
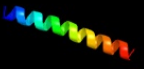
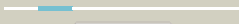

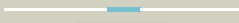












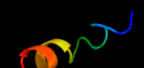






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2113 (- )_2372638_2373831
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	690096e40b93d49d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3fwbB_</a>	 Alignment		70.6	31	<b>PDB header:</b> cell cycle, transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear mrna export protein sac3; <b>PDBTitle:</b> sac3:sus1:cdc31 complex
2	<a href="#">c4ndlC_</a>	 Alignment		38.9	30	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> enh-c2b, computational designed homodimer; <b>PDBTitle:</b> computational design and experimental verification of a symmetric2 homodimer
3	<a href="#">d2axtz1</a>	 Alignment		34.8	21	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> PsbZ-like <b>Family:</b> PsbZ-like
4	<a href="#">d2obba1</a>	 Alignment		24.0	33	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
5	<a href="#">c4ndkA_</a>	 Alignment		23.4	33	<b>PDB header:</b> fluorescent protein, de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> e23p-yfp, gfp-like fluorescent chromoprotein fp506, <b>PDBTitle:</b> crystal structure of a computational designed engrailed homeodomain2 variant fused with yfp
6	<a href="#">d1b33n_</a>	 Alignment		19.7	36	<b>Fold:</b> Allophycocyanin linker chain (domain) <b>Superfamily:</b> Allophycocyanin linker chain (domain) <b>Family:</b> Allophycocyanin linker chain (domain)
7	<a href="#">d1dw0a_</a>	 Alignment		16.8	19	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
8	<a href="#">d1u6ra1</a>	 Alignment		14.4	42	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
9	<a href="#">d1gu2a_</a>	 Alignment		14.3	31	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
10	<a href="#">d1m15a1</a>	 Alignment		12.9	50	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
11	<a href="#">d1v8ca2</a>	 Alignment		12.9	56	<b>Fold:</b> TBP-like <b>Superfamily:</b> MoaD-related protein, C-terminal domain <b>Family:</b> MoaD-related protein, C-terminal domain

12	<a href="#">c5lqwL_</a>	Alignment		12.8	50	<b>PDB header:</b> splicing <b>Chain:</b> L: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc26; <b>PDBTitle:</b> yeast activated spliceosome
13	<a href="#">d1vrpa1</a>	Alignment		12.4	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
14	<a href="#">d1u6ka1</a>	Alignment		12.1	48	<b>Fold:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) <b>Superfamily:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) <b>Family:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
15	<a href="#">c5y0tD_</a>	Alignment		11.4	38	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> thermotoga maritima tmcal; <b>PDBTitle:</b> crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
16	<a href="#">d1g0wa1</a>	Alignment		11.2	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
17	<a href="#">d1i0ea1</a>	Alignment		11.0	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
18	<a href="#">d1crka1</a>	Alignment		10.9	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
19	<a href="#">d1qh4a1</a>	Alignment		10.3	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
20	<a href="#">d1qk1a1</a>	Alignment		10.2	40	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
21	<a href="#">d1oo2a_</a>	Alignment	not modelled	9.7	6	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
22	<a href="#">d1ttaa_</a>	Alignment	not modelled	9.2	13	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
23	<a href="#">d1f86a_</a>	Alignment	not modelled	8.5	12	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
24	<a href="#">c5ixiB_</a>	Alignment	not modelled	8.3	54	<b>PDB header:</b> cytokine <b>Chain:</b> B: <b>PDB Molecule:</b> chimera protein of interferon lambda receptor 1 and <b>PDBTitle:</b> structure of human jak1 ferm/sh2 in complex with ifn1r1/il10ra chimera
25	<a href="#">d1kgia_</a>	Alignment	not modelled	7.8	13	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Transthyretin (synonym: prealbumin) <b>Family:</b> Transthyretin (synonym: prealbumin)
26	<a href="#">c5y0nB_</a>	Alignment	not modelled	7.6	41	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0348 protein b4417_3650; <b>PDBTitle:</b> crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
27	<a href="#">c2dg7A_</a>	Alignment	not modelled	7.2	23	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
28	<a href="#">c6gcta_</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutral amino acid transporter b(0); <b>PDBTitle:</b> cryo-em structure of the human neutral amino acid transporter asct2

29	<a href="#">d1hf2a2</a>	Alignment	not modelled	6.8	16	<b>Fold:</b> Cell-division inhibitor MinC, N-terminal domain <b>Superfamily:</b> Cell-division inhibitor MinC, N-terminal domain <b>Family:</b> Cell-division inhibitor MinC, N-terminal domain
30	<a href="#">c3qvaB</a>	Alignment	not modelled	6.6	41	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transthyretin-like protein; <b>PDBTitle:</b> structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
31	<a href="#">c2l1nA</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the protein yp_399305.1
32	<a href="#">c5vkaC</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> no mechanoreceptor potential c isoform I; <b>PDBTitle:</b> structure of a mechanotransduction ion channel drosophila nompc in2 nanodisc
33	<a href="#">c2l3wA</a>	Alignment	not modelled	6.2	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> phycobilisome rod linker polypeptide; <b>PDBTitle:</b> solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
34	<a href="#">c4dh4A</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mif; <b>PDBTitle:</b> macrophage migration inhibitory factor toxoplasma gondii
35	<a href="#">c4z1mj</a>	Alignment	not modelled	6.1	44	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> bovine f1-atpase inhibited by three copies of the inhibitor protein2 if1 crystallised in the presence of thiophosphate.
36	<a href="#">c2qkwA</a>	Alignment	not modelled	6.1	63	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> structural basis for activation of plant immunity by2 bacterial effector protein avrpto
37	<a href="#">d2qkwa1</a>	Alignment	not modelled	6.1	63	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Avirulence protein AvrPto <b>Family:</b> Avirulence protein AvrPto
38	<a href="#">c4z1ml</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> bovine f1-atpase inhibited by three copies of the inhibitor protein2 if1 crystallised in the presence of thiophosphate.
39	<a href="#">c4tt3l</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> the pathway of binding of the intrinsically disordered mitochondrial2 inhibitor protein to f1-atpase
40	<a href="#">c3t5vE</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> nuclear mrna export protein thp1; <b>PDBTitle:</b> sac3:thp1:sem1 complex
41	<a href="#">c5ietA</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial proteasome activator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis atp-independent2 proteasome activator
42	<a href="#">c2h1xB</a>	Alignment	not modelled	6.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-hydroxyisourate hydrolase (formerly known as <b>PDBTitle:</b> crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
43	<a href="#">c3jcuz</a>	Alignment	not modelled	5.9	34	<b>PDB header:</b> membrane protein <b>Chain:</b> Z: <b>PDB Molecule:</b> photosystem ii reaction center protein z; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
44	<a href="#">c1ohhH</a>	Alignment	not modelled	5.7	40	<b>PDB header:</b> synthase <b>Chain:</b> H: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> bovine mitochondrial f1-atpase complexed with the inhibitor2 protein if1
45	<a href="#">d1smye</a>	Alignment	not modelled	5.5	38	<b>Fold:</b> RPB6/omega subunit-like <b>Superfamily:</b> RPB6/omega subunit-like <b>Family:</b> RNA polymerase omega subunit
46	<a href="#">c2cw1A</a>	Alignment	not modelled	5.5	60	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn4m; <b>PDBTitle:</b> solution structure of the de novo-designed lambda cro fold2 protein
47	<a href="#">c3zbeA</a>	Alignment	not modelled	5.5	8	<b>PDB header:</b> toxin-antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> paaa2; <b>PDBTitle:</b> e. coli o157 pare2-associated antitoxin 2 (paaa2)
48	<a href="#">c2rukA</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> solution structure of the complex between p53 transactivation domain 22 and tfiih p62 ph domain
49	<a href="#">d1x4ta1</a>	Alignment	not modelled	5.4	41	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> !SY1 domain-like <b>Family:</b> !SY1 N-terminal domain-like
50	<a href="#">c1pnbA</a>	Alignment	not modelled	5.3	8	<b>PDB header:</b> seed storage protein <b>Chain:</b> A: <b>PDB Molecule:</b> napin bnib; <b>PDBTitle:</b> structure of napin bnib, nmr, 10 structures
51	<a href="#">c1q90M</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome b6f complex subunit petm; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii