

Table S4: AB6 genome annotations acquired from protein sequence and homology analysis.

CDS	5'	3'	Strand	Putative Function	BLASTp Accession	E-value	Identity	Category	Functional Support
AB6_01	1	570	+	hypothetical protein	DAO51520.1	8.E-40	46.24%	hypothetical	
AB6_02	533	2,536	+	terminase large subunit	WWY66184.1	0.E+00	84.11%	lysogeny	PFAM:PF05876; PFAM:PF20454
AB6_03	2,547	2,753	+	head-tail joining protein	WWY66185.1	6.E-34	85.29%	virion structure & morphogenesis	NCBIFAM:NF047331
AB6_04	2,750	4,240	+	portal protein	WWY66186.1	0.E+00	81.62%	virion structure & morphogenesis	PFAM:PF05136
AB6_05	4,237	5,346	+	Clp protease	WWY66187.1	1.E-149	62.67%	virion structure & morphogenesis	CDD:cd07016
AB6_06	5,349	5,720	+	head decoration protein D	WWY66188.1	5.E-42	63.16%	virion structure & morphogenesis	PFAM:PF02924
AB6_07	5,797	6,792	+	major capsid protein	WWY66189.1	4.E-170	68.88%	virion structure & morphogenesis	PFAM:PF03864
AB6_08	6,794	7,084	+	head-tail attachment protein FII	WWY66190.1	3.E-39	70.53%	virion structure & morphogenesis	PFAM:PF05354
AB6_09	7,088	7,618	+	minor tail protein Z	WWY66191.1	5.E-84	68.75%	virion structure & morphogenesis	PFAM:PF06763
AB6_10	7,608	8,138	+	hypothetical protein	WWY66192.1	4.E-58	57.40%	hypothetical	
AB6_11	8,135	8,815	+	baseplate assembly protein V	WWY66193.1	1.E-101	64.29%	virion structure & morphogenesis	NCBI:TIGR01644
AB6_12	8,922	9,659	+	hypothetical protein	WP_186082680.1	4.E-178	100.00%	hypothetical	
AB6_13	9,722	9,919	+	hypothetical protein	WWY66194.1	1.E-07	42.00%	hypothetical	
AB6_14	9,922	10,254	+	baseplate wedge protein gp25	XOR69958.1	4.E-42	61.82%	virion structure & morphogenesis	PFAM:PF04965
AB6_15	10,251	11,147	+	baseplate assembly protein J	WWY66196.1	1.E-128	64.65%	virion structure & morphogenesis	PFAM:PF04865
AB6_16	11,137	11,715	+	tail protein I	WWY66197.1	4.E-96	71.28%	virion structure & morphogenesis	PFAM:PF09684
AB6_17	11,703	13,667	+	tail collar protein	UNY41680.1	2.E-178	55.77%	virion structure & morphogenesis	CATH:G3DSA:3.90.1340.10
AB6_18	13,681	14,406	+	tail fibre assembly protein	USM11628.1	5.E-73	54.09%	virion structure & morphogenesis	PFAM:PF02413
AB6_19	14,478	15,647	+	tail sheath protein	DAE46045.1	0.E+00	79.12%	virion structure & morphogenesis	PFAM:PF22671; PFAM:PF04984; PFAM:PF17482
AB6_20	15,657	16,160	+	tail tube protein	WWY66201.1	2.E-76	64.07%	virion structure & morphogenesis	PFAM:PF04985
AB6_21	16,242	16,544	+	tail assembly chaperone	WWY66202.1	1.E-30	57.00%	virion structure & morphogenesis	PFAM:PF10109
AB6_22	16,626	19,064	+	tail tape measure protein	DAE46041.1	0.E+00	69.02%	virion structure & morphogenesis	PFAM:PF10145
AB6_23	19,074	19,952	+	tail assembly protein	DAE46036.1	1.E-133	63.48%	virion structure & morphogenesis	PFAM:PF06995
AB6_24	19,960	20,133	+	tail protein X	WWY66205.1	4.E-23	71.93%	virion structure & morphogenesis	PFAM:PF05489
AB6_25	20,143	21,192	+	baseplate hub protein	DAE46046.1	0.E+00	75.86%	virion structure & morphogenesis	PFAM:PF05954
AB6_26	21,265	21,714	+	hypothetical protein	WGH15564.1	1.E-18	34.64%	hypothetical	
AB6_27	21,711	22,277	+	glycosyl hydrolase	ULR75146.1	6.E-91	70.72%	lysis & virulence	PFAM:PF05838; PFAM:PF09374; CDD:cd13926
AB6_28	22,280	22,903	+	hypothetical protein	UOF78607.1	3.E-20	34.92%	hypothetical	
AB6_29	23,063	23,848	+	DNA adenine methyltransferase	DAE46048.1	2.E-165	84.35%	DNA metabolism	CATH:G3DSA:1.10.1020.10; PFAM:PF02086
AB6_30	24,315	24,479	+	hypothetical protein	WP_244118616.1	1.E-77	100.00%	hypothetical	
AB6_31	24,564	26,573	+	ORC-CDC6 ATPase	DAD78761.1	9.E-15	20.90%	DNA metabolism	PFAM:PF24389
AB6_32	26,913	27,557	-	hypothetical protein	WP_186082693.1	1.E-155	100.00%	hypothetical	
AB6_33	27,561	28,112	-	hypothetical protein	DAY53150.1	2.E-05	38.46%	hypothetical	
AB6_34	28,773	30,575	+	OLD nuclease	DAN96970.1	2.E-50	28.41%	anti-phage defense	PANTHER:PTHR43581; PFAM:PF20469
AB6_35	30,886	31,986	+	HNH endonuclease	XOR15598.1	8.E-63	49.79%	DNA metabolism	CDD:cd00085
AB6_36	31,983	32,270	+	hypothetical protein	WP_186136537.1	4.E-17	75.00%	hypothetical	
AB6_37	32,585	33,661	+	tyrosine recombinase	DAG73198.1	0.E+00	75.78%	lysogeny	PROSITE:PS51898; CDD:cd00796
AB6_38	33,616	33,915	-	hypothetical protein	YP_010078789.1	1.E-32	58.82%	hypothetical	
AB6_39	33,903	34,352	-	hypothetical protein	YP_002221440.1	2.E-03	33.33%	hypothetical	
AB6_40	34,345	34,704	-	hypothetical protein	WWY66221.1	3.E-41	67.31%	hypothetical	
AB6_41	34,806	36,185	-	ParB-partition protein	WWY66222.1	4.E-165	57.35%	DNA metabolism	SSFAM:SSF110849; SSFAM:SSF109709
AB6_42	36,185	36,547	-	hypothetical protein	WWY66225.1	2.E-21	52.81%	hypothetical	
AB6_43	36,599	36,817	-	hypothetical protein	WP_186082665.1	3.E-43	100.00%	hypothetical	
AB6_44	36,955	37,209	-	hypothetical protein	WP_186142345.1	1.E-52	98.81%	hypothetical	
AB6_45	37,178	38,005	-	CI repressor protein	DAH83233.1	5.E-27	45.28%	lysogeny	CATH:G3DSA:1.10.260.40
AB6_46	38,064	38,606	+	hypothetical protein	WWY66227.1	4.E-92	83.03%	hypothetical	
AB6_47	38,644	38,976	+	hypothetical protein	WWY66228.1	3.E-29	55.45%	hypothetical	
AB6_48	39,135	41,636	+	virulence associated protein E	WWY66230.1	0.E+00	79.47%	lysis & virulence	PFAM:PF05272
AB6_49	41,853	42,623	+	Dna/Hsp40-family protein	WWY66231.1	2.E-85	57.03%	accessory	CDD:cd10719
AB6_50	42,872	43,978	+	RelA-SpoT family protein	DAN42088.1	1.E-65	39.08%	accessory	PFAM:PF04607
AB6_51	44,381	44,593	+	hypothetical protein	WP_341773643.1	2.E-39	95.71%	hypothetical	