

Table S3: AB1 genome annotations acquired from protein sequence and homology analysis.

CDS	5'end	3' end	Strand	Putative Function	BLASTp Accession	E-value	Identity	Category	Functional Support
AB1_01	1	1,953	+	terminase large subunit	WWY66184.1	0.E+00	84.31%	lysogeny	PFAM:PF05876; PFAM:PF20454
AB1_02	1,964	2,170	+	head-tail joining protein	WWY66185.1	6.E-34	85.29%	virion structure & morphogenesis	NCBI:NF047331
AB1_03	2,167	3,657	+	portal protein	WWY66186.1	0.E+00	80.40%	virion structure & morphogenesis	PFAM:PF05136
AB1_04	3,654	4,769	+	Clp protease	WWY66187.1	8.E-149	61.41%	virion structure & morphogenesis	PFAM:PF00574
AB1_05	4,799	5,143	+	head decoration protein D	WWY66188.1	7.E-42	63.16%	virion structure & morphogenesis	PFAM:PF02924
AB1_06	5,220	6,215	+	major capsid protein	WWY66189.1	2.E-169	68.58%	virion structure & morphogenesis	PFAM:PF03864
AB1_07	6,217	6,507	+	head-tail attachment protein FII	WWY66190.1	2.E-39	69.47%	virion structure & morphogenesis	PFAM:PF05354
AB1_08	6,511	7,041	+	minor tail protein Z	WWY66191.1	8.E-83	67.61%	virion structure & morphogenesis	PFAM:PF06763
AB1_09	7,031	7,561	+	hypothetical protein	WWY66192.1	2.E-58	57.40	hypothetical	
AB1_10	7,582	8,241	+	baseplate assembly protein V	WWY66193.1	3.E-95	61.93%	virion structure & morphogenesis	PFAM:PF04717
AB1_11	8,244	9,032	-	hypothetical protein	WP_186057531.1	0.E+00	98.85%	hypothetical	
AB1_12	9,147	9,347	+	hypothetical protein	WWY66194.1	7.E-08	47.06%	hypothetical	
AB1_13	9,350	9,682	+	baseplate wedge protein gp25	XOR69958.1	4.E-42	61.82%	virion structure & morphogenesis	PFAM:PF04965
AB1_14	9,679	10,575	+	baseplate assembly protein J	WWY66196.1	7.E-130	64.98%	virion structure & morphogenesis	PFAM:PF04865
AB1_15	10,565	11,143	+	tail protein I	WWY66197.1	3.E-96	71.28%	virion structure & morphogenesis	PFAM:PF09684
AB1_16	11,131	13,095	+	tail fiber protein	UNY41739.1	8.E-176	54.83%	virion structure & morphogenesis	PFAM:PF21446; PFAM:PF07484
AB1_17	13,109	13,819	+	tail fibre assembly protein	USM11628.1	2.E-72	58.06%	virion structure & morphogenesis	PFAM:PF02413
AB1_18	13,891	15,060	+	tail sheath protein	DAE46045.1	0.E+00	78.87%	virion structure & morphogenesis	PFAM:PF22671; PFAM:PF04984; PFAM:PF17482
AB1_19	15,071	15,574	+	tail tube protein	WWY66201.1	3.E-76	64.07%	virion structure & morphogenesis	PFAM:PF04985
AB1_20	15,656	15,958	+	tail assembly chaperone	WWY66202.1	4.E-31	57.00%	virion structure & morphogenesis	PFAM:PF10109
AB1_21	16,040	18,472	+	tail tape measure protein	WWY66203.1	0.E+00	68.72%	virion structure & morphogenesis	PFAM:PF10145
AB1_22	18,482	19,360	+	tail formation protein	DAE46036.1	6.E-134	63.82%	virion structure & morphogenesis	PIRSF:PIRSF011237
AB1_23	19,368	19,541	+	tail protein X	WWY66205.1	4.E-23	71.93%	virion structure & morphogenesis	PFAM:PF05489
AB1_24	19,551	20,600	+	baseplate hub protein	DAE46046.1	0.E+00	75.57%	virion structure & morphogenesis	PFAM:PF05954
AB1_25	20,672	21,121	+	putative membrane protein	WGH15564.1	1.E-18	34.64%	lysis & virulence	AA similarity, WGH15564.1
AB1_26	21,118	21,684	+	glycosyl hydrolase	ULR75146.1	5.E-91	70.72%	lysis & virulence	PFAM:PF05838; PFAM:PF09374
AB1_27	21,687	22,310	+	hypothetical protein	UOF78607.1	7.E-21	35.45%	hypothetical	
AB1_28	22,471	23,256	+	DNA adenine methyltransferase	WWY66210.1	1.E-164	83.59%	DNA metabolism	PFAM:PF02086
AB1_29	23,297	23,584	-	hypothetical protein	WP_369057405.1	4.E-60	100.00%	hypothetical	
AB1_30	23,581	23,994	-	hypothetical protein	WNO23848.1	1.E-30	47.48%	hypothetical	PFAM:PF10908
AB1_31	24,339	25,016	-	nitroreductase	WP_338000189.1	1.E-30	35.56%	lysogeny	CATH-Gene3D:G3DSA:3.40.109.10
AB1_32	24,991	25,587	-	queosine biosynthesis protein QueC	XOR87939.1	2.E-74	50.52%	accessory	PFAM:PF06508
AB1_33	25,584	26,717	-	nucleoside 2-deoxyribosyltransferase	XOR87938.1	9.E-74	36.95%	accessory	PFAM:PF00294; PFAM:PF05014
AB1_34	26,822	27,100	-	hypothetical protein	WP_369057402.1	1.E-55	98.91%	hypothetical	
AB1_35	27,406	28,476	+	hypothetical protein	WP_369057401.1	0.E+00	100.00%	hypothetical	
AB1_36	28,650	29,348	+	8-oxoguanine DNA glycosylase	XTP78316.1	9.E-04	32.18%	DNA metabolism	PFAM:PF22175
AB1_37	29,542	31,293	+	OLD nuclease	XOR94529.1	4.E-54	29.34%	anti-phage defense	PFAM:PF13175; PFAM:PF20469
AB1_38	31,335	33,065	+	UvrD helicase	XOR94528.1	1.E-16	26.80%	anti-phage defense	PFAM:PF00580
AB1_39	33,497	34,798	+	integrase	XDQ96023.1	0.E+00	62.50%	lysogeny	PFAM:PF00589
AB1_40	34,755	35,003	-	AlpA transcriptional regulator	YP_003090161.1	2.E-22	58.90%	lysogeny	PFAM:PF05930
AB1_41	35,000	35,392	-	hypothetical protein	WWY66221.1	4.E-44	70.87%	hypothetical	
AB1_42	35,494	36,531	-	ParB partition protein	WWY66222.1	2.E-137	65.75%	DNA metabolism	SSFAM:SSF110849; SSFAM:SSF109709
AB1_43	36,531	36,893	-	hypothetical protein	WWY66225.1	1.E-21	53.57%	hypothetical	
AB1_44	36,944	37,162	-	hypothetical protein	WP_105849413.1	4.E-42	100.00%	hypothetical	
AB1_45	37,291	37,626	-	hypothetical protein	WWY66226.1	2.E-10	44.93%	hypothetical	
AB1_46	37,697	38,248	-	CI repressor protein	DAR21306.1	1.E-17	41.07%	lysogeny	CATH:G3DSA:1.10.260.40; PROSITE:PSS0943
AB1_47	38,332	38,568	+	hypothetical protein	YP_002284394.1	2.E-08	42.86%	hypothetical	
AB1_48	38,646	39,188	+	hypothetical protein	WWY66227.1	2.E-92	83.64%	hypothetical	
AB1_49	39,196	39,558	+	hypothetical protein	WWY66228.1	3.E-35	57.50%	hypothetical	
AB1_50	39,819	42,326	+	virulence associated protein E	WWY66230.1	0.E+00	83.47%	lysis & virulence	PFAM:PF05272
AB1_51	42,547	43,320	+	DnaI/Hsp40 family protein	WWY66231.1	2.E-80	56.25%	accessory	SSFAM:SSF57938
AB1_52	43,540	43,734	+	hypothetical protein	MBU9166189.1	9.E-37	100%	hypothetical	
AB1_53	43,847	44,416	+	hypothetical protein	DAO51520.1	6.E-40	46.24%	hypothetical	