
















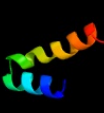

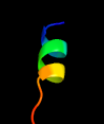

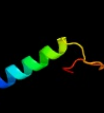


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2809 (- )_3115418_3115729
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	f7b04f9937d342f7

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3thgA_</a>	 Alignment		64.7	28	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain
2	<a href="#">d1v54e_</a>	 Alignment		28.7	43	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Cytochrome c oxidase subunit E <b>Family:</b> Cytochrome c oxidase subunit E
3	<a href="#">c2y69R_</a>	 Alignment		27.7	43	<b>PDB header:</b> electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> cytochrome c oxidase subunit 5a; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
4	<a href="#">c5uz9B_</a>	 Alignment		25.2	25	<b>PDB header:</b> immune system/rna <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated protein csy2; <b>PDBTitle:</b> cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
5	<a href="#">d2dkya1</a>	 Alignment		23.9	47	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
6	<a href="#">c5ji4A_</a>	 Alignment		18.7	44	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> w37; <b>PDBTitle:</b> solution structure of the de novo mini protein geehe_02
7	<a href="#">d2cs3a1</a>	 Alignment		18.1	83	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Variant RING domain
8	<a href="#">d2h80a1</a>	 Alignment		17.1	50	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
9	<a href="#">c6hu9r_</a>	 Alignment		16.2	24	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> R: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 7; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
10	<a href="#">d1izma_</a>	 Alignment		12.8	25	<b>Fold:</b> YgfB-like <b>Superfamily:</b> YgfB-like <b>Family:</b> YgfB-like
11	<a href="#">c4n71A_</a>	 Alignment		12.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted hd phosphohydrolase phnz; <b>PDBTitle:</b> x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz

12	<a href="#">c5o7yA_</a>	Alignment		11.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thebaine 6-o-demethylase; <b>PDBTitle:</b> thebaine 6-o-demethylase (t6odm) from papaver somniferum in complex2 with succinate
13	<a href="#">d1gtma2</a>	Alignment		9.9	26	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
14	<a href="#">d2i5ua1</a>	Alignment		9.2	6	<b>Fold:</b> DnaD domain-like <b>Superfamily:</b> DnaD domain-like <b>Family:</b> DnaD domain
15	<a href="#">c4gytB_</a>	Alignment		8.9	57	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lpg0076 protein from legionella pneumophila
16	<a href="#">d1bgva2</a>	Alignment		8.5	42	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
17	<a href="#">c5xyiU_</a>	Alignment		8.3	25	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> ribosomal protein s10p/s20e, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
18	<a href="#">d1u2ca2</a>	Alignment		8.3	23	<b>Fold:</b> Dystroglycan, domain 2 <b>Superfamily:</b> Dystroglycan, domain 2 <b>Family:</b> Dystroglycan, domain 2
19	<a href="#">d1bvua2</a>	Alignment		8.0	23	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
20	<a href="#">d1euza2</a>	Alignment		7.7	29	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
21	<a href="#">c2tmgD_</a>	Alignment	not modelled	7.4	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
22	<a href="#">c5k12F_</a>	Alignment	not modelled	7.3	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate dehydrogenase 1, mitochondrial; <b>PDBTitle:</b> cryo-em structure of glutamate dehydrogenase at 1.8 a resolution
23	<a href="#">c4kwyB_</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (cc_3750) from caulobacter2 crescentus cb15 at 2.40 a resolution
24	<a href="#">c5xcqB_</a>	Alignment	not modelled	7.1	31	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> vl-sarah(m24c) chimera; <b>PDBTitle:</b> crystal structure of p20.1 fv-clasp fragment with its antigen peptide
25	<a href="#">c3aoeC_</a>	Alignment	not modelled	7.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
26	<a href="#">c3aogA_</a>	Alignment	not modelled	6.8	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
27	<a href="#">c2kfeA_</a>	Alignment	not modelled	6.4	54	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> meucin-24; <b>PDBTitle:</b> solution structure of meucin-24
28	<a href="#">c3nohA_</a>	Alignment	not modelled	6.3	56	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptide binding protein; <b>PDBTitle:</b> crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a

						resolution
29	<a href="#">c2uwjF_</a>	Alignment	not modelled	6.2	56	<b>PDB header:</b> chaperone <b>Chain:</b> F; <b>PDB Molecule:</b> type iii export protein pscf; <b>PDBTitle:</b> structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
30	<a href="#">d1gp6a_</a>	Alignment	not modelled	6.1	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> Penicillin synthase-like
31	<a href="#">c3bjvA_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> rrmpa; <b>PDBTitle:</b> the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
32	<a href="#">d1g99a1</a>	Alignment	not modelled	6.0	37	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
33	<a href="#">d1c0ma1</a>	Alignment	not modelled	5.9	40	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
34	<a href="#">d1hwx2</a>	Alignment	not modelled	5.8	42	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
35	<a href="#">c2bmaA_</a>	Alignment	not modelled	5.7	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate dehydrogenase (nadp+); <b>PDBTitle:</b> the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
36	<a href="#">d1paaa_</a>	Alignment	not modelled	5.6	45	<b>Fold:</b> Phospholipase A2, PLA2 <b>Superfamily:</b> Phospholipase A2, PLA2 <b>Family:</b> Vertebrate phospholipase A2
37	<a href="#">c6gdjA_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> mto2; <b>PDBTitle:</b> crystal structure of mto2 twin-cysteine dimerisation domain
38	<a href="#">c2rt6A_</a>	Alignment	not modelled	5.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> primosomal replication protein n"; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for pric n-2 terminal domain
39	<a href="#">c3r2cJ_</a>	Alignment	not modelled	5.5	55	<b>PDB header:</b> transcription/rna <b>Chain:</b> J; <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
40	<a href="#">d2dmda1</a>	Alignment	not modelled	5.4	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
41	<a href="#">d1g4ia_</a>	Alignment	not modelled	5.3	45	<b>Fold:</b> Phospholipase A2, PLA2 <b>Superfamily:</b> Phospholipase A2, PLA2 <b>Family:</b> Vertebrate phospholipase A2
42	<a href="#">d1dpya_</a>	Alignment	not modelled	5.3	45	<b>Fold:</b> Phospholipase A2, PLA2 <b>Superfamily:</b> Phospholipase A2, PLA2 <b>Family:</b> Vertebrate phospholipase A2
43	<a href="#">d1gyza_</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> Ribosomal protein L20 <b>Family:</b> Ribosomal protein L20
44	<a href="#">c4xgiA_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
45	<a href="#">c3iz6J_</a>	Alignment	not modelled	5.2	24	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 40s ribosomal protein s20 (s10p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome