EG genomes minor tail proteins (2025; UMass Amherst)

Minor tail proteins:

BaconCheese

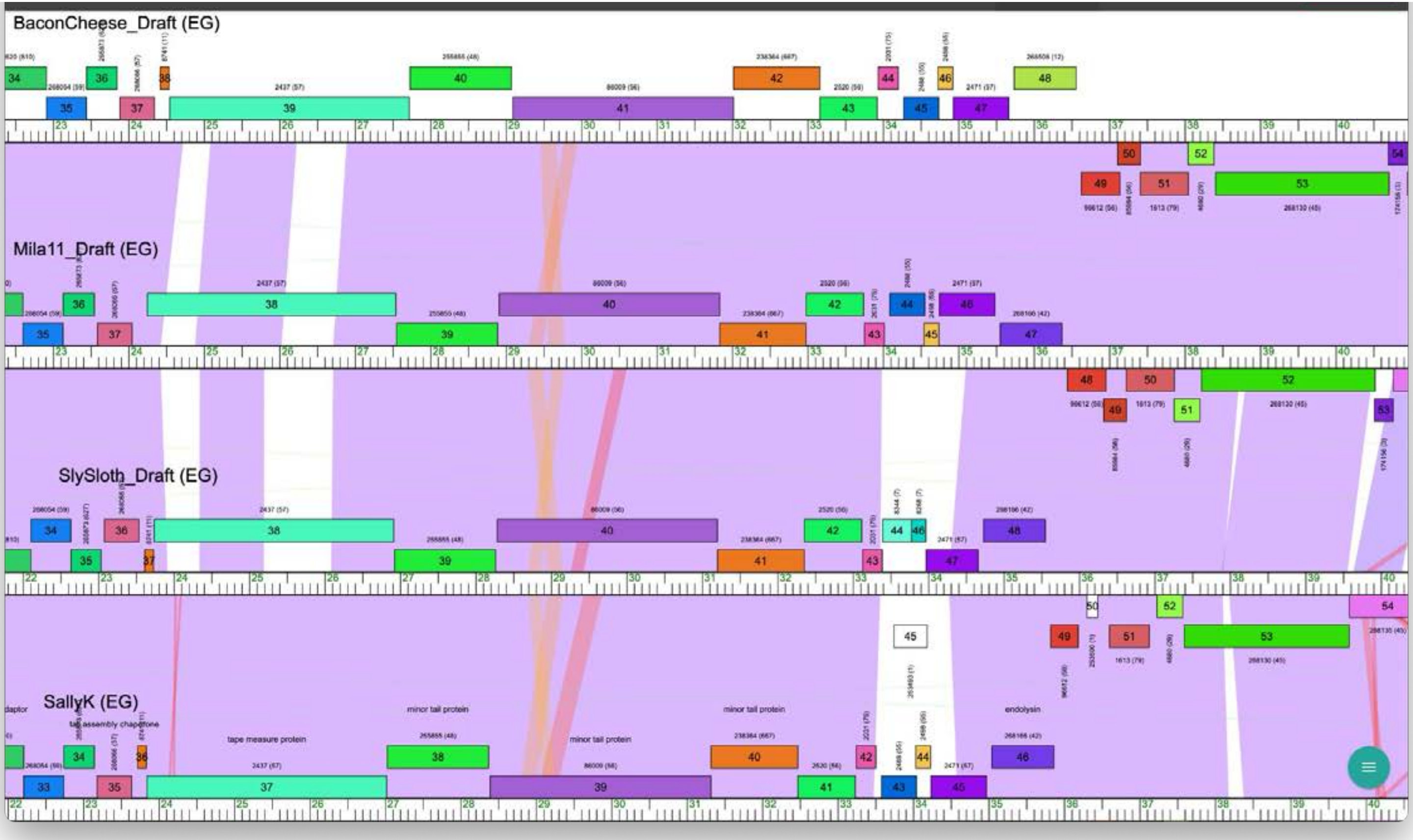
40,41,42,43

Mila11

39,40,41,42

Slysloth

39,40,41,42



BaconCheese40 is likely Dit (Distal tail tip protein)

Evidence:

Minor tail protein by synteny and HHPRED.

Alphafold server modeling as a hexamer looks consistent with that oligomer state.

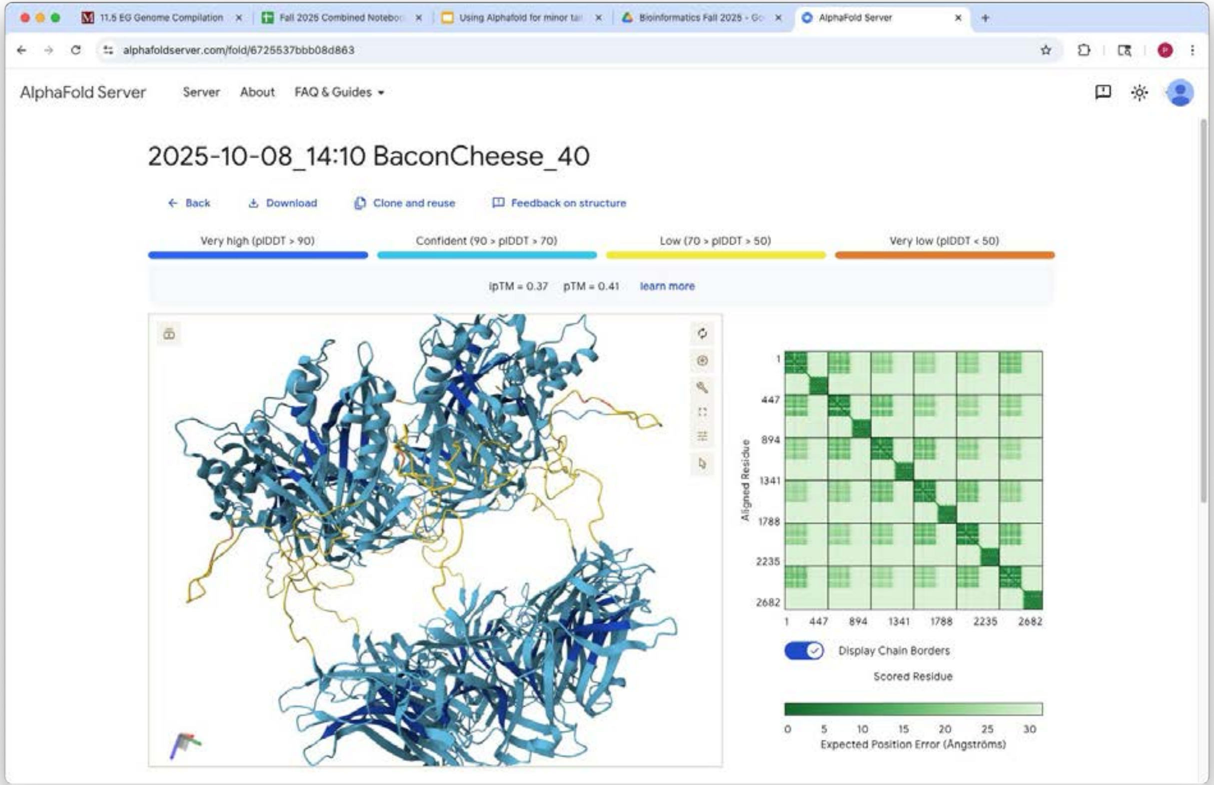
Foldseek search with the predicted hexamer pulls up other Dit orthologs.

Outer diameter of Dit is consistent with width of tail tube.

Alphafold modeling of BaconCheese_40 hexamer

pLDDT values are very high for the hexameric region (N-terminal portion)

PAE plots shows strong confidence (low error) in N-terminal hexamer



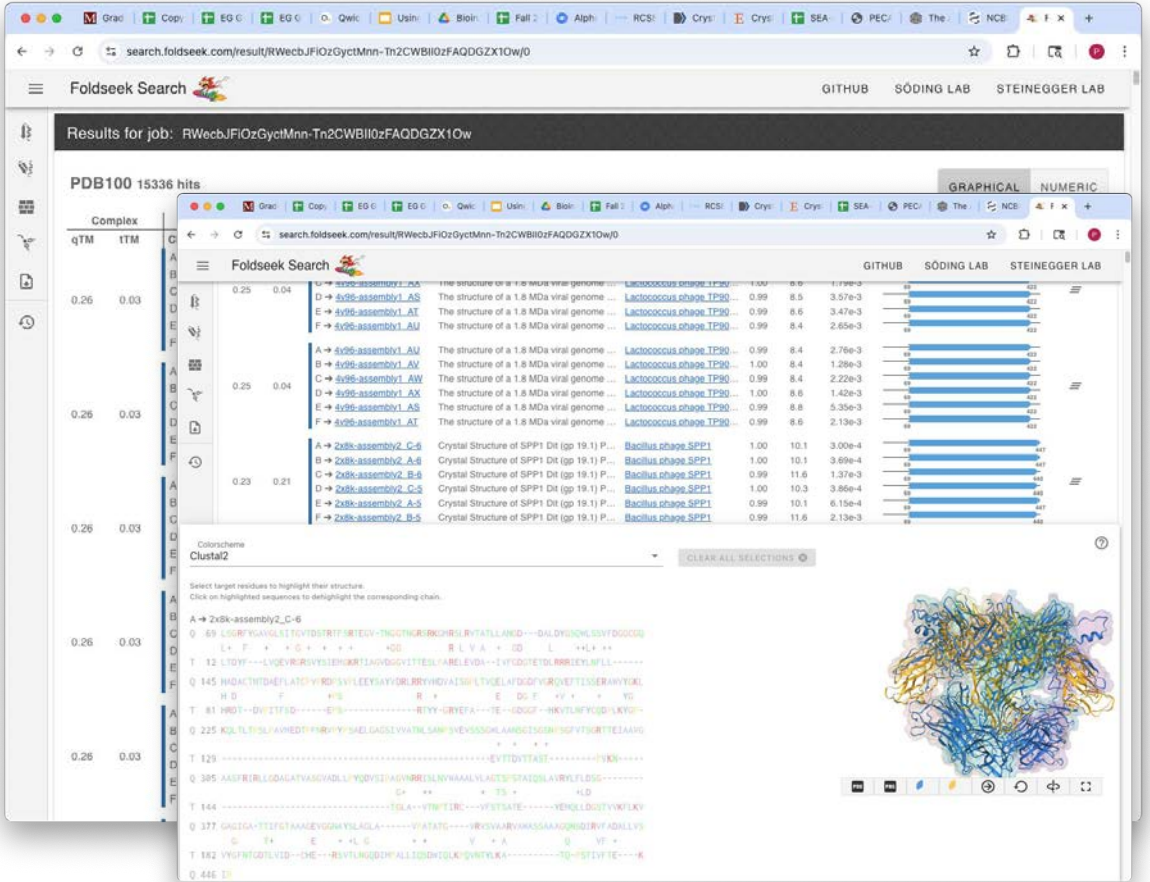
2025-10-08_14:10 BaconCheese_40

ipTM = 0.37 pTM = 0.41

Foldseek analysis of BaconCheese_40 hexamer

Foldseek multimer uses a structure of multiple proteins and looks for other known structures that are similar.

Doing this with BC_40 hexamers pulls up the dit protein for the bacteriophage SPP1 !



search.foldseek.com/result/RWecbJFiOzGyctMnn-Tn2CWBII0zFAQDGZX1Ow/0

Results for job: RWecbJFiOzGyctMnn-Tn2CWBII0zFAQDGZX1Ow

PDB100 15336 hits

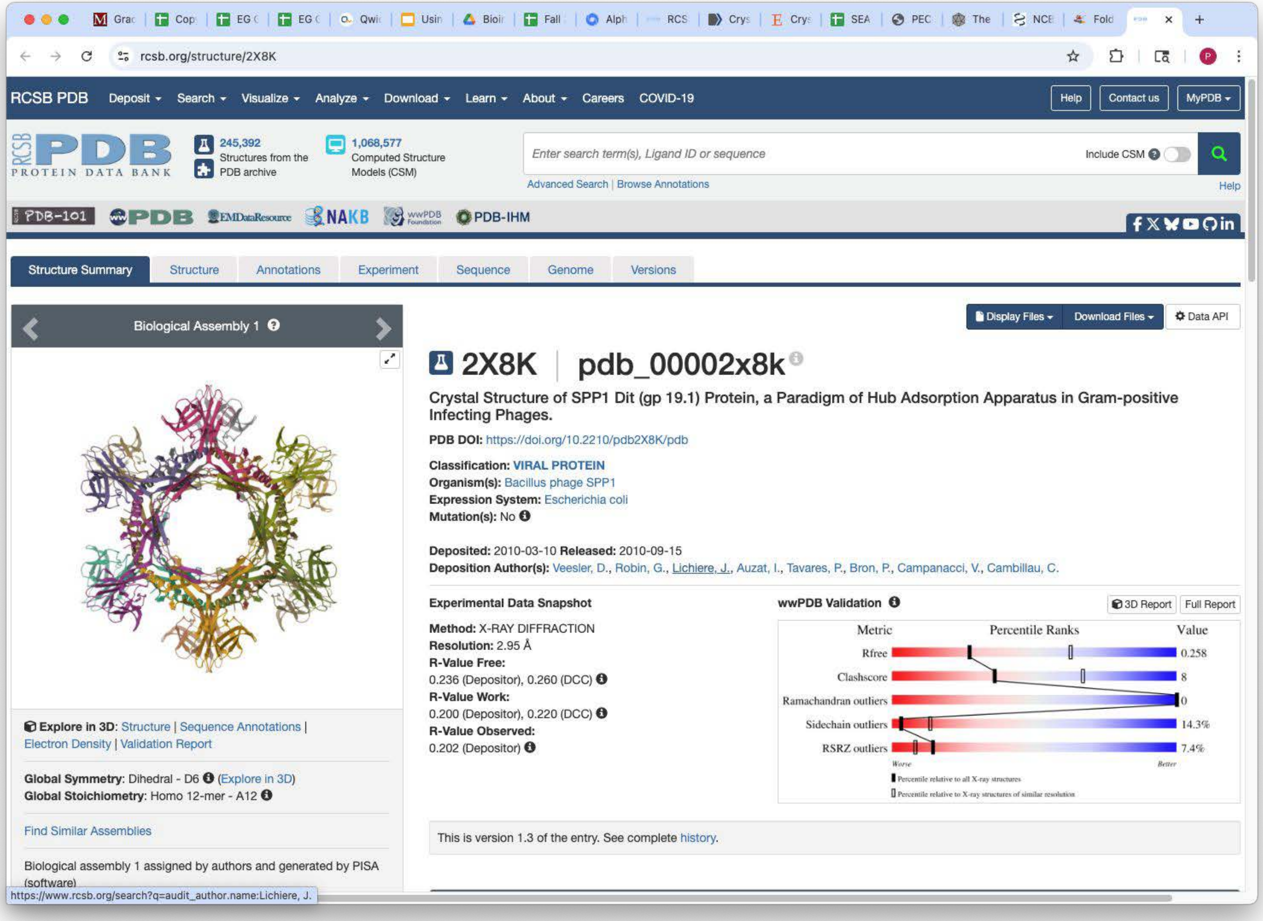
Complex qTM	tTM
0.26	0.03
0.26	0.03
0.26	0.03
0.26	0.03
0.26	0.03

0.25	0.04	D → 4v96-assembly1_AS	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.5	3.57e-3
		E → 4v96-assembly1_AT	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.6	3.47e-3
		F → 4v96-assembly1_AU	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.4	2.65e-3
0.25	0.04	A → 4v96-assembly1_AU	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.4	2.76e-3
		B → 4v96-assembly1_AV	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	1.00	8.4	1.28e-3
		C → 4v96-assembly1_AW	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.4	2.22e-3
		D → 4v96-assembly1_AX	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	1.00	8.6	1.42e-3
		E → 4v96-assembly1_AS	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.8	5.35e-3
		F → 4v96-assembly1_AT	The structure of a 1.8 MDa viral genome ...	Lactococcus phage TP90...	0.99	8.6	2.13e-3
0.23	0.21	A → 2x8k-assembly2_C-6	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	1.00	10.1	3.00e-4
		B → 2x8k-assembly2_A-6	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	1.00	10.1	3.69e-4
		C → 2x8k-assembly2_B-6	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	0.99	11.6	1.37e-3
		D → 2x8k-assembly2_C-5	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	1.00	10.3	3.86e-4
		E → 2x8k-assembly2_A-5	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	0.99	10.1	6.15e-4
		F → 2x8k-assembly2_B-5	Crystal Structure of SPP1 Dit (gp 19.1) P...	Bacillus phage SPP1	0.99	11.6	2.13e-3

Colorscheme: Clustal2

Select target residues to highlight their structure.
Click on highlighted sequences to dehighlight the corresponding chain.

A → 2x8k-assembly2_C-6



2X8K | pdb_00002x8k

Crystal Structure of SPP1 Dit (gp 19.1) Protein, a Paradigm of Hub Adsorption Apparatus in Gram-positive Infecting Phages.

PDB DOI: https://doi.org/10.2210/pdb2X8K/pdb

Classification: VIRAL PROTEIN
Organism(s): Bacillus phage SPP1
Expression System: Escherichia coli
Mutation(s): No

Deposited: 2010-03-10 **Released:** 2010-09-15
Deposition Author(s): Veesler, D., Robin, G., Lichiere, J., Auzat, I., Tavares, P., Bron, P., Campanacci, V., Cambillau, C.

Experimental Data Snapshot

Method: X-RAY DIFFRACTION
Resolution: 2.95 Å
R-Value Free:
0.236 (Depositor), 0.260 (DCC)
R-Value Work:
0.200 (Depositor), 0.220 (DCC)
R-Value Observed:
0.202 (Depositor)

wwPDB Validation

This is version 1.3 of the entry. See complete history.

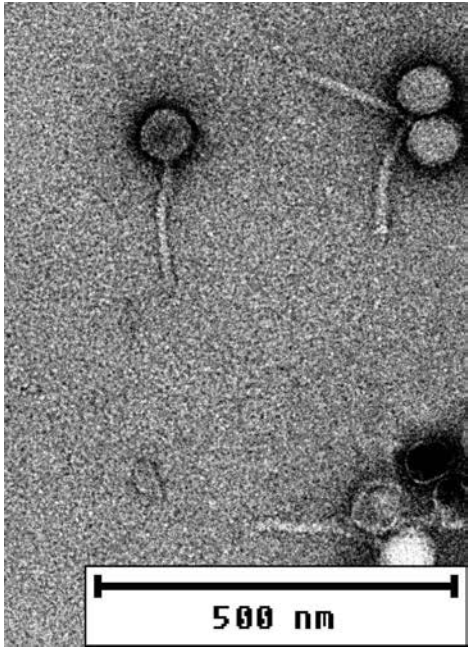
Explore in 3D: Structure | Sequence Annotations | Electron Density | Validation Report

Global Symmetry: Dihedral - D6 (Explore in 3D)
Global Stoichiometry: Homo 12-mer - A12

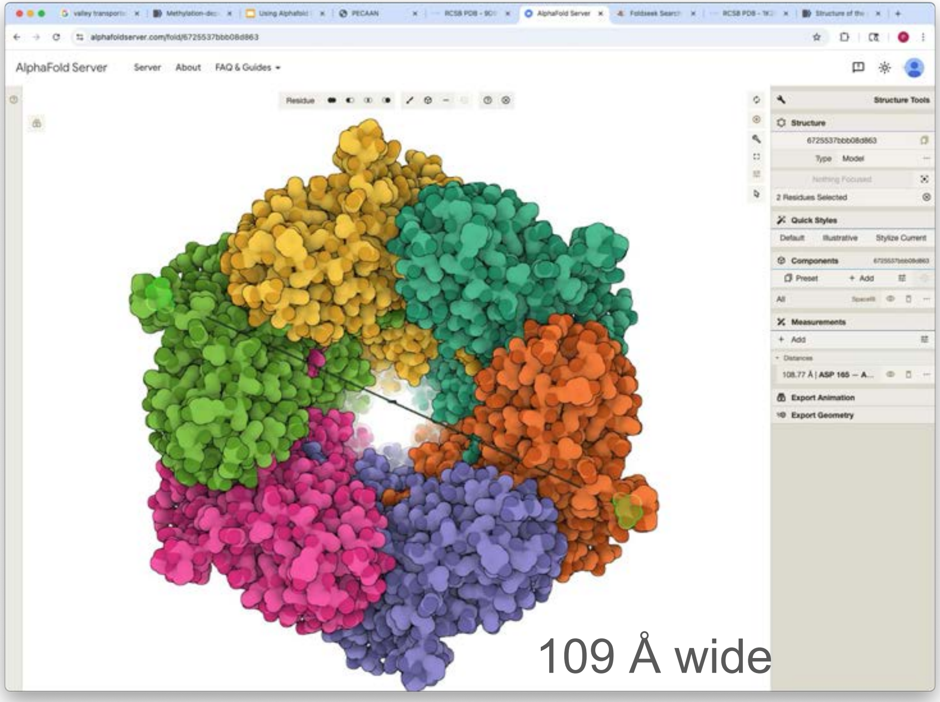
Find Similar Assemblies

Biological assembly 1 assigned by authors and generated by PISA (software)

Tail-tube width and Dit outer diameter measurements



Measuring tube width:
113 +/- 17 Å (n=10)
(BaconCheese Tues_C2_24.jpg)


alphafoldserver.com/fold/6725537bbb08d863

6725537bbb08d863

Type Model

2 Residues Selected

108.77 Å | ASP 165 — A...

109 Å wide

BaconCheese gp40 hexamer modeling

BaconCheese42 is likely baseplate hub

Evidence:

Minor tail protein by synteny and HHPRED.

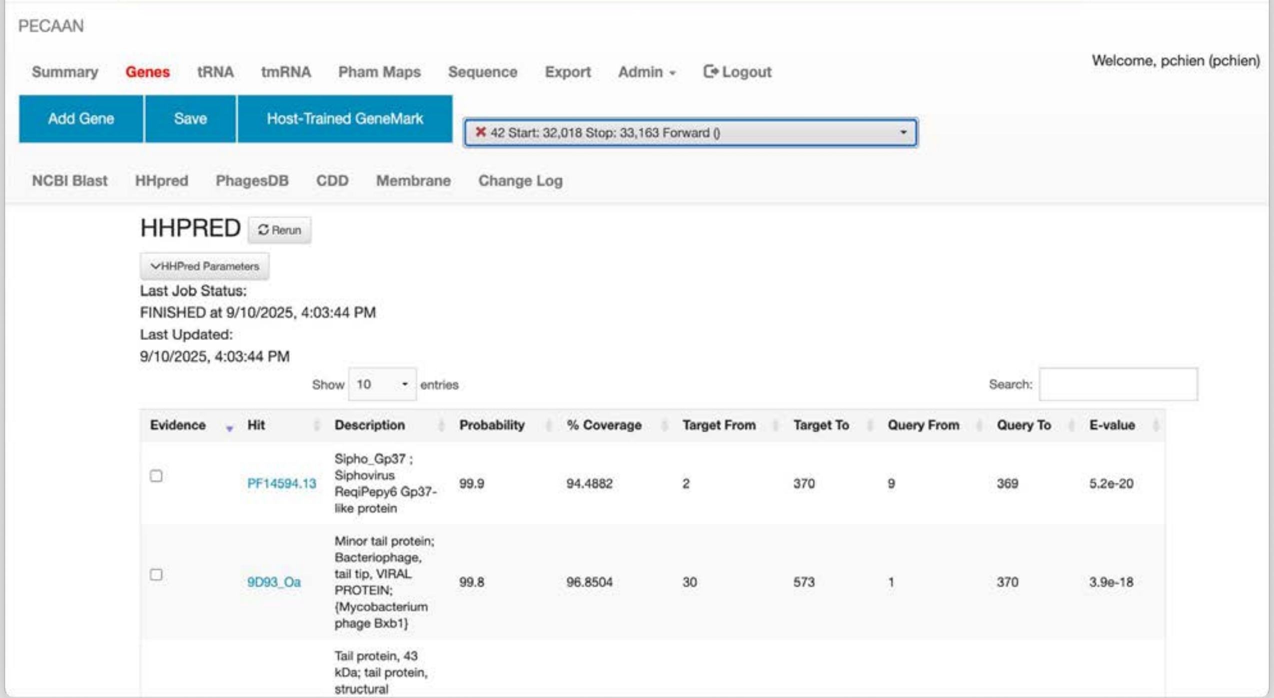
Alphafold server modeling as a trimer looks consistent with that oligomer state.

Foldseek search with the predicted trimer pulls up other baseplate hub.

HHPRED

Baconcheese 42 looks like baseplate hub from Bxb1

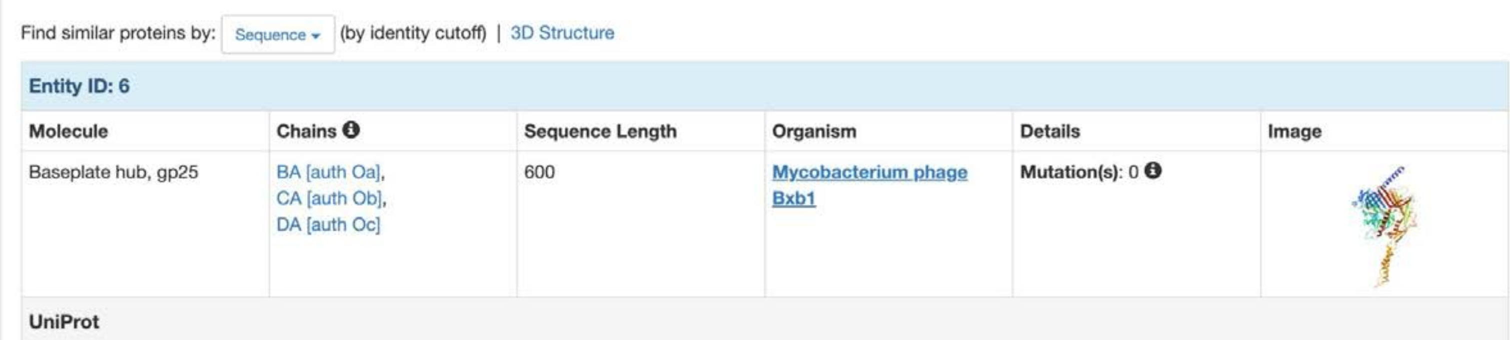
(98% probability)



HHPRED

Last Job Status:
FINISHED at 9/10/2025, 4:03:44 PM
Last Updated:
9/10/2025, 4:03:44 PM

Evidence	Hit	Description	Probability	% Coverage	Target From	Target To	Query From	Query To	E-value
☐	PF14594.13	Sipho_Gp37 ; Siphovirus ReqiPepy6 Gp37-like protein	99.9	94.4882	2	370	9	369	5.2e-20
☐	9D93_Oa	Minor tail protein; Bacteriophage, tail tip, VIRAL PROTEIN; {Mycobacterium phage Bxb1}	99.8	96.8504	30	573	1	370	3.9e-18
		Tail protein, 43 kDa; tail protein, structural							

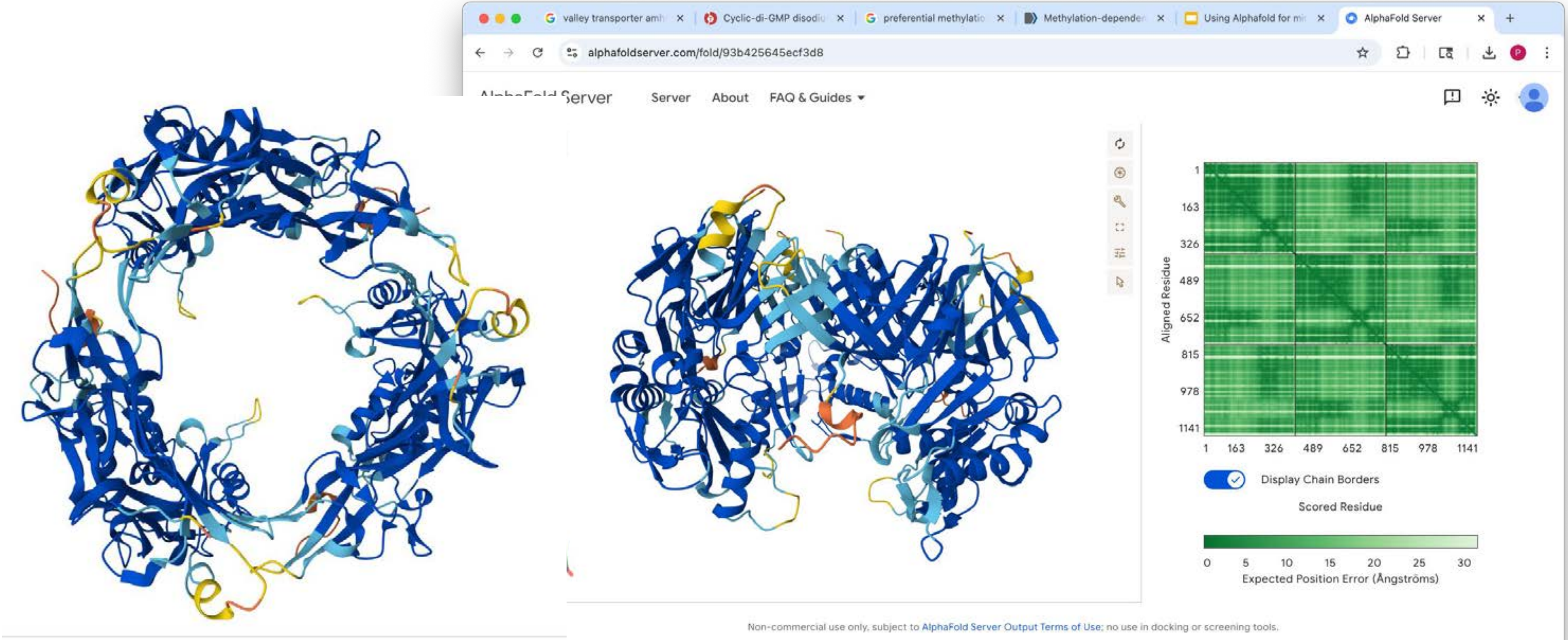


Entity ID: 6

Molecule	Chains	Sequence Length	Organism	Details	Image
Baseplate hub, gp25	BA [auth Oa], CA [auth Ob], DA [auth Oc]	600	Mycobacterium phage Bxb1	Mutation(s): 0	

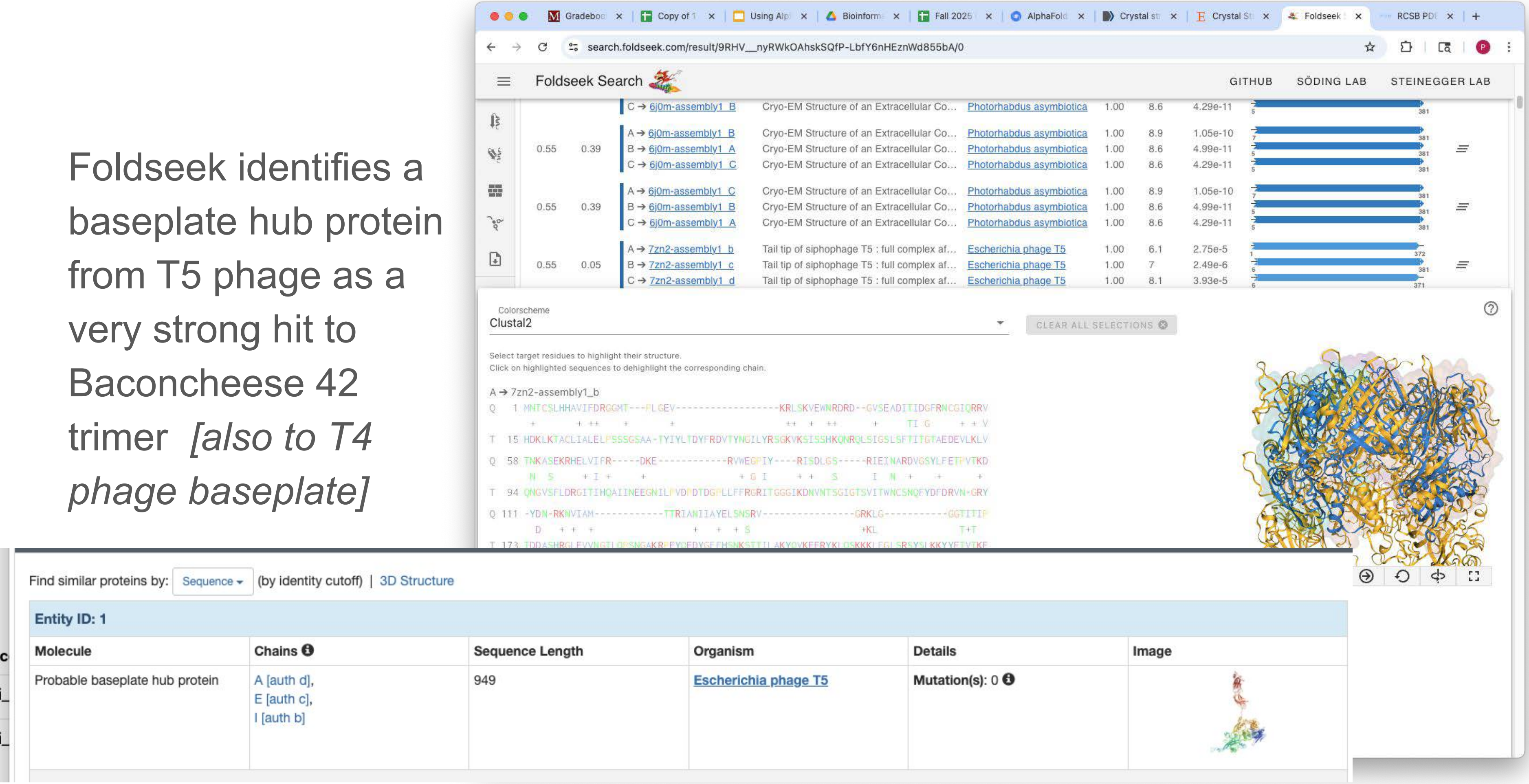
UniProt

Alphafold results modeling as a trimer - fits very well.



Non-commercial use only, subject to AlphaFold Server Output Terms of Use; no use in docking or screening tools.

Foldseek identifies a baseplate hub protein from T5 phage as a very strong hit to Baconcheese 42 trimer *[also to T4 phage baseplate]*



		C → 6j0m-assembly1_B	Cryo-EM Structure of an Extracellular Co…	Photorhabdus asymbiotica	1.00	8.6	4.29e-11
0.55	0.39	A → 6j0m-assembly1_B B → 6j0m-assembly1_A C → 6j0m-assembly1_C	Cryo-EM Structure of an Extracellular Co… Cryo-EM Structure of an Extracellular Co… Cryo-EM Structure of an Extracellular Co…	Photorhabdus asymbiotica Photorhabdus asymbiotica Photorhabdus asymbiotica	1.00 1.00 1.00	8.9 8.6 8.6	1.05e-10 4.99e-11 4.29e-11
0.55	0.39	A → 6j0m-assembly1_C B → 6j0m-assembly1_B C → 6j0m-assembly1_A	Cryo-EM Structure of an Extracellular Co… Cryo-EM Structure of an Extracellular Co… Cryo-EM Structure of an Extracellular Co…	Photorhabdus asymbiotica Photorhabdus asymbiotica Photorhabdus asymbiotica	1.00 1.00 1.00	8.9 8.6 8.6	1.05e-10 4.99e-11 4.29e-11
0.55	0.05	A → 7zn2-assembly1_b B → 7zn2-assembly1_c C → 7zn2-assembly1_d	Tail tip of siphophage T5 : full complex af… Tail tip of siphophage T5 : full complex af… Tail tip of siphophage T5 : full complex af…	Escherichia phage T5 Escherichia phage T5 Escherichia phage T5	1.00 1.00 1.00	6.1 7 8.1	2.75e-5 2.49e-6 3.93e-5

Select target residues to highlight their structure.
Click on highlighted sequences to dehighlight the corresponding chain.

A → 7zn2-assembly1_b

```
Q   1 MNTCSLHHAVIFDRGGMT---PLGEV------------------KRLSKVEWNRDRD--GVSEADITIDGFRNCGIQRRV
        +      + ++    +       +                  ++  +  ++       +     TI G     + + V
T  15 HDKLKTACLIALELPSSSGSAA-TYIYLTDYFRDVTYNGILYRSGKVKSISSHKQNRQLSIGSLSFTITGTAEDEVLKLV

Q  58 TNKASEKRHELVIFR-----DKE------------RVWEGPIY----RISDLGS-----RIEINARDVGSYLFETPVTKD
        N  S     + I +     +             + G I     + +  S      I  N +    +     +
T  94 QNGVSFLDRGITIHQAIINEEGNILPVDPDTDGPLLFFRGRITGGGIKDNVNTSGIGTSVITWNCSNQFYDFDRVN-GRY

Q 111 -YDN-RKNVIAM------------TTRIANIIAYELSNSRV---------------GRKLG-----------GGTITIP
         D   + +  +               +    +  + S                +KL             T+T
```

Find similar proteins by: Sequence (by identity cutoff) | 3D Structure

Entity ID: 1

Molecule	Chains	Sequence Length	Organism	Details	Image
Probable baseplate hub protein	A [auth d], E [auth c], I [auth b]	949	Escherichia phage T5	Mutation(s): 0	

BaconCheese43 is likely tailspike protein

Evidence:

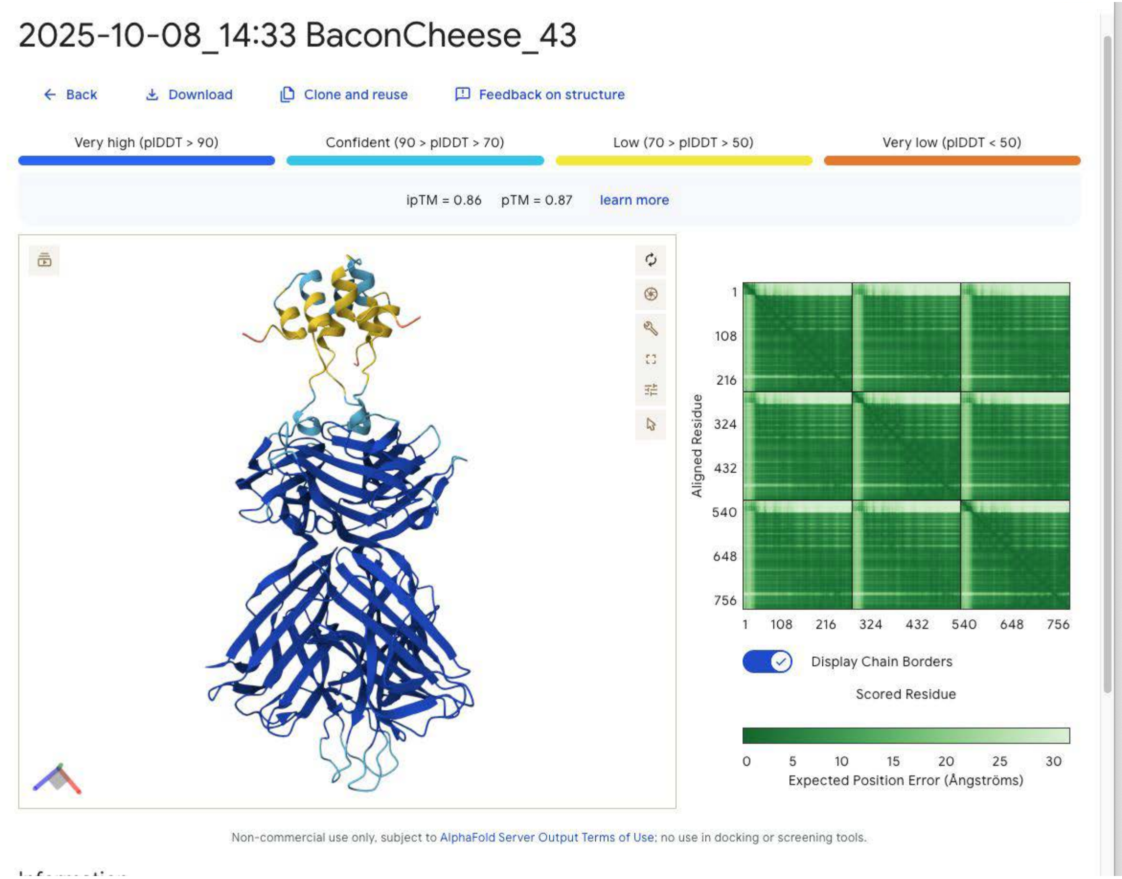
Immediately following other minor tail proteins.

Alphafold server modeling as a trimer looks consistent with the C-terminal end of the spike proteins from other phages

Foldseek search with the predicted trimer pulls up other tail spikes

HHPRED is not strong evidence for tailspike or anything (best is 52%)

Alphafold modeling of BaconCheese 43 trimer



2025-10-08_14:33 BaconCheese_43

ipTM = 0.86 pTM = 0.87

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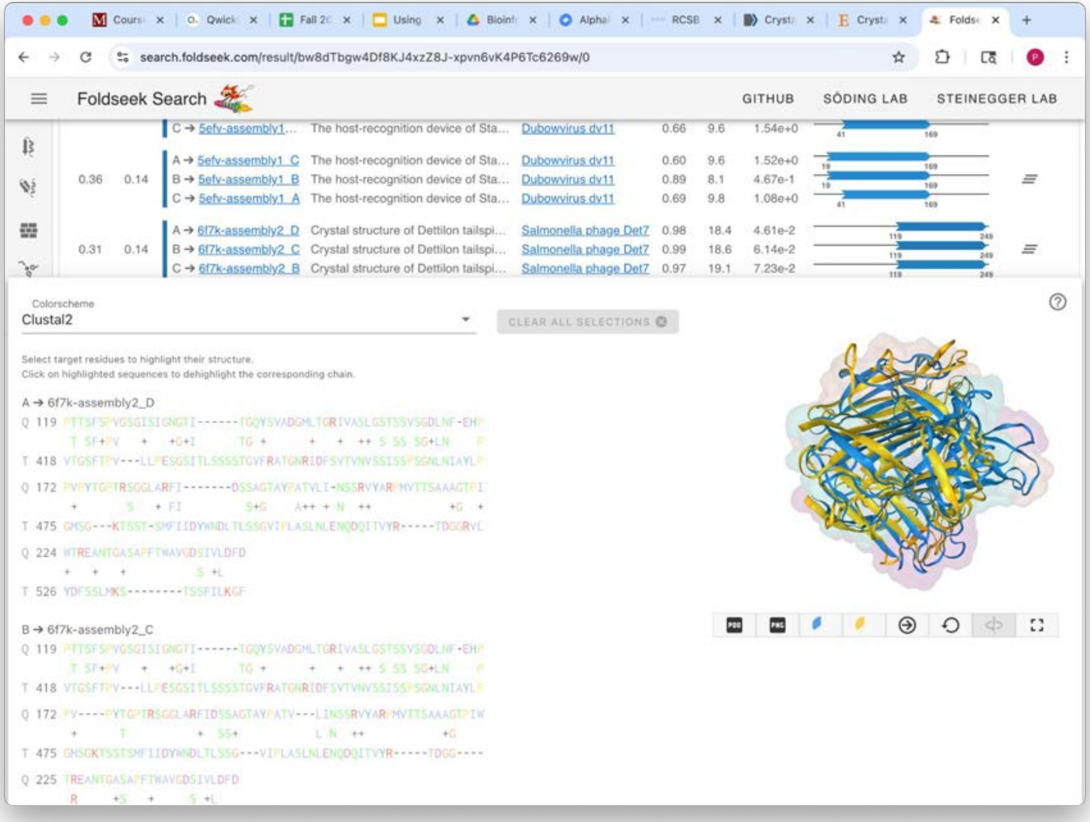
Foldseek-multimer with trimers of BaconCheese 43

Using Foldseek reveals a very strong hit with Tailspike protein from other phages



		C → 5efv-assembly1…	The host-recognition device of Sta…	Dubowvirus dv11	0.66	9.6	1.54e+0
0.36	0.14	A → 5efv-assembly1_C	The host-recognition device of Sta…	Dubowvirus dv11	0.60	9.6	1.52e+0
		B → 5efv-assembly1_B	The host-recognition device of Sta…	Dubowvirus dv11	0.89	8.1	4.67e-1
		C → 5efv-assembly1_A	The host-recognition device of Sta…	Dubowvirus dv11	0.69	9.8	1.08e+0
0.31	0.14	A → 6f7k-assembly2_D	Crystal structure of Dettilon tailspi…	Salmonella phage Det7	0.98	18.4	4.61e-2
		B → 6f7k-assembly2_C	Crystal structure of Dettilon tailspi…	Salmonella phage Det7	0.99	18.6	6.14e-2
		C → 6f7k-assembly2_B	Crystal structure of Dettilon tailspi…	Salmonella phage Det7	0.97	19.1	7.23e-2

Select target residues to highlight their structure.
Click on highlighted sequences to dehighlight the corresponding chain.

A → 6f7k-assembly2_D

```
Q 119 PTTSFSPVGSGISIGNGTI------TGQYSVADGMLTGRIVASLGSTSSVSGDLNF-EHP
        T SF+PV   +   +G+I      TG +      +   +  ++ S SS SG+LN    P
T 418 VTGSFTPV---LLPESGSITLSSSSTGVFRATGNRIDFSVTVNVSSISSPSGNLNIAYLP

Q 172 PVPYTGPTRSGGLARFI-------DSSAGTAYPATVLI-NSSRVYARPMVTTSAAAGTPI
        +       S   + FI       S+G    A++ + N  ++             +G  +
T 475 GMSG---KTSST-SMFIIDYWNDLTLSSGVIPLASLNLENQDQITVYR-----TDGGRVL

Q 224 WTREANTGASAPFTWAVGDSIVLDFD
      +    +    +           S +L
T 526 YDFSSLMKS--------TSSFILKGF
```

B → 6f7k-assembly2_C

```
Q 119 PTTSFSPVGSGISIGNGTI------TGQYSVADGMLTGRIVASLGSTSSVSGDLNF-EHP
        T SF+PV   +   +G+I      TG +      +   +  ++ S SS SG+LN    P
T 418 VTGSFTPV---LLPESGSITLSSSSTGVFRATGNRIDFSVTVNVSSISSPSGNLNIAYLP

Q 172 PV----PYTGPTRSGGLARFIDSSAGTAYPATV---LINSSRVYARPMVTTSAAAGTPIW
        +       T           +  SS+               L N  ++           +G
T 475 GMSGKTSSTSMFIIDYWNDLTLSSG---VIPLASLNLENQDQITVYR-----TDGG----

Q 225 TREANTGASAPFTWAVGDSIVLDFD
       R    +S   +      S +L
```

Final assessments for EG genomes

Distal tip protein:

BaconCheese 40

Mila11 39

Slysloth 39

Baseplate hub:

BaconCheese 42

Mila11 41

Slysloth 41

Tail spike protein:

BaconCheese 43

Mila11 42

Slysloth 42