50E-27	94	100	BAA97605.1
20	34815	35480	221		ORF20 [bacteriophage phi ETA]	4.00E-127	98	100	BAA97606.1
51	35482	35811	109						
31	36076	35666	136						
18	36139	36909	256	DNA replication	DnaA analog [Bacteriophage LL-H]	3.80E-48	38	100	AAL77546.1
17	36919	37698	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	2.00E-149	99	100	AAL82346.1
101	37692	37853	53		unknown [S. aureus subsp. aureus Mu50]	1.50E-06	50	98	BAB57032.1
64	37866	38087	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
32	38097	38501	134		ORF25 [bacteriophage phi ETA]	4.70E-71	93	100	BAA97611.1
82	38506	38691	61		ORF26 [bacteriophage phi ETA]	3.20E-25	87	100	BAA97612.1
47	38692	38997	101		unknown [S. agalactiae NEM316]	2.80E-06	33	91	CAD45858.1
97	39125	39289	54		unknown [S. aureus phage phi 11]	2.60E-06	100	42	AAL82249.1
58	39246	39482	78		unknown [S. aureus subsp. aureus MRSA252]	8.70E-25	68	100	CAG41062.1
62	39486	39728	80		unknown [S. aureus subsp. aureus MRSA252]	2.90E-41	96	100	CAG41061.1

Bacteriophage 69 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
60	39740	39997	85		orf 52 [S. aureus bacteriophage PVL]	2.70E-39	98	96	BAA31925.1
79	39984	40154	56						
26	40147	40653	168		ORF34 [bacteriophage phi ETA]	2.80E-61	71	100	BAA97620.1
89	40690	40863	57		unknown [S. aureus subsp. aureus MSSA476]	6.50E-26	98	100	CAG42695.1
72	40880	41086	68		unknown [S. aureus subsp. aureus Mu50]	1.50E-32	99	100	BAB57039.1
71	41083	41286	67		unknown [S. aureus subsp. aureus Mu50]	1.50E-32	100	100	BAB57041.1
61	41279	41515	78		unknown [S. aureus subsp. aureus Mu50]	1.20E-39	99	100	BAB57042.1
34	41508	41894	128		orf31 [S. aureus prophage phiPV83]	4.30E-67	99	99	BAA97838.1
90	41891	42064	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	1.40E-23	93	100	AAL82255.1
120	42065	42211	48		unknown [S. aureus subsp. aureus Mu50]	1.30E-08	97	60	BAB57045.1
30	42226	42645	139	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	3.10E-19	38	96	AAL82256.1

Bacteriophage 53

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
28	156	596	146	Small terminase	small terminase [S. aureus phage phi 11]	3.30E-77	99	100	AAL82257.1
9	517	1860	447	Large terminase	large terminase [S. aureus phage phi 11]	0	99	100	AAL82258.1
114	698	838	46						
6	1871	3406	511	Portal	Portal protein [S. pyogenes MGAS10394]	1.20E-93	41	95	AAT87695.1
14	3413	4408	331	Head morphogenesis	putative minor head protein [C. difficile phage phiC2]	3.80E-12	32	40	AAS02083.1
96	4481	4651	56		unknown [S. aureus subsp. aureus Mu50]	2.30E-23	96	100	BAB57051.1
23	4760	5380	206	Penicillin binding	penicillin-binding protein [B. cereus ATCC 10987]	1.30E-07	30	66	AAS40607.1
23	4760	5380	206	Minor structural protein	minor structural protein 2 [Bacteriophage Tuc2009]	2.20E-07	25	100	AAK19862.1
11	5394	6368	324	Major capsid	head protein [S. aureus phage phi 11]	0	99	100	AAL82262.1
57	6390	6677	95		unknown [S. aureus subsp. aureus Mu50]	4.00E-48	100	100	BAB57055.1
48	6686	7018	110		unknown [S. aureus subsp. aureus Mu50]	1.30E-56	100	100	BAB57056.1
45	7317	7664	115		unknown [S. aureus subsp. aureus Mu50]	5.80E-62	99	100	BAB57058.1
38	7676	8059	127		unknown [S. aureus subsp. aureus Mu50]	1.90E-70	99	100	BAB57059.1
25	8078	8659	193	Major tail	Major tail protein [S. pyogenes MGAS10394]	1.30E-19	35	82	AAT87691.1
131	8217	8321	34						
40	8721	9086	121		unknown [S. aureus phage phi 11]	1.10E-60	99	100	AAL82268.1
46	9116	9460	114		unknown [S. aureus phage phi 11]	6.40E-61	100	100	AAL82269.1
1	9477	12941	1154	Tape measure protein	tape measure protein [S. aureus phage phi 11]	0	95	78	AAL82270.1
128	10807	10667	46						
12	12954	13901	315		ORF54 [bacteriophage phi ETA]	3.20E-21	32	60	BAA97640.1
157	13604	13485	39						
3	13910	15811	633	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	2.20E-15	24	39	AAT86193.1
74	15624	15833	69						
2	15826	17736	636	Minor structural protein	minor structural protein [S. aureus phage phiP68]	2.10E-37	27	76	AAO83891.1
161	16826	16942	38						
5	17736	19559	607		ORF57 [bacteriophage phi ETA]	0	82	100	BAA97643.1
70	19033	19254	73						
37	19559	19936	125		ORF58 [bacteriophage phi ETA]	6.10E-61	93	100	BAA97644.1
88	19937	20119	60		ORF59 [bacteriophage phi ETA]	8.40E-26	91	95	BAA97645.1
192	20119	20220	33						
52	20159	20458	99		unknown [S. aureus temperate phage phiSLT]	7.60E-52	100	100	BAB21751.1
4	20595	22493	632	Peptidoglycan hydrolase	cell wall hydrolase [S. aureus phage phi 11]	0	99	100	AAL82277.1

Bacteriophage 53 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
10	22506	23678	390	Tail fiber	tail fiber [S. aureus phage phi 11]	0	99	100	AAL82278.1
98	22708	22580	42						
34	23684	24079	131		ORF63 [bacteriophage phi ETA]	9.10E-70	97	100	BAA97649.1
51	24135	24437	100	Holin	holin [S. aureus temperate phage phiSLT]	4.90E-51	100	100	BAB21752.1
7	24449	25903	484	Amidase	amidase [S. aureus subsp. Aureus MRSA252]	0	100	100	CAG40495.1
180	25569	25676	35						
16	26518	27354	278						
8	29029	27644	461	Integrase; Recombinase; Resolvase	site-specific recombinase for integration and excision [bacteriophage phi-105]	8.20E-62	34	100	BAA36658.1
89	29138	29317	59	Excisionase	excisionase [S. aureus subsp. Aureus Mu50]	3.80E-26	97	100	BAB57010.1
13	30229	29297	310		unknown [S. aureus subsp. Aureus Mu50]	5.00E-173	97	100	BAB57011.1
103	30536	30369	55		unknown [S. aureus phage phi 12]	7.30E-25	100	98	AAL82284.1
20	31325	30606	239	Repressor	cI-like repressor [S. aureus phage phi 11]	1.00E-132	99	100	AAL82233.1
73	31467	31685	72	Repressor; DNA-binding	cro-like repressor [S. aureus phage phi 11]	2.30E-36	100	100	AAL82234.1
17	31701	32489	262	Antirepressor	anti-repressor [S. aureus phage phi 11]	8.00E-144	98	99	AAL82235.1
81	32506	32700	64		unknown [S. aureus subsp. Aureus MRSA252]	5.60E-06	48	100	CAG40551.1
62	32753	32929	58		orf 10 [S. aureus prophage phiPV83]	1.30E-21	88	100	BAA97817.1
64	33134	32904	76		orf 11 [S. aureus prophage phiPV83]	1.70E-36	97	100	BAA97818.1
130	33193	33321	42						
83	33314	33475	53		putative exported protein [S. aureus subsp. Aureus MSSA476]	3.80E-21	89	100	CAG43717.1
176	33444	33334	36						
54	33567	33827	86		ORF15 [bacteriophage phi ETA]	1.20E-44	98	100	BAA97601.1
71	33837	34058	73		ORF16 [bacteriophage phi ETA]	2.70E-21	63	100	BAA97602.1
24	34051	34674	207	Topoisomerase I	prophage pi2 protein 11, topoisomerase [L. lactis subsp. Lactis Il1403]	3.00E-20	36	85	AAK05116.1
30	34674	35102	142	ssDNA-binding	single strand DNA-binding protein [S. aureus prophage phiPV83]	1.60E-76	98	100	BAA97825.1
21	35116	35790	224		unknown [S. aureus subsp. Aureus Mu50]	3.00E-129	98	100	BAB57028.1
162	35787	35903	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
19	36818	37588	256	DNA replication	DnaA analog [Bacteriophage LL-H]	2.90E-40	38	100	AAL77546.1
18	37598	38377	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	9.00E-151	100	100	AAL82346.1
108	38371	38529	52		unknown [S. aureus subsp. Aureus Mu50]	2.20E-21	90	100	BAB57032.1
66	38542	38763	73		ORF24 [bacteriophage phi ETA]	5.00E-36	99	100	BAA97610.1
33	38773	39180	135	Endodeoxyribonuclease RusA	unknown [S. aureus subsp. Aureus N315]	1.60E-71	94	99	BAB43067.1
86	39180	39365	61		ORF26 [bacteriophage phi ETA]	5.80E-27	93	100	BAA97612.1
41	39366	39725	119	DNA-binding	putative DNA-binding protein [S. aureus subsp. Aureus MSSA476]	1.20E-11	37	100	CAG42686.1

Bacteriophage 53 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
61	39725	39979	84		unknown [S. aureus subsp. Aureus MRSA252]	3.10E-43	99	100	CAG40537.1
60	39985	40227	80		unknown [S. aureus subsp. aureus MRSA252]	2.10E-39	94	100	CAG41061.1
32	40242	40643	133		unknown [S. aureus subsp. aureus MSSA476]	8.70E-57	81	100	CAG42690.1
44	40640	40987	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93	100	AAL82351.1
49	40984	41292	102		unknown [S. aureus subsp. aureus MSSA476]	5.70E-52	96	100	CAG42692.1
63	41285	41521	78		unknown [S. aureus subsp. aureus MSSA476]	1.30E-36	96	100	CAG42693.1
26	41526	42038	170	dUTPase	dUTP pyrophosphatase [S. aureus subsp. aureus Mu50]	5.50E-68	79	100	BAB58136.1
78	42075	42281	68		unknown [S. aureus subsp. aureus MRSA252]	4.20E-30	93	100	CAG41056.1
76	42278	42481	67						
50	42474	42710	78		unknown [S. aureus subsp. aureus Mu50]	1.30E-36	94	100	BAB57042.1
35	42703	43089	128		orf31 [S. aureus prophage phiPV83]	4.30E-67	99	99	BAA97838.1
93	43086	43259	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	6.70E-23	91	100	AAL82255.1
120	43260	43406	48		unknown [S. aureus subsp. aureus Mu50]	6.30E-08	96	58	BAB57045.1
31	43430	43852	140	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	3.10E-75	99	100	AAL82256.1

Bacteriophage 85

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
28	152	646	164	Small terminase	putative small terminase [S. aureus subsp. aureus MRSA252]	5.50E-35	46	100	CAG39405.1
8	649	1944	431	Large terminase	putative terminase, large subunit - phage associated [S. pyogenes M1 GAS]	3.00E-172	71	94	AAK33879.1
6	1955	3493	512	Portal	portal protein [S. pyogenes MGAS10394]	5.10E-92	40	96	AAT87695.1
12	3611	4495	294	Minor head	putative minor head protein [C. difficile phage phiC2]	3.20E-12	32	45	AAS02083.1
98	4568	4738	56		unknown [S. aureus subsp. aureus Mu50]	2.10E-24	100	100	BAB57051.1
24	4873	5487	204	Structural; Immunoglobulin binding	putative scaffold protein [LactoB. johnsonii prophage Lj965]	3.70E-12	29	100	AAR27459.1
					EMML15=M-like immunoglobulin-binding protein [S. pyogenes, EF1949, type M15, Peptide Partial, 217 aa]	1.50E-08	27	67	AAB31196.1
10	5501	6475	324	Major capsid	head protein [S. aureus phage phi 11]	0	99	100	AAL82262.1
59	6497	6784	95		unknown [S. aureus subsp. aureus Mu50]	4.00E-48	100	100	BAB57055.1
49	6793	7125	110		unknown [S. aureus subsp. aureus Mu50]	1.30E-56	100	100	BAB57056.1
47	7424	7771	115		unknown [S. aureus subsp. aureus Mu50]	5.80E-62	99	100	BAB57058.1
41	7783	8166	127		unknown [S. aureus subsp. aureus Mu50]	6.40E-71	100	100	BAB57059.1
25	8185	8766	193	Major tail	Major tail protein [S. pyogenes MGAS10394]	9.70E-20	35	82	AAT87691.1
126	8324	8428	34						
44	8828	9193	121		unknown [S. aureus subsp. aureus Mu50]	2.80E-61	100	100	BAB57061.1
48	9223	9567	114		unknown [S. aureus phage phi 11]	6.40E-61	100	100	AAL82269.1
1	9584	13048	1154	Minor tail	tape measure protein [S. aureus phage phi 11]	0	94	78	AAL82270.1
150	10914	10795	39						
11	13061	14008	315		ORF54 [bacteriophage phi ETA]	3.20E-21	32	60	BAA97640.1
3	14017	15918	633	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	2.20E-15	24	39	AAT86193.1
75	15773	15940	55						
2	15933	17843	636	Minor structural protein	minor structural protein [S. aureus phage phiP68]	1.90E-38	28	76	AAO83891.1
5	17843	19666	607		ORF57 [bacteriophage phi ETA]	0	89	100	BAA97643.1
72	19140	19361	73						
40	19666	20043	125		ORF58 [bacteriophage phi ETA]	6.10E-61	93	100	BAA97644.1
88	20044	20226	60		ORF594 [bacteriophage phi ETA]	3.20E-25	89	95	BAA97645.1
54	20267	20566	99		unknown [S. aureus temperate phage phiSLT]	3.90E-48	93	100	BAB21751.1
4	20703	22601	632	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	99	100	AAL82277.1
76	21148	21258	36						
9	22614	23852	412	Tail fiber	tail fiber [S. aureus subsp. aureus Mu50]	0	98	100	BAB57072.1
102	22816	22688	42						

Bacteriophage 85 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
38	23858	24253	131		ORF63 [bacteriophage phi ETA]	1.40E-70	98	100	BAA97649.1
32	24309	24746	145	Holin	holin [S. aureus subsp. Aureus Mu50]	1.70E-75	97	100	BAB57074.1
21	24727	25368	213	Amidase	amidase [S. aureus subsp. Aureus Mu50]	3.00E-115	95	95	BAB57075.1
84	25085	25264	59	Amidase	amidase [bacteriophage 80 alpha]	4.10E-12	73	76	AAB39699.1
27	25503	25943	146	HNH endonuclease	putative HNH homing endonuclease [bacteriophage bIL170]	1.40E-11	32	93	AAC27227.1
18	26393	27106	237	Amidase	amidase [S. aureus subsp. Aureus Mu50]	1.00E-142	100	100	BAB57075.1
128	27652	27515	45						
52	27773	28084	103						
42	28203	28454	83						
7	29986	28601	461	Integrase; Recombinase; Resolvase	site-specific recombinase for integration and excision [bacteriophage phi-105]	8.20E-62	34	100	BAA36658.1
19	30873	30193	226		unknown [S. aureus subsp. Aureus Mu50]	1.10E-31	37	100	BAB56579.1
30	31366	30905	153		unknown [S. aureus subsp. Aureus MRSA252]	1.20E-80	96	99	CAG40556.1
50	31714	31388	108	Repressor	putative phage regulatory protein [S. aureus subsp. Aureus MSSA476]	2.40E-34	63	100	CAG42672.1
79	31877	32086	69	Repressor	putative phage regulatory protein [S. aureus subsp. Aureus MSSA476]	2.10E-10	51	94	CAG42673.1
13	32126	33007	293	ParB-like nuclease	ParB-like nuclease domain protein [T. denticola ATCC 35405]	6.10E-16	43	36	AAS12707.1
16	33000	33767	255		unknown [E. faecalis V583]	1.10E-15	25	100	AAO82012.1
51	33057	32737	106						
97	33838	34008	56						
134	34027	34158	43						
74	34206	33997	69						
92	34262	34438	58		orf 10 [S. aureus prophage phiPV83]	1.30E-21	88	100	BAA97817.1
67	34643	34413	76		orf 11 [S. aureus prophage phiPV83]	1.70E-36	97	100	BAA97818.1
125	34702	34830	42						
82	34823	34984	53		putative exported protein [S. aureus subsp. Aureus MSSA476]	3.80E-21	89	100	CAG43717.1
164	34953	34843	36						
56	35076	35336	86		ORF15 [bacteriophage phi ETA]	4.30E-45	99	100	BAA97601.1
73	35346	35567	73		ORF16 [bacteriophage phi ETA]	4.50E-37	100	100	BAA97602.1
23	35560	36183	207	Topoisomerase	prophage pi2 protein 11, topoisomerase [L. lactis subsp. Lactis Il1403]	3.00E-20	36	85	AAK05116.1
33	36183	36611	142	ssDNA-binding	single strand DNA-binding protein [S. aureus prophage phiPV83]	1.60E-76	98	100	BAA97825.1
20	36625	37299	224		unknown [S. aureus subsp. Aureus Mu50]	3.00E-129	98	100	BAB57028.1
154	37296	37412	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
17	38326	39069	247	DNA replication	DnaA analog [Bacteriophage LL-H]	2.50E-22	30	100	AAL77546.1
15	39079	39858	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	4.00E-149	99	100	AAL82346.1

Bacteriophage 85 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
108	39852	40010	52		unknown [S. aureus subsp. aureus Mu50]	2.20E-21	90	100	BAB57032.1
69	40023	40244	73		ORF24 [bacteriophage phi ETA]	5.00E-36	99	100	BAA97610.1
37	40254	40661	135	Endodeoxyribonuclease RusA	unknown [S. aureus subsp. aureus N315]	1.60E-71	94	99	BAB43067.1
85	40661	40846	61		ORF26 [bacteriophage phi ETA]	5.80E-27	93	100	BAA97612.1
45	40847	41206	119	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.20E-11	37	100	CAG42686.1
63	41206	41460	84		unknown [S. aureus subsp. aureus MRSA252]	3.10E-43	99	100	CAG40537.1
62	41466	41708	80		unknown [S. aureus subsp. aureus MRSA252]	2.10E-39	94	100	CAG41061.1
36	41723	42124	133		unknown [S. aureus subsp. aureus MSSA476]	3.00E-57	82	100	CAG42690.1
46	42121	42468	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93	100	AAL82351.1
53	42465	42773	102		unknown [S. aureus subsp. aureus MSSA476]	3.20E-50	94	100	CAG42692.1
65	42766	43002	78		unknown [S. aureus subsp. aureus MSSA476]	1.30E-36	96	100	CAG42693.1
26	43007	43549	180	dUTPase	dUTPase [S. aureus phage phi 12]	5.80E-98	100	100	AAL82303.1
111	43586	43738	50		ORF35 [bacteriophage phi ETA]	2.50E-20	94	100	BAA97621.1
34	43826	44248	140	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	1.20E-74	98	100	AAL82256.1

Bacteriophage 2638A

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
31	52	399	115		unknown [S. pyogenes SSI-1]	2.30E-10	41	80	BAC64238.1
5	396	2057	553	Large terminase	phage Large terminase [S. aureus bacteriophage phi 77]	2.00E-175	53	100	AAM49610.1
11	2072	3229	385	Portal	portal protein [Bacteriophage T5]	8.50E-06	22	97	AAS77191.1
13	3144	4043	299	Clp protease	putative Clp protease [S. aureus subsp. Aureus MRSA252]	2.70E-27	35	79	CAG41046.1
9	4103	5290	395	Major capsid	major capsid protein a [Bacteriophage PSA]	3.40E-50	34	90	CAC85561.1
36	5308	5598	96		unknown [S. aureus subsp. Aureus MRSA252]	1.50E-18	53	84	CAG41043.1
27	5588	5950	120		unknown [S. aureus subsp. Aureus MRSA252]	1.90E-33	52	100	CAG41042.1
23	5947	6348	133		unknown [S. aureus subsp. Aureus Mu50]	5.90E-29	48	94	BAB58121.1
14	6759	7664	301	Major tail; beta-1,3-glucanase	putative phagelike major tail protein [B. licheniformis ATCC 14580] beta-1,3-glucanase [B. circulans]	2.10E-11 1.10E-10	27 39	67 29	AAU25062.1 AAC60453.1
96	7727	7891	54						
28	7906	8265	119		unknown [S. aureus subsp. Aureus MRSA252]	1.30E-29	52	99	CAG41037.1
94	8325	8459	44		unknown [S. aureus subsp. Aureus MRSA252]	8.70E-05	53	97	CAG41036.1
1	8512	14538	2008	Tape measure protein	tail length tape measure protein [S. aureus phage phi 13]	0	31	84	AAL82371.1
6	14535	16019	494		unknown [S. aureus subsp. Aureus MRSA252]	3.00E-162	55	99	CAG41034.1
2	16035	19499	1154	Minor structural protein	structural protein [S. aureus phage phi 13]	0	62	53	AAL82373.1
97	19496	19660	54						
38	19707	19994	95		orf 22 [S. aureus bacteriophage PVL]	8.40E-06	32	82	BAA31895.1
35	20017	20310	97		unknown [S. aureus prophage phiPV83]	4.70E-17	47	93	BAA97863.1
41	20445	20693	82						
7	20695	22155	486	Amidase	N-acetylmuramoyl-L-alanine amidase [Staphylococcus phage Twort]	9.30E-64	41	73	CAA69021.1
150	22685	22566	39						
58	22715	22915	66		unknown [S. aureus subsp. Aureus MRSA252]	8.80E-12	57	84	CAG40141.1
12	24198	23161	345	Integrase	integrase [S. aureus subsp. Aureus N315]	1.00E-147	69	100	BAB43090.1
15	24908	24255	217	Nuclease	MEMBRANE NUCLEASE, LIPOPROTEIN [M. pulmonis]	2.20E-05	23	85	CAC13866.1
16	25582	24962	206	LexA repressor	LexA repressor [B. cereus ATCC 14579]	7.40E-24	37	91	AAP10633.1
52	25745	25987	80	Transcriptional regulator	Transcriptional regulator, Cro/CI family [S. pyogenes MGAS10394]	6.00E-10	46	86	AAT87724.1
55	26007	26231	74						
76	26410	26234	58						
33	26477	26800	107		unknown [S. aureus subsp. Aureus MSSA476]	4.90E-32	59	97	CAG43718.1
30	27055	27411	118	ATPase	ATPase involved in DNA repair [T. tengcongensis MB4]	6.40E-05	30	99	AAM23562.1
10	27408	28574	388		unknown [S. aureus subsp. Aureus MRSA252]	7.00E-178	77	100	CAG40542.1

Bacteriophage 2638A (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
18	28603	29157	184		unknown [S. aureus phage phi 12]	2.70E-82	81	100	AAL82292.1
4	29215	31176	653	DNA-directed DNA polymerase	putative DNA polymerase [S. aureus subsp. aureus MSSA476]	0	88	100	CAG42684.1
59	31188	31391	67						
85	31384	31557	57						
48	32010	32261	83		unknown [S. aureus subsp. aureus MRSA252]	5.30E-19	52	97	CAG40535.1
74	32265	32450	61						
29	32447	32797	116	Sensor	possible sensor protein [S. aureus phage phi 13]	1.40E-20	41	100	AAL82351.1
21	32794	33177	127						
80	33178	33357	59						
82	33358	33534	58						
44	33524	33790	88		unknown [E. faecalis V583]	1.00E-06	40	68	AAO81853.1
101	33792	33947	51						
19	33940	34479	179	dUTPase	putative dUTP pyrophosphatase [S. aureus subsp. aureus MRSA252]	2.00E-58	65	100	CAG41057.1
51	34516	34758	80						
63	34755	34949	64		unknown [S. aureus subsp. aureus MRSA252]	3.20E-09	68	68	CAG41056.1
40	34940	35221	93		unknown [C. perfringens str. 13]	5.10E-11	53	59	BAB80820.1
113	35218	35361	47						
54	35361	35588	75						
83	35588	35764	58						
3	35801	38251	816	Virulence-associated; DNA primase/helicase	virulence-associated protein E [B. cereus ATCC 10987] putative DNA primase/helicase [S. pyogenes phage 315.6]	0 1.60E-93	43 41	98 56	AAS39320.1 AAM80049.1
152	38536	38652	38						
37	38609	38905	98		unknown [S. aureus subsp. aureus MSSA476]	1.40E-34	67	97	CAG42703.1
8	38889	40247	452	SNF helicase; DEAD/DEAH box helicase	phage helicase [S. aureus phage phi 12] SNF2 domain protein [E. faecalis V583]	0 4.00E-140	82 55	93 99	AAL82307.1 AAO80193.1
20	40261	40746	161		orf 61 [S. aureus bacteriophage PVL]	2.70E-23	41	82	BAA31934.1
26	40893	41216	107	HNH endonuclease	prophage LambdaBa02, HNH endonuclease family protein [B. anthracis str. 'Ames Ancestor']	3.30E-12	40	94	AAT33216.1

Bacteriophage 77

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
37	102	446	114		unknown [S. aureus subsp. aureus MRSA252]	1.20E-59	100	100	CAG41049.1
3	443	2104	553	Large terminase	phage large terminase [S. aureus bacteriophage phi 77]	0	100	100	AAM49610.1
8	2120	3307	395	Portal	putative portal protein [Bacteriophage T5]	6.80E-06	22	97	AAU05287.1
15	3291	4028	245	Clp protease	putative Clp protease [S. aureus subsp. aureus MRSA252]	1.00E-131	98	100	CAG41046.1
6	4051	5196	381	Major capsid	major capsid protein a [Bacteriophage PSA]	7.80E-36	30	100	CAC85561.1
45	5216	5500	94		unknown [S. aureus subsp. aureus MRSA252]	8.90E-48	98	100	CAG41044.1
33	5758	6120	120	Head-tail adaptor	unknown [S. aureus subsp. aureus MRSA252]	9.90E-67	100	100	CAG41042.1
29	6117	6521	134		unknown [S. aureus subsp. aureus N315]	7.10E-59	81	100	BAB43047.1
27	6518	6925	135		unknown [S. aureus subsp. aureus MRSA252]	9.20E-75	99	100	CAG41040.1
20	6926	7570	214	Major tail	putative phagelike major tail protein [B. licheniformis ATCC 14580]	2.00E-06	29	75	AAU25062.1
34	7886	8236	116		unknown [S. aureus subsp. aureus MRSA252]	6.30E-61	100	100	CAG41037.1
100	8263	8424	53		unknown [S. aureus subsp. aureus MRSA252]	1.10E-23	100	100	CAG41036.1
1	8481	13010	1509	Tape measure protein	tail length tape measure protein [S. aureus phage phi 13]	0	51	100	AAL82371.1
4	13007	14491	494		unknown [S. aureus subsp. aureus N315]	0	100	100	BAB43042.1
2	14507	18292	1261	Minor structural protein	structural protein [S. aureus phage phi 13]	0	99	97	AAL82373.1
109	18282	18434	50		orf 55 [S. aureus prophage phiPV83]	1.50E-22	100	100	BAA97861.1
44	18481	18768	95		orf 22 [S. aureus bacteriophage PVL]	8.60E-43	92	100	BAA31895.1
58	18892	19122	76		unknown [S. aureus temperate phage phiSLT]	2.20E-15	46	100	BAB21751.1
35	19258	19560	100	Holin	holin [S. aureus bacteriophage PVL]	1.70E-51	100	100	BAA31897.1
5	19572	21026	484	Amidase	amidase [S. aureus subsp. aureus MRSA252]	0	100	100	CAG40495.1
7	23076	21871	401	Integrase	phage integrase [S. aureus subsp. aureus MSSA476]	0	85	100	CAG42666.1
17	23982	23269	237		unknown [S. aureus subsp. aureus MRSA252]	4.60E-18	29	100	CAG39388.1
85	24242	24060	60		unknown [S. aureus phage phi 12]	3.10E-28	100	100	AAL82284.1
11	25208	24441	255	Repressor	cI-like repressor [S. aureus phage phi 13]	4.00E-128	90	99	AAL82333.1
77	25357	25605	82	Repressor	repressor-like protein [S. aureus phage phi 13]	5.40E-19	61	86	AAL82334.1
46	25663	25935	90		77ORF046 [Bacteriophage 77]	1.10E-45	100	100	AAR87914.1
10	26092	26889	265	Antirepressor; DNA-binding	antirepressor [S. aureus prophage phiPV83]	1.00E-145	98	100	BAA97816.1
23	26903	27346	147		orf 7 [S. aureus prophage phiPV83]	1.60E-76	97	100	BAA97814.1
117	27361	27501	46		orf 8 [S. aureus prophage phiPV83]	1.00E-18	100	100	BAA97815.1
66	27703	27494	69		77ORF066 [Bacteriophage 77]	2.60E-32	100	100	AAR87924.1
14	27760	28512	250	Antirepressor	putative anti repressor [S. aureus subsp. aureus MRSA252]	4.00E-122	90	100	CAG41079.1
65	28528	28746	72		orf 10 [S. aureus prophage phiPV83]	4.10E-06	86	38	BAA97817.1

Bacteriophage 77 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
48	28776	29039	87	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.20E-47	100	100	CAG42677.1
102	29051	29212	53		putative exported protein [S. aureus subsp. aureus MSSA476]	1.70E-21	91	100	CAG43717.1
43	29304	29564	86		orf 39 [S. aureus bacteriophage PVL]	2.50E-45	100	100	BAA31913.1
64	29574	29795	73		unknown [S. aureus subsp. aureus Mu50]	5.90E-37	100	100	BAB57024.1
12	29788	30576	262		ORF17 [bacteriophage phi ETA]	1.70E-99	67	98	BAA97603.1
22	30605	31156	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.50E-61	63	100	AAL82241.1
18	31169	31840	223		ORF20 [bacteriophage phi ETA]	3.00E-128	99	100	BAA97606.1
151	31837	31953	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
9	32803	31946	285		unknown phage protein [S. pyogenes MGAS10394]	4.20E-22	36	58	AAT86873.1
16	32867	33610	247	DNA replication	DnaA analog [Bacteriophage LL-H]	1.10E-22	30	100	AAL77546.1
13	33620	34399	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	5.00E-149	99	100	AAL82346.1
104	34393	34551	52		unknown [S. aureus subsp. aureus Mu50]	2.20E-21	90	100	BAB57032.1
59	34564	34785	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
28	34795	35199	134		orf 22 [S. aureus prophage phiPV83]	4.60E-74	99	100	BAA97829.1
80	35204	35389	61		ORF26 [bacteriophage phi ETA]	1.50E-27	95	100	BAA97612.1
178	35390	35491	33		77ORF178 [Bacteriophage 77]	4.30E-15	100	100	AAR87941.1
41	35454	35753	99	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	9.10E-13	55	71	CAG42686.1
50	35753	36007	84		unknown [S. aureus subsp. aureus MRSA252]	5.30E-43	99	100	CAG40537.1
49	36013	36255	80		unknown [S. aureus subsp. aureus MSSA476]	1.60E-39	94	100	CAG42688.1
70	36269	36475	68		unknown [S. aureus subsp. aureus MSSA476]	5.60E-35	100	100	CAG42689.1
30	36478	36879	133		unknown [S. aureus subsp. aureus MSSA476]	4.60E-58	83	100	CAG42690.1
36	36876	37223	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93	100	AAL82351.1
39	37220	37528	102		unknown [S. aureus subsp. aureus MSSA476]	2.00E-52	96	100	CAG42692.1
53	37521	37757	78		unknown [S. aureus subsp. aureus MSSA476]	1.30E-36	96	100	CAG42693.1
21	37762	38304	180	dUTPase	dUTPase [S. aureus phage phi 12]	5.80E-98	100	100	AAL82303.1
69	38341	38547	68		unknown [S. aureus subsp. aureus Mu50]	1.60E-29	87	100	BAB57039.1
74	38544	38738	64		unknown [S. aureus subsp. aureus Mu50]	6.10E-29	97	100	BAB57040.1
72	38735	38938	67		unknown [S. aureus subsp. aureus Mu50]	1.50E-32	100	100	BAB57041.1
51	38931	39167	78		unknown [S. aureus subsp. aureus Mu50]	5.80E-37	94	100	BAB57042.1
31	39160	39546	128		ORF36 [bacteriophage phi ETA]	2.40E-62	92	100	BAA97622.1
112	39543	39692	49	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	8.20E-16	75	100	AAL82255.1
108	39692	39844	50		orf 58 [S. aureus bacteriophage PVL]	1.10E-20	100	100	BAA31931.1
19	39851	40501	216		orf 59 [S. aureus bacteriophage PVL]	7.00E-121	100	100	BAA31932.1

Bacteriophage 77 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
71	40498	40701	67		putative exported protein [S. aureus subsp. aureus MRSA252]	2.20E-31	99	100	CAG41053.1
26	40729	41145	138	Transcriptional activator RinA	unknown [S. aureus subsp. aureus MRSA252]	1.50E-77	99	100	CAG41052.1
40	41377	41676	99	HNH endonuclease; Electron transporter	putative electron transporter [B. licheniformis ATCC 14580]	6.10E-09	42	73	AAU25074.1
					prophage LambdaBa02, HNH endonuclease family protein [B. anthracis str. 'Ames Ancestor']	6.10E-09	39	92	AAT33216.1

Bacteriophage 42e

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
43	47	352	101	Small terminase	terminase-small subunit [S. aureus phage phi 12]	5.80E-52	100	100	AAL82310.1
3	342	2033	563	Large terminase	large terminase [S. aureus subsp. aureus MW2]	0	100	100	BAB95266.1
8	2047	3276	409	Portal	portal protein [S. aureus subsp. aureus MW2]	0	100	100	BAB95265.1
15	3260	4033	257	Clp protease	scaffolding protease [S. aureus phage phi 12]	1.00E-142	100	100	AAL82313.1
9	4045	5208	387	Major capsid	prophage LambdaBa02, major capsid protein, putative [B. anthracis str. 'Ames Ancestor']	5.10E-99	51	97	AAT33211.1
172	5156	5266	36						
55	5277	5555	92	DNA packaging	unknown [S. aureus temperate phage phiSLT]	9.00E-48	100	100	BAB21736.1
110	5395	5532	45						
42	5567	5899	110		unknown [S. aureus subsp. aureus MSSA476]	4.70E-59	100	100	CAG42713.1
34	5896	6297	133		unknown [S. aureus subsp. aureus MW2]	1.80E-70	100	100	BAB95260.1
35	6298	6693	131		unknown [S. aureus temperate phage phiSLT]	9.10E-70	100	100	BAB21739.1
21	6728	7369	213	Major tail	major tail protein [S. aureus phage phi 12]	8.00E-122	100	100	AAL82318.1
83	7227	7427	66						
28	7461	7916	151	Major tail	major tail protein [S. aureus phage phi 12]	1.80E-81	100	100	AAL82319.1
41	7974	8324	116		unknown [S. aureus temperate phage phiSLT]	2.80E-61	100	100	BAB21742.1
103	8366	8524	52		unknown [S. aureus bacteriophage phi 3A]	3.10E-23	100	100	AAM49604.1
1	8538	14738	2066	Tail fiber	tail fiber protein [S. aureus phage phi 12]	0	100	100	AAL82321.1
25	12928	12422	168						
106	13576	13719	47						
14	14738	15562	274	Holin	holin-like protein [S. aureus phage phi 12]	7.00E-160	100	100	AAL82322.1
4	15571	17154	527	Minor structural protein	minor structural protein, putative [Listeria monocytogenes str. 4b F2365]	1.20E-32	36	43	AAT02929.1
52	17154	17444	96		unknown [S. aureus subsp. aureus MSSA476]	2.50E-50	100	100	CAG42723.1
2	17460	19370	636	Minor structural protein	minor structural protein [S. aureus phage phiP68]	1.20E-37	27	85	AAO83891.1
5	19370	20836	488		unknown [S. aureus subsp. aureus MW2]	0	99	100	BAB95250.1
36	20836	21225	129		unknown [S. aureus subsp. aureus MSSA476]	3.50E-61	91	100	CAG42726.1
97	21218	21382	54		unknown [S. aureus subsp. aureus MSSA476]	5.60E-25	96	100	CAG42727.1
47	21428	21727	99		unknown [S. aureus temperate phage phiSLT]	1.40E-50	96	100	BAB21751.1
87	21922	22056	44		putative membrane protein [S. aureus subsp. aureus MSSA476]	2.40E-15	98	100	CAG43677.1
61	22258	22512	84	Holin	holin [S. aureus phage phi 13]	2.90E-41	95	100	AAL82376.1
17	22524	23279	251	Amidase	amidase [S. aureus phage phi 13]	7.00E-150	97	100	AAL82377.1

Bacteriophage 42e (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
10	23467	24561	364	Staphylokinase	streptokinase precursor [Streptococcus dysgalactiae subsp. Equisimilis]	5.80E-25	25	100	AAC83933.1
161	24868	24767	33						
48	24989	25300	103						
37	25287	25670	127						
12	26860	25883	325	IMP dehydrogenase/GMP reductase	putative GMP reductase [S. aureus subsp. Aureus MSSA476]	0	100	100	CAG43055.1
11	28235	27198	345	Integrase	integrase [S. aureus subsp. Aureus N315]	0	94	100	BAB43090.1
26	28799	28302	165		ORF2 [bacteriophage phi ETA]	3.80E-23	61	50	BAA97588.1
31	29214	28789	141		ORF3 [bacteriophage phi ETA]	1.20E-74	97	100	BAA97589.1
22	29883	29299	194		putative lipoprotein [S. aureus subsp. Aureus MRSA252]	2.80E-11	44	41	CAG40557.1
18	30658	29939	239	Repressor	cI-like repressor [S. aureus phage phi 11]	3.00E-134	100	100	AAL82233.1
76	30800	31018	72	DNA-binding; Repressor	cro-like repressor [S. aureus phage phi 11]	2.30E-36	100	100	AAL82234.1
49	31033	31341	102	BAG domain	77ORF046 [Bacteriophage 77]	4.10E-42	92	88	AAR87914.1
13	31498	32289	263	Antirepressor	anti-repressor [S. aureus phage phi 11]	2.00E-147	100	100	AAL82235.1
71	32290	32514	74		unknown [S. aureus phage phi 11]	2.00E-37	100	100	AAL82236.1
29	32556	33005	149		unknown [S. aureus phage phi 11]	1.00E-81	100	100	AAL82237.1
72	33019	33240	73		unknown [S. aureus subsp. Aureus Mu50]	1.40E-33	99	100	BAB57021.1
98	33233	33394	53		putative exported protein [S. aureus subsp. Aureus MSSA476]	3.60E-24	100	100	CAG43717.1
175	33363	33253	36						
59	33496	33756	86		ORF15 [bacteriophage phi ETA]	1.20E-44	98	100	BAA97601.1
27	33770	34249	159		orf 16 [S. aureus prophage phiPV83]	6.00E-84	98	100	BAA97823.1
20	34249	34887	212	ssDNA-binding; Recombination	recombination protein [temperate phage PhiNIH1.1]	2.70E-40	50	86	AAL15054.1
32	34887	35312	141	ssDNA-binding	single strand DNA-binding protein [S. aureus prophage phiPV83]	5.90E-71	94	100	BAA97825.1
19	35326	36000	224		unknown [S. aureus subsp. Aureus Mu50]	1.00E-128	98	100	BAB57028.1
16	35993	36748	251	DnaD and phage-associated domain	unknown [B. cereus ZK]	4.20E-36	51	62	AAU16814.1
40	36748	37104	118						
7	37101	38342	413	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	0	100	100	AAL82244.1
78	38339	38554	71						
73	38558	38779	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
33	38790	39194	134		ORF25 [bacteriophage phi ETA]	7.10E-75	99	100	BAA97611.1
88	39199	39384	61		orf 23 [S. aureus prophage phiPV83]	1.10E-25	92	100	BAA97830.1
58	39385	39654	89	Repressor	HTH DNA-binding protein [S. aureus phage phi 11]	5.50E-45	100	100	AAL82248.1
64	40015	40263	82		orf 51 [S. aureus bacteriophage PVL]	6.10E-39	94	96	BAA31924.1
60	40275	40526	83		orf 52 [S. aureus bacteriophage PVL]	4.20E-40	100	98	BAA31925.1

Bacteriophage 42e (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
24	40501	41028	175	dUTPase	dUTPase [S. aureus bacteriophage PVL]	3.30E-95	100	100	BAA31926.1
81	41065	41271	68		unknown [S. aureus subsp. aureus MRSA252]	4.90E-31	96	100	CAG41056.1
38	41268	41624	118		orf31 [S. aureus prophage phiPV83]	2.10E-48	77	100	BAA97838.1
112	41621	41773	50	Transcriptional activator RinB	transcriptional activator rinB [S. aureus phage phi 12]	1.90E-20	92	100	AAL82304.1
69	41841	42041	66		putative exported phage protein [S. aureus subsp. aureus MRSA252]	4.20E-30	100	100	CAG40524.1
198	41899	41798	33						
23	42093	42656	187	Virulence associated E; DNA primase/helicase	virulence-associated protein E [B. cereus ATCC 10987]	9.90E-43	52	78	AAS39320.1
					putative DNA primase/helicase - phage associated [S. pyogenes phage 315.6]	2.40E-33	42	82	AAM80049.1
62	42635	42889	84	Virulence associated E	virulence-associated protein E [B. cereus ATCC 10987]	1.80E-06	40	85	AAS39320.1
147	43035	42913	40		unknown [S. aureus subsp. aureus MW2]	3.80E-16	93	100	BAB95272.1
191	43096	42992	34						
53	43230	43520	96		unknown [S. aureus subsp. aureus MSSA476]	7.70E-52	99	100	CAG42703.1
6	43501	44868	455	DEAD/DEAH box helicase	phage helicase [S. aureus phage phi 12]	0	97	92	AAL82307.1
155	44657	44761	34						
30	44881	45318	145	Transcriptional activator RinA	phage regulatory protein [S. aureus subsp. aureus MRSA252]	4.20E-77	97	100	CAG40520.1
46	45475	45789	104	HNH endonuclease; Electron transporter	putative electron transporter [B. licheniformis ATCC 14580]	8.30E-19	52	89	AAU25074.1
					prophage LambdaBa02, HNH endonuclease family protein [B. anthracis str. 'Ames Ancestor']	1.60E-14	46	85	AAT33216.1

Bacteriophage 3A

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
37	117	422	101	Small terminase	small terminase [S. aureus subsp. aureus MRSA252]	5.80E-52	100	100	CAG40518.1
5	412	2103	563	Large terminase; Homing endonucleases	large terminase [S. aureus subsp. aureus MSSA476]	0	100	100	CAG42708.1
10	2117	3346	409	Portal	portal protein [S. aureus temperate phage phiSLT]	0	100	100	BAB21733.1
15	3330	4103	257	Clp protease	scaffolding protease [S. aureus phage phi 12]	6.00E-141	99	100	AAL82313.1
11	4115	5278	387	Major capsid	prophage LambdaBa02, major capsid protein, putative [B. anthracis str. 'Ames Ancestor']	3.30E-98	51	97	AAT33211.1
46	5347	5625	92	DNA packaging	unknown [S. aureus temperate phage phiSLT]	2.00E-47	99	100	BAB21736.1
97	5465	5602	45						
36	5637	5969	110		unknown [S. aureus temperate phage phiSLT]	1.60E-59	100	100	BAB21737.1
28	5966	6367	133		unknown [S. aureus subsp. aureus MW2]	9.90E-69	97	100	BAB95260.1
29	6368	6763	131		unknown [S. aureus temperate phage phiSLT]	1.40E-67	97	100	BAB21739.1
17	6798	7439	213	Major tail	major tail protein [S. aureus phage phi 12]	1.00E-119	98	100	AAL82318.1
23	7531	7986	151	Major tail	major tail protein [S. aureus temperate phage phiSLT]	1.80E-81	100	100	BAB21741.1
34	8044	8394	116		unknown [S. aureus temperate phage phiSLT]	2.40E-60	98	100	BAB21742.1
1	8608	13557	1649	Tape measure protein	tail fiber protein [S. aureus phage phi 12]	0	99	99	AAL82321.1
22	12998	12492	168						
13	13581	14807	408	Tail fiber	tail fiber protein [S. aureus phage phi 12]	0	98	100	AAL82321.1
14	14807	15631	274	Holin	holin-like protein [S. aureus phage phi 12]	9.00E-160	100	100	AAL82322.1
6	15640	17223	527	Minor structural protein	minor structural protein, putative [Listeria monocytogenes str. 4b F2365]	4.20E-33	36	45	AAT02929.1
44	17223	17513	96		unknown [S. aureus subsp. aureus MSSA476]	2.50E-50	100	100	CAG42723.1
4	17529	19439	636	Minor structural protein	minor structural protein [S. aureus phage phiP68]	7.20E-38	27	87	AAO83891.1
7	19439	20905	488		unknown [S. aureus subsp. aureus MW2]	0	100	100	BAB95250.1
30	20905	21294	129		unknown [S. aureus subsp. aureus MSSA476]	7.30E-67	100	100	CAG42726.1
89	21287	21451	54		unknown [S. aureus subsp. aureus MSSA476]	1.50E-25	100	100	CAG42727.1
41	21497	21796	99		unknown [S. aureus temperate phage phiSLT]	7.60E-52	100	100	BAB21751.1
35	21932	22234	100	Holin	holin [S. aureus bacteriophage PVL]	6.40E-51	99	100	BAA31897.1
8	22245	23699	484	Amidase	amidase [S. aureus temperate phage phiSLT]	0	96	100	BAB21753.1
21	24089	24604	171	Gamma-hemolysin; Leucocidin S	Panton-Valentine leukocidin chain S precursor [S. aureus subsp. aureus MW2]	1.00E-93	99	97	BAB95244.1
					gamma-hemolysin component C precursor [S. aureus subsp. aureus MRSA252]	1.10E-68	74	99	CAG41490.1
18	24609	25223	204	Na/K-ATPase	Na/K ATPase [S. aureus phage phi 12]	1.00E-107	96	100	AAL82283.1
130	25345	25220	41						

Bacteriophage 3A (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
74	25585	25403	60		unknown [S. aureus phage phi 12]	3.10E-28	100	100	AAL82284.1
53	26131	26361	76						
16	26342	25656	228	Repressor	cI-like repressor [S. aureus phage phi 11]	2.00E-92	78	100	AAL82233.1
70	26540	26752	70						
24	26800	27243	147		unknown [S. aureus subsp. aureus MRSA252]	2.90E-78	99	100	CAG40553.1
88	27258	27407	49		unknown [S. aureus subsp. aureus MRSA252]	1.50E-22	100	100	CAG40552.1
63	27660	27448	70						
77	27730	27927	65		unknown [S. aureus subsp. aureus MRSA252]	9.10E-33	100	100	CAG40551.1
31	28294	27914	126		unknown [S. aureus subsp. aureus MRSA252]	9.30E-70	100	100	CAG40550.1
54	28361	28606	81		unknown [S. aureus subsp. aureus MRSA252]	3.50E-42	100	100	CAG40549.1
32	28940	28575	121		unknown [S. aureus subsp. aureus MRSA252]	4.10E-65	100	100	CAG40548.1
67	28995	29210	71		unknown [S. aureus subsp. aureus MRSA252]	4.00E-33	100	100	CAG40547.1
48	29235	29498	87	Homeodomain-like	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	3.90E-46	97	100	CAG42677.1
93	29511	29672	53		putative exported protein [S. aureus subsp. aureus MSSA476]	1.20E-22	94	100	CAG43717.1
38	29751	30074	107		unknown [S. aureus subsp. aureus MRSA252]	4.30E-52	93	100	CAG40544.1
33	30089	30451	120		unknown [S. aureus subsp. aureus MRSA252]	1.90E-57	95	100	CAG40543.1
12	30448	31614	388		unknown [S. aureus subsp. aureus MSSA476]	0	99	100	CAG42682.1
19	31640	32197	185		unknown [S. aureus subsp. aureus MRSA252]	4.00E-100	99	100	CAG40541.1
3	32266	34218	650	DNA-directed DNA polymerase	putative DNA polymerase [S. aureus subsp. aureus MRSA252]	0	98	100	CAG40540.1
79	34231	34416	61		unknown [S. aureus subsp. aureus MRSA252]	1.80E-28	100	100	CAG40539.1
27	34416	34817	133	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MRSA252]	7.80E-74	99	100	CAG40538.1
50	34817	35071	84		unknown [S. aureus subsp. aureus MRSA252]	1.30E-41	95	100	CAG40537.1
49	35062	35319	85		unknown [S. aureus subsp. aureus MRSA252]	1.60E-39	94	94	CAG41061.1
26	35330	35740	136		unknown [S. aureus subsp. aureus MSSA476]	1.90E-40	61	99	CAG42690.1
47	35740	36015	91		unknown [S. aureus subsp. aureus MSSA476]	3.40E-31	85	80	CAG42692.1
52	36008	36256	82		orf 52 [S. aureus bacteriophage PVL]	1.60E-39	98	100	BAA31925.1
20	36249	36782	177	dUTPase	dUTP pyrophosphatase [S. aureus subsp. aureus Mu50]	7.00E-93	96	100	BAB58136.1
55	36819	37064	81		orf 54 [S. aureus bacteriophage PVL]	8.50E-33	88	96	BAA31927.1
71	37061	37267	68		unknown [S. aureus subsp. aureus MRSA252]	1.40E-30	94	100	CAG41056.1
91	37264	37416	50	Transcriptional activator RinB	transcriptional activator rinB [S. aureus phage phi 12]	9.40E-20	92	100	AAL82304.1
59	37484	37684	66		putative exported phage protein [S. aureus subsp. aureus MRSA252]	7.20E-30	98	100	CAG40524.1
2	37736	40183	815	Virulence-associated E; DNA primase/helicase	virulence-associated protein E [B. cereus ATCC 10987] putative DNA primase/helicase - phage associated [S. pyogenes phage 315.6]	0 3.20E-94	44 37	97 74	AAS39320.1 AAM80049.1

Bacteriophage 3A (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
76	40329	40129	66		unknown [S. aureus subsp. aureus MW2]	5.00E-15	90	59	BAB95272.1
45	40524	40814	96		unknown [S. aureus subsp. aureus MSSA476]	2.70E-52	100	100	CAG42703.1
9	40795	42162	455	DEAD/DEAH box helicase	phage helicase [S. aureus phage phi 12]	0	100	92	AAL82307.1
137	41951	42055	34						
25	42175	42612	145	Transcriptional activator RinA	phage regulatory protein [S. aureus subsp. aureus MRSA252]	8.40E-78	98	100	CAG40520.1
40	42769	43083	104	HNH endonuclease; Electron transporter	putative electron transporter [B. licheniformis ATCC 14580] prophage LambdaBa02, HNH endonuclease family protein [B. anthracis str. 'Ames Ancestor']	1.40E-18 2.80E-14	52 46	89 85	AAU25074.1 AAT33216.1

Bacteriophage 47

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
38	48	353	101	Small terminase	terminase-small subunit [S. aureus phage phi 12]	5.80E-52	100	100	AAL82310.1
5	343	2034	563	Large terminase	large terminase [S. aureus subsp. aureus MSSA476]	0	99	100	CAG42708.1
9	2048	3277	409	Portal	portal protein [S. aureus temperate phage phiSLT]	0	100	100	BAB21733.1
16	3261	4034	257	Clp protease	scaffolding protease [S. aureus phage phi 12]	1.00E-142	100	100	AAL82313.1
10	4046	5209	387	Major capsid	prophage LambdaBa02, major capsid protein, putative [B. anthracis str. 'Ames Ancestor']	5.10E-99	51	97	AAT33211.1
159	5157	5267	36						
46	5278	5556	92	DNA packaging	unknown [S. aureus temperate phage phiSLT]	9.00E-48	100	100	BAB21736.1
96	5396	5533	45						
36	5568	5900	110		unknown [S. aureus subsp. aureus MSSA476]	4.70E-59	100	100	CAG42713.1
28	5897	6298	133		unknown [S. aureus subsp. aureus MW2]	1.80E-70	100	100	BAB95260.1
29	6299	6694	131		unknown [S. aureus temperate phage phiSLT]	1.20E-69	99	100	BAB21739.1
18	6729	7370	213	Major tail	major tail protein [S. aureus phage phi 12]	8.00E-122	100	100	AAL82318.1
24	7462	7917	151	Major tail	major tail protein [S. aureus phage phi 12]	1.80E-81	100	100	AAL82319.1
33	7975	8325	116		unknown [S. aureus temperate phage phiSLT]	2.80E-61	100	100	BAB21742.1
93	8367	8525	52		unknown [S. aureus bacteriophage phi 3A]	3.10E-23	100	100	AAM49604.1
1	8539	14739	2066	Tail fiber	tail fiber protein [S. aureus phage phi 12]	0	100	100	AAL82321.1
95	13577	13720	47						
6	15572	17155	527	Minor structural protein	minor structural protein, putative [L. monocytogenes str. 4b F2365]	7.20E-33	36	45	AAT02929.1
43	17155	17445	96		unknown [S. aureus subsp. aureus MSSA476]	9.40E-50	99	100	CAG42723.1
4	17461	19371	636	Minor structural protein	minor structural protein [Staphylococcus phage 44AHJD]	7.20E-38	27	87	AAO83869.1
45	19371	19625	84		unknown [S. aureus subsp. aureus MW2]	9.40E-24	98	66	BAB95250.1
40	19671	19970	99		unknown [S. aureus temperate phage phiSLT]	1.70E-51	99	100	BAB21751.1
34	20106	20408	100	Holin	holin [S. aureus phage phi 12]	2.90E-51	100	100	AAL82329.1
7	20419	21873	484	Amidase	peptidoglycan hydrolase [S. aureus phage phi 12]	0	100	100	AAL82330.1
125	21539	21670	43						
103	22231	22368	45						
14	22489	23325	278						
71	23570	23782	70		unknown [S. aureus subsp. aureus MW2]	9.30E-06	81	38	BAB95308.1
11	25030	23825	401	Integrase	integrase [S. aureus phage phi 12]	0	100	100	AAL82282.1
19	25156	25770	204	Na/K-ATPase	Na/K ATPase [S. aureus phage phi 12]	1.00E-112	100	100	AAL82283.1
136	25892	25767	41						

Bacteriophage 47 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
83	26131	25949	60		unknown [S. aureus phage phi 12]	3.10E-28	100	100	AAL82284.1
13	27147	26227	306	DNA polymerase III; Exonuclease	probable DNA polymerase III epsilon chain [C. perfringens str. 13]	7.20E-47	38	99	BAB81107.1
20	27777	27163	204	LexA repressor	LexA repressor [B. cereus ATCC 14579]	5.00E-25	35	100	AAP10633.1
60	27949	28176	75		unknown [E. faecalis V583]	2.40E-06	36	100	AAO82185.1
17	28202	28978	258	Antirepressor	similar to anti-repressor [S. aureus subsp. aureus Mu50]	6.00E-134	93	99	BAB57017.1
30	28515	28126	129						
65	28994	29212	72						
52	29262	29507	81		unknown [S. aureus subsp. aureus MRSA252]	1.00E-41	99	100	CAG40549.1
31	29841	29476	121		unknown [S. aureus temperate phage phiSLT]	4.10E-65	100	100	BAB21704.1
67	29896	30111	71		unknown [S. aureus temperate phage phiSLT]	2.60E-32	99	100	BAB21705.1
47	30136	30399	87	DNA-binding; Homeodomain-like	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	3.90E-46	97	100	CAG42677.1
92	30412	30573	53		putative exported protein [S. aureus subsp. aureus MRSA252]	2.60E-22	94	100	CAG41074.1
161	30542	30432	36						
37	30652	30975	107		unknown [S. aureus subsp. aureus MRSA252]	1.30E-53	97	100	CAG40544.1
32	30990	31352	120		unknown [S. aureus subsp. aureus MW2]	4.50E-59	98	100	BAB95293.1
12	31349	32515	388		unknown [S. aureus subsp. aureus MSSA476]	0	97	100	CAG42682.1
22	32541	33098	185		unknown [S. aureus phage phi 12]	1.00E-100	100	100	AAL82292.1
3	33158	35119	653	DNA-directed DNA polymerase	DNA polymerase A domain [S. aureus phage phi 12]	0	100	99	AAL82293.1
81	35132	35317	61		unknown [S. aureus subsp. aureus MSSA476]	1.80E-28	100	100	CAG42685.1
26	35317	35718	133	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	5.60E-72	97	100	CAG42686.1
48	35718	35975	85		unknown [S. aureus phage phi 12]	4.80E-44	100	100	AAL82296.1
68	35978	36178	66		unknown [S. aureus subsp. aureus MRSA252]	2.10E-29	92	100	CAG40536.1
73	36449	36655	68		unknown [S. aureus subsp. aureus MSSA476]	5.30E-33	97	100	CAG42689.1
35	37056	37403	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93	100	AAL82351.1
41	37400	37708	102		unknown [S. aureus subsp. aureus MSSA476]	8.90E-53	97	100	CAG42692.1
53	37701	37937	78		unknown [S. aureus subsp. aureus MSSA476]	1.30E-36	96	100	CAG42693.1
21	37942	38484	180	dUTPase	dUTPase [S. aureus phage phi 12]	5.80E-98	100	100	AAL82303.1
79	38521	38709	62		orf 55 [S. aureus bacteriophage PVL]	1.50E-27	92	100	BAA31928.1
74	38684	38884	66		orf 56 [S. aureus bacteriophage PVL]	1.10E-30	100	100	BAA31929.1
90	38884	39039	51	Transcriptional activator RinB	transcriptional activator rinB [S. aureus phage phi 12]	7.60E-22	100	100	AAL82304.1
57	39107	39307	66		putative exported phage protein [S. aureus subsp. aureus MRSA252]	4.20E-30	100	100	CAG40524.1
2	39359	41806	815	Virulence-associated E; DNA primase/helicase	virulence-associated protein E [B. cereus ATCC 10987] putative DNA primase/helicase [S. pyogenes phage 315.6]	0 7.20E-94	44 37	97 71	AAS39320.1 AAM80049.1
143	41952	41830	40		unknown [S. aureus subsp. aureus MW2]	3.80E-16	93	100	BAB95272.1

Bacteriophage 47 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
185	42013	41909	34						
44	42147	42437	96		phi related protein [S. aureus phage phi 12]	2.70E-52	100	100	AAL82306.1
8	42418	43785	455	SNF Helicase; DEAD/DEAH box helicase	phage helicase [S. aureus phage phi 12]	0	100	92	AAL82307.1
25	43798	44235	145	Transcriptional activator RinA	phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.20E-79	99	100	CAG42705.1
39	44392	44706	104	HNH endonuclease; Electron transporter	putative electron transporter [B. licheniformis ATCC 14580] prophage LambdaBa02, HNH endonuclease family protein [B. anthracis str. 'Ames Ancestor']	1.40E-18 2.80E-14	52 46	89 85	AAU25074.1 AAT33216.1

Bacteriophage 37

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
35	22	453	143	Small terminase	putative small terminase [S. pyogenes phage 315.6]	2.00E-34	57	95	AAM80043.1
9	453	1712	419	Large terminase	putative large terminase [S. pyogenes phage 315.5]	1.00E-117	75	63	AAM79934.1
7	1718	3124	468	Portal	portal protein [Bacteriophage SPP1]	1.30E-67	35	97	CAA39541.1
11	3096	4040	314	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	5.00E-122	69	98	BAA97628.1
23	4167	4760	197	Minor capsid	ORF43 (minor capsid protein) [bacteriophage phi ETA]	1.90E-71	63	100	BAA97629.1
13	4779	5603	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	9.00E-67	49	97	AAL15075.1
53	5616	5897	93	Rho termination factor, N-terminal	unknown [S. pyogenes phage 315.5]	1.90E-13	45	100	AAM79928.1
50	5897	6193	98	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.90E-26	53	100	BAA97632.1
47	6195	6530	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	2.50E-36	59	100	BAA97633.1
40	6517	6930	137		ORF48 [bacteriophage phi ETA]	3.10E-43	65	84	BAA97634.1
106	6740	6892	50						
38	6942	7364	140		ORF49 [bacteriophage phi ETA]	4.30E-37	52	100	BAA97635.1
24	7368	7931	187	Major tail	ORF50 [bacteriophage phi ETA]	4.40E-35	48	85	BAA97636.1
26	7989	8486	165		ORF51 [bacteriophage phi ETA]	4.90E-31	41	96	BAA97637.1
1	8838	11843	1001	Minor tail; Tape measure protein	tape measure protein [S. aureus phage phi 11]	0	43	92	AAL82270.1
22	11862	12776	304		ORF54 [bacteriophage phi ETA]	2.30E-53	38	100	BAA97640.1
153	12704	12573	43						
8	12785	14287	500	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	9.80E-24	25	57	AAT86193.1
3	14290	16953	887	Pre-neck appendage	pre-neck appendage protein	3.00E-129	37	86	AAA32285.1
5	16946	18442	498		unknown [S. aureus subsp. aureus MRSA252]	1.80E-41	29	76	CAG40500.1
29	18456	18818	120						
143	18808	18942	44						
32	18954	19397	147						
43	19390	19779	129						
72	19790	19563	75						
4	19829	21748	639	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	57	100	AAL82277.1
2	21761	24346	861	Tail fiber; Collagen helix repeat	tail fiber [S. aureus phage phi 11]	3.70E-48	37	39	AAL82278.1
37	24389	24811	140	Holin	holin [S. aureus phage phi 11]	8.70E-46	61	100	AAL82280.1
78	24597	24764	55						
6	24792	26237	481	Amidase	amidase [S. aureus phage phi 11]	0	83	100	AAL82281.1
80	26114	25917	65						

Bacteriophage 37 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
10	27951	26923	342	Integrase	integrase [S. aureus subsp. aureus MW2]	2.00E-100	50	100	BAB95804.1
14	28803	28015	262		unknown [S. aureus subsp. aureus MW2]	3.00E-129	85	99	BAB95635.1
31	29271	28816	151		unknown [S. aureus subsp. aureus MW2]	1.00E-68	80	100	BAB95634.1
69	29522	29289	77		unknown [S. epidermidis ATCC 12228]	1.10E-24	65	100	AAO04167.1
52	29829	29572	85		unknown [S. epidermidis ATCC 12228]	6.50E-17	46	94	AAO05977.1
39	30303	29881	140		unknown [S. aureus]	4.60E-39	56	100	AAL04145.1
133	30460	30317	47						
19	31106	30480	208	LexA repressor	LexA repressor [B. cereus ATCC 14579]	7.00E-22	32	100	AAP10633.1
71	31258	31485	75	Repressor					
110	31396	31238	52						
33	31505	31951	148		unknown [S. aureus subsp. aureus MRSA252]	5.60E-32	49	100	CAG40553.1
16	31965	32738	257	Antirepressor	anti-repressor [S. aureus phage phi 11]	2.30E-93	69	100	AAL82235.1
66	32739	32975	78		unknown [S. aureus subsp. aureus Mu50]	1.20E-05	39	84	BAB58186.1
137	32988	33128	46						
48	33318	33088	76		orf 11 [S. aureus prophage phiPV83]	1.80E-06	29	100	BAA97818.1
49	33365	33667	100		unknown [S. aureus subsp. aureus MSSA476]	1.40E-10	31	99	CAG43718.1
76	33680	33895	71						
92	33725	33549	58						
62	34000	34239	79						
59	34232	34486	84		unknown [S. aureus subsp. aureus Mu50]	2.50E-21	63	85	BAB57024.1
18	34449	35087	212	ssDNA-binding	unknown [S. aureus temperate phage phiSLT]	1.00E-79	69	100	BAB21711.1
34	35084	35530	148	ssDNA-binding	ssDNA-binding protein [S. aureus bacteriophage PVL]	2.00E-50	63	100	BAA31919.1
17	35543	36220	225		unknown [S. aureus temperate phage phiSLT]	7.00E-101	75	99	BAB21713.1
45	36210	36560	116						
12	36553	37335	260	DNA replication	DnaA analog [Bacteriophage LL-H]	4.30E-15	39	53	AAL77546.1
15	37337	38113	258	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	5.30E-82	59	100	AAL82346.1
87	38107	38295	62		unknown [S. aureus subsp. aureus Mu50]	1.10E-06	41	79	BAB57032.1
42	38279	38686	135	Endodeoxyribonuclease RusA	unknown [S. aureus subsp. aureus MSSA476]	8.90E-46	61	99	CAG43708.1
105	38687	38878	63						
89	38818	38630	62						
25	38891	39415	174	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.30E-06	30	64	CAG42686.1
166	39085	38963	40						
28	39416	39886	156		unknown [S. aureus subsp. aureus MSSA476]	6.60E-08	43	44	CAG42687.1

Bacteriophage 37 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
83	39887	40081	64						
27	40071	40535	154	Sensor	possible sensor protein [S. aureus phage phi 13]	1.30E-08	33	97	AAL82351.1
41	40552	40959	135	Sensor	possible sensor protein [S. aureus phage phi 13]	7.10E-11	33	95	AAL82351.1
58	40946	41152	68						
30	41142	41570	142						
65	41570	41806	78						
36	41806	42228	140	dUTPase	dUTPase [S. aureus bacteriophage PVL]	8.50E-25	40	100	BAA31926.1
88	42270	42458	62						
56	42464	42730	88						
98	42723	42899	58	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	5.20E-07	46	100	AAL82255.1
95	42899	43081	60						
44	43074	43478	134		unknown [B. cereus ATCC 14579]	7.20E-11	30	99	AAP10629.1

Bacteriophage EW

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
36	32	412	126		unknown [S. pyogenes SSI-1]	1.40E-09	39	70	BAC63628.1
9	396	1661	421	Large terminase	putative large terminase [Bacteriophage A118]	3.60E-45	31	100	CAB53788.1
8	1667	3091	474	Portal	portal protein [Bacteriophage SPP1]	3.60E-73	35	100	CAA39541.1
12	3054	4001	315	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	4.00E-133	75	98	BAA97628.1
147	3974	4108	44						
74	4112	4336	74						
22	4451	5047	198	Minor capsid	minor capsid protein [Bacteriophage phig1e]	5.80E-15	24	100	CAA66737.1
15	5064	5891	275	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	2.80E-60	48	94	AAL15075.1
55	5910	6191	93	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	1.60E-20	51	100	BAA97631.1
52	6191	6487	98	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.40E-32	67	100	BAA97632.1
43	6492	6827	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	3.40E-33	57	100	BAA97633.1
33	6814	7221	135		ORF48 [bacteriophage phi ETA]	2.10E-47	74	85	BAA97634.1
29	7233	7655	140		ORF49 [bacteriophage phi ETA]	4.90E-41	62	95	BAA97635.1
23	7659	8201	180	Major tail	ORF50 [bacteriophage phi ETA]	2.00E-42	49	100	BAA97636.1
99	8264	8767	167		ORF51 [bacteriophage phi ETA]	2.80E-61	68	96	BAA97637.1
57	8818	9096	92		ORF52 [bacteriophage phi ETA]	1.40E-16	44	100	BAA97638.1
1	9100	12027	975	Tape measure protein	tape measure protein [S. aureus phage phi 11]	0	44	94	AAL82270.1
196	11210	11320	36						
38	12040	12972	310		ORF54 [bacteriophage phi ETA]	2.00E-102	59	100	BAA97640.1
6	12985	14844	619	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	4.20E-27	28	47	AAT86193.1
159	14678	14806	42						
5	14856	16586	576		ORF56 [bacteriophage phi ETA]	3.90E-11	28	23	BAA97642.1
4	16601	18337	578		ORF572 [bacteriophage phi ETA]	7.60E-31	28	54	BAA97643.1
44	18334	18666	110						
148	18663	18797	44						
51	18820	19116	98		unknown [S. aureus temperate phage phiSLT]	4.00E-16	43	90	BAB21751.1
3	19244	21136	630	Amidase	cell wall hydrolase [S. aureus subsp. aureus Mu50]	0	52	100	BAB57071.1
39	19335	19592	85						
2	21153	23879	908	Tail fiber	tail fiber [S. aureus subsp. aureus Mu50]	3.00E-56	53	22	BAB57072.1
63	22012	21761	83	Structural	collagen-like protein [B. thuringiensis serovar israelensis]	1.50E-08	52	50	AAB16964.1
164	22792	22667	41						

Bacteriophage EW (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
27	23925	24359	144	Holin	holin [S. aureus phage phi 11]	2.60E-42	65	92	AAL82280.1
7	24340	25788	482	Amidase	amidase [S. aureus phage phi 11]	0	77	99	AAL82281.1
165	24701	24808	35						
11	28263	27229	344	Integrase	integrase [S. aureus phage phi 13]	8.10E-82	42	98	AAL82331.1
14	29158	28325	277		unknown [N. europaea ATCC 19718]	1.20E-74	50	97	CAD86410.1
25	29660	29196	154		unknown [S. aureus subsp. aureus Mu50]	1.30E-48	61	99	BAB57012.1
47	30013	29684	109	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.20E-35	67	98	CAG42672.1
71	30178	30387	69	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	8.20E-10	48	94	CAG42673.1
13	30426	31337	303	ParB-like nuclease	ParB-like nuclease domain protein [Treponema denticola ATCC 35405]	2.20E-16	42	34	AAS12707.1
17	31330	32100	256		unknown [E. faecalis V583]	1.10E-15	25	100	AAO82012.1
100	32160	32339	59		ORF8 [bacteriophage phi ETA]	8.20E-21	78	100	BAA97594.1
65	32568	32329	79						
16	32625	33401	258	Antirepressor	antirepressor [S. aureus temperate phage phiSLT]	3.70E-75	74	66	BAB21701.1
79	33436	33585	49						
133	33733	33876	47		unknown [S. aureus subsp. aureus MSSA476]	1.70E-16	91	97	CAG43720.1
82	34084	34290	68						
20	34545	33886	219		unknown [S. aureus subsp. aureus Mu50]	6.00E-105	87	98	BAB57020.1
40	34693	34998	101		unknown [S. epidermidis ATCC 12228]	4.30E-07	31	84	AAO05105.1
123	35003	35158	51						
154	35348	35229	39						
61	35390	35659	89						
77	35656	35874	72		unknown [S. aureus subsp. aureus Mu50]	2.10E-13	49	98	BAB57024.1
21	35871	36494	207	ssDNA-binding; Recombination	recombination protein [temperate phage PhiNIH1.1]	6.30E-39	45	100	AAL15054.1
34	36494	36892	132	ssDNA-binding	single strand DNA-binding protein [S. aureus subsp. aureus Mu50]	1.10E-19	39	100	BAB57026.1
19	36904	37575	223		unknown [S. aureus temperate phage phiSLT]	4.10E-95	73	99	BAB21713.1
84	37572	37778	68	Repressor	transcriptional regulator [S. pneumoniae TIGR4]	3.80E-07	38	92	AAK75240.1
18	37771	38475	234	DnaD and phage-associated domain	putative replication protein [L. phage BK5-T]	2.20E-09	31	61	AAK56827.1
41	38480	38827	115						
10	38820	40058	412	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	4.00E-115	53	98	AAL82244.1
78	40055	40273	72						
31	40260	40676	138	Endodeoxyribonuclease RusA	unknown [S. aureus subsp. aureus Mu50]	4.80E-28	49	86	BAB58142.2
26	40678	41106	142						
90	41106	41300	64						

Bacteriophage EW (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
46	41293	41601	102		unknown [S. aureus subsp. aureus N315]	2.90E-11	47	79	BAB43065.1
72	41598	41810	70						
101	41823	42002	59						
37	42021	42401	126		unknown [S. aureus subsp. aureus MRSA252]	3.70E-18	40	100	CAG40534.1
69	42398	42637	79						
58	42621	42896	91		unknown [N. farcinica IFM 10152]	3.80E-14	43	90	BAD56358.1
35	42880	43239	119	Staphylococcus nuclease	Staphylococcal nuclease family protein [L. interrogans serovar lai str. 56601]	7.00E-12	35	85	AAN50918.1
114	43487	43648	53		unknown [S. aureus subsp. aureus MW2]	4.20E-20	85	100	BAB95281.1
24	43659	44168	169	dUTPase	dUTPase [S. aureus phage phi 11]	9.60E-57	68	100	AAL82253.1
201	44110	44217	35						
204	44222	44329	35						
127	44330	44479	49						
30	44479	44898	139	Transcriptional activator RinA	Phage transcriptional activator [S. pyogenes MGAS10394]	2.10E-07	31	94	AAT86175.1

Bacteriophage 96

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
27	194	655	153		ORF39 [bacteriophage phi ETA]	7.10E-44	82	69	BAA97625.1
9	648	1871	407	Large terminase	terminase, large subunit [Bacteriophage EJ-1]	1.70E-28	26	97	CAE82121.1
7	1868	3292	474	Portal	phage portal protein [C. tetani E88]	1.80E-32	27	94	AAO36104.1
12	3261	4214	317	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	2.00E-157	89	97	BAA97628.1
66	4216	4422	68						
46	4277	4083	64						
19	4525	5109	194	Structural	putative scaffold protein [LactoB. johnsonii prophage Lj965]	8.80E-05	24	92	AAR27459.1
13	5126	6040	304	Major capsid	major capsid protein [Bacteriophage A118]	1.70E-64	44	99	CAB53792.1
132	6049	6195	48						
41	6201	6551	116	Head morphogenesis	phage related protein [B. subtilis phage PBSX]	3.10E-07	32	83	AAU23019.1
44	6554	6898	114	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	5.50E-36	61	96	BAA97633.1
29	6849	7298	149		ORF48 [bacteriophage phi ETA]	3.00E-41	64	77	BAA97634.1
81	7108	7308	66						
31	7311	7736	141		ORF49 [bacteriophage phi ETA]	3.50E-39	58	99	BAA97635.1
20	7737	8294	185	Major tail	ORF50 [bacteriophage phi ETA]	1.30E-42	50	98	BAA97636.1
39	8502	8867	121		ORF51[bacteriophage phi ETA]	2.10E-32	58	95	BAA97637.1
1	9200	12343	1047	Tape measure protein	tape measure protein [S. aureus phage phi 11]	3.00E-165	38	87	AAL82270.1
34	11133	10729	134						
17	12201	11482	239						
102	12764	12946	60						
43	12943	13299	118		ORF54 [bacteriophage phi ETA]	6.10E-56	84	100	BAA97640.1
3	13310	15196	628	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	4.40E-24	25	48	AAT86193.1
2	15209	17107	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	2.20E-39	28	77	AAO83891.1
5	17107	18930	607		ORF57 [bacteriophage phi ETA]	0	78	100	BAA97643.1
74	18404	18625	73						
38	18930	19307	125		ORF58 [bacteriophage phi ETA]	3.20E-62	94	100	BAA97644.1
104	19308	19484	58		ORF59 [bacteriophage phi ETA]	5.00E-26	93	98	BAA97645.1
52	19525	19824	99		77ORF058 [Bacteriophage 77]	3.90E-32	86	76	AAR87920.1
4	19961	21835	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
10	21848	23020	390	Tail fiber	tail fiber [S. aureus phage phi 11]	0	98	100	AAL82278.1
33	23026	23421	131		ORF63 [bacteriophage phi ETA]	2.60E-69	96	100	BAA97649.1

Bacteriophage 96 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
50	23477	23779	100	Holin	holin [S. aureus bacteriophage PVL]	1.70E-51	100	100	BAA31897.1
6	23790	25244	484	Amidase	amidase [S. aureus subsp. aureus MSSA476]	0	99	100	CAG42730.1
186	25521	25420	33						
59	25992	26198	68		unknown [S. aureus subsp. aureus MRSA252]	6.70E-20	68	95	CAG40141.1
89	26213	26413	66						
11	27945	26896	349	Integrase	integrase [S. aureus subsp. aureus MSSA476]	1.10E-54	35	95	CAG43729.1
25	28509	28006	167		putative lipoprotein [S. aureus subsp. aureus MRSA252]	9.70E-14	36	88	CAG40557.1
26	29004	28513	163						
28	29483	29025	152		unknown [S. aureus subsp. aureus MRSA252]	4.80E-85	100	100	CAG40556.1
47	29831	29505	108	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	2.40E-34	63	100	CAG42672.1
85	29994	30203	69	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.60E-10	51	94	CAG42673.1
16	30242	30967	241	Antirepressor	anti-repressor [S. aureus phage phi 11]	2.20E-52	57	85	AAL82235.1
86	30992	31201	69						
92	31215	31376	53		putative exported protein [S. aureus subsp. aureus MSSA476]	1.50E-22	94	100	CAG43717.1
45	31469	31798	109						
48	31779	32039	86		orf 39 [S. aureus bacteriophage PVL]	9.90E-26	62	100	BAA31913.1
22	32052	32588	178	Chromosome segregation	chromosome segregation SMC protein [OceanoB. iheyensis HTE831]	3.30E-05	24	84	BAC13484.1
14	32589	33368	259		ORF17 [bacteriophage phi ETA]	2.00E-144	99	100	BAA97603.1
21	33398	33952	184	ssDNA-binding	ssb [S. aureus phage phi 11]	7.00E-105	100	100	AAL82241.1
18	33965	34636	223		ORF20 [bacteriophage phi ETA]	2.00E-127	98	100	BAA97606.1
15	34629	35384	251	DnaD and phage-associated domain	unknown [B. cereus ZK]	4.20E-36	51	62	AAU16814.1
42	35384	35740	118						
8	35737	36978	413	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	0	99	100	AAL82244.1
78	36975	37190	71						
73	37194	37415	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
32	37426	37830	134		ORF25 [bacteriophage phi ETA]	7.10E-75	99	100	BAA97611.1
100	37835	38020	61		orf 23 [S. aureus prophage phiPV83]	1.10E-25	92	100	BAA97830.1
61	38021	38278	85	Repressor	HTH DNA-binding protein [S. aureus phage phi 11]	8.40E-41	100	96	AAL82248.1
40	38290	38649	119	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.10E-12	37	100	CAG42686.1
60	38649	38906	85		unknown [S. aureus subsp. aureus MSSA476]	2.60E-42	98	98	CAG42687.1
80	38909	39109	66		unknown [S. aureus subsp. aureus MRSA252]	2.70E-29	94	100	CAG40536.1
64	39124	39366	80		unknown [S. aureus subsp. aureus MRSA252]	1.60E-39	94	100	CAG40535.1

Bacteriophage 96 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
35	39381	39773	130		unknown [S. aureus subsp. aureus MRSA252]	1.70E-71	100	100	CAG40534.1
94	39770	39961	63		unknown [S. aureus subsp. aureus MRSA252]	5.60E-30	100	100	CAG40533.1
30	39961	40392	143		unknown [S. aureus subsp. aureus MRSA252]	5.00E-78	99	100	CAG40532.1
65	40385	40636	83		unknown [S. aureus subsp. aureus MRSA252]	7.90E-39	94	100	CAG41059.1
93	40626	40799	57		unknown [S. aureus subsp. aureus MW2]	8.50E-26	100	100	BAB95283.1
55	40800	41081	93		unknown [S. aureus subsp. aureus MW2]	6.20E-49	98	100	BAB95282.1
114	41082	41243	53		unknown [S. aureus subsp. aureus MW2]	2.80E-24	98	100	BAB95281.1
23	41258	41791	177		unknown [S. aureus subsp. aureus MW2]	6.20E-97	98	100	BAB95280.1
97	41828	42016	62		orf 55 [S. aureus bacteriophage PVL]	2.20E-26	90	100	BAA31928.1
217	41877	41978	33						
79	41991	42200	69		orf 56 [S. aureus bacteriophage PVL]	8.70E-28	98	91	BAA31929.1
62	42197	42433	78		unknown [S. aureus subsp. aureus Mu50]	8.10E-39	97	100	BAB57042.1
24	42367	41861	168						
37	42423	42809	128		unknown [S. aureus subsp. aureus Mu50]	1.50E-67	99	100	BAB57043.1
105	42809	42982	57	Transcriptional activator RinB	int gene activator RinB [S. aureus subsp. aureus Mu50]	2.70E-24	98	100	BAB57044.1
36	42983	43384	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage ROSA

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
34	140	520	126		unknown[S. pyogenes phage 315.5]	4.90E-10	39	73	AAM79936.1
8	504	1769	421	Large terminase	putative large terminase [S. pyogenes phage 315.5]	3.00E-115	74	61	AAM79934.1
7	1770	3194	474	Portal	portal protein [Bacteriophage SPP1]	3.70E-65	34	100	CAA39541.1
11	3151	4110	319	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	3.00E-156	87	98	BAA97628.1
20	4223	4822	199	Minor capsid	minor capsid protein [Bacteriophage phig1e]	1.30E-17	29	100	CAA66737.1
13	4844	5668	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	1.10E-61	49	97	AAL15075.1
44	5685	6011	108	Rho termination factor, N-terminal domain	ORF45 [bacteriophage phi ETA]	2.10E-51	94	100	BAA97631.1
47	6011	6325	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	7.90E-54	97	100	BAA97632.1
43	6318	6653	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	5.00E-37	63	99	BAA97633.1
49	6604	6906	100		ORF48 [bacteriophage phi ETA]	3.10E-13	55	56	BAA97634.1
19	6991	7650	219	Early protein	possible Early Protein (E6) [Prochlorococcus marinus str. MIT 9313]	3.90E-05	31	53	CAE20971.1
27	8036	8461	141		ORF49 [bacteriophage phi ETA]	3.50E-39	58	99	BAA97635.1
21	8462	9019	185		ORF50 [bacteriophage phi ETA]	1.30E-42	50	98	BAA97636.1
36	9086	9592	168		ORF51 [bacteriophage phi ETA]	7.00E-44	56	98	BAA97637.1
124	9772	9921	49						
1	9925	13068	1047	Tape measure protein	tape measure protein [S. aureus phage phi 11]	1.00E-162	37	87	AAL82270.1
39	13083	14024	313		ORF54 [bacteriophage phi ETA]	7.00E-146	78	100	BAA97640.1
3	14035	15921	628	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	4.40E-24	25	48	AAT86193.1
2	15934	17832	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	2.40E-38	27	76	AAO83891.1
5	17832	19655	607		ORF57 [bacteriophage phi ETA]	0	78	100	BAA97643.1
32	19655	20032	125		ORF58 [bacteriophage phi ETA]	1.10E-62	94	100	BAA97644.1
103	20033	20209	58		ORF59 [bacteriophage phi ETA]	5.00E-26	93	98	BAA97645.1
51	20250	20549	99		unknown [S. aureus temperate phage phiSLT]	3.30E-31	63	100	BAB21751.1
4	20686	22560	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
10	22573	23745	390	Tail	tail fiber [S. aureus phage phi 11]	0	99	100	AAL82278.1
31	23751	24146	131		ORF63 [bacteriophage phi ETA]	9.10E-70	97	100	BAA97649.1
50	24202	24504	100	Holin	holin [S. aureus temperate phage phiSLT]	4.90E-51	100	100	BAB21752.1
6	24516	25970	484	Amidase	amidase [S. aureus subsp. aureus MRSA252]	0	100	100	CAG40495.1
198	25630	25743	37						
9	28020	26815	401	Integrase	phage integrase [S. aureus subsp. aureus MSSA476]	0	85	100	CAG42666.1

Bacteriophage ROSA (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
98	28131	28310	59	Excisionase	excisionase [S. aureus subsp. aureus Mu50]	3.80E-26	97	100	BAB57010.1
207	28432	28325	35		unknown [S. aureus]	1.80E-05	77	85	AAL04145.1
25	28927	28436	163						
26	29409	28948	153		unknown [S. aureus temperate phage phiSLT]	3.50E-83	97	100	BAB21699.1
46	29745	29422	107	Repressor	phage repressor [S. aureus subsp. aureus MW2]	3.90E-53	97	100	BAB95301.1
63	29909	30157	82	Repressor	putative Cro-like repressor - phage associated [S. pyogenes phage 315.5]	7.00E-11	52	79	AAM79956.1
114	30172	30333	53						
42	30571	30326	81						
17	30627	31379	250	Antirepressor	putative anti repressor [S. aureus subsp. aureus MRSA252]	7.00E-124	91	100	CAG41079.1
74	31395	31613	72		orf 10 [S. aureus prophage phiPV83]	4.10E-06	86	38	BAA97817.1
58	31643	31906	87	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.20E-47	100	100	CAG42677.1
115	31918	32079	53		putative exported protein [S. aureus subsp. aureus MSSA476]	1.70E-21	91	100	CAG43717.1
193	32048	31938	36						
53	32171	32431	86		orf 39 [S. aureus bacteriophage PVL]	2.50E-45	100	100	BAA31913.1
72	32441	32662	73		unknown [S. aureus subsp. aureus Mu50]	5.90E-37	100	100	BAB57024.1
14	32655	33443	262		ORF17 [bacteriophage phi ETA]	1.70E-99	67	98	BAA97603.1
22	33472	34023	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.50E-61	63	100	AAL82241.1
168	33654	33535	39						
80	33812	34015	67		ORF19 [bacteriophage phi ETA]	1.10E-30	99	100	BAA97605.1
91	34036	34224	62		ORF20 [bacteriophage phi ETA]	5.60E-22	100	79	BAA97606.1
24	34217	34708	163		ORF20 [bacteriophage phi ETA]	4.40E-93	98	100	BAA97606.1
171	34705	34821	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
12	35671	34814	285		unknown [S. pyogenes MGAS10394]	4.20E-22	36	58	AAT86873.1
16	35736	36506	256	DNA replication	DnaA analog [Bacteriophage LL-H]	3.80E-40	38	100	AAL77546.1
15	36516	37295	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	6.00E-150	99	100	AAL82346.1
117	37289	37447	52		unknown [S. aureus subsp. aureus Mu50]	2.20E-21	90	100	BAB57032.1
68	37460	37681	73		ORF24 [bacteriophage phi ETA]	5.00E-36	99	100	BAA97610.1
30	37691	38098	135	Endodeoxyribonuclease RusA	orf 48 [S. aureus bacteriophage PVL]	2.40E-67	88	99	BAA31922.1
95	38098	38283	61		ORF26 [bacteriophage phi ETA]	5.80E-27	93	100	BAA97612.1
38	38284	38643	119	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.20E-11	37	100	CAG42686.1
62	38643	38897	84		unknown [S. aureus subsp. aureus MRSA252]	3.10E-43	99	100	CAG40537.1
61	38897	39145	82		unknown [S. aureus subsp. aureus N315]	3.20E-40	94	100	BAB43064.1
29	39160	39564	134		unknown [S. aureus subsp. aureus MSSA476]	2.80E-71	97	99	CAG42690.1

Bacteriophage ROSA (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
41	39561	39908	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93	100	AAL82351.1
48	39905	40213	102		unknown [S. aureus subsp. aureus MSSA476]	8.90E-53	97	100	CAG42692.1
59	40206	40460	84		orf 52 [S. aureus bacteriophage PVL]	1.10E-37	94	97	BAA31925.1
92	40447	40617	56						
23	40610	41140	176	dUTPase	putative dUTP pyrophosphatase [S. aureus subsp. aureus MRSA252]	9.10E-85	87	100	CAG41057.1
54	41177	41464	95		unknown [S. aureus subsp. aureus MRSA252]	4.30E-18	75	58	CAG40528.1
33	41457	41843	128		orf31 [S. aureus prophage phiPV83]	2.20E-63	92	99	BAA97838.1
105	41840	42013	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	1.00E-23	95	100	AAL82255.1
37	42014	42379	121						
128	42380	42526	48		unknown [S. aureus subsp. aureus Mu50]	6.30E-08	96	58	BAB57045.1
28	42550	42972	140	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	1.20E-71	94	99	AAL82256.1

Bacteriophage 71

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
41	66	446	126		unknown [S. pyogenes SSI-1]	4.90E-10	39	73	BAC63628.1
8	430	1695	421	Large terminase	putative large terminase [Bacteriophage A118]	4.70E-45	31	100	CAB53788.1
6	1696	3120	474	Portal	portal protein [Bacteriophage SPP1]	3.70E-65	34	100	CAA39541.1
12	3077	4036	319	Head morphogenesis; Minor head	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	8.00E-156	87	98	BAA97628.1
					phage related minor head protein [B. subtilis phage PBSX]	3.40E-63	43	95	AAU23011.1
20	4149	4748	199	Minor capsid	minor capsid protein [Bacteriophage phig1e]	1.30E-17	29	100	CAA66737.1
14	4770	5594	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	1.10E-61	49	97	AAL15075.1
50	5611	5937	108	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	2.10E-51	94	100	BAA97631.1
51	5937	6251	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	7.90E-54	97	100	BAA97632.1
49	6244	6579	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	9.40E-60	97	100	BAA97633.1
46	6566	6979	137	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	3.40E-05	32	59	AAR27382.1
97	6765	6941	58						
32	6992	7429	145	Inorganic pyrophosphatase	ORF49 [bacteriophage phi ETA]	3.80E-78	99	100	BAA97635.1
23	7416	7976	186		ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
28	8038	8532	164		ORF51 [bacteriophage phi ETA]	1.00E-89	100	100	BAA97637.1
48	8553	8894	113		ORF52 [bacteriophage phi ETA]	1.60E-59	98	100	BAA97638.1
1	8897	11866	989	Tape measure protein	tape measure protein [S. aureus phage phi 11]	2.00E-165	37	93	AAL82270.1
13	11881	12816	311		ORF54 [bacteriophage phi ETA]	1.00E-177	97	100	BAA97640.1
3	12827	14713	628	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	7.10E-22	25	46	AAT86193.1
2	14726	16624	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	1.40E-38	27	76	AAO83891.1
5	16624	18447	607		ORF57 [bacteriophage phi ETA]	0	82	100	BAA97643.1
40	18447	18824	125		ORF58 [bacteriophage phi ETA]	2.60E-64	98	100	BAA97644.1
96	18824	19000	58		ORF59 [bacteriophage phi ETA]	1.10E-28	100	98	BAA97645.1
53	19041	19340	99		unknown [S. aureus temperate phage phiSLT]	6.70E-48	93	100	BAB21751.1
4	19477	21351	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
10	21364	22536	390	Tail fiber	tail fiber [S. aureus phage phi 11]	0	99	100	AAL82278.1
36	22542	22937	131		ORF63 [bacteriophage phi ETA]	9.10E-70	97	100	BAA97649.1
56	22992	23267	91	Holin	holin [bacteriophage bIL285]	4.10E-16	49	79	AAK08286.1
7	23254	24666	470	Amidase	amidase [S. aureus subsp. aureus MSSA476]	4.70E-89	49	78	CAG42730.1
24	25284	24727	185	Beta-lactamase	probable beta-lactamase [S. aureus subsp. aureus Mu50]	1.60E-26	41	100	BAB57977.1
21	25804	26391	195						

Bacteriophage 71 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
31	26388	26843	151						
11	28216	27167	349	Integrase	integrase [S. aureus subsp. aureus Mu50]	0	100	100	BAB57009.1
42	28645	28274	123		ORF2 [bacteriophage phi ETA]	1.10E-65	100	100	BAA97588.1
33	29060	28635	141		ORF3 [bacteriophage phi ETA]	2.80E-76	99	100	BAA97589.1
30	29539	29078	153		unknown [S. aureus temperate phage phiSLT]	1.20E-83	99	100	BAB21699.1
67	30018	30254	78						
22	30124	29552	190	Repressor	repressor [S. aureus temperate phage phiSLT]	9.00E-55	100	54	BAB21700.1
92	30268	30447	59		ORF8 [bacteriophage phi ETA]	8.50E-26	95	100	BAA97594.1
29	31030	30548	160		ORF9 [bacteriophage phi ETA]	5.00E-86	100	100	BAA97595.1
17	31090	31839	249	Antirepressor	anti repressor [S. aureus bacteriophage PVL]	8.00E-138	99	100	BAA31909.1
132	31855	31998	47		unknown [S. aureus subsp. aureus Mu50]	8.00E-19	100	100	BAB57019.1
72	32194	32406	70						
19	32661	32008	217		ORF12 [bacteriophage phi ETA]	3.60E-56	54	99	BAA97598.1
74	32732	32953	73	Transcriptional regulator	orf 12 [S. aureus prophage phiPV83]	1.70E-31	95	100	BAA97819.1
105	32946	33107	53		putative exported protein [S. aureus subsp. aureus MRSA252]	6.20E-24	100	100	CAG41074.1
195	33076	32966	36						
54	33200	33460	86		ORF15 [bacteriophage phi ETA]	4.30E-45	99	100	BAA97601.1
75	33470	33691	73		unknown [S. aureus subsp. aureus Mu50]	2.00E-21	63	100	BAB57024.1
16	33684	34472	262		ORF17 [bacteriophage phi ETA]	3.00E-100	67	98	BAA97603.1
25	34501	35052	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.50E-61	63	100	AAL82241.1
174	34683	34564	39						
81	34841	35044	67		ORF19 [bacteriophage phi ETA]	1.10E-30	99	100	BAA97605.1
18	35065	35757	230		ORF20 [bacteriophage phi ETA]	6.00E-126	97	96	BAA97606.1
15	35729	36526	265	DnaD and phage-associated domain; Replisome organizer	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	7.00E-05	21	69	CAG43710.1
43	36526	36882	118						
9	36879	38120	413	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	0	99	100	AAL82244.1
78	38117	38332	71						
69	38335	38556	73		ORF24 [bacteriophage phi ETA]	5.00E-36	99	100	BAA97610.1
35	38567	38971	134		ORF25 [bacteriophage phi ETA]	4.60E-74	98	100	BAA97611.1
90	38976	39161	61		orf 23 [S. aureus prophage phiPV83]	2.40E-25	90	100	BAA97830.1
44	39162	39518	118		unknown [S. aureus subsp. aureus MRSA252]	4.00E-39	65	98	CAG41062.1
65	39522	39764	80		orf 51 [S. aureus bacteriophage PVL]	6.60E-41	96	100	BAA31924.1
34	39778	40182	134		unknown [S. aureus subsp. aureus MSSA476]	5.10E-49	66	100	CAG42690.1

Bacteriophage 71 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
57	40182	40457	91		unknown [S. aureus subsp. aureus MSSA476]	2.20E-30	85	80	CAG42692.1
62	40450	40704	84		unknown [S. aureus subsp. aureus MW2]	4.60E-39	96	97	BAB95284.1
88	40691	40861	56						
26	40854	41363	169	dUTPase	dUTPase [S. aureus phage phi 11]	4.20E-89	97	100	AAL82253.1
64	41400	41645	81		orf 54 [S. aureus bacteriophage PVL]	8.50E-33	88	96	BAA31927.1
118	41642	41794	50		ORF35 [bacteriophage phi ETA]	8.80E-18	93	92	BAA97621.1
27	41787	42245	152						
144	42258	42431	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	3.70E-21	86	100	AAL82255.1
38	42432	42833	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage 55

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
38	266	637	123		ORF39 [bacteriophage phi ETA]	1.70E-63	100	100	BAA97625.1
9	627	1838	403	Large terminase	putative phage terminase [N. farcinica IFM 10152]	4.00E-38	31	100	BAD58781.1
6	1852	3270	472	Portal	portal protein [Bacteriophage SPP1]	1.10E-72	35	100	CAA39541.1
11	3227	4189	320	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	0	99	100	BAA97628.1
190	4029	4136	35						
46	4210	3941	89						
21	4287	4883	198	Minor capsid	minor capsid protein [Bacteriophage phig1e]	1.70E-19	30	97	CAA66737.1
13	4904	5728	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	9.60E-61	49	97	AAL15075.1
45	5745	6071	108	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	5.10E-53	96	100	BAA97631.1
47	6071	6385	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.20E-54	98	100	BAA97632.1
43	6378	6713	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	1.40E-60	98	100	BAA97633.1
41	6700	7113	137	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	2.60E-05	32	59	AAR27382.1
88	6899	7075	58						
30	7126	7563	145	Inorganic pyrophosphatase	ORF49 [bacteriophage phi ETA]	4.20E-77	99	100	BAA97635.1
22	7550	8110	186	Major tail	ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
26	8172	8666	164		ORF51 [bacteriophage phi ETA]	1.00E-89	100	100	BAA97637.1
42	8687	9028	113		ORF52 [bacteriophage phi ETA]	2.40E-60	100	100	BAA97638.1
1	9031	12000	989	Tape measure protein	tape measure protein [S. aureus phage phi 11]	3.00E-165	37	93	AAL82270.1
15	11942	11139	267						
12	12015	12950	311		ORF54 [bacteriophage phi ETA]	4.00E-180	98	100	BAA97640.1
3	12961	14844	627	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	1.60E-21	25	46	AAT86193.1
2	14857	16755	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	9.30E-38	27	77	AAO83891.1
5	16755	18578	607		ORF57 [bacteriophage phi ETA]	0	88	100	BAA97643.1
66	18052	18273	73						
36	18578	18955	125		ORF58 [bacteriophage phi ETA]	5.30E-65	99	100	BAA97644.1
90	18959	19132	57		ORF59 [bacteriophage phi ETA]	1.10E-28	100	100	BAA97645.1
49	19172	19471	99		ORF60 [bacteriophage phi ETA]	1.80E-48	93	100	BAA97646.1
4	19608	21482	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
8	21495	22733	412	Tail fiber	tail fiber [S. aureus subsp. aureus Mu50]	0	92	100	BAB57072.1
92	21697	21569	42						
35	22738	23133	131		ORF63 [bacteriophage phi ETA]	2.20E-63	89	100	BAA97649.1

Bacteriophage 55 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
31	23189	23626	145	Holin	holin [S. aureus phage phi 11]	6.00E-76	98	100	AAL82280.1
7	23607	25052	481	Amidase	amidase [S. aureus phage phi 11]	0	99	100	AAL82281.1
171	23965	24072	35	Amidase	amidase [bacteriophage 80 alpha]	8.10E-06	79	82	AAB39699.1
187	25518	25628	36		unknown [S. aureus subsp. aureus Mu50]	1.10E-13	97	100	BAB57077.1
73	25630	25815	61	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MRSA252]	3.60E-21	79	100	CAG40305.1
137	26040	25903	45						
48	26161	26472	103						
37	26459	26842	127						
10	28231	27182	349	Integrase	integrase [S. aureus subsp. aureus Mu50]	0	99	100	BAB57009.1
131	28745	28602	47						
25	28797	28297	166		putative lipoprotein [S. aureus subsp. aureus MSSA476]	4.70E-13	33	90	CAG42670.1
28	29276	28815	153		unknown [S. aureus]	1.60E-67	83	100	AAL04144.1
44	29627	29298	109	Repressor	transcriptional regulator, Cro/CI family [E. faecalis V583]	1.70E-08	30	100	AAO81213.1
54	29804	30052	82	Cro repressor					
29	30065	30508	147		unknown [S. aureus subsp. aureus MRSA252]	4.00E-35	51	100	CAG40553.1
82	30859	31044	61	Repressor; Helix-turn-helix motif	ORF10 [bacteriophage phi ETA]	3.40E-27	100	100	BAA97596.1
18	31046	31801	251	Antirepressor	anti repressor [S. aureus subsp. aureus Mu50]	7.00E-140	99	100	BAB58156.1
126	31817	31960	47		unknown [S. aureus subsp. aureus Mu50]	8.90E-18	96	100	BAB57019.1
67	32156	32368	70						
20	32623	31970	217		ORF12 [bacteriophage phi ETA]	3.60E-56	54	99	BAA97598.1
68	32694	32915	73	Transcriptional regulator	ORF13 [bacteriophage phi ETA]	8.00E-34	100	100	BAA97599.1
99	32908	33069	53		putative exported protein [S. aureus subsp. aureus MRSA252]	1.20E-22	94	100	CAG41074.1
56	33161	33421	86		orf 39 [S. aureus bacteriophage PVL]	1.20E-44	99	100	BAA31913.1
27	33436	33915	159		orf 16 [S. aureus prophage phiPV83]	2.10E-84	99	100	BAA97823.1
17	33915	34688	257	AAA ATPase	ORF17 [bacteriophage phi ETA]	9.90E-57	42	100	BAA97603.1
24	34718	35269	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.20E-61	63	100	AAL82241.1
167	34900	34781	39						
72	35058	35261	67		ORF19 [bacteriophage phi ETA]	1.10E-30	99	100	BAA97605.1
19	35282	35974	230		ORF20 [bacteriophage phi ETA]	2.00E-125	97	96	BAA97606.1
14	35946	36767	273	Replisome organizer	putative replisome organizer [L. bacteriophage 4268]	5.10E-06	22	96	AAM83050.1
16	36780	37565	261	DNA replication	dnaC [S. aureus phage phi 13]	7.70E-57	45	91	AAL82346.1
103	37562	37720	52		unknown [S. aureus subsp. aureus Mu50]	8.40E-21	90	100	BAB57032.1
64	37733	37954	73		unknown [S. aureus temperate phage phiSLT]	3.20E-35	96	100	BAB21717.1

Bacteriophage 55 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
33	37964	38368	134		ORF25 [bacteriophage phi ETA]	1.20E-74	99	100	BAA97611.1
83	38373	38558	61		orf 23 [S. aureus prophage phiPV83]	7.90E-24	90	100	BAA97830.1
40	38559	38927	122		orf 50 [S. aureus bacteriophage PVL]	3.10E-60	93	100	BAA31923.1
60	38931	39173	80		orf 51 [S. aureus bacteriophage PVL]	1.40E-38	93	100	BAA31924.1
32	39187	39591	134		unknown [S. aureus subsp. aureus MSSA476]	5.10E-49	66	100	CAG42690.1
52	39591	39866	91		orf 27 [S. aureus prophage phiPV83]	5.00E-30	85	80	BAA97834.1
57	39859	40107	82		unknown [S. aureus subsp. aureus MRSA252]	2.30E-38	96	100	CAG40531.1
23	40100	40636	178		unknown [S. aureus subsp. aureus MSSA476]	9.60E-98	99	100	CAG42694.1
59	40673	40918	81		orf 54 [S. aureus bacteriophage PVL]	8.50E-33	88	96	BAA31927.1
71	40915	41121	68		ORF35 [bacteriophage phi ETA]	1.40E-30	94	100	BAA97621.1
84	41118	41291	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	6.70E-23	93	100	AAL82255.1
34	41292	41693	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1
58	41877	41623	84						

Bacteriophage 29

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
95	385	552	55		ORF39 [bacteriophage phi ETA]	5.20E-23	98	100	BAA97625.1
9	545	1753	402	Large terminase	ORF40 (putative large subunit terminase) [bacteriophage phi ETA]	0	100	100	BAA97626.1
6	1707	3185	492	Portal	ORF41 (portal protein) [bacteriophage phi ETA]	0	99	98	BAA97627.1
13	3124	4104	326	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	8.00E-180	98	98	BAA97628.1
42	4125	3856	89						
26	4202	4726	174	Minor capsid	ORF43 (minor capsid protein) [bacteriophage phi ETA]	6.50E-72	85	93	BAA97629.1
153	4599	4721	40						
12	4738	5697	319						
41	5714	6040	108	Rho termination factor, N-terminal	unknown [S. pyogenes phage 315.5]	4.20E-07	36	95	AAM79928.1
43	6040	6354	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.80E-53	95	100	BAA97632.1
40	6347	6682	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	9.40E-60	97	100	BAA97633.1
50	6669	7082	137		ORF48 [bacteriophage phi ETA]	2.50E-64	97	84	BAA97634.1
92	6868	7044	58						
28	7095	7532	145		ORF49 [bacteriophage phi ETA]	2.90E-78	99	100	BAA97635.1
23	7519	8079	186	Major tail	ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
27	8141	8635	164		ORF51 [bacteriophage phi ETA]	3.90E-89	99	100	BAA97637.1
39	8656	8997	113		ORF52 [bacteriophage phi ETA]	2.40E-60	100	100	BAA97638.1
1	9000	12143	1047	Tape measure protein	tape measure protein [S. aureus phage phi 11]	5.00E-165	37	87	AAL82270.1
16	12085	11282	267						
14	12158	13093	311		ORF54 [bacteriophage phi ETA]	6.00E-180	98	100	BAA97640.1
3	13104	14990	628	Endopeptidase	endopeptidase [S. pyogenes MGAS10394]	9.30E-22	25	46	AAT86193.1
2	15003	16901	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	1.20E-37	27	76	AAO83891.1
5	16901	18724	607		unknown [S. aureus bacteriophage phi 53]	0	94	100	AAM49605.1
66	18198	18419	73						
34	18724	19101	125		ORF58 [bacteriophage phi ETA]	6.70E-60	91	100	BAA97644.1
84	19102	19284	60		ORF59 [bacteriophage phi ETA]	3.80E-26	93	95	BAA97645.1
44	19325	19624	99		ORF60 [bacteriophage phi ETA]	7.60E-52	100	100	BAA97646.1
4	19761	21635	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
10	21648	22820	390	Tail	tail fiber [S. aureus phage phi 11]	0	98	100	AAL82278.1
32	22826	23221	131		ORF63 [bacteriophage phi ETA]	4.50E-69	97	100	BAA97649.1
29	23277	23714	145	Holin	holin [S. aureus phage phi 11]	1.20E-76	99	100	AAL82280.1

Bacteriophage 29 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
7	23695	25140	481	Amidase	amidase [S. aureus phage phi 11]	0	100	100	AAL82281.1
80	24053	24232	59	Amidase	amidase [bacteriophage 80 alpha]	3.80E-18	96	76	AAB39699.1
173	25416	25315	33						
130	25686	25549	45						
20	25816	26478	220						
21	26493	27134	213						
11	28523	27477	348	Integrase	integrase [S. aureus phage phi 11]	0	98	100	AAL82229.1
86	28636	28815	59	Excisionase	excisionase [S. aureus subsp. aureus Mu50]	3.80E-26	97	100	BAB57010.1
33	29196	28795	133		unknown [S. aureus subsp. aureus Mu50]	3.80E-68	97	100	BAB57011.1
72	29728	29525	67		unknown [S. aureus subsp. aureus Mu50]	4.20E-30	97	94	BAB57011.1
22	30393	29764	209	LexA repressor	LexA repressor [B. cereus ATCC 14579]	4.30E-27	35	100	AAP10633.1
49	30547	30774	75	DNA-binding; Repressor	unknown [LactoB. plantarum WCFS1]	7.70E-05	32	74	CAD63511.1
102	30797	30958	53						
56	31199	30951	82						
82	31638	31823	61	Helix-turn-helix motif	ORF10 [bacteriophage phi ETA]	3.40E-27	100	100	BAA97596.1
18	31825	32568	247	Antirepressor	anti repressor [S. aureus subsp. aureus N315]	5.00E-122	90	100	BAB43081.1
91	32593	32769	58		orf 10 [S. aureus prophage phiPV83]	2.30E-23	93	100	BAA97817.1
58	32974	32744	76		orf 11 [S. aureus prophage phiPV83]	4.50E-37	99	100	BAA97818.1
67	33045	33266	73	Transcriptional regulator	orf 12 [S. aureus prophage phiPV83]	8.30E-31	93	100	BAA97819.1
101	33259	33420	53		putative exported protein [S. aureus subsp. aureus MSSA476]	8.10E-24	98	100	CAG43717.1
191	33389	33279	36						
48	33517	33777	86		orf 39 [S. aureus bacteriophage PVL]	1.60E-44	98	100	BAA31913.1
64	33787	34008	73		unknown [S. aureus subsp. aureus Mu50]	9.20E-22	63	100	BAB57024.1
17	34001	34789	262		ORF17 [bacteriophage phi ETA]	1.70E-99	67	98	BAA97603.1
24	34818	35369	183	ssDNA-binding	ssb [S. aureus phage phi 11]	1.50E-61	63	100	AAL82241.1
71	35158	35361	67		ORF19 [bacteriophage phi ETA]	1.10E-30	99	100	BAA97605.1
19	35382	36074	230		ORF20 [bacteriophage phi ETA]	1.00E-126	98	96	BAA97606.1
15	36046	36852	268	DnaD and phage-associated domain; Replisome organizer	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	3.20E-05	20	78	CAG43710.1
38	36852	37208	118						
8	37205	38446	413	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	0	99	100	AAL82244.1
69	38443	38658	71						
65	38662	38883	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
31	38894	39298	134		ORF25 [bacteriophage phi ETA]	6.00E-74	99	100	BAA97611.1

Bacteriophage 29 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
83	39303	39488	61		orf 23 [S. aureus prophage phiPV83]	7.10E-25	90	100	BAA97830.1
35	39489	39860	123		putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	2.00E-11	43	76	CAG42686.1
55	39861	40109	82		unknown [S. aureus subsp. aureus N315]	3.30E-37	89	100	BAB43064.1
54	40114	40371	85		orf 52 [S. aureus bacteriophage PVL]	1.20E-39	99	96	BAA31925.1
25	40364	40873	169	dUTPase	dUTPase [S. aureus bacteriophage PVL]	7.00E-92	100	100	BAA31926.1
60	40910	41146	78		unknown [S. aureus temperate phage phiSLT]	2.60E-37	100	97	BAB21724.1
61	41171	41407	78		unknown [S. aureus temperate phage phiSLT]	2.80E-39	99	100	BAB21725.1
85	41397	41573	58	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	3.90E-23	90	100	AAL82255.1
37	41574	41939	121						
118	41940	42086	48		unknown [S. aureus subsp. aureus Mu50]	6.30E-08	96	58	BAB57045.1
30	42111	42533	140	Transcriptional activator RinA	rinA [S. aureus phage phi 11]	1.20E-71	94	99	AAL82256.1

Bacteriophage 52A

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
94	462	629	55		ORF39 [bacteriophage phi ETA]	1.20E-22	96	100	BAA97625.1
9	622	1830	402	Large terminase	putative phage terminase [Nocardia farcinica IFM 10152]	2.00E-37	31	100	BAD58781.1
6	1784	3262	492	Portal	portal protein [Bacteriophage SPP1]	1.00E-73	35	99	CAA39541.1
12	3201	4181	326	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	2.00E-180	98	98	BAA97628.1
47	4202	3933	89						
25	4279	4803	174	Minor capsid	ORF43 (minor capsid protein) [bacteriophage phi ETA]	6.50E-72	85	93	BAA97629.1
142	4676	4798	40						
11	4815	5774	319	ATP-binding					
45	5791	6117	108	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	1.20E-43	82	100	BAA97631.1
48	6117	6431	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.40E-53	96	100	BAA97632.1
43	6424	6759	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	6.10E-59	95	100	BAA97633.1
41	6809	7159	116	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	6.40E-05	38	52	AAR27382.1
88	6945	7121	58						
30	7172	7609	145		ORF49 [bacteriophage phi ETA]	1.20E-76	98	100	BAA97635.1
21	7596	8156	186	Major tail	ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
27	8218	8712	164		ORF51 [bacteriophage phi ETA]	3.00E-89	99	100	BAA97637.1
1	9077	12220	1047	Tape measure protein	tape measure protein [S. aureus phage phi 11]	4.00E-166	37	87	AAL82270.1
14	12235	13170	311		ORF54 [bacteriophage phi ETA]	0	99	100	BAA97640.1
3	13181	15067	628	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	7.10E-22	25	46	AAT86193.1
2	15080	16978	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	5.40E-38	27	77	AAO83891.1
155	16068	16184	38						
5	16978	18801	607		ORF57 [bacteriophage phi ETA]	0	82	100	BAA97643.1
71	18275	18496	73						
38	18801	19178	125		ORF58 [bacteriophage phi ETA]	2.00E-59	91	100	BAA97644.1
84	19179	19361	60		ORF59 [bacteriophage phi ETA]	3.80E-26	93	95	BAA97645.1
49	19402	19701	99		unknown [S. aureus temperate phage phiSLT]	7.60E-52	100	100	BAB21751.1
4	19838	21712	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
8	21725	22963	412	Tail fiber	tail fiber [S. aureus subsp. aureus Mu50]	0	98	100	BAB57072.1
36	22968	23363	131		ORF63 [bacteriophage phi ETA]	9.10E-70	97	100	BAA97649.1
31	23419	23856	145	Holin	holin [S. aureus subsp. aureus Mu50]	5.10E-75	96	100	BAB57074.1
7	23837	25282	481	Amidase	amidase [S. aureus phage phi 11]	0	99	100	AAL82281.1
157	24195	24302	35	Amidase	amidase [bacteriophage 80 alpha]	8.10E-06	79	82	AAB39699.1

Bacteriophage 52A (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
13	26059	26853	264						
19	26860	27597	245		unknown [S. aureus subsp. aureus MRSA252]	1.30E-23	41	57	CAG40307.1
10	29329	28124	401	Integrase	phage integrase [S. aureus subsp. aureus MSSA476]	0	85	100	CAG42666.1
26	29893	29393	166		putative lipoprotein [S. aureus subsp. aureus MRSA252]	2.80E-13	37	83	CAG40557.1
28	30388	29897	163						
29	30867	30409	152		unknown [S. aureus subsp. aureus MRSA252]	4.80E-85	100	100	CAG40556.1
54	31215	30937	92	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.20E-28	66	100	CAG42672.1
72	31378	31587	69	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.60E-10	51	94	CAG42673.1
18	31626	32351	241	Antirepressor	anti-repressor [S. aureus phage phi 11]	5.00E-52	57	85	AAL82235.1
73	32376	32585	69						
79	32599	32760	53		putative exported protein [S. aureus subsp. aureus MSSA476]	4.40E-22	91	100	CAG43717.1
171	32729	32619	36						
46	32853	33170	105						
44	33175	33435	86		orf 39 [S. aureus bacteriophage PVL]	2.60E-26	66	100	BAA31913.1
23	33448	33984	178	Chromosome segregation	chromosome segregation SMC protein [OceanoB. iheyensis HTE831]	3.30E-05	24	84	BAC13484.1
16	33985	34764	259		ORF17 [bacteriophage phi ETA]	6.00E-145	99	100	BAA97603.1
22	34794	35348	184	ssDNA-binding	ssb [S. aureus phage phi 11]	7.00E-105	100	100	AAL82241.1
20	35361	36053	230		ORF20 [bacteriophage phi ETA]	1.00E-126	98	96	BAA97606.1
15	36025	36840	271	Replisome organizer	putative replisome organizer [Lactococcus bacteriophage 4268]	7.10E-08	22	100	AAM83050.1
17	36850	37623	257	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	7.00E-127	86	100	AAL82346.1
98	37617	37778	53		unknown [S. aureus subsp. aureus Mu50]	1.80E-07	52	98	BAB57032.1
68	37791	38012	73		ORF24 [bacteriophage phi ETA]	1.30E-36	100	100	BAA97610.1
32	38022	38447	141	DNA N-6-adenine-methyltransferase	prophage LambdaSo, DNA modification methyltransferase, putative [Shewanella oneidensis MR-1]	2.90E-17	37	100	AAN56016.1
33	38444	38848	134		ORF25 [bacteriophage phi ETA]	1.70E-73	96	100	BAA97611.1
83	38853	39038	61		ORF26 [bacteriophage phi ETA]	2.00E-27	95	100	BAA97612.1
40	39039	39401	120	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	7.00E-12	53	55	CAG42686.1
62	39402	39650	82		unknown [S. aureus subsp. aureus MRSA252]	2.50E-40	96	96	CAG41061.1
61	39664	39912	82		orf 52 [S. aureus bacteriophage PVL]	4.20E-40	100	100	BAA31925.1
24	39887	40414	175	dUTPase	dUTPase [S. aureus bacteriophage PVL]	3.30E-95	100	100	BAA31926.1
63	40451	40696	81		orf 54 [S. aureus bacteriophage PVL]	8.80E-38	100	96	BAA31927.1
74	40693	40899	68		ORF35 [bacteriophage phi ETA]	1.50E-32	100	100	BAA97621.1
85	40896	41069	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	4.00E-23	93	100	AAL82255.1
35	41070	41471	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage 88

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
28	143	631	162	Small terminase	putative small terminase [S. aureus subsp. aureus MRSA252]	7.40E-32	48.67	92	CAG39405.1
8	615	1880	421	Large terminase	terminase [Bacteriophage SPP1]	4.00E-141	59.47	99	CAA39537.1
90	754	566	62						
7	1881	3305	474	Portal	portal protein [Bacteriophage SPP1]	6.90E-72	33.74	100	CAA39541.1
11	3262	4224	320	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	6.00E-180	98.12	100	BAA97628.1
48	4245	3976	89						
23	4322	4918	198	Minor capsid	minor capsid protein [Bacteriophage phig1e]	4.60E-20	30.41	97	CAA66737.1
15	4939	5763	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	9.60E-61	48.5	97	AAL15075.1
47	5780	6106	108	Head-tail adaptor	ORF45 [bacteriophage phi ETA]	1.50E-52	96.3	100	BAA97631.1
49	6106	6420	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.60E-54	98.08	100	BAA97632.1
46	6413	6748	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	1.40E-60	98.2	100	BAA97633.1
43	6735	7148	137	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	2.60E-05	32.1	59	AAR27382.1
96	6934	7110	58						
32	7161	7598	145	Inorganic pyrophosphatase	ORF49 [bacteriophage phi ETA]	4.20E-77	98.62	100	BAA97635.1
26	7585	8145	186		ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
29	8207	8701	164		ORF51 [bacteriophage phi ETA]	1.00E-89	100	100	BAA97637.1
45	8722	9063	113		ORF52 [bacteriophage phi ETA]	2.40E-60	100	100	BAA97638.1
1	9066	12035	989	Tape measure protein	tape measure protein [S. aureus phage phi 11]	2.00E-165	36.88	93	AAL82270.1
13	12050	12985	311		ORF54 [bacteriophage phi ETA]	1.00E-179	98.07	100	BAA97640.1
3	12996	14882	628	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	9.30E-22	25.43	46	AAT86193.1
2	14895	16793	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	3.20E-38	27.27	76	AAO83891.1
5	16793	18616	607		ORF57 [bacteriophage phi ETA]	0	77.92	100	BAA97643.1
70	18090	18311	73						
41	18616	18993	125		ORF58 [bacteriophage phi ETA]	1.10E-62	94.4	100	BAA97644.1
97	18994	19170	58		ORF59 [bacteriophage phi ETA]	5.00E-26	92.98	98	BAA97645.1
53	19211	19510	99		unknown [S. aureus temperate phage phiSLT]	3.30E-31	62.63	100	BAB21751.1
4	19647	21521	624	Amidase	peptidoglycan hydrolase [S. aureus bacteriophage phi 53]	0	58.76	100	AAM49609.1
9	21534	22772	412	Tail	tail fiber [S. aureus subsp. aureus Mu50]	0	97.82	100	BAB57072.1
36	22778	23173	131		ORF63 [bacteriophage phi ETA]	9.10E-70	96.95	100	BAA97649.1
33	23229	23666	145	Holin	holin [S. aureus phage phi 11]	1.20E-76	98.62	100	AAL82280.1
6	23647	25092	481	Amidase	amidase [S. aureus subsp. aureus Mu50]	0	99.79	100	BAB57075.1

Bacteriophage 88 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
87	24005	24184	59	Amidase	amidase [bacteriophage 80 alpha]	4.10E-12	73.33	76	AAB39699.1
24	25481	26068	195						
31	26065	26520	151						
10	27892	26846	348	Integrase	integrase [S. aureus phage phi 11]	0	97.99	100	AAL82229.1
12	28883	27954	309		putative lipoprotein [S. aureus subsp. aureus MSSA476]	6.40E-35	37.02	76	CAG42523.1
30	29360	28902	152		unknown [S. aureus subsp. aureus MRSA252]	4.80E-85	100	100	CAG40556.1
50	29696	29382	104	Repressor	putative phage regulatory protein [S. aureus subsp. aureus MSSA476]	1.50E-20	46.6	99	CAG42672.1
64	29849	30061	70	Repressor					
19	30138	30902	254	Antirepressor	anti-repressor [S. aureus phage phi 11]	6.00E-121	83.85	100	AAL82235.1
124	31144	31287	47		unknown [S. aureus subsp. aureus Mu50]	1.80E-18	97.87	100	BAB57019.1
73	31486	31277	69		unknown [S. aureus temperate phage phiSLT]	3.40E-32	100	100	BAB21703.1
71	31557	31778	73	Transcriptional regulator	orf 12 [S. aureus prophage phiPV83]	2.30E-33	97.26	100	BAA97819.1
107	31771	31932	53		putative exported protein [S. aureus subsp. aureus MSSA476]	1.50E-22	94.34	100	CAG43717.1
188	31901	31791	36						
58	32025	32285	86		unknown [S. aureus subsp. aureus MSSA476]	6.20E-44	97.67	100	CAG43716.1
72	32295	32516	73		unknown [S. aureus subsp. aureus Mu50]	1.30E-36	98.63	100	BAB57024.1
21	32509	33132	207	Topoisomerase	prophage pi2 protein 11, topoisomerase [Lactococcus lactis subsp. lactis Il1403]	3.00E-20	35.96	85	AAK05116.1
35	33132	33557	141	ssDNA-binding	single strand DNA-binding protein [S. aureus prophage phiPV83]	7.00E-72	94.37	100	BAA97825.1
27	33568	34119	183	HNH endonuclease	prophage LambdaSa2, HNH endonuclease family protein [Streptococcus agalactiae 2603V/R]	7.70E-21	39.34	100	AAN00738.1
20	34120	34794	224		orf 19 [S. aureus prophage phiPV83]	4.00E-125	95.93	98	BAA97826.1
169	34791	34907	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
14	35757	34900	285		unknown phage protein [S. pyogenes MGAS10394]	4.20E-22	35.93	58	AAT86873.1
18	35822	36592	256	DNA replication	DnaA analog [Bacteriophage LL-H]	8.40E-40	37.46	100	AAL77546.1
17	36602	37381	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	5.00E-147	97.68	100	AAL82346.1
108	37375	37536	53		unknown [S. aureus subsp. aureus Mu50]	1.80E-07	51.92	98	BAB57032.1
67	37549	37770	73		ORF24 [bacteriophage phi ETA]	5.00E-36	98.63	100	BAA97610.1
34	37780	38205	141	DNA N-6-adenine-methyltransferase	prophage LambdaSo, DNA modification methyltransferase, putative [Shewanella oneidensis MR-1]	2.20E-17	37.01	100	AAN56016.1
37	38202	38606	134		ORF25 [bacteriophage phi ETA]	6.00E-74	97.76	100	BAA97611.1
91	38611	38796	61		ORF26 [bacteriophage phi ETA]	4.00E-28	96.72	100	BAA97612.1
22	38797	39420	207	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.10E-14	33.97	75	CAG42686.1
62	39421	39669	82		orf 51 [S. aureus bacteriophage PVL]	6.10E-39	93.67	96	BAA31924.1
44	40080	40427	115	Sensor	possible sensor protein [S. aureus phage phi 13]	2.80E-56	93.04	100	AAL82351.1

Bacteriophage 88 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
52	40424	40732	102		unknown [S. aureus subsp. aureus MSSA476]	7.00E-50	93.14	100	CAG42692.1
60	40725	40973	82		orf 52 [S. aureus bacteriophage PVL]	1.50E-37	93.9	100	BAA31925.1
25	40966	41526	186	Winged helix DNA-binding domain	unknown [S. aureus subsp. aureus MRSA252]	4.10E-49	56.99	100	CAG40530.1
56	41563	41850	95		unknown [S. aureus temperate phage phiSLT]	6.00E-20	85.19	56	BAB21724.1
65	41843	42079	78		unknown [S. aureus subsp. aureus Mu50]	8.10E-39	97.44	100	BAB57042.1
40	42069	42458	129		orf31 [S. aureus prophage phiPV83]	3.30E-67	98.44	99	BAA97838.1
100	42455	42628	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	4.00E-23	92.98	100	AAL82255.1
39	42629	43030	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage 92

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
27	140	628	162	Small terminase	putative wmall terminase [S. aureus subsp. aureus MRSA252]	7.40E-32	49	92	CAG39405.1
9	612	1877	421	Large terminase	putative large terminase [S. pyogenes phage 315.5]	5.00E-117	75	62	AAM79934.1
92	751	563	62						
7	1878	3302	474	Portal	portal protein [Bacteriophage SPP1]	6.90E-72	34	100	CAA39541.1
141	2135	2004	43						
11	3259	4221	320	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	6.00E-180	98	100	BAA97628.1
50	4242	3973	89						
24	4319	4915	198	Minor capsid	minor capsid protein [Bacteriophage phig1e]	4.60E-20	30	97	CAA66737.1
14	4936	5760	274	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	9.60E-61	49	97	AAL15075.1
48	5777	6103	108	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	1.50E-52	96	100	BAA97631.1
51	6103	6417	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	1.60E-54	98	100	BAA97632.1
46	6410	6745	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	1.40E-60	98	100	BAA97633.1
43	6732	7145	137	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	2.60E-05	32	59	AAR27382.1
98	6931	7107	58						
30	7158	7595	145	Inorganic pyrophosphatase	ORF49 [bacteriophage phi ETA]	4.20E-77	99	100	BAA97635.1
26	7582	8142	186		ORF50 [bacteriophage phi ETA]	5.00E-103	100	100	BAA97636.1
28	8204	8698	164		ORF51 [bacteriophage phi ETA]	1.00E-89	100	100	BAA97637.1
45	8719	9060	113		ORF52 [bacteriophage phi ETA]	2.40E-60	100	100	BAA97638.1
1	9063	12032	989	Tape measure protein	tape measure protein [S. aureus phage phi 11]	2.00E-165	37	93	AAL82270.1
15	11974	11171	267						
12	12047	12982	311		ORF54 [bacteriophage phi ETA]	1.00E-179	98	100	BAA97640.1
3	12993	14879	628	Endopeptidase	phage endopeptidase [S. pyogenes MGAS10394]	9.30E-22	25	46	AAT86193.1
2	14892	16790	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	3.20E-38	27	76	AAO83891.1
5	16790	18613	607		ORF57 [bacteriophage phi ETA]	0	78	100	BAA97643.1
72	18087	18308	73						
39	18613	18990	125		ORF58 [bacteriophage phi ETA]	1.10E-62	94	100	BAA97644.1
99	18991	19167	58		ORF59 [bacteriophage phi ETA]	5.00E-26	93	98	BAA97645.1
57	19208	19507	99		unknown [S. aureus temperate phage phiSLT]	3.30E-31	63	100	BAB21751.1
4	19644	21518	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
10	21531	22703	390	Tail	tail fiber [S. aureus phage phi 11]	0	99	100	AAL82278.1
35	22709	23104	131		ORF63 [bacteriophage phi ETA]	5.90E-69	96	100	BAA97649.1

Bacteriophage 92 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
31	23160	23597	145	Holin	holin [S. aureus phage phi 11]	1.20E-76	99	100	AAL82280.1
6	23578	25023	481	Amidase	amidase [S. aureus phage phi 11]	0	99	100	AAL82281.1
89	23936	24115	59	Amidase	amidase [bacteriophage 80 alpha]	3.80E-18	96	76	AAB39699.1
113	24659	24814	51						
53	25420	25731	103						
40	25718	26101	127						
8	27633	26248	461	Integrase; Recombinase; Resolvase	site-specific recombinase for integration and excision [bacteriophage phi-105]	4.10E-61	34	100	BAA36658.1
20	28520	27840	226		unknown [S. aureus subsp. aureus Mu50]	1.10E-31	37	100	BAB56579.1
19	29275	28556	239	Repressor	cI-like repressor [S. aureus phage phi 11]	3.00E-133	99	100	AAL82233.1
73	29417	29635	72	Repressor; DNA-binding	cro-like repressor [S. aureus phage phi 11]	6.60E-36	100	98	AAL82234.1
18	29651	30388	245	Antirepressor	anti-repressor [S. aureus phage phi 11]	2.80E-58	63	83	AAL82235.1
77	30401	30610	69						
86	30624	30785	53		putative exported protein [S. aureus subsp. aureus MRSA252]	1.20E-22	96	100	CAG41074.1
182	30754	30644	36						
52	30800	31114	104						
47	31179	31508	109						
49	31489	31749	86		orf 39 [S. aureus bacteriophage PVL]	2.60E-26	63	100	BAA31913.1
29	31764	32243	159		orf 16 [S. aureus prophage phiPV83]	5.10E-83	97	100	BAA97823.1
22	32243	32881	212	Recombination	recombination protein [temperate phage PhiNIH1.1]	3.50E-40	51	86	AAL15054.1
33	32881	33303	140	ssDNA-binding	single strand DNA-binding protein [S. aureus prophage phiPV83]	4.70E-68	89	100	BAA97825.1
21	33317	33991	224		orf 19 [S. aureus prophage phiPV83]	3.00E-124	95	98	BAA97826.1
174	33520	33407	37						
164	33988	34104	38		77ORF151 [Bacteriophage 77]	6.80E-13	100	100	AAR87940.1
13	34954	34097	285		unknown [S. pyogenes MGAS10394]	4.20E-22	36	58	AAT86873.1
17	35019	35789	256	DNA replication	DnaA analog [Bacteriophage LL-H]	8.40E-40	37	100	AAL77546.1
16	35799	36578	259	DNA replication protein DnaC	dnaC [S. aureus phage phi 13]	5.00E-147	98	100	AAL82346.1
107	36572	36733	53		77ORF104 [Bacteriophage 77]	2.80E-08	52	98	AAR87935.1
107	36572	36733	53		unknown [S. aureus subsp. aureus Mu50]	1.80E-07	52	98	BAB57032.1
70	36746	36967	73		ORF24 [bacteriophage phi ETA]	5.00E-36	99	100	BAA97610.1
32	36977	37402	141	DNA N-6-adenine-methyltransferase	prophage LambdaSo, DNA modification methyltransferase, putative [Shewanella oneidensis MR-1]	2.20E-17	37	100	AAN56016.1
34	37399	37803	134		ORF25 [bacteriophage phi ETA]	6.00E-74	98	100	BAA97611.1
93	37808	37993	61		ORF26 [bacteriophage phi ETA]	4.00E-28	97	100	BAA97612.1
23	37994	38617	207	DNA-binding	putative DNA-binding protein [S. aureus subsp. aureus MSSA476]	1.10E-14	34	75	CAG42686.1

Bacteriophage 92 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
66	38618	38866	82		orf 51 [S. aureus bacteriophage PVL]	6.10E-39	94	96	BAA31924.1
36	38879	39280	133		unknown [S. aureus subsp. aureus MSSA476]	7.60E-53	75	100	CAG42690.1
44	39277	39624	115		unknown [S. aureus phage phi 12]	4.90E-61	100	100	AAL82300.1
55	39621	39929	102		unknown [S. aureus subsp. aureus MSSA476]	7.00E-50	93	100	CAG42692.1
64	39922	40170	82		orf 52 [S. aureus bacteriophage PVL]	1.50E-37	94	100	BAA31925.1
25	40163	40723	186		unknown [S. aureus subsp. aureus MRSA252]	4.10E-49	57	100	CAG40530.1
59	40760	41047	95		unknown [S. aureus temperate phage phiSLT]	6.00E-20	85	56	BAB21724.1
68	41040	41276	78		unknown [S. aureus subsp. aureus Mu50]	8.10E-39	97	100	BAB57042.1
38	41266	41655	129		orf31 [S. aureus prophage phiPV83]	3.30E-67	98	99	BAA97838.1
100	41652	41825	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	4.00E-23	93	100	AAL82255.1
37	41826	42227	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage X2

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
41	89	469	126		unknown [S. pyogenes phage 315.5]	4.90E-10	39	73	AAM79936.1
9	453	1718	421	Large terminase	putative large terminase [S. pyogenes phage 315.5]	2.00E-116	74	62	AAM79934.1
7	1719	3143	474	Portal	portal protein [Bacteriophage SPP1]	1.20E-71	34	100	CAA39541.1
11	3100	4062	320	Head morphogenesis	ORF42 (product required for head morphogenesis) [bacteriophage phi ETA]	6.00E-180	98	100	BAA97628.1
191	3902	4009	35						
49	4083	3814	89						
22	4160	4750	196	Minor capsid	minor capsid protein [Bacteriophage phig1e]	4.30E-15	28	97	CAA66737.1
13	4768	5580	270	Major capsid	major capsid protein [temperate phage PhiNIH1.1]	2.70E-44	39	98	AAL15075.1
128	5339	5521	60						
47	5597	5923	108	Rho termination factor, N-terminal	ORF45 [bacteriophage phi ETA]	7.80E-54	97	100	BAA97631.1
50	5923	6237	104	Head morphogenesis	ORF46 (product required for head morphogenesis) [bacteriophage phi ETA]	9.40E-55	98	100	BAA97632.1
46	6230	6565	111	Head-tail adaptor	ORF47 [bacteriophage phi ETA]	2.90E-61	99	100	BAA97633.1
44	6615	6965	116	Major tail	putative major tail protein [LactoB. johnsonii prophage Lj928]	6.40E-05	38	52	AAR27382.1
94	6751	6927	58						
30	6978	7415	145		ORF49 [bacteriophage phi ETA]	7.10E-77	98	100	BAA97635.1
24	7402	7962	186		ORF50 [bacteriophage phi ETA]	7.00E-102	99	100	BAA97636.1
28	8024	8518	164		ORF51 [bacteriophage phi ETA]	1.00E-89	100	100	BAA97637.1
45	8539	8880	113		ORF52 [bacteriophage phi ETA]	5.40E-60	99	100	BAA97638.1
1	8883	11852	989	Tape measure protein	tape measure protein [S. aureus phage phi 11]	2.00E-166	37	93	AAL82270.1
12	11867	12802	311		ORF54 [bacteriophage phi ETA]	2.00E-178	98	100	BAA97640.1
4	12813	14699	628	Endopeptidase	Phage endopeptidase [S. pyogenes MGAS10394]	1.20E-21	25	46	AAT86193.1
3	14712	16610	632	Minor structural protein	minor structural protein [S. aureus phage phiP68]	3.20E-38	28	77	AAO83891.1
166	15700	15816	38						
6	16610	18433	607		ORF57 [bacteriophage phi ETA]	0	81	100	BAA97643.1
135	17907	18047	46						
40	18433	18810	125		ORF58 [bacteriophage phi ETA]	1.00E-55	84	100	BAA97644.1
89	18811	18993	60		ORF59 [bacteriophage phi ETA]	1.00E-23	86	95	BAA97645.1
53	19033	19338	101		unknown [S. aureus phage phi 11]	4.30E-31	62	100	AAL82276.1
53	19033	19338	101		unknown [S. aureus temperate phage phiSLT]	7.30E-31	60	100	BAB21751.1
5	19475	21349	624	Amidase	cell wall hydrolase [S. aureus phage phi 11]	0	58	100	AAL82277.1
207	20880	20981	33						

Bacteriophage X2 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
2	21362	23374	670	Tail fiber	tail fiber [S. aureus phage phi 11]	3.10E-71	62	30	AAL82278.1
26	23425	23862	145	Holin	holin [S. aureus phage phi 11]	3.30E-74	94	100	AAL82280.1
18	23843	24484	213	Amidase	amidase [S. aureus phage phi 11]	6.00E-115	94	95	AAL82281.1
27	24514	25059	181	HNH endonuclease	prophage LambdaSa2, HNH endonuclease family protein [S. agalactiae 2603V/R]	7.60E-21	36	99	AAN00738.1
19	25590	26222	210	Amidase	amidase [S. aureus phage phi 11]	1.00E-115	91	100	AAL82281.1
74	25858	26013	51						
171	26400	26299	33						
8	28207	26822	461	Integrase; Recombinase; Resolvase	site-specific recombinase for integration and excision [bacteriophage phi-105]	8.20E-62	33	100	BAA36658.1
83	28316	28513	65		unknown [S. pyogenes MGAS8232]	6.40E-10	46	100	AAL98050.1
35	28917	28510	135						
31	29348	28911	145		unknown [S. pneumoniae TIGR4]	1.30E-09	29	93	AAK75994.1
15	30105	29380	241		unknown [C. perfringens str. 13]	1.20E-37	42	76	BAB79844.1
110	30284	30123	53	Repressor	cI-like repressor [S. aureus phage phi 12]	9.90E-14	76	86	AAL82286.1
112	30590	30742	50						
21	30825	30223	200	LexA Repressor	cI-like repressor [S. aureus phage phi 12]	2.20E-62	64	100	AAL82286.1
32	31021	31236	71		unknown [B. cereus ATCC 14579]	6.90E-09	43	95	AAP10632.1
102	31252	31419	55						
29	31952	31470	160		ORF9 [bacteriophage phi ETA]	1.00E-83	98	100	BAA97595.1
87	32398	32583	61	Repressor	ORF10 [bacteriophage phi ETA]	3.40E-27	100	100	BAA97596.1
16	32585	33292	235	Antirepressor	antirepressor [S. aureus prophage phiPV83]	1.90E-56	94	48	BAA97816.1
138	33307	33444	45						
103	33428	33595	55		putative exported protein [S. aureus subsp. aureus MSSA476]	2.60E-22	96	94	CAG43717.1
184	33558	33448	36						
48	33596	33916	106		orf 14 [S. aureus prophage phiPV83]	9.00E-58	100	100	BAA97821.1
62	34008	34268	86		ORF15 [bacteriophage phi ETA]	4.30E-45	99	100	BAA97601.1
76	34278	34499	73		unknown [S. aureus subsp. aureus Mu50]	5.90E-37	100	100	BAB57024.1
20	34492	35115	207	Topoisomerase	prophage pi2 protein 11, topoisomerase [L. lactis subsp. lactis Il1403]	3.00E-20	36	85	AAK05116.1
33	35115	35534	139	ssDNA-binding	single strand DNA-binding protein [S. aureus subsp. aureus Mu50]	4.90E-65	87	100	BAB57026.1
17	35548	36222	224		unknown [S. aureus subsp. aureus Mu50]	3.00E-126	96	100	BAB57028.1
14	36215	36979	254	DnaD and phage-associated domain	unknown [S. aureus phage phi 11]	7.80E-22	43	64	AAL82243.1
42	36979	37335	118						
10	37332	38573	413	DnaB-like helicase	helicase DnaB [S. aureus phage phi 11]	0	99	100	AAL82244.1

Bacteriophage X2 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
78	38570	38785	71						
72	38788	39009	73		ORF24 [bacteriophage phi ETA]	3.80E-36	99	100	BAA97610.1
36	39020	39424	134		orf 22 [S. aureus prophage phiPV83]	1.30E-73	99	100	BAA97829.1
88	39429	39614	61		ORF26 [bacteriophage phi ETA]	4.00E-28	97	100	BAA97612.1
54	39615	39920	101		unknown [S. agalactiae NEM316]	2.20E-06	33	91	CAD45858.1
43	40048	40404	118		unknown [S. aureus subsp. aureus MRSA252]	3.40E-38	63	98	CAG41062.1
67	40408	40650	80		orf 51 [S. aureus bacteriophage PVL]	2.10E-39	94	100	BAA31924.1
34	40661	41071	136		unknown [S. aureus subsp. aureus MSSA476]	7.80E-50	72	99	CAG42690.1
58	41071	41346	91		unknown [S. aureus subsp. aureus MSSA476]	1.00E-30	85	80	CAG42692.1
65	41339	41587	82		unknown [S. aureus subsp. aureus MRSA252]	5.70E-37	93	100	CAG41059.1
23	41580	42140	186		unknown [S. aureus subsp. aureus MRSA252]	3.80E-47	55	100	CAG40530.1
77	42177	42395	72		unknown [S. aureus subsp. aureus Mu50]	3.60E-26	88	88	BAB57039.1
70	42379	42615	78		unknown [S. aureus subsp. aureus Mu50]	1.20E-29	76	100	BAB57042.1
90	42608	42781	57	Transcriptional activator RinB	rinB [S. aureus phage phi 11]	5.20E-23	91	100	AAL82255.1
38	42782	43183	133		ORF38 [bacteriophage phi ETA]	3.60E-71	100	100	BAA97624.1

Bacteriophage K

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
10	13	1830	605	Large terminase	large terminase [B. subtilis phage 1102phi1-3]	ORF35	0	57	94	AAS45252.1
39	1823	2644	273			ORF36	1.00E-153	100	100	AAS91583.1
85	2801	3280	159			ORF37	1.20E-84	100	100	AAO47483.1
23	3373	4515	380	S-layer protein; Clumping factor	S-layer protein [C. thermocellum]	ORF38	2.60E-15	31	56	CAA47841.1
					Clumping factor B [S. aureus subsp. aureus Mu50]		3.20E-13	31	35	BAB58792.1
112	4579	4941	120			ORF39	2.90E-58	100	94	AAO47486.1
108	4950	5330	126			ORF40	9.60E-67	99	97	AAO47487.1
14	5523	7025	500	Portal	phage portal protein, HK97 family [Wolbachia endosymbiont of D. melanogaster]	ORF41	2.10E-05	23	44	AAS14672.1
47	7252	7992	246	Major capsid		ORF42	3.00E-137	100	100	AAO47489.1
28	8011	8961	316	Topoisomerase; Autolysin	DNA topoisomerase IV subunit A [M. penetrans HF-2]	ORF43	1.40E-16	23	95	BAC44437.1
28	8011	8961	316		putative autolysin [S. cohnii]		1.90E-13	19	100	CAC83649.1
17	9077	10468	463	Major capsid	major capsid protein [Staphylococcus phage Twort]	ORF44	0	82	98	AAQ62708.1
139	10560	10856	98							
30	10869	11777	302			ORF45	5.00E-179	100	100	AAO47492.1
33	11791	12669	292			ORF46	1.00E-170	100	100	AAO47493.1
60	12747	13289	180			ORF47	1.00E-115	100	100	AAO47494.1
38	13308	14144	278			ORF48	1.00E-156	100	100	AAO47495.1
183	14146	14361	71		ORF7 [Bacteriophage A511]		1.00E-12	48	100	CAA62545.1
11	14388	16151	587	Major tail	major tail sheath protein [Bacteriophage A511]	ORF49	0	58	100	CAA62546.1
99	16224	16652	142			ORF50	1.60E-76	100	100	AAO47497.1
264	16749	16889	46							
89	16932	17390	152			ORF51	4.80E-85	100	100	AAO47498.1
197	17403	17597	64							
129	17679	17990	103			ORF100	2.50E-55	100	100	AAO47549.1
88	18122	18580	152			ORF53	5.30E-84	100	100	AAO47500.1
73	18624	19160	178							
1	19213	23271	1352	Tape measure protein	tail tape meausure protein [P. syringae pv. tomato str. DC3000]	ORF55	9.40E-17	23	64	AAO56871.1
109	22202	21825	125		proline-rich mucin homolog [M. tuberculosis]		1.40E-09	32	100	AAD41594.1
5	23344	25776	810	Secretory antigen; Autolysin	secretory antigen SsaA-like protein [S. epidermidis ATCC 12228]	ORF56	2.40E-33	49	20	AAO05088.1
					autolysin precursor [S. epidermidis ATCC 12228]		4.40E-19	24	61	AAO05873.1
32	25790	26677	295			ORF57	5.00E-172	100	100	AAO47506.1

Bacteriophage K (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
4	26677	29223	848	Glycerophosphoryl diester phosphodiesterase	glycerophosphoryl diester phosphodiesterase [B. subtilis]	ORF58	7.30E-41	38	29	CAA81292.1
42	29330	30121	263			ORF59	4.00E-149	100	100	AAO47508.1
75	30121	30645	174			ORF60	2.10E-94	100	100	AAO47509.1
52	30645	31349	234			ORF61	3.00E-131	100	100	AAO47510.1
26	31364	32410	348			ORF62	0	100	100	AAS91584.1
3	32431	35490	1019			ORF63	0	100	100	AAO47511.1
76	35601	36122	173			ORF64	7.10E-95	100	100	AAO47512.1
2	36143	39601	1152	Virulence-associated	Virulence-associated protein [B. henselae str. Houston-1]	ORF65	4.60E-65	25	100	CAF27126.1
115	37698	37348	116							
234	39650	39808	52							
8	39809	41731	640			ORF66	0	100	100	AAO47515.1
110	41754	42128	124			ORF67	2.00E-67	100	100	AAO47516.1
18	42135	43511	458			ORF68	0	100	100	AAO47517.1
12	43603	45351	582	DEAD/DEAH box helicase	putative helicase [S. enterica subsp. enterica serovar Typhi str. CT18]	ORF69	9.30E-37	33	48	CAD09945.1
13	45363	46976	537			ORF70	0	100	100	AAO47519.1
16	46969	48411	480	AAA ATPase	gp41 DNA primase-helicase subunit [Aeromonas phage 65]	ORF71	2.40E-16	23	92	AAR90925.1
27	48490	49527	345	Exonuclease	ATP-dependent dsDNA exonuclease [A. aeolicus VF5]	ORF72	6.80E-12	23	100	AAC07689.1
102	49527	49904	125			ORF73	1.00E-71	100	100	AAO47522.1
9	49904	51823	639	Exonuclease	putative exonuclease subunit 2 [Y. pestis biovar Medievalis str. 91001]	ORF74	1.30E-55	25	100	AAS58684.1
63	51823	52419	198			ORF84	1.00E-111	100	100	AAO47533.1
25	52434	53501	355	DNA Primase	DNA primase [T. tengcongensis MB4]	ORF76	9.00E-15	26	100	AAM24950.1
117	53568	53906	112							
93	53906	54358	150	Penicillin-binding	penicillin-binding protein [B. thuringiensis serovar konkukian str. 97-27]	ORF77	4.70E-05	30	83	AAT63192.1
62	54345	54953	202			ORF78	3.00E-118	100	100	AAO47527.1
97	54970	55362	130	Ribonucleotide reductase; NrdI	NrdI protein involved in ribonucleotide reductase function [S. aureus subsp. aureus Mu50]	ORF79	1.40E-14	35	83	BAB56892.1
6	55377	57491	704	Ribonucleotide reductase large subunit	large subunit ribonucleotide reductase [Staphylococcus phage Twort]	ORF80	0	73	100	AAM00816.1
24	57505	58554	349	Ribonucleotide reductase small subunit	ribonucleoside-diphosphate reductase minor subunit [S. epidermidis ATCC 12228]	ORF81	2.40E-95	55	92	AAO04111.1
120	58572	58901	109			ORF82	4.40E-57	100	100	AAO47531.1
119	58873	59205	110			ORF83	3.50E-54	100	96	AAO47532.1
64	59412	60008	198			ORF75	4.00E-111	100	100	AAO47524.1

Bacteriophage K (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
133	60018	60323	101							
34	60399	61271	290			ORF86/ORF88/ORF90	8.00E-168	100	100	AAO47535.1
78	61464	61949	161			ORF87	1.60E-92	100	96	AAO47536.1
19	62085	63428	447	DNA polymerase I	DNA polymerase [Bacteriophage Bastille]	ORF86/ORF88/ORF90	5.30E-34	39	47	AAO93094.1
40	63696	64403	235	HNH endonuclease	putative HNH homing endonuclease [bacteriophage bIL170]	ORF89	5.60E-24	38	72	AAC27227.1
36	64637	65497	286	DNA-directed DNA polymerase	DNA polymerase I [T. thermosulfurigenes]	ORF86/ORF88/ORF90	6.90E-33	34	79	AAR11873.1
164	65566	65808	80							
83	65825	66307	160			ORF91	7.00E-88	100	100	AAO47540.1
20	66394	67665	423			ORF92	0	100	100	AAO47541.1
21	67725	68981	418	RecA bacterial DNA recombination protein	recA protein [P. gingivalis W83]	ORF93	7.50E-27	29	81	AAQ66027.1
114	68985	69338	117			ORF115	1.80E-63	100	100	AAO47564.1
54	69325	69987	220			ORF94	1.00E-124	100	100	AAO47543.1
57	70115	70747	210			ORF95	5.00E-118	100	100	AAO47544.1
77	70761	71282	173	Major tail	phi12 major tail protein-like protein [S. aureus bacteriophage phi 3A]	ORF96	1.80E-21	40	78	AAM49601.1
173	71297	71524	75							
155	71620	71880	86							
45	71884	72639	251			ORF97	1.00E-144	100	100	AAO47546.1
22	72632	73882	416	Metallophosphoesterase		ORF98	0	100	100	AAO47547.1
111	73896	74264	122			ORF99	1.30E-63	100	100	AAO47548.1
127	74251	74562	103			ORF113	4.20E-55	100	100	AAO47563.1
72	74626	75162	178			ORF54	2.00E-101	100	100	AAO47501.1
44	75155	75922	255			ORF101	2.00E-150	100	100	AAO47550.1
94	75900	76346	148			ORF102	1.40E-80	100	100	AAO47551.1
35	76346	77209	287							
46	77581	78312	243			ORF103	2.00E-133	100	100	AAO47553.1
90	78330	78788	152			ORF104	6.90E-84	100	100	AAO47554.1
95	78853	79296	147			ORF105	9.20E-80	100	100	AAO47555.1
51	79313	80017	234			ORF106	5.00E-132	100	100	AAO47556.1
101	80079	80477	132			ORF107	1.30E-71	100	100	AAO47557.1
165	80624	80866	80							
86	80871	81341	156							
191	81623	81823	66							

Bacteriophage K (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
142	81824	82114	96							
130	82206	82514	102			ORF109	1.70E-51	100	100	AAO47559.1
29	82511	83419	302	Phosphoribosyl transferase	phosphoribosyl transferase domain protein [S. oneidensis MR-1]	ORF110	6.40E-16	30	79	AAN55031.1
15	83437	84906	489	Nicotinate phosphoribosyltransferase	putative nicotinamide phosphoribosyl transferase [H. ducreyi]	ORF111	2.00E-138	53	98	AAR87771.1
159	84985	85230	81							
104	85247	85642	131			ORF112	1.20E-69	100	100	AAO47562.1
161	85639	85890	83							
138	85955	86251	98							
128	86255	86566	103			ORF52	2.60E-52	100	100	AAO47499.1
136	86572	86871	99			ORF114	1.40E-53	100	100	AAS91585.1
171	86950	87177	75				5.50E-11	52	81	AAO47545.1
171	86950	87177	75	Major tail	phi12 major tail protein-like protein [S. aureus bacteriophage phi 3A]	ORF96	6.80E-09	47	85	AAM49601.1
196	87205	87399	64							
113	87418	87771	117							
107	87790	88176	128			ORF116	1.10E-70	100	100	AAO47565.1
137	88858	89157	99			ORF117	5.30E-05	35	100	AAO47566.1
143	89465	89752	95							
122	89752	90078	108			ORF34	1.40E-55	100	100	AAO47481.1
141	90094	90387	97			ORF117	3.20E-05	34	100	AAO47566.1
156	90391	90648	85							
166	90726	90965	79							
116	90976	91323	115			ORF118	6.20E-64	100	100	AAO47567.1
118	91870	91532	112							
131	92181	92489	102							
87	92574	93044	156			ORF108	3.10E-82	100	100	AAO47558.1
211	93103	93276	57							
151	93276	93545	89							
169	93621	93851	76							
400	93925	94026	33							
167	94384	94148	78							
160	94818	94564	84							
201	95012	94821	63							

Bacteriophage K (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
82	95494	95009	161			ORF1	6.60E-86	100	100	AAO47447.1
98	95918	95487	143			ORF2	4.80E-81	100	100	AAO47448.1
71	96474	95932	180			ORF3	1.00E-102	100	100	AAO47449.1
81	96974	96486	162	GTP cyclohydrolase	GTP cyclohydrolase II [V. vulnificus CMCP6]	ORF4	2.80E-07	26	91	AAO08077.1
103	97385	96987	132			ORF5	2.10E-74	100	100	AAO47451.1
50	98089	97382	235	Serine/threonine-specific protein phosphatase	serine/threonine protein phosphatase [C. burnetii RSA 493]	ORF6	2.30E-14	27	94	AAO90036.1
68	98743	98189	184			ORF7	2.00E-103	100	100	AAO47453.1
126	99076	98759	105			ORF96	1.50E-07	41	82	AAO47545.1
69	100610	100062	182			ORF8	1.00E-101	100	100	AAO47455.1
181	100832	100614	72							
199	101027	100833	64							
49	101754	101017	245			ORF9	3.00E-137	100	100	AAO47456.1
387	101921	101817	34							
163	102181	101933	82							
106	102563	102174	129			ORF10	2.00E-72	100	100	AAO47457.1
219	102835	102662	57	Immunodominant antigen A	immunodominant antigen A [S. aureus subsp. aureus MSSA476]		4.40E-06	40	92	CAG44271.1
84	103358	102876	160			ORF11	1.80E-88	100	100	AAO47458.1
70	103950	103408	180			ORF12	3.40E-98	100	100	AAO47459.1
172	104083	104310	75							
74	104483	103950	177			ORF13	2.00E-100	100	100	AAO47460.1
227	104650	104486	54							
147	104928	104653	91							
37	105773	104928	281			ORF14	2.00E-158	100	100	AAO47461.1
65	106369	105785	194	AAA ATPase	predicted AAA family ATPase [M. penetrans HF-2]	ORF15	9.70E-20	40	80	BAC44370.1
148	106913	106638	91							
124	107384	107058	108							
100	107793	107377	138			ORF16	1.20E-74	100	100	AAO47463.1
135	108229	107927	100	DNA-binding	putative DNA-binding protein [S. thermophilus bacteriophage SFi18]	ORF17	1.90E-15	43	93	AAF63096.1
204	108417	108229	62							
230	108622	108461	53							
7	110670	108622	682			ORF18	0	100	100	AAO47466.1
154	111011	110748	87							

Bacteriophage K (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	Genbank gene name	E-value	% Identity	% Length of Match	Accession
66	111786	111208	192			ORF19	6.00E-102	100	100	AAO47465.1
59	112405	111779	208			ORF20	1.00E-118	100	100	AAO47467.1
31	113294	112398	298	DNA ligase	possible homolog of eukaryotic DNA ligase III [N. europaea ATCC 19718]	ORF21	2.80E-08	28	59	CAD85795.1
48	114327	113587	246	PhoH-like protein	PhoH-related protein [N. meningitidis MC58]	ORF22	5.10E-15	35	75	AAF41256.1
61	114993	114379	204			ORF23	2.00E-119	100	100	AAO47470.1
91	115467	115009	152	RNase H	RNase HI related protein [M. maripaludis S2]	ORF24	6.60E-18	37	90	CAF30393.1
203	115615	115424	63							
55	116279	115638	213			ORF25	1.00E-116	100	100	AAO47472.1
170	116499	116269	76	Transcription regulator	transcription regulator (putative) [LactoB. plantarum WCFS1]		7.00E-06	39	81	CAD64381.1
174	116729	116502	75							
53	117531	116839	230	Immunodominant antigen A	immunodominant antigen A [S. epidermidis ATCC 12228]	ORF26	5.90E-15	32	100	AAO05768.1
56	118353	117718	211			ORF27	6.00E-125	100	100	AAO47474.1
43	119211	118420	263	B-cell receptor associated; Transposase; Band 7 protein	B-cell receptor associated protein-related protein [S. pyogenes SSI-1] bacteriophage/transposase fusion protein [B. pseudomallei K96243] Band 7 protein [P. marinus str. MIT 9313]	ORF28	6.50E-27 2.50E-18 1.20E-09	29 26 22	96 96 90	BAC64245.1 CAH37855.1 CAE21083.1
132	119519	119211	102			ORF29	3.70E-51	100	100	AAO47476.1
58	120261	119632	209	Amidase	amidase [S. aureus phage phi 11]	ORF30/ORF32	4.80E-55	53	99	AAL82281.1
80	121032	120532	166	HNH endonuclease; Intron encoded nuclease domain	putative HNH homing endonuclease [bacteriophage bIL170]	ORF31	3.50E-16	34	96	AAC27227.1
41	121995	121192	267	Amidase	N-acetylmuramoyl-L-alanine amidase [Staphylococcus phage Twort]	ORF30/ORF32	1.40E-48	43	93	CAA69021.1
79	122498	121995	167	Holin	holTW [Staphylococcus phage Twort]	ORF33	2.20E-42	62	86	CAA69020.1
210	122768	122583	61							
180	124533	124315	72							
187	125220	125011	69							
189	125439	125233	68							
152	126464	126730	88							
145	126708	126986	92							
123	127067	127393	108			ORF117	6.20E-59	100	100	AAO47566.1

Bacteriophage G1

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
10	13	1830	605	Large terminase	large terminase [B. subtilis phage 1102phi1-3]	0	57	94	AAS45252.1
40	1844	2644	266		ORF36 [Staphylococcus phage K]	4.00E-147	99	100	AAS91583.1
235	2622	2804	60						
91	2801	3280	159		ORF37 [Staphylococcus phage K]	1.20E-84	100	100	AAO47483.1
23	3322	4521	399	S-layer protein; Clumping factor; Structural	S-layer protein [C. thermocellum]	1.60E-15	27	59	CAA47841.1
					Clumping factor B [S. aureus subsp. aureus Mu50]	3.10E-14	30	33	BAB58792.1
					fibrinogen and keratin-10 binding surface anchored protein [S. aureus subsp. aureus MRSA252]	4.40E-13	29	33	CAG41687.1
112	4124	4492	122						
120	4598	4948	116		ORF39 [Staphylococcus phage K]	1.50E-57	99	97	AAO47486.1
115	4966	5337	123		ORF40 [Staphylococcus phage K]	9.80E-67	99	100	AAO47487.1
14	5341	7032	563	Portal	phage portal protein, HK97 family [Wolbachia endosymbiont of Drosophila melanogaster]	2.40E-05	23	39	AAS14672.1
48	7226	7999	257	Major capsid	ORF42 [Staphylococcus phage K]	2.00E-143	100	100	AAO47489.1
29	8018	8974	318	Topoisomerase; Autolysin; Internalin	DNA topoisomerase IV subunit A [M. penetrans HF-2]	3.30E-18	23	100	BAC44437.1
					putative autolysin [S. cohnii]	5.90E-15	19	100	CAC83649.1
					fimbriae-associated protein Fap1 [S. parasanguinis]	8.50E-14	24	89	AAC79868.1
					Internalin protein [B. cereus ATCC 14579]	4.60E-12	24	81	AAP07572.1
16	9090	10481	463	Major capsid	major capsid protein [Staphylococcus phage Twort]	0	82	98	AAQ62708.1
151	10573	10869	98						
30	10882	11790	302		ORF45 [Staphylococcus phage K]	5.00E-179	100	100	AAO47492.1
34	11804	12682	292		ORF46 [Staphylococcus phage K]	1.00E-170	100	100	AAO47493.1
62	12682	13302	206		ORF47 [Staphylococcus phage K]	1.00E-115	100	100	AAO47494.1
39	13321	14157	278		ORF48 [Staphylococcus phage K]	1.00E-156	100	100	AAO47495.1
202	14159	14374	71		ORF7 [Bacteriophage A511]	1.00E-12	48	100	CAA62545.1
11	14401	16164	587	Major tail	major tail sheath protein [Bacteriophage A511]	0	58	100	CAA62546.1
105	16237	16665	142		ORF50 [Staphylococcus phage K]	1.60E-76	100	100	AAO47497.1
293	16762	16902	46						
93	16945	17403	152		ORF51 [Staphylococcus phage K]	4.80E-85	100	100	AAO47498.1
215	17416	17610	64						
141	17692	18003	103		ORF52 [Staphylococcus phage K]	2.60E-52	100	100	AAO47499.1
95	18135	18593	152		ORF53 [Staphylococcus phage K]	5.30E-84	100	100	AAO47500.1
95	18135	18593	152		ORF9 [Bacteriophage A511]	1.40E-28	40	97	CAA62548.1

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
74	18637	19173	178		ORF54 [Staphylococcus phage K]	2.00E-101	100	100	AAO47501.1
1	19226	23284	1352	Tape measure protein	tail tape meausure protein [P. syringae pv. tomato str. DC3000]	5.50E-17	23	63	AAO56871.1
311	21441	21575	44						
285	21579	21722	47						
5	23363	25789	808	Amidase; Secretory antigen	secretory antigen SsaA-like protein [S. epidermidis ATCC 12228] N-acetylmuramoyl-L-alanine amidase, family 4 [E. faecalis V583]	2.40E-33 2.80E-13	49 28	20 39	AAO05088.1
33	25803	26690	295		ORF57 [Staphylococcus phage K]	5.00E-172	100	100	AAO47506.1
4	26690	29236	848	Glycerophosphoryl diester phosphodiesterase	glycerophosphoryl diester phosphodiesterase [B. subtilis]	7.30E-41	38	29	CAA81292.1
43	29343	30134	263		ORF59 [Staphylococcus phage K]	4.00E-149	100	100	AAO47508.1
78	30134	30658	174		ORF60 [Staphylococcus phage K]	7.90E-94	99	100	AAO47509.1
52	30658	31362	234	LysM domain	ORF61 [Staphylococcus phage K]	3.00E-131	100	100	AAO47510.1
27	31377	32423	348		ORF62 [Staphylococcus phage K]	0	100	100	AAS91584.1
3	32444	35503	1019		ORF63 [Staphylococcus phage K]	0	100	100	AAO47511.1
79	35614	36135	173		ORF64 [Staphylococcus phage K]	7.10E-95	100	100	AAO47512.1
2	36156	39614	1152	Virulence-associated	Virulence-associated protein [B. henselae str. Houston-1]	4.60E-65	25	100	CAF27126.1
262	39663	39821	52						
8	39822	41744	640		ORF66 [Staphylococcus phage K]	0	100	100	AAO47515.1
117	41767	42141	124		ORF67 [Staphylococcus phage K]	2.00E-67	100	100	AAO47516.1
17	42148	43524	458		ORF68 [Staphylococcus phage K]	0	100	100	AAO47517.1
12	43616	45364	582	Type III restriction enzyme; DEAD/DEAH box helicase	putative helicase [S. enterica subsp. enterica serovar Typhi str. CT18]	9.30E-37	33	48	CAD09945.1
13	45376	46989	537		ORF70 [Staphylococcus phage K]	0	100	100	AAO47519.1
15	46982	48424	480	AAA ATPase	gp41 DNA primase-helicase subunit [Aeromonas phage 65]	2.40E-16	23	92	AAR90925.1
28	48503	49540	345	Exonuclease	ATP-dependent dsDNA exonuclease [Aquifex aeolicus VF5]	6.80E-12	23	100	AAC07689.1
110	49540	49917	125		ORF73 [Staphylococcus phage K]	1.00E-71	100	100	AAO47522.1
9	49917	51836	639	Exonuclease	putative exonuclease [Yersinia pestis KIM]	1.30E-55	25	100	AAC82670.1
67	51836	52432	198		ORF75 [Staphylococcus phage K]	4.00E-111	100	100	AAO47524.1
26	52447	53514	355	DNA primase	DNA primase (bacterial type) [Thermoanaerobacter tengcongensis MB4]	9.00E-15	26	100	AAM24950.1
127	53581	53919	112						
98	53919	54371	150	Penicillin-binding	penicillin-binding protein [B. thuringiensis serovar konkukian str. 97-27]	4.70E-05	30	83	AAT63192.1
64	54358	54966	202		ORF78 [Staphylococcus phage K]	6.00E-118	100	100	AAO47527.1
102	54983	55375	130	Ribonucleotide reductase; NrdI	NrdI protein involved in ribonucleotide reductase function [S. aureus subsp. aureus Mu50]	1.40E-14	35	83	BAB56892.1

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
6	55390	57504	704	Ribonucleotide reductase large subunit	large subunit ribonucleotide reductase [Staphylococcus phage Twort]	0	73	100	AAM00816.1
25	57770	58567	265	Ribonucleotide reductase minor subunit	ribonucleoside-diphosphate reductase minor subunit [S. epidermidis ATCC 12228]	5.30E-69	54	95	AAO04111.1
130	58585	58914	109		ORF82 [Staphylococcus phage K]	4.40E-57	100	100	AAO47531.1
129	58907	59218	103		ORF83 [Staphylococcus phage K]	2.00E-52	100	100	AAO47532.1
66	59425	60021	198		ORF84 [Staphylococcus phage K]	1.00E-111	100	100	AAO47533.1
147	60031	60336	101	Integration host factor; Histone-like bacterial DNA-binding protein	putative integration host factor [Parachlamydia sp. UWE25]	2.80E-06	31	93	CAF23892.1
35	60412	61284	290	DNA polymerase	ORF86/ORF88/ORF90 [Staphylococcus phage K]	8.00E-168	100	100	AAO47535.1
81	61450	61962	170		ORF87 [Staphylococcus phage K]	1.90E-92	100	91	AAO47536.1
19	62098	63441	447	DNA polymerase I	DNA polymerase [Bacteriophage Bastille]	3.10E-34	39	47	AAO93094.1
388	63002	63112	36						
41	63709	64416	235	HNH endonuclease	putative HNH homing endonuclease [bacteriophage bIL170]	5.60E-24	38	72	AAC27227.1
37	64650	65510	286	DNA-directed DNA polymerase	DNA polymerase I [T. thermosulfurigenes]	6.90E-33	34	79	AAR11873.1
181	65579	65821	80						
89	65838	66320	160		ORF91 [Staphylococcus phage K]	7.00E-88	100	100	AAO47540.1
20	66407	67678	423		ORF92 [Staphylococcus phage K]	0	100	100	AAO47541.1
21	67738	68994	418	RecA bacterial DNA recombination protein	recA protein [P. gingivalis W83]	7.50E-27	29	81	AAQ66027.1
121	68998	69351	117						
56	69338	70000	220	RNA polymerase sigma	ORF94 [Staphylococcus phage K]	1.00E-124	100	100	AAO47543.1
59	70128	70760	210		ORF95 [Staphylococcus phage K]	5.00E-118	100	100	AAO47544.1
80	70783	71295	170	Major tail	phi12 major tail protein-like protein [S. aureus bacteriophage phi 3A]	1.70E-21	40	79	AAM49601.1
189	71310	71537	75	Major tail	phi12 major tail protein-like protein [S. aureus bacteriophage phi 3A]	6.80E-09	47	85	AAM49601.1
174	71633	71893	86						
46	71897	72652	251		ORF97 [Staphylococcus phage K]	1.00E-144	100	100	AAO47546.1
22	72645	73895	416	Metallophosphoesterase	ORF98 [Staphylococcus phage K]	0	100	100	AAO47547.1
118	73909	74277	122		ORF99 [Staphylococcus phage K]	1.30E-63	100	100	AAO47548.1
143	74264	74575	103		ORF100 [Staphylococcus phage K]	2.50E-55	100	100	AAO47549.1
75	74639	75175	178						
45	75168	75935	255		ORF101 [Staphylococcus phage K]	4.00E-150	100	100	AAO47550.1
99	75913	76359	148		ORF102 [Staphylococcus phage K]	1.40E-80	100	100	AAO47551.1
36	76359	77222	287						
47	77594	78325	243		ORF103 [Staphylococcus phage K]	2.00E-133	100	100	AAO47553.1
94	78343	78801	152		ORF104 [Staphylococcus phage K]	7.60E-83	99	100	AAO47554.1

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
100	78866	79309	147		ORF105 [Staphylococcus phage K]	9.20E-80	100	100	AAO47555.1
53	79326	80030	234		ORF106 [Staphylococcus phage K]	5.00E-132	100	100	AAO47556.1
108	80092	80490	132		ORF107 [Staphylococcus phage K]	1.30E-71	100	100	AAO47557.1
182	80637	80879	80						
252	80884	81048	54		ORF108 [Staphylococcus phage K]	3.10E-23	100	100	AAO47558.1
240	81250	81426	58						
76	81416	81949	177						
241	82120	82296	58						
152	82289	82585	98						
219	82633	82815	60						
119	82828	83196	122						
124	83209	83556	115						
162	83556	83834	92						
140	83904	84209	101						
122	84224	84574	116		unknown [S. aureus subsp. aureus MSSA476]	2.20E-05	28	98	CAG42397.1
65	84574	85176	200						
237	85190	85369	59						
107	85596	85997	133						
173	85999	86259	86						
333	86190	86294	34						
157	86311	86598	95						
362	86609	86725	38						
170	86715	86978	87						
236	87055	87234	59						
171	87249	87512	87						
137	87515	87832	105						
55	87833	88513	226		ORF108 [Staphylococcus phage K]	2.20E-06	100	11	AAO47558.1
216	87849	87655	64						
263	88602	88760	52						
211	88795	88995	66						
155	88996	89286	96						
144	89378	89686	102		ORF109 [Staphylococcus phage K]	1.70E-51	100	100	AAO47559.1
31	89683	90591	302	Phosphoribosyl transferase	phosphoribosyl transferase domain protein [S. oneidensis MR-1]	6.40E-16	30	79	AAN55031.1

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
18	90609	91973	454	Nicotinate phosphoribosyltransferase	putative nicotinamide phosphoribosyl transferase [H. ducreyi]	3.00E-134	54	99	AAR87771.1
178	92157	92402	81						
113	92422	92814	130		ORF112 [Staphylococcus phage K]	9.80E-64	91	99	AAO47562.1
194	92816	93037	73						
142	93103	93414	103		ORF113 [Staphylococcus phage K]	5.90E-49	86	100	AAO47563.1
82	93417	93926	169						
131	93928	94257	109						
139	94451	94765	104						
225	94780	94947	55						
445	94984	95085	33						
150	96032	96331	99		ORF117 [Staphylococcus phage K]	5.30E-05	35	100	AAO47566.1
231	96347	96532	61						
156	96639	96929	96						
158	96929	97216	95						
154	97216	97509	97		ORF117 [Staphylococcus phage K]	3.20E-05	34	100	AAO47566.1
175	97513	97770	85						
183	97848	98087	79						
125	98098	98445	115		ORF118 [Staphylococcus phage K]	6.20E-64	100	100	AAO47567.1
128	98992	98654	112						
145	99303	99611	102						
159	99817	100101	94						
221	100176	100367	63						
312	100576	100442	44						
85	101172	100684	162	HNH endonuclease	putative HNH endonuclease [Enterobacteria phage T1]	8.20E-07	35	53	AAP49937.1
297	101568	101699	43						
135	101867	102190	107						
92	102616	103086	156						
234	103145	103318	57						
166	103318	103587	89						
247	103386	103216	56						
226	103672	103851	59						
450	103935	104036	33						
184	104421	104185	78						

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
88	104908	104423	161						
109	105328	104921	135						
103	105759	105328	143						
224	105953	105762	63						
87	106435	105950	161		ORF1 [Staphylococcus phage K]	3.60E-84	99	100	AAO47447.1
104	106859	106428	143		ORF2 [Staphylococcus phage K]	4.80E-81	100	100	AAO47448.1
73	107415	106873	180		ORF3 [Staphylococcus phage K]	4.00E-102	99	100	AAO47449.1
86	107915	107427	162	GTP cyclohydrolase	GTP cyclohydrolase II [V. vulnificus CMCP6]	2.80E-07	26	91	AAO08077.1
111	108326	107928	132		ORF5 [Staphylococcus phage K]	2.10E-74	100	100	AAO47451.1
51	109030	108323	235	Serine/threonine-specific protein phosphatase	serine/threonine protein phosphatase [C. burnetii RSA 493]	1.20E-13	27	94	AAO90036.1
70	109684	109130	184		ORF7 [Staphylococcus phage K]	2.00E-103	100	100	AAO47453.1
138	110017	109700	105		ORF96 [Staphylococcus phage K]	1.50E-07	41	82	AAO47545.1
71	111551	111003	182		ORF8 [Staphylococcus phage K]	1.00E-101	100	100	AAO47455.1
201	111773	111555	72						
218	111968	111774	64						
50	112695	111958	245		ORF9 [Staphylococcus phage K]	3.00E-137	100	100	AAO47456.1
437	112862	112758	34						
180	113113	112874	79						
114	113504	113115	129		ORF10 [Staphylococcus phage K]	2.00E-72	100	100	AAO47457.1
245	113776	113603	57	Immunodominant antigen A	immunodominant antigen A [S. aureus subsp. aureus MSSA476]	4.40E-06	40	92	CAG44271.1
90	114299	113817	160		ORF11 [Staphylococcus phage K]	1.80E-88	100	100	AAO47458.1
72	114891	114349	180		ORF12 [Staphylococcus phage K]	3.40E-98	100	100	AAO47459.1
77	115424	114891	177		ORF13 [Staphylococcus phage K]	2.00E-100	100	100	AAO47460.1
256	115591	115427	54						
163	115869	115594	91						
38	116714	115869	281		ORF14 [Staphylococcus phage K]	2.00E-158	100	100	AAO47461.1
24	117844	116726	372	Nitric oxide reductase	nitric-oxide reductase [S. epidermidis ATCC 12228]	3.30E-07	26	71	AAO04689.1
24	117844	116726	372	Porphyrin biosynthesis	putative porphyrin biosynthetic protein [S. enterica subsp. enterica serovar Typhi str. CT18]	5.70E-07	24	70	CAD09883.1
134	118324	117998	108						
106	118733	118317	138		ORF16 [Staphylococcus phage K]	1.20E-74	100	100	AAO47463.1
149	119169	118867	100	DNA-binding	putative DNA-binding protein [S. thermophilus bacteriophage SFi18]	1.90E-15	43	93	AAF63096.1
228	119357	119169	62						
259	119562	119401	53						

Bacteriophage G1 (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
309	121318	121181	45						
7	121610	119562	682		ORF18 [Staphylococcus phage K]	0	100	100	AAO47466.1
172	121951	121688	87						
68	122726	122148	192		ORF19 [Staphylococcus phage K]	6.00E-102	100	100	AAO47465.1
61	123345	122719	208		ORF20 [Staphylococcus phage K]	1.00E-118	100	100	AAO47467.1
32	124234	123338	298	DNA ligase/mRNA capping enzyme	possible homolog of eukaryotic DNA ligase III [N. europaea ATCC 19718]	2.80E-08	28	59	CAD85795.1
49	125267	124527	246	PhoH-like protein	PhoH-related protein [N. meningitidis MC58]	5.10E-15	35	75	AAF41256.1
63	125933	125319	204		ORF23 [Staphylococcus phage K]	2.00E-119	100	100	AAO47470.1
96	126374	125949	141	RNase H	RNase HI related protein [M. maripaludis S2]	3.40E-18	37	97	CAF30393.1
222	126555	126364	63						
57	127219	126578	213		ORF25 [Staphylococcus phage K]	1.00E-116	100	100	AAO47472.1
187	127439	127209	76	Helix-turn-helix motif	transcription regulator (putative) [LactoB. plantarum WCFS1]	7.00E-06	39	81	CAD64381.1
190	127669	127442	75						
54	128471	127779	230	Transglycosylase-like; Immunodominant antigen A	immunodominant antigen A [S. epidermidis ATCC 12228]	5.90E-15	32	100	AAO05768.1
58	129293	128658	211		ORF27 [Staphylococcus phage K]	6.00E-125	100	100	AAO47474.1
44	130151	129360	263	Prohibitin; Band 7 protein	B-cell receptor associated protein-related protein [S. pyogenes SSI-1]	6.50E-27	29	96	BAC64245.1
					Band 7 protein [P. marinus str. MIT 9313]	1.20E-09	22	90	CAE21083.1
146	130459	130151	102		ORF29 [Staphylococcus phage K]	3.70E-51	100	100	AAO47476.1
60	131201	130572	209	Amidase	amidase [S. aureus phage phi 11]	4.80E-55	53	99	AAL82281.1
84	131972	131472	166	HNH endonuclease; Intron encoded nuclease domain	putative HNH homing endonuclease [bacteriophage bIL170]	3.50E-16	34	96	AAC27227.1
42	132935	132132	267	Amidase	N-acetylmuramoyl-L-alanine amidase [Staphylococcus phage Twort]	1.40E-48	43	93	CAA69021.1
83	133438	132935	167	Holin	holTW [Staphylococcus phage Twort]	2.20E-42	62	86	CAA69020.1
233	133708	133523	61						
200	135473	135255	72						
207	136540	136331	69						
209	136885	136553	110						
169	137523	137257	88						
168	137664	138050	128						
161	138028	138306	92						
133	138303	138713	136		ORF34 [Staphylococcus phage K]	1.20E-55	100	79	AAO47481.1

Bacteriophage Twort

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
97	764	1165	133	Group I Intron	group I intron [Bacteriophage Tuc2009]	1.10E-11	35	92	AAK19864.1
36	1284	2144	286	Large terminase	large terminase [B. subtilis phage 1102phi1-3]	3.30E-67	49	89	AAS45252.1
39	2157	2948	263		ORF36 [Staphylococcus phage K]	3.90E-56	45	97	AAS91583.1
57	2935	3570	211		ORF37 [Staphylococcus phage K]	3.20E-62	75	72	AAO47483.1
29	3606	4577	323	Structural	cell surface protein precursor [LactoB. plantarum WCFS1]	1.90E-21	36	44	CAD62863.1
205	4663	5019	118		ORF39 [Staphylococcus phage K]	5.00E-18	46	96	AAO47486.1
121	5028	5408	126		ORF40 [Staphylococcus phage K]	9.40E-46	70	97	AAO47487.1
12	5389	7119	576	Portal	phage portal protein, HK97 family [Wolbachia endosymbiont of D. melanogaster]	2.90E-06	22	40	AAS14672.1
40	7268	8053	261	Capsid	major capsid protein [Staphylococcus phage Twort]	6.20E-06	57	20	AAQ62708.1
28	8059	9054	331	Topoisomerase; Initiation factor; Virulence-associated; Internalin	DNA topoisomerase IV subunit A [M. penetrans HF-2] initiation factor IF-2 [A. aeolicus VF5] virulent strain associated lipoprotein [B. burgdorferi] Internalin protein [B. cereus ATCC 14579]	3.50E-18 1.00E-17 2.30E-17 5.60E-16	24 33 23 29	94 70 77 75	BAC44437.1 AAC07794.1 AAD09328.1 AAP07572.1
16	9146	10534	462	Major capsid	major capsid protein [Staphylococcus phage Twort]	0	100	100	AAQ62708.1
286	10485	10619	44						
138	10621	10890	89						
32	10902	11813	303		ORF45 [Staphylococcus phage K]	6.00E-149	82	100	AAO47492.1
34	11825	12712	295		ORF46 [Staphylococcus phage K]	3.00E-126	73	99	AAO47493.1
55	12712	13356	214		ORF47 [Staphylococcus phage K]	8.40E-66	57	96	AAO47494.1
37	13387	14214	275		ORF48 [Staphylococcus phage K]	2.00E-105	69	98	AAO47495.1
185	14204	14413	69		ORF7 [Bacteriophage A511]	1.30E-12	60	79	CAA62545.1
11	14434	16197	587	Major tail	major tail sheath protein [Bacteriophage A511]	0	58	100	CAA62546.1
203	15647	15456	63						
106	16272	16637	121		unknown [Staphylococcus phage Twort]	1.80E-60	99	95	AAD31276.1
18	17654	18967	437	Group I Intron	group I intron [Bacteriophage Tuc2009]	7.70E-06	30	32	AAK19864.1
172	18363	18142	73						
245	19026	19184	52						
219	19132	19311	59						
83	19347	19802	151		ORF51 [Staphylococcus phage K]	8.70E-31	44	98	AAO47498.1
125	19849	20154	101		ORF52 [Staphylococcus phage K]	3.80E-19	49	92	AAO47499.1
229	20237	20689	150		ORF53 [Staphylococcus phage K]	1.40E-41	54	100	AAO47500.1
81	20763	21221	152		ORF54 [Staphylococcus phage K]	5.20E-31	44	100	AAO47501.1
2	21272	25081	1269	Purine NTPase	purine NTPase, putative [A. fulgidus DSM 4304]	2.80E-07	18	22	AAB90211.1

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
7	25129	27543	804	Amidase; Secretory antigen	secretory antigen SsaA-like protein [S. epidermidis ATCC 12228]	2.20E-18	35	28	AAO05088.1
					N-acetylmuramoyl-L-alanine amidase, family 4 [E. faecalis V583]	1.80E-12	41	11	AAO81590.1
87	25182	24748	144						
319	27431	27550	39						
35	27547	28413	288		ORF57 [Staphylococcus phage K]	1.80E-41	33	100	AAO47506.1
10	28410	30224	604	Purine NTPase	purine NTPase [M. jannaschii DSM 2661]	8.00E-07	23	44	AAB99331.1
277	28975	29115	46						
41	30314	31093	259		ORF59 [Staphylococcus phage K]	4.40E-68	50	100	AAO47508.1
72	31090	31623	177		ORF60 [Staphylococcus phage K]	9.00E-48	54	96	AAO47509.1
50	31613	32317	234		ORF61 [Staphylococcus phage K]	2.20E-89	68	100	AAO47510.1
26	32331	33377	348		ORF62 [Staphylococcus phage K]	2.00E-129	65	99	AAS91584.1
5	33388	36519	1043	Anti-receptor	putative anti-receptor [S. thermophilus bacteriophage Sfi11]	1.30E-05	30	16	AAC34416.1
381	33418	33308	36						
73	36604	37113	169		ORF64 [Staphylococcus phage K]	3.30E-57	63	100	AAO47512.1
3	37130	40585	1151	Virulence-associated	Virulence-associated protein [B. henselae str. Houston-1]	1.30E-54	23	96	CAF27126.1
232	40636	40803	55						
24	40803	41852	349		ORF66 [Staphylococcus phage K]	9.40E-17	26	93	AAO47515.1
107	41868	42233	121		ORF67 [Staphylococcus phage K]	6.30E-13	35	89	AAO47516.1
17	42242	43570	442		ORF68 [Staphylococcus phage K]	5.20E-66	35	100	AAO47517.1
6	43659	46673	1004	Helicase; Gyrase; Protein splicing (intein) site	putative helicase [S. enterica subsp. enterica serovar Typhi str. CT18]	2.80E-34	33	28	CAD09945.1
					DNA gyrase subunit A [M. flavescens]	3.30E-19	22	46	CAA92433.1
13	46679	48166	495		ORF70 [Staphylococcus phage K]	2.00E-114	43	100	AAO47519.1
14	48153	49595	480	DNA Helicase; AAA ATPase	DNA primase-helicase subunit [Enterobacteria phage RB49]	6.70E-14	24	82	AAL87839.2
27	49656	50675	339	Endonuclase; Exonuclease	gp47 recombination endonuclease subunit [Enterobacteria phage T4]	2.50E-11	24	100	AAD42475.1
					putative DNA repair exonuclease [S. aureus subsp. aureus MSSA476]	4.30E-11	25	81	CAG43570.1
401	49807	49703	34						
109	50732	51094	120		ORF73 [Staphylococcus phage K]	1.40E-23	56	72	AAO47522.1
9	51098	53008	636	Exonuclease; ABC transporter	putative exonuclease subunit 2 [Y. pestis biovar Medievalis str. 91001]	1.10E-54	26	100	AAS58684.1
					ABC transporter [Y. pestis KIM]	9.60E-51	25	100	AAC13199.1
65	53011	53598	195		ORF75 [Staphylococcus phage K]	2.10E-38	44	100	AAO47524.1
23	53611	54672	353	DNA primase	DNA primase (bacterial type) [T. tengcongensis MB4]	3.20E-12	24	97	AAM24950.1
310	54913	55035	40						
89	55035	55466	143		ORF77 [Staphylococcus phage K]	2.40E-32	47	100	AAO47526.1

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
63	55456	56055	199		ORF78 [Staphylococcus phage K]	2.40E-77	65	100	AAO47527.1
99	56071	56463	130	Flavodoxin/nitric oxide synthase; NrdI	NrdI protein involved in ribonucleotide reductase function [S. aureus subsp. aureus Mu50]	2.30E-12	32	86	BAB56892.1
45	56474	57217	247	Ribonucleotide reductase large subunit	large subunit ribonucleotide reductase [Staphylococcus phage Twort]	2.00E-133	99	97	AAM00816.1
33	57767	58669	300	Ribonucleotide reductase large subunit	large subunit ribonucleotide reductase [Staphylococcus phage Twort]	2.00E-169	100	98	AAM00816.1
52	58841	59572	243	HNH endonuclease	HNH endonuclease I-TwoI [Staphylococcus phage Twort]	4.00E-141	100	100	AAM00817.1
371	59547	59657	36						
118	59778	60104	108	Ribonucleotide reductase alpha subunit	large subunit ribonucleotide reductase [Staphylococcus phage Twort]	2.00E-57	99	100	AAM00816.1
25	60120	61169	349	Ribonucleotide reductase beta subunit	ribonucleoside-diphosphate reductase minor subunit [S. epidermidis ATCC 12228]	6.10E-93	53	92	AAO04111.1
139	61182	61451	89						
252	61234	61079	51						
123	61453	61761	102		ORF83 [Staphylococcus phage K]	2.70E-33	62	100	AAO47532.1
64	61841	62563	240		ORF84 [Staphylococcus phage K]	5.80E-85	74	82	AAO47533.1
129	62563	62859	98	Histone-like bacterial DNA-binding protein	probable DNA-binding protein HU [Pirellula sp.]	1.10E-05	28	96	CAD73100.1
110	62939	63250	103						
4	63253	66456	1067	DNA-directed DNA polymerase	DNA-directed DNA polymerase I [T. maritima MSB8]	2.50E-49	26	49	AAD36686.1
186	66506	66709	67						
77	66694	67176	160		ORF91 [Staphylococcus phage K]	7.50E-50	60	100	AAO47540.1
22	67248	68342	364		ORF92 [Staphylococcus phage K]	1.20E-99	47	100	AAO47541.1
155	68485	68730	81						
19	68745	69968	407	RecA bacterial DNA recombination protein	recA-like protein [P. gingivalis]	1.70E-23	27	74	AAC72890.1
112	69961	70308	115						
58	70301	70936	211	RNA polymerase sigma	ORF94 [Staphylococcus phage K]	5.10E-68	61	100	AAO47543.1
58	70301	70936	211	RNA polymerase sigma	unknown [Bacteriophage SPO1]	9.80E-11	32	59	CAA25950.1
407	70924	71025	33						
56	71007	71645	212		ORF95 [Staphylococcus phage K]	6.90E-73	64	100	AAO47544.1
178	72199	72414	71	Major tail	phi12 major tail protein-like protein [S. aureus bacteriophage phi 3A]	7.60E-08	46	91	AAM49601.1
131	72515	72757	80						
47	72757	73491	244		ORF97 [Staphylococcus phage K]	1.90E-38	37	100	AAO47546.1
20	73484	74719	411	Metallophosphoesterase	ORF98 [Staphylococcus phage K]	3.00E-132	56	100	AAO47547.1
105	74729	75094	121		ORF99 [Staphylococcus phage K]	1.30E-13	28	99	AAO47548.1

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
71	75147	75683	178						
43	75676	76422	248		ORF101 [Staphylococcus phage K]	2.90E-98	70	99	AAO47550.1
93	76406	76825	139		ORF102 [Staphylococcus phage K]	1.30E-44	65	99	AAO47551.1
38	76827	77633	268						
48	77972	78700	242		ORF103 [Staphylococcus phage K]	1.60E-85	66	100	AAO47553.1
79	78716	79180	154		ORF104 [Staphylococcus phage K]	1.10E-28	42	100	AAO47554.1
88	79238	79669	143		ORF105 [Staphylococcus phage K]	2.00E-34	50	100	AAO47555.1
54	79679	80353	224		ORF106 [Staphylococcus phage K]	3.70E-27	34	100	AAO47556.1
96	80346	80741	131		ORF107 [Staphylococcus phage K]	1.10E-22	42	96	AAO47557.1
366	80412	80299	37						
157	80877	81116	79						
168	81116	81340	74						
237	81337	81501	54						
190	81498	81704	68						
21	81885	82994	369	Insertion sequence; Transposase	transposase [C. tetani E88]	9.00E-140	66	100	AAO36394.1
132	83366	83644	92						
67	83723	84286	187						
111	84303	84659	118						
195	84673	84873	66						
84	84887	85339	150						
102	85420	85794	124						
130	85776	86069	97						
82	86438	86893	151						
174	86883	87095	70						
117	87158	87490	110						
170	88236	88508	90						
44	88523	89269	248		unknown [E. ictaluri]	3.70E-13	25	69	AAT77726.1
95	89367	89774	135						
75	90005	90502	165						
162	90560	90793	77						
127	90817	91119	100						
114	91387	91731	114						
227	91768	91941	57						
200	91938	92126	62						

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
179	92137	92352	71						
175	92349	92567	72						
206	92579	92767	62						
30	92964	93914	316						
137	94575	94847	90						
197	95037	95234	65						
94	95378	95794	138						
113	96373	96020	117						
408	96577	96678	33						
192	96697	96900	67						
253	96902	97054	50						
173	97072	97260	62						
62	98432	97830	200		ORF2 [Staphylococcus phage K]	1.60E-36	51	71	AAO47448.1
148	98746	98492	84						
171	99049	98828	73						
104	99431	99060	123						
8	101685	99421	754	Serine/threonine-specific protein phosphatase	2',3'-cyclic nucleotide 3'-phosphodiesterase [F. nucleatum subsp. nucleatum ATCC 25586]	5.00E-111	37	96	AAL93718.1
126	101992	101687	101						
146	102249	101992	85	DNA packaging	unknown [Bacteriophage SPP1]	6.10E-15	52	100	CAA39540.1
49	102953	102246	235	Serine/threonine-specific protein phosphatase	serine/threonine protein phosphatase [C. burnetii RSA 493]	3.30E-16	30	95	AAO90036.1
217	103259	103077	60						
68	103824	103267	185		ORF8 [Staphylococcus phage K]	7.90E-29	42	100	AAO47455.1
101	104270	103887	127		ORF14 [S. thermophilus bacteriophage 7201]	3.20E-22	75	50	AAF43507.1
86	104720	104280	146						
53	105412	104729	227						
166	105711	105505	68						
159	105955	105719	78						
85	106320	105952	122	Sensor	possible sensor protein [S. aureus phage phi 13]	1.20E-11	39	100	AAL82351.1
76	106814	106317	165		unknown [LactoB. bacteriophage phi adh]	2.60E-32	48	78	CAB52497.1
152	106975	106727	82		unknown [S. pyogenes M1 GAS]	6.60E-09	46	71	AAK33631.1
404	107256	107152	34						
103	108139	107765	124	Staphylococcal nuclease	Staphylococcal nuclease family protein [L. interrogans serovar lai str. 56601]	1.60E-08	31	86	AAN50918.1

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
124	108488	108180	102						
300	108881	108753	42						
1	112707	108565	1380	Structural	putative membrane-anchored cell surface protein [B. pseudomallei K96243]	3.40E-06	19	56	CAH38912.1
80	113172	112708	154		ORF11 [Staphylococcus phage K]	9.00E-31	44	98	AAO47458.1
326	113360	113241	39						
120	113667	113353	104						
98	114061	113660	133		ORF16 [Staphylococcus phage K]	1.10E-14	38	100	AAO47463.1
91	114637	114212	141	dUTPase	deoxyuridine 5-triphosphate nucleotidohydrolase [C. tetani E88]	2.40E-24	46	100	AAO35779.1
236	114814	114647	55						
191	114957	114814	47						
150	115255	115004	83						
122	115584	115267	105	Amidase	N-acetylmuramoyl-L-alanine amidase (autolysine) [OceanoB. iheyensis HTE831]	7.80E-09	34	90	BAC12176.1
230	115812	115982	56						
61	116167	115550	205		ORF19 [Staphylococcus phage K]	4.90E-60	59	92	AAO47465.1
60	116787	116167	206		ORF20 [Staphylococcus phage K]	2.10E-79	68	100	AAO47467.1
78	117260	116793	155		unknown [M. hyopneumoniae 232]	1.80E-05	30	99	AAV27515.1
141	117536	117273	87						
340	118343	118459	38						
46	118344	117607	245	PhoH ATP-dependent phosphate regulator	PhoH protein (phosphate starvation inducible protein) [L. pneumophila subsp. pneumophila str. Philadelphia 1]	1.30E-15	29	95	AAU28890.1
51	119140	118472	222	Immunodominant antigen A	immunodominant antigen A [S. aureus subsp. aureus MRSA252]	1.60E-46	46	100	CAG41627.1
70	119768	119232	178		ORF23 [Staphylococcus phage K]	2.30E-22	37	93	AAO47470.1
90	120199	119774	141	RNase H	RNase HI related protein [M. maripaludis S2]	1.60E-20	42	92	CAF30393.1
213	120381	120196	61						
66	120965	120393	190	EF-hand	ORF25 [Staphylococcus phage K]	2.70E-19	30	88	AAO47472.1
184	121170	120958	70	DNA-binding; Repressor					
134	121458	121234	74						
69	121601	122128	175	HNH endonuclease	putative HNH homing endonuclease [bacteriophage bIL170]	1.10E-10	33	65	AAC27202.1
15	123559	122156	467	Amidase	N-acetylmuramoyl-L-alanine amidase [Staphylococcus phage Twort]	0	100	100	CAA69021.1
176	124082	123525	185	Holin	holTW [Staphylococcus phage Twort]	1.00E-104	99	100	CAA69020.1
221	124334	124155	59						
180	125499	125284	71						
222	126037	125834	67						

Bacteriophage Twort (continued)

ORF	Start (nt)	End (nt)	Size (aa)	Predicted Function	Representative similarity to proteins in database	E-value	% Identity	% Length of Match	Accession
158	126722	126402	106						
149	127039	126788	83						
140	127270	127533	87						
133	127508	127786	92						
92	127779	128192	137		ORF34 [Staphylococcus phage K]	1.20E-29	57	79	AAO47481.1
151	128207	128446	79	Large terminase	large terminase [B. subtilis phage 1102phi1-3]	1.00E-17	51	86	AAS45252.1
31	128937	129887	316	Group I Intron	group I intron [Bacteriophage Tuc2009]	1.40E-21	26	93	AAK19864.1
59	129991	130623	210	Large terminase	large terminase [B. subtilis phage 1102phi1-3]	2.50E-59	52	98	AAS45252.1
212	130310	130125	61						