

Phyre²

Email k.butela@pitt.edu
 Description NEhalo_gp3
 Date Mon Jul 2 15:29:48 BST 2018
 Unique Job ID 61e7530f85d267d2
 Sequence MGPVVPKRSD ... [Download FASTA](#)
 Job Type **normal**
 Job Expiry 30 days

 Download zip of all results

Summary

[Top model](#)

Model (left) based on template [c2ev2B](#)

[Top template information](#)

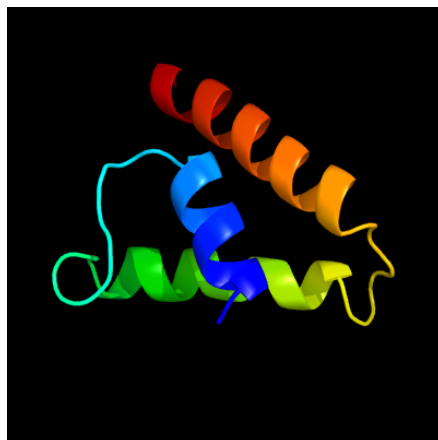


Image coloured by rainbow N → C terminus
 Model dimensions (Å): **X**:27.619 **Y**:31.819 **Z**:33.953

PDB header:lyase
Chain: B; **PDB Molecule:**hypothetical protein rv1264/mt1302;
PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5

[Confidence and coverage](#)

Confidence: **82.0%** Coverage: **40%**

58 residues (40% of your sequence) have been modelled with 82.0% 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](#)


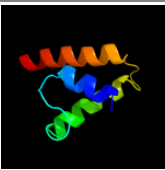

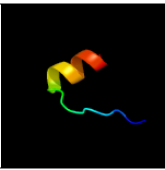



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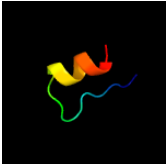
Secondary structure and disorder prediction [\[Show\]](#)


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

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



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ev2B ○○	 Alignment		82.0	12	PDB header: lyase Chain: B; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5 <input type="button" value="Run Investigator"/>
2	d2p5zx2 ○○	 Alignment		40.6	22	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like <input type="button" value="Run Investigator"/>
3	c2p5zX ○○	 Alignment		29.2	22	PDB header: structural genomics, unknown function Chain: X; PDB Molecule: type vi secretion system component; PDBTitle: the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5 <input type="button" value="Run Investigator"/>
4	c4mtkD ○○	 Alignment		25.7	6	PDB header: toxin

					Chain: D: PDB Molecule: vgrg1; PDBTitle: crystal structure of pa0091 vgrg1, the central spike of the type vi2 secretion system	<input type="button" value="Run Investigator"/>
5	c3h3pT <input type="radio"/> <input type="checkbox"/>	<input type="button" value="Alignment"/>	18.6	15	PDB header: immune system Chain: T: PDB Molecule: 4e10_s0_1tjlc_004_n; PDBTitle: crystal structure of hiv epitope-scaffold 4e10 fv complex	<input type="button" value="Run Investigator"/>
6	d1wrua2 <input type="radio"/> <input type="checkbox"/>	<input type="button" value="Alignment"/>	11.9	0	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like	<input type="button" value="Run Investigator"/>



Binding site prediction

The confidence in the top model (c2ev2B_ 82.0% 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 for **non-commercial use** only

Commercial users please contact [Michael Sternberg](#)

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](#)

