

Phyre2.2

Email bcshaefer@yahoo.com
Description Factor_C_FULL_L_polyphemus
Date Sun Nov 23 22:42:31 GMT 2025
Unique Job ID 52bf6f1440d4399e
Sequence MVLASFLVSG ... [Download FASTA](#)
Job Type **normal**
Job Expiry **30 days**



Summary

Top model

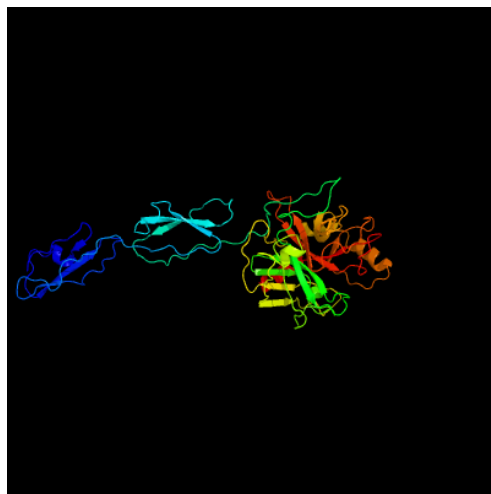


Image coloured by rainbow N → C terminus
Model dimensions (Å): **X**:94.444 **Y**:61.156 **Z**:87.977

Model (left) based on template [c9ekeD_](#)

Top template information

PDB header: immune system,hydrolase
Chain: D: **PDB Molecule:** Complement C1r subcomponent
PDBTitle: structure of a c1r zymogen fragment bound to salo, y51f mutant
PDB Entry: [PDBe](#) [RCSB](#) [PDBj](#)

Confidence and coverage

Confidence: **100.0%** Coverage: **35%**

358 residues (35% of your sequence) have been modelled with 100.0% confidence by the single highest scoring template.

Additional confident templates have been detected (see [Domain analysis](#)) which cover other regions of your sequence.

727 residues (71%) could be modelled at >90% confidence using multiple-templates.

You may wish to try resubmitting your sequence in "intensive" mode to model more of your sequence.

3D viewing

[Interactive 3D view in JSmol](#)

For other options to view your downloaded structure offline see the [FAQ](#)

Sequence analysis

[View PSI-Blast Pseudo-Multiple Sequence Alignment](#)

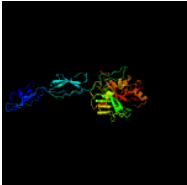
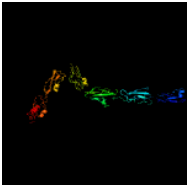
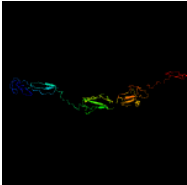
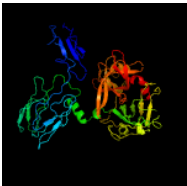
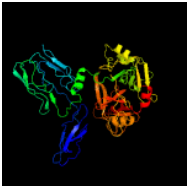
[Download FASTA version](#)

Secondary structure and disorder prediction [\[Show\]](#)

Domain analysis [\[Show\]](#)

Detailed template information [\[Hide\]](#)



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c9ekeD_ ○ □	 Alignment		100.0	30	PDB header: immune system,hydrolase Chain: D: PDB Molecule: Complement C1r subcomponent PDBTitle: structure of a c1r zymogen fragment bound to salo, y51f mutant PDB Entry: PDBe RCSB PDBj Run Investigator
2	c5o35C_ ○ □	 Alignment		99.8	21	PDB header: immune system Chain: C: PDB Molecule: Complement factor H, Complement factor H PDBTitle: structure of complement proteins complex PDB Entry: PDBe RCSB PDBj Run Investigator
3	c7nydD_ ○ □	 Alignment		99.4	18	PDB header: immune system Chain: D: PDB Molecule: Complement component C7 PDBTitle: cryoem structure of 2c9-smac PDB Entry: PDBe RCSB PDBj Run Investigator
4	c8eokC_ ○ □	 Alignment		99.9	25	PDB header: immune system Chain: C: PDB Molecule: Complement factor B PDBTitle: structure of the c3bb proconvertase in complex with lufaxin and factor xa PDB Entry: PDBe RCSB PDBj Run Investigator
5	c7jtnA_ ○ □	 Alignment		99.9	24	PDB header: immune system/dna Chain: A: PDB Molecule: Complement factor B PDBTitle: human complement factor b inhibited by a slow off-rate modified aptamer of 29 bases PDB Entry: PDBe RCSB PDBj Run Investigator
						PDB header: immune system Chain: D: PDB Molecule: Complement factor B PDBTitle: cobra venom factor (cvf) in complex with human factor b PDB Entry: PDBe RCSB PDBj

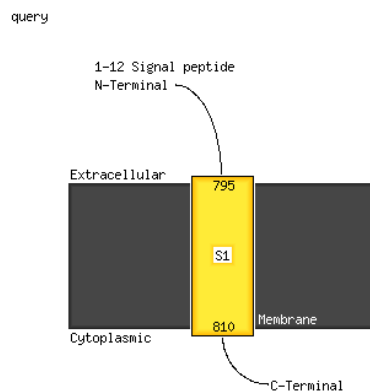
[Generate superposition of selected models](#)

Binding site prediction

Automated 3DLigandsite submission is temporarily suspended due to server load. However you may submit models directly to 3DLigandSite [HERE](#)

Transmembrane helix prediction

Transmembrane helices have been predicted in your sequence to adopt the topology shown below



Phyre is **now FREE** for commercial users!

All images and data generated by Phyre2 are free to use in any publication with acknowledgement

Accessibility Statement

Please cite: Phyre2.2: A Community Resource for Template-based Protein Structure Prediction

Powell HR *et al.* Journal of Molecular Biology (2025) *in press* DOI: <https://doi.org/10.1016/j.jmb.2025.168960>

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Michael Sternberg

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Phyre2.2

Email bcshaefer@yahoo.com
Description Factor_C_FULL_T_tridentatus
Date Sun Nov 23 22:40:29 GMT 2025
Unique Job ID 559d595a415dceab
Sequence MVLASFLVSG ... [Download FASTA](#)
Job Type **normal**
Job Expiry **30 days**



Summary

Top model

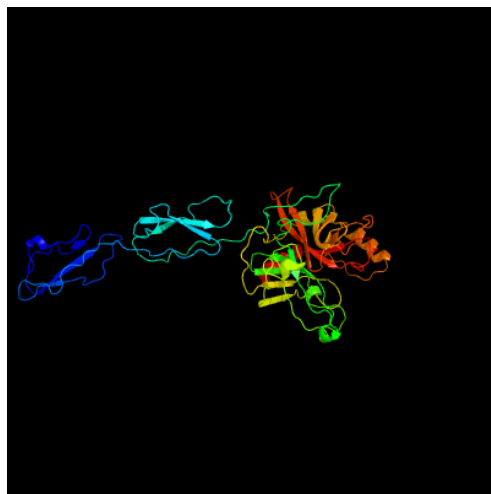


Image coloured by rainbow N → C terminus
Model dimensions (Å): **X**:95.522 **Y**:63.545 **Z**:90.290

Model (left) based on template [c9ekeD_](#)

Top template information

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-

Confidence and coverage

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358 residues (35% of your sequence) have been modelled with 100.0% confidence by the single highest scoring template.

Additional confident templates have been detected (see [Domain analysis](#)) which cover other regions of your sequence.

708 residues (69%) could be modelled at >90% confidence using multiple-templates.

You may wish to try resubmitting your sequence in "intensive" mode to model more of your sequence.

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Sequence analysis

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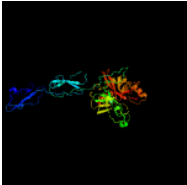
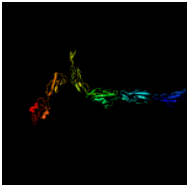
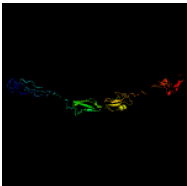
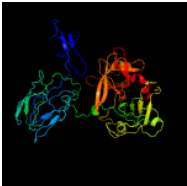
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						PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: Mannan-binding lectin serine protease 1 light chain Run Investigator

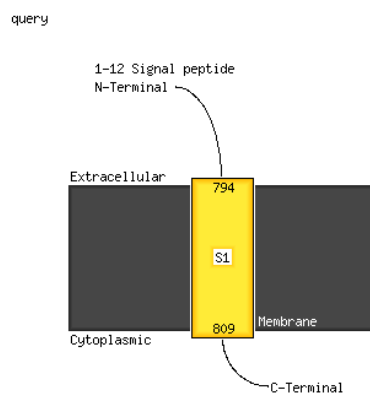
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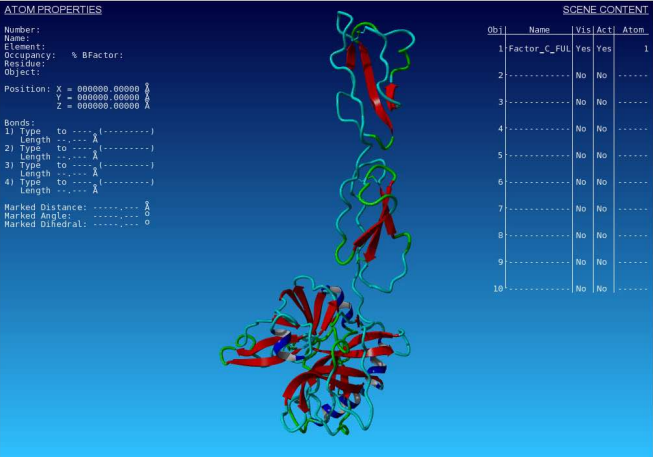
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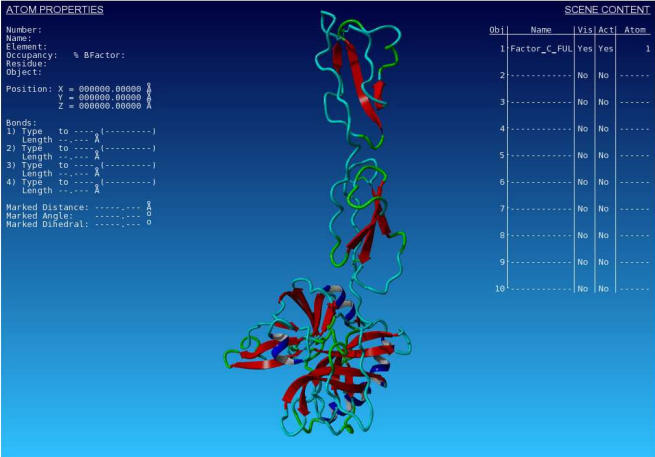
Powell HR *et al.* Journal of Molecular Biology (2025) *in press* DOI: <https://doi.org/10.1016/j.jmb.2025.168960>

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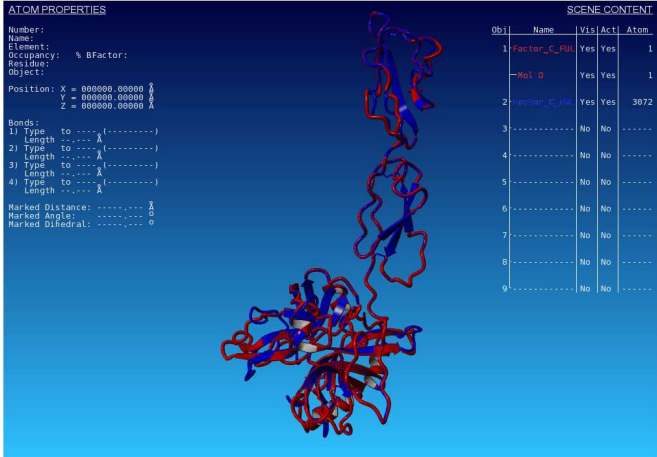




T. tridentatus Factor C (aa 576-1019)
Model based on template c9ekeD



L. polyphemus Proclotting factor (aa 577-1020)
Model based on template c9ekeD



Alignment between predicted structures:
1 (Factor C T tridentatus, red) and
2 (Factor C Limulus, blue)
Calpha RMSD of 0.479 Å over 359 aligned
residues with 90.25 % sequence identity.