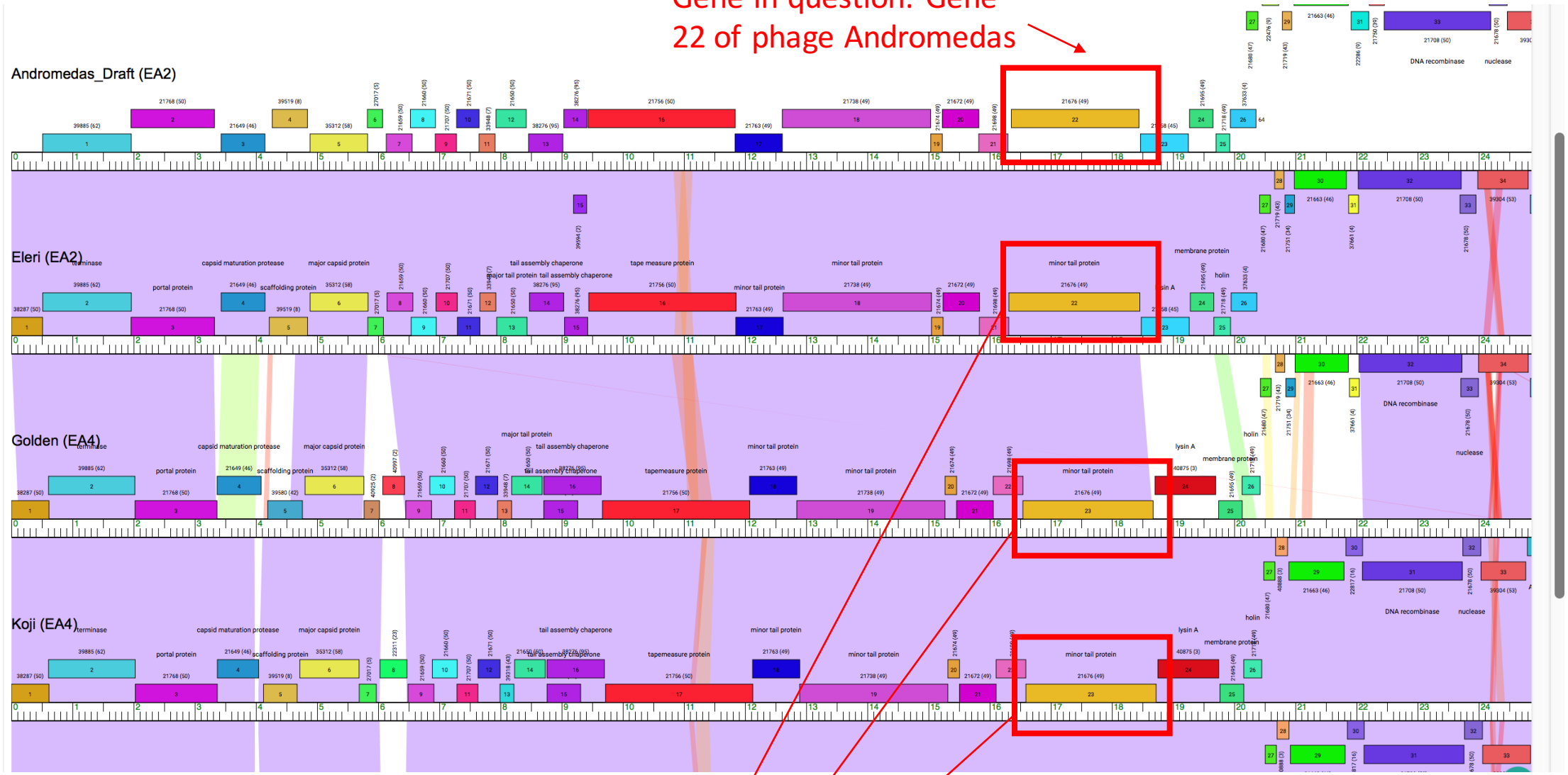
Gene in question: Gene 22 of phage Andromedas



Other members of the pham in EA phages have function as “minor tail protein”

HHPred results suggest chitinase/hydrolase. Coverage is not great but good probability/E-value for these hits. No hits show tail protein.

Show 25 entries

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
1	5WUS_A	Chitinase; Ostrinia furnacalis, chitinase, three-dimensional structure; 2.201A {Ostrinia furnacalis}	100	7.9e-35	30.1	288	460
2	3W4R_A	Chitinase (E.C.3.2.1.14); insect, glycosyl hydrolase, chitin, HYDROLASE; HET: NAG; 1.7A {Ostrinia furnacalis}	100	2.3e-34	32.1	286	554
3	5WV8_A	Chitinase; Ostrinia furnacalis, chitinase, three-dimensional structure; 2.042A {Ostrinia furnacalis}	100	4.3e-33	32.4	287	482
4	4TXG_A	Family 18 Glycoside Hydrolase (E.C.3.2.1.14); Chitinase Family GH18 Chitinase, HYDROLASE; HET: CS; 1.75A {Chromobacterium violaceum}	100	1.5e-32	28.1	288	793
5	3ALF_A	Chitinase, class V; chitinase, HYDROLASE; HET: EDO, PO4; 1.2A {Nicotiana tabacum}	100	3.4e-31	31.1	287	353
6	3AQU_D	At4g19810 (E.C.3.2.1.14); stress response, TIM barrel, Hydrolase; HET: FLC; 2.01A {Arabidopsis thaliana}	100	9.5e-31	31.4	278	356
7	1EDQ_A	CHITINASE A (E.C. 3.2.1.14); BETA-ALPHA (TIM) BARREL, HYDROLASE; 1.55A {Serratia marcescens} SCOP: c.1.8.5, d.26.3.1, b.1.18.2	100	7.3e-31	32	272	540
8	1VF8_A	secretory protein; Ym1, chitinase, chi-lectin, structural	100	1.3e-30	31.1	284	377

NCBI BLAST returns lots of hits for phage Minor Tail Proteins, but...

Description	Max score	Total score	Query cover	E value	Ident	Accession
minor tail protein [Microbacterium phage Eleri]	1429	1429	100%	0.0	99%	AUX83360.1
minor tail protein [Microbacterium phage Golden]	1182	1182	100%	0.0	81%	AVJ49770.1
minor tail protein [Microbacterium phage Koji]	1152	1152	100%	0.0	79%	AVJ49921.1
minor tail protein [Microbacterium phage Nattles]	1117	1117	99%	0.0	76%	AVJ50496.1
minor tail protein [Microbacterium phage Gelo]	1115	1115	99%	0.0	76%	AVO25201.1
minor tail protein [Microbacterium phage Baines]	1112	1112	99%	0.0	76%	AUX82735.1
minor tail protein [Microbacterium phage Bonino]	1112	1112	99%	0.0	76%	AVJ49225.1
minor tail protein [Microbacterium phage Aubergine]	1111	1111	99%	0.0	76%	AUX82610.1
minor tail protein [Microbacterium phage Bandik]	1109	1109	99%	0.0	76%	AVR56045.1
minor tail protein [Microbacterium phage Ludgate]	1109	1109	99%	0.0	76%	AUX83047.1
minor tail protein [Microbacterium phage AxiPup]	1109	1109	99%	0.0	76%	AUX82672.1
minor tail [Microbacterium phage AlexAdler]	1108	1108	99%	0.0	76%	AVO24414.1
minor tail protein [Microbacterium phage Peep]	1108	1108	99%	0.0	76%	AUX83109.1
minor tail protein [Microbacterium phage Knox]	1108	1108	99%	0.0	76%	AUX82984.1
minor tail protein [Microbacterium phage StingRay]	1107	1107	99%	0.0	76%	AVJ51468.1
minor tail protein [Microbacterium phage Raptor]	1107	1107	99%	0.0	76%	AVR56440.1
minor tail protein [Microbacterium phage Ilzat]	1106	1106	99%	0.0	76%	AUX83487.1
minor tail protein [Microbacterium phage Etna]	1093	1093	99%	0.0	74%	AVR56288.1
minor tail protein [Microbacterium phage Peppino]	1087	1087	99%	0.0	74%	AUX83173.1
minor tail protein [Microbacterium phage Hamlet]	1086	1086	99%	0.0	74%	AUX82859.1
minor tail protein [Microbacterium phage Raccoon]	1086	1086	99%	0.0	74%	AUX83236.1
minor tail protein [Microbacterium phage BeeBee8]	1083	1083	99%	0.0	74%	AVR56109.1

A little further down in the hits the returns start to be for hydrolase, glycosyl hydrolase still with good E-values

hypothetical protein [Haloglycomyces albus]	184	184	44%	4e-48	39%	WP_025272627.1
Predicted glycosyl hydrolase [[[Eubacterium] siraeum V10Sc8a]	188	348	94%	9e-47	36%	CBL33601.1
glycosyl hydrolase [Anaerotruncus colihominis]	187	346	94%	3e-46	36%	WP_087298891.1
glycosyl hydrolase [Ruminococcaceae bacterium CPB6]	187	340	97%	3e-46	35%	WP_086035475.1
glycosyl hydrolase [Coprothermobacter proteolyticus]	186	334	96%	3e-46	35%	WP_107689621.1
hypothetical protein FC14_GL000854 [Lactobacillus agilis DSM 20509]	186	334	96%	4e-46	35%	KRM65835.1
glycosyl hydrolase-like protein [Thermoanaerobacter sp. X561]	186	334	96%	4e-46	35%	EFK83711.1
glycosyl hydrolase [[Ruminococcus] torques]	186	346	94%	5e-46	36%	WP_055159014.1
glycosyl hydrolase [Clostridium tertium]	186	331	96%	5e-46	35%	WP_097033523.1
glycosyl hydrolase-like protein [Thermoanaerobacter sp. X514]	186	333	96%	5e-46	35%	ABY92561.1
MULTISPECIES: glycosyl hydrolase [Thermoanaerobacter]	186	334	96%	6e-46	35%	WP_038016876.1
glycosyl hydrolase [Agathobaculum desmolans]	186	338	95%	6e-46	35%	WP_034972281.1
glycosyl hydrolase [Lactobacillus agilis]	186	333	96%	6e-46	35%	WP_056975872.1
hypothetical protein HMPREF1025_02675 [Lachnospiraceae bacterium 3_1_46FAA]	185	333	97%	8e-46	33%	EGG81722.1
glycosyl hydrolase [Lachnospiraceae bacterium 3_1_46FAA]	185	332	97%	9e-46	33%	WP_084763859.1