
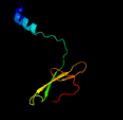
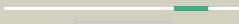






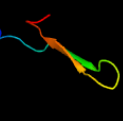











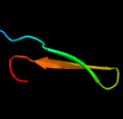


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1431 (-) _1608089_1609858
Date	Wed Jul 31 22:05:54 BST 2019
Unique Job ID	6f47f2552738af1c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2r6gf1</a>	 Alignment		58.5	12	<b>Fold:</b> MaIF N-terminal region-like <b>Superfamily:</b> MaIF N-terminal region-like <b>Family:</b> MaIF N-terminal region-like
2	<a href="#">d1fo1a2</a>	 Alignment		40.0	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Non-canonical RBD domain
3	<a href="#">c3hi2C_</a>	 Alignment		35.9	24	<b>PDB header:</b> dna binding protein/toxin <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator mqa2(ygit); <b>PDBTitle:</b> structure of the n-terminal domain of the e. coli antitoxin mqa2 (ygit/b3021) in complex with the e. coli toxin mqs2 (ygiu/b3022)
4	<a href="#">c3lzkC_</a>	 Alignment		34.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarylacetoacetate hydrolase family protein; <b>PDBTitle:</b> the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
5	<a href="#">c2l6pA_</a>	 Alignment		32.6	15	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phac1, phac2 and phad genes; <b>PDBTitle:</b> nmr solution structure of the protein np_253742.1
6	<a href="#">d1kpta_</a>	 Alignment		32.1	16	<b>Fold:</b> Yeast killer toxins <b>Superfamily:</b> Yeast killer toxins <b>Family:</b> Virally encoded KP4 toxin
7	<a href="#">d1b4ra_</a>	 Alignment		28.8	67	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PKD domain <b>Family:</b> PKD domain
8	<a href="#">c2hija_</a>	 Alignment		28.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ykff; <b>PDBTitle:</b> solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
9	<a href="#">d2hija1</a>	 Alignment		28.1	25	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain <b>Family:</b> Ykff-like
10	<a href="#">c5jpa_</a>	 Alignment		25.9	20	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> u3 small nucleolar rna-associated protein 21; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
11	<a href="#">c2l6nA_</a>	 Alignment		24.2	22	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_001092504.1; <b>PDBTitle:</b> nmr solution structure of the protein yp_001092504.1

12	<a href="#">c2ifoA_</a>	Alignment		24.1	10	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> inovirus; <b>PDBTitle:</b> model-building studies of inovirus: genetic variations on a2 geometric theme
13	<a href="#">d1tisa_</a>	Alignment		22.7	18	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
14	<a href="#">c2zpaB_</a>	Alignment		22.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ypfi; <b>PDBTitle:</b> crystal structure of trna(met) cytidine acetyltransferase
15	<a href="#">c2xu9A_</a>	Alignment		22.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> laccase; <b>PDBTitle:</b> crystal structure of laccase from thermus thermophilus hb27
16	<a href="#">d1wgoa_</a>	Alignment		21.6	33	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PKD domain <b>Family:</b> PKD domain
17	<a href="#">c3iynR_</a>	Alignment		20.4	44	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
18	<a href="#">c6rdf7_</a>	Alignment		19.9	46	<b>PDB header:</b> proton transport <b>Chain:</b> 7: <b>PDB Molecule:</b> mitochondrial atp synthase associated protein asa7; <b>PDBTitle:</b> cryoem structure of polytomella f-atp synthase, primary rotary state2 3, monomer-masked refinement
19	<a href="#">c1x27F_</a>	Alignment		19.5	23	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase lck; <b>PDBTitle:</b> crystal structure of lck sh2-sh3 with sh2 binding site of2 p130cas
20	<a href="#">c2vldA_</a>	Alignment		19.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease nucs; <b>PDBTitle:</b> crystal structure of a repair endonuclease from pyrococcus abyssi
21	<a href="#">c3iynQ_</a>	Alignment	not modelled	18.7	44	<b>PDB header:</b> virus <b>Chain:</b> Q: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
22	<a href="#">d1c0pa1</a>	Alignment	not modelled	18.0	13	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> D-aminoacid oxidase, N-terminal domain
23	<a href="#">c3gzaA_</a>	Alignment	not modelled	16.7	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like fold; <b>PDBTitle:</b> crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
24	<a href="#">c4nc6A_</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> rab gtpase-activating protein 1; <b>PDBTitle:</b> tbc domain of human rab gtpase-activating protein 1
25	<a href="#">c4xedA_</a>	Alignment	not modelled	16.6	33	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase m14, carboxypeptidase a; <b>PDBTitle:</b> pkd domain of m14-like peptidase from thermoplasmatales archaeon scgc2 ab-540-f20
26	<a href="#">c3luuA_</a>	Alignment	not modelled	16.0	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
27	<a href="#">c4l9dB_</a>	Alignment	not modelled	15.2	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> protease; <b>PDBTitle:</b> crystal structure of the pkd1 domain from vibrio cholerae2 metalloprotease prtV
						<b>Fold:</b> Immunoglobulin-like beta-sandwich

28	<a href="#">d1l0qa1</a>	Alignment	not modelled	15.0	67	<b>Superfamily:</b> PKD domain <b>Family:</b> PKD domain
29	<a href="#">c5ubdB_</a>	Alignment	not modelled	14.8	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rctb replication initiator protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain (domain 1) of rctb, rctb-1-2 124-148m
30	<a href="#">c1avoA_</a>	Alignment	not modelled	14.5	46	<b>PDB header:</b> proteasome activator <b>Chain:</b> A: <b>PDB Molecule:</b> 11s regulator; <b>PDBTitle:</b> proteasome activator reg(alpha)
31	<a href="#">d1vkwa_</a>	Alignment	not modelled	14.4	71	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> Putative nitroreductase TM1586
32	<a href="#">c2wsf_</a>	Alignment	not modelled	14.3	53	<b>PDB header:</b> photosynthesis <b>Chain:</b> F: <b>PDB Molecule:</b> photosystem i reaction center subunit iii, chloroplastic; <b>PDBTitle:</b> improved model of plant photosystem i
33	<a href="#">c4kp3C_</a>	Alignment	not modelled	13.5	15	<b>PDB header:</b> motor protein/protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> riip-like protein 2; <b>PDBTitle:</b> crystal structure of myova-gtd in complex with two cargos
34	<a href="#">c4z9nB_</a>	Alignment	not modelled	13.4	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
35	<a href="#">d1c3ha_</a>	Alignment	not modelled	13.2	29	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
36	<a href="#">c5hbaA_</a>	Alignment	not modelled	12.9	23	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> globular domain of zebrafish complement 1qa protein
37	<a href="#">c5tvf_</a>	Alignment	not modelled	12.5	18	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> s-adenosylmethionine decarboxylase proenzyme-like, <b>PDBTitle:</b> crystal structure of trypanosoma brucei adometdc/prozyme heterodimer2 in complex with inhibitor cgp 40215
38	<a href="#">d1j2b_</a>	Alignment	not modelled	12.5	39	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> GAT-like domain <b>Family:</b> GAT domain
39	<a href="#">c3oakD_</a>	Alignment	not modelled	12.3	80	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> crystal structure of a spn1 (iws1)-spt6 complex
40	<a href="#">c6aemB_</a>	Alignment	not modelled	12.2	67	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> pkd domain; <b>PDBTitle:</b> crystal structure of the pkd1 domain of vibrio anguillarum epp
41	<a href="#">d1oz9a_</a>	Alignment	not modelled	12.2	22	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Predicted metal-dependent hydrolase
42	<a href="#">c3oakC_</a>	Alignment	not modelled	11.8	80	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> crystal structure of a spn1 (iws1)-spt6 complex
43	<a href="#">c3nhnA_</a>	Alignment	not modelled	11.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase hck; <b>PDBTitle:</b> crystal structure of the src-family kinase hck sh3-sh2-linker2 regulatory region
44	<a href="#">d1pk6c_</a>	Alignment	not modelled	11.7	24	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
45	<a href="#">d1f28a_</a>	Alignment	not modelled	11.7	16	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
46	<a href="#">c2l73A_</a>	Alignment	not modelled	11.6	17	<b>PDB header:</b> oxidoreductase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase organizer 1; <b>PDBTitle:</b> structure of the noxo1b px domain
47	<a href="#">d1rgoa2</a>	Alignment	not modelled	11.6	33	<b>Fold:</b> CCCH zinc finger <b>Superfamily:</b> CCCH zinc finger <b>Family:</b> CCCH zinc finger
48	<a href="#">c4whnB_</a>	Alignment	not modelled	11.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> apxc; <b>PDBTitle:</b> structure of toxin-activating acyltransferase (taat)
49	<a href="#">c5xywD_</a>	Alignment	not modelled	11.4	71	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> gd21652; <b>PDBTitle:</b> crystal structure of drosophila simulans rhino chromoshadow domain in2 complex with n-terminal domain
50	<a href="#">c2wltA_</a>	Alignment	not modelled	11.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
51	<a href="#">d1pj3a2</a>	Alignment	not modelled	11.0	18	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
52	<a href="#">d1dula_</a>	Alignment	not modelled	10.9	17	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain
53	<a href="#">d1gq2a2</a>	Alignment	not modelled	10.9	18	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
54	<a href="#">c4kt0F_</a>	Alignment	not modelled	10.8	47	<b>PDB header:</b> electron transport <b>Chain:</b> F: <b>PDB Molecule:</b> photosystem i subunit iii; <b>PDBTitle:</b> crystal structure of a virus like photosystem i from the2



						<b>Family:</b> S-adenosylmethionine synthetase
81	<a href="#">c1yewl_</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
82	<a href="#">c3rgbA_</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase subunit b2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from 2 methylcoccus capsulatus (bath)
83	<a href="#">c4ediC_</a>	Alignment	not modelled	8.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> ethanolamine utilization protein; <b>PDBTitle:</b> disulfide bonded eutl from clostridium perfringens
84	<a href="#">c2q74B_</a>	Alignment	not modelled	8.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol-1-monophosphatase; <b>PDBTitle:</b> mycobacterium tuberculosis suhb
85	<a href="#">d2p02a3</a>	Alignment	not modelled	8.8	16	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
86	<a href="#">d2bp3a1</a>	Alignment	not modelled	8.8	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
87	<a href="#">c4f3jA_</a>	Alignment	not modelled	8.7	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> complement c1q tumor necrosis factor-related protein 5; <b>PDBTitle:</b> crystal structure of trimeric gc1q domain of human c1qtnf5 associated2 with late-onset retinal macular degeneration
88	<a href="#">c2kzwA_</a>	Alignment	not modelled	8.6	67	<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 q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
89	<a href="#">d1pk6a_</a>	Alignment	not modelled	8.6	24	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
90	<a href="#">c3rfrl_</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from 2 methylcystis sp. strain m
91	<a href="#">c1l0qC_</a>	Alignment	not modelled	8.4	67	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> surface layer protein; <b>PDBTitle:</b> tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
92	<a href="#">d1u5la_</a>	Alignment	not modelled	8.4	36	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
93	<a href="#">d1fngb2</a>	Alignment	not modelled	8.3	24	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
94	<a href="#">d1ttja_</a>	Alignment	not modelled	8.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
95	<a href="#">d3c7ba2</a>	Alignment	not modelled	8.3	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
96	<a href="#">d1vhib_</a>	Alignment	not modelled	8.3	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
97	<a href="#">d1mxaa3</a>	Alignment	not modelled	8.3	23	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
98	<a href="#">c3b89A_</a>	Alignment	not modelled	8.3	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> crystal structure of rrna methylase from escherichia coli
99	<a href="#">c4esjA_</a>	Alignment	not modelled	8.3	31	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> type-2 restriction enzyme dpni; <b>PDBTitle:</b> restriction endonuclease dpni in complex with target dna