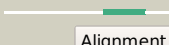

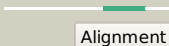
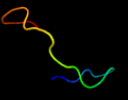
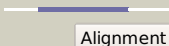
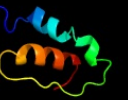
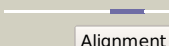

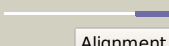

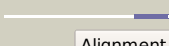

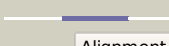
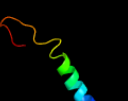
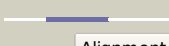
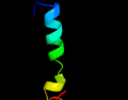
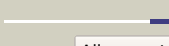


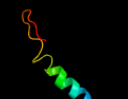




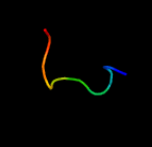

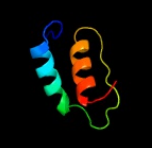
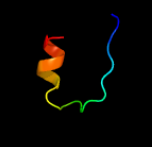

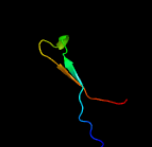



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0492A (-) _583378_583707
Date	Fri Jul 26 01:50:03 BST 2019
Unique Job ID	825f2337fc3108fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xg8D_</a>	 Alignment		46.7	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> pipx; <b>PDBTitle:</b> structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942
2	<a href="#">c3n5bB_</a>	 Alignment		43.7	33	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> asr0485 protein; <b>PDBTitle:</b> the complex of pii and pipx from anabaena
3	<a href="#">d1y0ba1</a>	 Alignment		13.4	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
4	<a href="#">c2n5qA_</a>	 Alignment		13.1	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine-rich peptide js1; <b>PDBTitle:</b> solution structure of cystein-rich peptide js1 from jasminum sambac
5	<a href="#">c6az5A_</a>	 Alignment		12.9	57	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k
6	<a href="#">c2x5sB_</a>	 Alignment		11.8	67	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-1-phosphate guanylyltransferase; <b>PDBTitle:</b> crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
7	<a href="#">c1iz1L_</a>	 Alignment		10.9	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> photosystem ii: subunit psbb; <b>PDBTitle:</b> crystal structure of photosystem ii
8	<a href="#">d1k1xa1</a>	 Alignment		10.8	23	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> 4-alpha-glucanotransferase, domain 2
9	<a href="#">d2i00a1</a>	 Alignment		8.8	29	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
10	<a href="#">c1iz1B_</a>	 Alignment		8.8	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> photosystem ii: subunit psbb; <b>PDBTitle:</b> crystal structure of photosystem ii
11	<a href="#">c5vocB_</a>	 Alignment		8.5	25	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein I; <b>PDBTitle:</b> crystal structure of hcmv pentamer in complex with neutralizing2 antibody 8i21 - low resolution dataset for initial phasing by sad

12	<a href="#">d2ozga1</a>	Alignment		8.2	45	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
13	<a href="#">c2wj9A_</a>	Alignment		8.1	15	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> intergenic-region protein; <b>PDBTitle:</b> ardb
14	<a href="#">c5lcsA_</a>	Alignment		8.1	40	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gallinacin-7; <b>PDBTitle:</b> nmr structure of chicken avbd7 defensin
15	<a href="#">c2mwdA_</a>	Alignment		7.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation regulator 1; <b>PDBTitle:</b> nmr structure of fbp28 ww2 mutant y438r dndc
16	<a href="#">d1vcha1</a>	Alignment		7.8	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
17	<a href="#">c4lu0A_</a>	Alignment		7.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.
18	<a href="#">c4ewcA_</a>	Alignment		7.3	86	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleoprotein; <b>PDBTitle:</b> crystal structure of the infectious salmon anemia virus nucleoprotein
19	<a href="#">c3h6qA_</a>	Alignment		7.2	25	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> macrocyprin 1a; <b>PDBTitle:</b> macrocyprin, a beta-trefoil cysteine protease inhibitor
20	<a href="#">d1rzhh2</a>	Alignment		7.0	50	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
21	<a href="#">d1o60a_</a>	Alignment	not modelled	6.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
22	<a href="#">c1zr7A_</a>	Alignment	not modelled	6.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> huntingtin-interacting protein hypa/fbp11; <b>PDBTitle:</b> solution structure of the first ww domain of fbp11
23	<a href="#">c4ng2E_</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lasr lbd-qsla complex from pseudomonas aeruginosa
24	<a href="#">c4z1bA_</a>	Alignment	not modelled	6.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> structure of h204a mutant kdo8ps from h.pylori
25	<a href="#">c1zcoA_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
26	<a href="#">d1l9bh2</a>	Alignment	not modelled	6.3	50	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
27	<a href="#">c6h8qH_</a>	Alignment	not modelled	6.2	67	<b>PDB header:</b> cell cycle <b>Chain:</b> H: <b>PDB Molecule:</b> sister chromatid cohesion protein 1; <b>PDBTitle:</b> structural basis for scc3-dependent cohesin recruitment to chromatin
28	<a href="#">c1izlC_</a>	Alignment	not modelled	6.2	26	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii

29	<a href="#">d1qbjc_</a>	Alignment	not modelled	6.0	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
30	<a href="#">d2hv2a1</a>	Alignment	not modelled	6.0	21	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
31	<a href="#">c6eznE_</a>	Alignment	not modelled	5.8	55	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
32	<a href="#">c6dnsA_</a>	Alignment	not modelled	5.5	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-endofucoidanase; <b>PDBTitle:</b> endo-fucoidan hydrolase mffcna9 from glycoside hydrolase family 107
33	<a href="#">c2axtc_</a>	Alignment	not modelled	5.5	26	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> photosystem ii cp43 protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
34	<a href="#">d2axtc1</a>	Alignment	not modelled	5.5	26	<b>Fold:</b> Photosystem II antenna protein-like <b>Superfamily:</b> Photosystem II antenna protein-like <b>Family:</b> Photosystem II antenna protein-like
35	<a href="#">d1d9ea_</a>	Alignment	not modelled	5.4	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
36	<a href="#">d2rm0w1</a>	Alignment	not modelled	5.4	19	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
37	<a href="#">c6cxhC_</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> particulate methane monooxygenase, c subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylomicrobium alcaliphilum 20z
38	<a href="#">c6hb2B_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein hgh1; <b>PDBTitle:</b> structure of hgh1, crystal form i, selenomethionine derivative
39	<a href="#">c2mweA_</a>	Alignment	not modelled	5.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation regulator 1; <b>PDBTitle:</b> nmr structure of fbp28 ww2 mutant y438r, l453a dncd
40	<a href="#">c3fs2A_</a>	Alignment	not modelled	5.2	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 bruceiella melitensis at 1.85a resolution