

Table S5: AB2 genome annotations acquired from protein sequence and homology analysis.

CDS	5'	3'	Strand	Putative Function	BLASTp Accession	E-value	Identity	Category	Functional Support
AB2_01	1	504	+	terminase small subunit	YP_003090177.1	2.E-85	73.62%	lysogeny	similar to AA sequence, YP_003090177.1 and YP_010082062.1
AB2_02	549	2,192	+	terminase large subunit	DAG84110.1	0.E+00	72.14%	lysogeny	PFAM:PF03354; PFAM:PF20441
AB2_03	2,189	3,463	+	portal protein	YP_003090179.1	9.E-152	52.13%	virion structure & morphogenesis	PFAM:PF04860
AB2_04	3,432	4,193	+	Clp protease	YP_003090180.1	2.E-74	54.20%	virion structure & morphogenesis	PFAM:PF00574
AB2_05	4,256	5,542	+	capsid protein	DAX83085.1	4.E-176	59.39%	virion structure & morphogenesis	PFAM:PF05065
AB2_06	5,599	5,964	+	hypothetical protein	WP_369062920.1	8.E-78	100.00%	hypothetical	
AB2_07	5,977	6,516	+	head-tail connector protein	YP_003090182.1	1.E-21	41.56%	virion structure & morphogenesis	CATH:G3DSA:1.10.3230.30
AB2_08	6,519	6,875	+	head completion protein	XRX02929.1	5.E-29	49.15%	virion structure & morphogenesis	PFAM:PF05521
AB2_09	6,868	7,110	+	hypothetical protein	WP_186270404.1	4.E-48	100.00%	hypothetical	
AB2_10	7,097	7,447	+	tail completion protein	XRX02930.1	1.E-29	52.21%	virion structure & morphogenesis	PFAM:PF11367
AB2_11	7,511	7,939	+	tail tube protein	DAG46823.1	3.E-41	52.63%	virion structure & morphogenesis	PFAM:PF16460
AB2_12	7,946	8,317	+	tail assembly chaperone	CAB4153270.1	1.E-22	43.86%	virion structure & morphogenesis	CATH:G3DSA:3.30.2220.20
AB2_13	8,332	8,631	+	minor tail protein T	DAG46839.1	2.E-26	45.83%	virion structure & morphogenesis	PFAM:PF06223
AB2_14	8,631	9,038	+	tail component	DAG84104.1	2.E-13	36.22%	virion structure & morphogenesis	PFAM:PF04883
AB2_15	9,328	12,150	+	tail tape measure protein	DAH83217.1	1.E-39	36.16%	virion structure & morphogenesis	PFAM:PF09718
AB2_16	12,143	12,484	+	tail tip protein M	UYE89890.1	1.E-41	61.61%	virion structure & morphogenesis	InterPro:IPR010265
AB2_17	12,491	13,669	+	hypothetical protein	UYE89889.1	2.E-45	42.11%	hypothetical	
AB2_18	13,666	14,349	+	tail tip protein L	NP_94504.1	7.E-127	74.01%	virion structure & morphogenesis	PFAM:PF05100
AB2_19	14,350	15,099	+	tail tip assembly protein K	WNO23865.1	1.E-126	69.64%	virion structure & morphogenesis	UniProt:P03729; PROSITE:PS51935; PFAM:PF14464
AB2_20	15,096	15,692	+	tail assembly protein I	NP_536376.1	1.E-81	63.96%	virion structure & morphogenesis	PFAM:PF06805
AB2_21	15,689	19,090	+	viral tip-attachment protein J	YP_355397.1	0.E+00	64.20%	virion structure & morphogenesis	PFAM:PF2480; PFAM:PF09327
AB2_22	19,090	19,374	+	hypothetical protein	UOL48386.1	3.E-06	36.08%	hypothetical	
AB2_23	19,376	20,110	+	hypothetical protein	DAL63675.1	4.E-07	29.63%	hypothetical	
AB2_24	20,120	20,482	+	hypothetical protein	DAX65569.1	6.E-12	36.56%	hypothetical	
AB2_25	20,544	20,903	+	hypothetical protein	WP_036029969.1	9.E-81	100.00%	hypothetical	
AB2_26	20,900	21,196	+	hypothetical protein	WP_186042159.1	1.E-61	100.00%	hypothetical	
AB2_27	21,193	21,687	+	hypothetical protein	XOS39714.1	6.E-63	62.20%	hypothetical	
AB2_28	21,684	22,010	+	hypothetical protein	WP_186270413.1	2.E-64	100.00%	hypothetical	
AB2_29	21,979	22,218	+	Rz-like spanin	XRX03430.1	8.E-02	62.71%	lysis & virulence	PROSITE:PS51257
AB2_30	22,404	23,192	+	DNA adenine methyltransferase	DAE46048.1	6.E-160	80.15%	DNA metabolism	PFAM:PF02086
AB2_31	23,231	23,848	-	hypothetical protein	NP_536388.1	2.E-30	43.09%	hypothetical	
AB2_32	24,183	25,196	+	integrase	WNL50560.1	5.E-110	51.48%	lysogeny	PFAM:PF24624; PFAM:PF00589
AB2_33	25,193	25,492	-	hypothetical protein	UEW68564.1	6.E-49	82.47%	hypothetical	
AB2_34	25,495	25,860	-	DUF4031-domain containing protein	NP_944277.1	2.E-37	61.61%	hypothetical	PFAM:PF13223
AB2_35	25,878	26,663	-	hypothetical protein	QXV72216.1	1.E-52	67.36%	hypothetical	
AB2_36	26,660	27,460	-	ParB partition protein	YP_003090162.1	7.E-142	73.48%	DNA metabolism	PFAM:PF02195
AB2_37	27,463	28,236	-	PRTRC system ThfF protein	UEW68563.1	4.E-142	79.59%	plasmid associated	NCBI:TIGR03736
AB2_38	28,236	28,433	-	hypothetical protein	WP_186270392.1	3.E-40	100.00%	hypothetical	
AB2_39	28,613	29,425	-	PRTRC system protein A	UEW68562.1	3.E-112	62.02%	plasmid associated	NCBI:TIGR03735
AB2_40	29,427	30,155	-	PRTRC system protein B	UEW68561.1	6.E-95	60.42	plasmid associated	NCBI:TIGR03737
AB2_41	30,152	31,225	-	PRTRC system protein F	UEW68560.1	3.E-103	47.97%	plasmid associated	NCBI:TIGR03742
AB2_42	31,222	31,407	-	hypothetical protein	DAH61494.1	9.E-09	44.26%	hypothetical	
AB2_43	31,412	31,798	-	PRTRC system protein C	DAH61472.1	3.E-54	65.41%	plasmid associated	NCBI:TIGR03738
AB2_44	31,810	32,370	-	PRTRC system protein E	UEW68557.1	2.E-43	53.50%	plasmid associated	NCBI:TIGR03741
AB2_45	32,376	32,870	+	hypothetical protein	BET72104.1	4.E-56	90.84%	hypothetical	
AB2_46	32,962	33,228	-	hypothetical protein	WP_186270423.1	5.E-57	100.00%	hypothetical	
AB2_47	33,347	33,472	-	hypothetical protein	WP_279606935.1	1.E-19	100.00%	hypothetical	
AB2_48	33,718	34,071	-	hypothetical protein	WP_155301489.1	5.E-78	100.00%	hypothetical	
AB2_49	34,091	34,825	-	LexA peptidase	YP_001293383.1	3.E-22	32.42%	lysogeny	CDD:cd06529
AB2_50	34,886	35,140	+	lambda CI repressor	DAM00921.1	5.E-17	53.73%	lysogeny	SSFAM:SSF47413
AB2_51	35,143	35,400	-	hypothetical protein	DAH61483.1	7.E-33	63.53%	hypothetical	
AB2_52	35,428	35,934	+	regulatory protein CII	DAG84130.1	6.E-103	85.12%	lysogeny	PFAM:PF06892
AB2_53	35,974	36,225	+	hypothetical protein	WP_155301488.1	3.E-49	96.39%	hypothetical	
AB2_54	36,215	36,421	-	hypothetical protein	WP_155301487.1	3.E-42	100.00%	hypothetical	
AB2_55	36,587	37,948	+	DnaB-like replicative helicase	DAG84112.1	0.E+00	85.65%	DNA metabolism	PFAM:PF00772; PFAM:PF03796
AB2_56	37,991	38,989	+	hypothetical protein	YP_003090173.1	2.E-145	62.14%	hypothetical	
AB2_57	39,170	39,412	+	hypothetical protein	UEW68544.1	3.E-27	65.75%	hypothetical	
AB2_58	39,547	39,930	+	HNH endonuclease	YP_003090176.1	3.E-48	59.50%	lysogeny	PFAM:PF01844