


















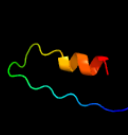

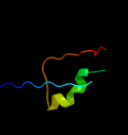


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3606c\_(foK)\_4048360\_4048926  
 Date Fri Aug 9 18:20:29 BST 2019  
 Unique Job ID 4d79a8982616aa3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1cbka_</a>	 Alignment		100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK <b>Family:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
2	<a href="#">c3qbcB_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine <b>PDBTitle:</b> structure and design of a new pterin site inhibitor of s. aureus hppk
3	<a href="#">c2qx0A_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 7,8-dihydro-6-hydroxymethylpterin- <b>PDBTitle:</b> crystal structure of yersinia pestis hppk (ternary complex)
4	<a href="#">d1f9ya_</a>	 Alignment		100.0	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK <b>Family:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
5	<a href="#">c2bmbA_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> folic acid synthesis protein fol1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
6	<a href="#">c3mcnA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine <b>PDBTitle:</b> crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
7	<a href="#">c2cg8B_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroneopterin aldolase 6-hydroxymethyl-7,8- <b>PDBTitle:</b> the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
8	<a href="#">c5z79F_</a>	 Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> hydroxymethyl-dihydropterin pyrophosphokinase- <b>PDBTitle:</b> crystal structure analysis of the hppk-dhps in complex with substrates
9	<a href="#">c6ohkA_</a>	 Alignment		22.7	9	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of fusobacterium nucleatum flavodoxin mutant k13g2 bound to flavin mononucleotide
10	<a href="#">c2m6rA_</a>	 Alignment		20.7	23	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> apo_yqca
11	<a href="#">d2bcgg3</a>	 Alignment		16.8	16	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GDI-like

12	<a href="#">c2wc1A_</a>	Alignment		16.0	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
13	<a href="#">c5f4bB_</a>	Alignment		14.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p)h dehydrogenase (quinone); <b>PDBTitle:</b> structure of b. abortus wrba-related protein a (wrpa)
14	<a href="#">c5ns5A_</a>	Alignment		14.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidase glij; <b>PDBTitle:</b> cys-gly dipeptidase glij in complex with cu2+ and zn2+
15	<a href="#">c2inpD_</a>	Alignment		12.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> phenol hydroxylase component phl; <b>PDBTitle:</b> structure of the phenol hydroxylase-regulatory protein2 complex
16	<a href="#">c5f5mB_</a>	Alignment		11.8	41	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> crystal structure of marburg virus nucleoprotein core domain
17	<a href="#">c6o58C_</a>	Alignment		11.5	27	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> human mcu-emre complex, dimer of channel
18	<a href="#">d1d5ta2</a>	Alignment		11.1	20	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GDI-like
19	<a href="#">c1unvB_</a>	Alignment		10.9	21	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
20	<a href="#">c1unvA_</a>	Alignment		10.9	21	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
21	<a href="#">c1u9gA_</a>	Alignment	not modelled	10.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(8)l(9)
22	<a href="#">c1unzB_</a>	Alignment	not modelled	9.6	21	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
23	<a href="#">c1unzA_</a>	Alignment	not modelled	9.6	21	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
24	<a href="#">c2hnbA_</a>	Alignment	not modelled	8.9	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein mioc; <b>PDBTitle:</b> solution structure of a bacterial holo-flavodoxin
25	<a href="#">c1u9gB_</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(8)l(9)
26	<a href="#">d1t6ca1</a>	Alignment	not modelled	8.4	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
27	<a href="#">c1w5kA_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
28	<a href="#">c1w5kD_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> four helix bundle <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
						<b>PDB header:</b> four helix bundle

29	<a href="#">c1w5kC_</a>	Alignment	not modelled	7.3	22	<b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
30	<a href="#">c1w5kB_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> an anti-parallel four helix bundle
31	<a href="#">d1vl2a2</a>	Alignment	not modelled	7.2	18	<b>Fold:</b> Argininosuccinate synthetase, C-terminal domain <b>Superfamily:</b> Argininosuccinate synthetase, C-terminal domain <b>Family:</b> Argininosuccinate synthetase, C-terminal domain
32	<a href="#">d1h2vc2</a>	Alignment	not modelled	7.0	20	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
33	<a href="#">c2zdiC_</a>	Alignment	not modelled	7.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> prefoldin subunit alpha; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
34	<a href="#">c1unyA_</a>	Alignment	not modelled	7.0	25	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
35	<a href="#">d1fxkc_</a>	Alignment	not modelled	6.7	14	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
36	<a href="#">c2la3A_</a>	Alignment	not modelled	6.2	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
37	<a href="#">c4xtbA_</a>	Alignment	not modelled	6.2	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter
38	<a href="#">d1hn0a4</a>	Alignment	not modelled	5.9	33	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain
39	<a href="#">c3u80A_</a>	Alignment	not modelled	5.7	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase, type ii; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
40	<a href="#">d1om2a_</a>	Alignment	not modelled	5.4	25	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Mitochondrial import receptor subunit Tom20 <b>Family:</b> Mitochondrial import receptor subunit Tom20
41	<a href="#">d1a9xa4</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
42	<a href="#">c1eiyA_</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of phenylalanyl-trna synthetase from thermus2 thermophilus complexed with cognate trnaphe
43	<a href="#">c6c6kD_</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> interferon-induced protein with tetratricopeptide repeats <b>PDBTitle:</b> structural basis for preferential recognition of cap 0 rna by a human2 ifit1-iftit3 protein complex
44	<a href="#">d1n7oa3</a>	Alignment	not modelled	5.2	38	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain
45	<a href="#">c5b88A_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dead; <b>PDBTitle:</b> rrm-like domain of dead-box protein, csda
46	<a href="#">d1cb8a3</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain
47	<a href="#">d1x1ia3</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Hyaluronate lyase-like, central domain