

Table S6: AB4 genome annotations acquired from protein sequence and homology analysis.

CDS	5'	3'	Strand	Putative Function	BLASTp Accession	E-value	Identity	Category	Functional Support
AB4_01	1	1,059	-	portal protein	YP_010664104.1	0.E+00	80.91%	virion structure & morphogenesis	NCBIFAM:TIGR01540
AB4_02	1,056	2,825	-	terminase large subunit	UNY41721.1	0.E+00	86.42%	lysogeny	PFAM:PF17289;PFAM:PF03237;PFAM:PF06056
AB4_03	2,929	3,789	+	capsid scaffolding protein	UNY41778.1	3.E-135	70.74%	virion structure & morphogenesis	PFAM:PF05929
AB4_04	3,029	3,143	-	tRNA-Val				tRNA	
AB4_04	3,818	4,837	+	major capsid protein	QWY84949.1	0.E+00	72.92%	virion structure & morphogenesis	PFAM:PF05125
AB4_05	4,834	5,523	+	terminase small subunit	XRXY06447.1	4.E-95	66.52%	lysogeny	PFAM:PF05944
AB4_06	5,622	6,101	+	head completion protein	UNY41725.1	2.E-70	70.44%	virion structure & morphogenesis	PFAM:PF05926
AB4_07	6,101	6,307	+	tail protein	UNY41666.1	2.E-37	85.29%	virion structure & morphogenesis	PFAM:PF05489
AB4_08	6,321	6,665	+	putative holin	YP_010664112.1	6.E-56	83.33%	lysis & virulence	PFAM:PF16931
AB4_09	6,667	6,939	+	putative holin	XRXY03276.1	4.E-31	73.33%	lysis & virulence	PFAM:PF05449
AB4_10	6,936	7,748	+	endolysin	YP_001111074.1	3.E-143	74.81%	lysis & virulence	PFAM:PF11860;PFAM:PF01471
AB4_11	7,745	8,176	+	LysB protein	UNY41670.1	2.E-37	56.91%	lysis & virulence	NCBIFAM:TIGR03495
AB4_12	8,151	8,285	+	LysC protein	YP_010114052.1	8.E-15	70.45%	lysis & virulence	NCBIFAM:NF038368
AB4_13	8,278	8,694	+	tail completion protein R	XRXY06482.1	3.E-52	62.50%	virion structure & morphogenesis	PFAM:PF06891
AB4_14	8,682	9,152	+	virion morphogenesis protein	XRXY03272.1	2.E-63	63.69%	virion structure & morphogenesis	PFAM:PF05069
AB4_15	9,132	9,908	-	DNA methylase	YP_004306440.1	1.E-135	72.87%	DNA metabolism	PFAM:PF01555
AB4_16	10,078	10,776	+	baseplate assembly protein V	UNY41792.1	3.E-114	72.41%	virion structure & morphogenesis	PFAM:PF04717
AB4_17	10,773	11,135	+	baseplate wedge protein	UNY41793.1	4.E-61	74.17%	virion structure & morphogenesis	PFAM:PF04965
AB4_18	11,132	12,037	+	baseplate assembly protein J	UNY41794.1	3.E-176	79.40%	virion structure & morphogenesis	PFAM:PF04865
AB4_19	12,030	12,572	+	tail protein I	XRXY04640.1	5.E-102	80.34%	virion structure & morphogenesis	PFAM:PF09684
AB4_20	12,569	15,172	+	long tail fibre protein	UNY41680.1	0.E+00	54.65%	virion structure & morphogenesis	PFAM:PF21446
AB4_21	15,191	15,826	+	tail fibre assembly protein	UNY41681.1	1.E-94	70.94%	virion structure & morphogenesis	PFAM:PF02413
AB4_22	15,865	17,037	+	tail sheath protein	UNY41798.1	0.E+00	82.05%	virion structure & morphogenesis	PFAM:PF22671;PFAM:PF04984;PFAM:PF17482
AB4_23	17,054	17,563	+	tail tube protein	UNY41683.1	5.E-87	72.78%	virion structure & morphogenesis	PFAM:PF04985
AB4_24	17,617	17,958	+	tail assembly protein E	XRXY03261.1	6.E-46	76.64%	virion structure & morphogenesis	PFAM:PF10109;InterPro:IPR019289
AB4_25	17,967	18,086	+	tail assembly protein E'	YP_004306430.1	6.E-14	86.49%	virion structure & morphogenesis	PFAM:PF06528
AB4_26	18,083	21,322	+	tape measure protein	UNY41686.1	0.E+00	59.36%	virion structure & morphogenesis	PANTHER:PTHR37813
AB4_27	21,336	21,785	+	tail protein GpU	XRXY03067.1	4.E-63	74.81%	virion structure & morphogenesis	PFAM:PF06995
AB4_28	21,830	22,867	+	baseplate hub protein	UNY41688.1	0.E+00	75.07%	virion structure & morphogenesis	PFAM:PF05954
AB4_29	22,893	23,171	-	hypothetical protein	WP_186134993.1	4.E-54	100.00%	hypothetical	
AB4_30	23,328	23,852	-	lambda repressor-like protein	DAH82860.1	2.E-63	62.35%	lysogeny	SSFAM:SSF47413;CDD:cd00093
AB4_31	23,894	24,109	+	transcriptional regulator	YP_004306424.1	7.E-22	70.15%	lysogeny	HHPred 99.19% PDBe 2k1o Transcriptional regulator
AB4_32	24,119	24,316	+	hypothetical protein	UNY41692.1	1.E-34	86.15%	hypothetical	
AB4_33	24,356	24,559	+	hypothetical protein	YP_004306422.1	5.E-30	79.10%	hypothetical	
AB4_34	24,547	24,795	+	transcriptional regulator	YP_004306421.1	4.E-49	92.68%	lysogeny	PFAM:PF04606
AB4_35	24,885	25,097	+	hypothetical protein	XRXY06508.1	2.E-15	53.03%	hypothetical	
AB4_36	25,100	25,303	+	hypothetical protein	YP_004306372.1	1.E-28	76.12%	hypothetical	
AB4_37	25,345	25,539	+	hypothetical protein	YP_010109814.1	2.E-19	62.50%	hypothetical	
AB4_38	25,536	25,907	+	hypothetical protein	USM11647.1	2.E-48	67.86%	hypothetical	
AB4_39	26,160	28,955	+	DNA primase	YP_004306368.1	0.E+00	90.40%	DNA metabolism	HHPred 99.97% PDB 5DGK Active helicase
AB4_40	28,996	29,403	-	hypothetical protein	CAI8735375.1	4.E-23	53.68%	hypothetical	
AB4_41	29,823	30,899	+	tyrosine integrase	UNY41702.1	0.E+00	80.95%	lysogeny	PFAM:PF00589
AB4_42	31,184	31,723	-	DUF5129-domain containing protein	MEK6422291.1	7.E-126	100.00%	hypothetical	PFAM:PF17173
AB4_43	31,892	32,431	+	PAAR domain-containing protein	YP_010109826.1	2.E-77	67.05%	lysis & virulence	CDD:cd14739
AB4_44	32,428	33,135	+	VRR-NUC domain-containing protein	XRXY03909.1	9.E-73	54.34%	lysis & virulence	PFAM:PF08774
AB4_45	33,154	34,242	+	Type VI immunity for VRR-NUC	ABY40565.1	1.E-119	62.41%	lysis & virulence	PFAM:PF11876
AB4_46	34,222	34,665	-	hypothetical protein	YP_010668207.1	4.E-15	52.00%	hypothetical	

