

Emotion\_draft\_16: potentially baseplate?  
Currently all other members of pham call minor tail protein.

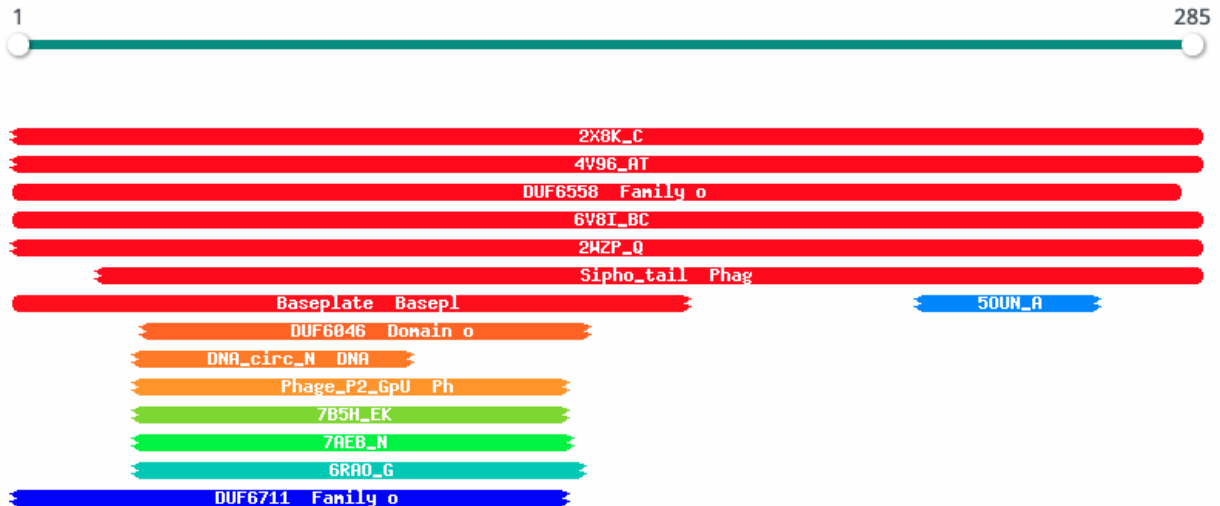
### Emotion\_draft\_16:

MAEGDFDLNGYKMGLGYDVVVESFDPGSAEWITQDAVAPVGGRRNFGADYASGPTWVLDLAT  
DTHDAASARAALAGAARAWRPSGLATPGYEAILKYTIGGETRRVYGRPRKFAPIANGVSASGV  
MLATAEFVTSEAFTHAEEARSLTVGLVPVESGGFTSPLISPITTVAGSQRQGLIDVGGDAPAPM  
TITIQQPVSGPKVSSSGWYFSLPSLSLAYDQSVTIDTRKGTVRRNDGANLGGLLSRGSTRLVDA  
RLKTGAVEFIYSGTDQTATSTATVTWRPTYHAL

[PhagesDB for gene Emotion\\_draft\\_16](#)

**HHpred results:** [https://toolkit.tuebingen.mpg.de/jobs/Emotion\\_16](https://toolkit.tuebingen.mpg.de/jobs/Emotion_16)

- ✓ 11 Start: 7,354 Stop: 7,758 Forward (tail terminator)
- ✓ 12 Start: 7,771 Stop: 8,325 Forward (major tail protein)
- ✓ 13 Start: 8,425 Stop: 8,691 Forward (tail assembly chaperone)
- ✓ 14 Start: 8,425 Stop: 9,035 Forward (tail assembly chaperone)
- ✗ (Not Included) Start: 8,825 Stop: 8,688 Reverse ()
- ✓ 15 Start: 9,044 Stop: 11,284 Forward (tape measure protein)
- ✓ 16 Start: 11,297 Stop: 12,160 Forward (minor tail protein)
- ✓ 17 Start: 12,170 Stop: 13,147 Forward (minor tail protein)
- ✓ 18 Start: 13,147 Stop: 14,427 Forward (minor tail protein)
- ✓ 19 Start: 14,446 Stop: 17,979 Forward (minor tail protein)
- ✓ 20 Start: 18,061 Stop: 18,345 Forward (NKF)



Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
<input type="checkbox"/> 1	<a href="#">2X8K_C</a>	HYPOTHETICAL PROTEIN 19.1; VIRAL PROTEIN, DISTAL TAIL PROTEIN; 2.95A {BACILLUS PHAGE SPP1}	99.97	2.9e-27	194.89	25.7	236	252
<input type="checkbox"/> 2	<a href="#">4V96_AT</a>	ORF46; Distal tail protein, Receptor-binding protein, Phage baseplate, host adsorption apparatus, genome injection devic	99.95	1e-25	186.07	24.7	230	253
<input type="checkbox"/> 3	<a href="#">PF20195.1</a>	; DUF6558 ; Family of unknown function (DUF6558)	99.95	3.1e-25	184.58	24.5	240	266
<input type="checkbox"/> 4	<a href="#">6V8I_BC</a>	Distal Tail Protein, gp58; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha}	99.94	1.8e-24	182.91	25.1	260	315
<input type="checkbox"/> 5	<a href="#">2WZP_Q</a>	LACTOCOCCAL PHAGE P2 ORF15; BASEPLATE, VIRAL PROTEIN; 2.6A {LACTOCOCCUS PHAGE P2}	99.88	4.3e-19	151.09	27.2	259	326
<input type="checkbox"/> 6	<a href="#">PF05709.14</a>	; Siphon_tail ; Phage tail protein	99.8	1e-16	150.05	25.4	245	671
<input type="checkbox"/> 7	<a href="#">PF16774.8</a>	; Baseplate ; Baseplate protein	99.34	1.6e-10	90.32	14.5	147	167

Both 4v96 and 2WZP link to manuscripts that discuss crystal structures of baseplate proteins. These appear to be large proteins with many chains, so perhaps it isn't sufficient to call this (even part of) a baseplate on the basis of a hit to just one or two chains?

PDB: [4V96](#)

PDB: [2WZP](#)

\*I don't see any HHpred hits that line up with the evidence entries for the example baseplate J or baseplate wedge genes, Alice\_133 and RosiePosie\_38.

Alice\_133 HHpred: [https://toolkit.tuebingen.mpg.de/jobs/Alice\\_133](https://toolkit.tuebingen.mpg.de/jobs/Alice_133)

RosiePosie\_38 HHpred: [https://toolkit.tuebingen.mpg.de/jobs/RosiePosie\\_38](https://toolkit.tuebingen.mpg.de/jobs/RosiePosie_38)