

Phyre²

Email sally.dixon@maine.edu
Description Undefined
Date Mon Jul 15 09:58:36 BST 2019
Unique Job ID 5f330e02b2f74e20
Sequence MSKQDNRPTK ... [Download FASTA](#)
Job Type **normal**
Job Expiry 30 days



Summary

[Top model](#)

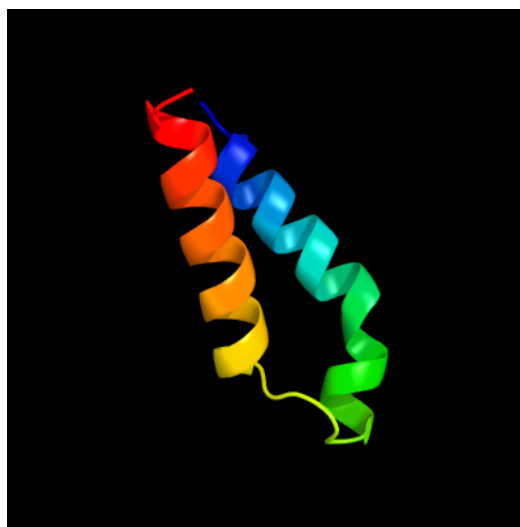


Image coloured by rainbow N → C terminus
Model dimensions (Å): X:27.002 Y:39.872 Z:32.950

Model (left) based on template [c4psoH](#)

[Top template information](#)

PDB header: dna binding protein
Chain: H: **PDB Molecule:** ssdna binding protein;
PDBTitle: crystal structure of apethermo-dbp-rp2 bound to ssdna dt10

[Confidence and coverage](#)

Confidence: **54.9%** Coverage: **49%**
44 residues (49% of your sequence) have been modelled with 54.9% confidence by the single highest scoring template.



You may wish to submit your sequence to [Phyrealarm](#). This will automatically scan your sequence every week for new potential templates as they appear in the Phyre2 library.

Please note: You must be registered and logged in to use Phyrealarm.

[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](#)


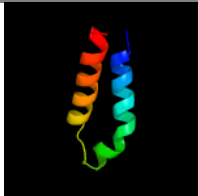

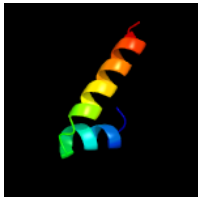

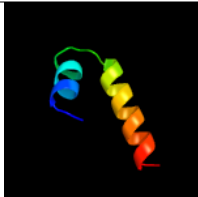

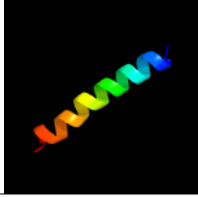





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Secondary structure and disorder prediction [\[Show\]](#)

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

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



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4psoH ○ □	 Alignment		54.9	18	PDB header: dna binding protein Chain: H: PDB Molecule: ssdna binding protein; PDBTitle: crystal structure of apethermo-dbp-rp2 bound to ssdna dt10 Run Investigator
2	c3l6tB ○ □	 Alignment		28.3	17	PDB header: hydrolase Chain: B: PDB Molecule: mobilization protein trai; PDBTitle: crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain Run Investigator
3	d1p4da ○ □	 Alignment		24.8	20	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain Run Investigator
4	c3iynQ ○ □	 Alignment		21.7	16	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5 Run Investigator
5	c4pupB ○ □	 Alignment		21.4	27	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from burkholderia cenocepacia j2315 Run Investigator
6	c1aq5B ○ □	 Alignment		20.9	14	PDB header: coiled-coil Chain: B: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures Run Investigator
						PDB header: coiled-coil Chain: C: PDB Molecule: cartilage matrix protein;

[Generate superposition of selected models](#) ⓘ

Binding site prediction

The confidence in the top model (c4psoH_ 54.9% confidence) was considered too low (<90%) for submission to [3DLigandSite](#)

You may manually submit your model to 3DLigandSite, but please be aware that results may be misleading

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

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

Please cite: The Phyre2 web portal for protein modeling, prediction and analysis.

Kelley LA *et al.* *Nature Protocols* 10, 845-858 (2015)[[pdf](#)] [[Citation link](#)]

If you use the binding site predictions from 3DLigandSite, **please also cite:**

3DLigandSite: predicting ligand-binding sites using similar structures.

Wass MN, Kelley LA and Sternberg MJ *Nucleic Acids Research* 38, W469-73 (2010) [[PubMed](#)]

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Component software

Template detection: [HHpred 1.51](#)
Secondary structure prediction: [Psi-pred 2.5](#)
Disorder prediction: [Disopred 2.4](#)
Transmembrane prediction: [Memsat_SVM](#)
Multi-template modelling and *ab initio*: [Poing 1.0](#)

