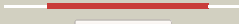
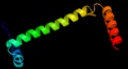

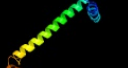
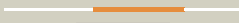
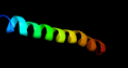





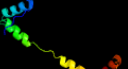



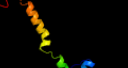











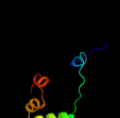





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1494_(-)_1686277_1686579
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	29d6f404eb9823ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xe3E_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase/antitoxin <b>Chain:</b> E; <b>PDB Molecule:</b> probable antitoxin maze4; <b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
2	<a href="#">c5xe3F_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase/antitoxin <b>Chain:</b> F; <b>PDB Molecule:</b> probable antitoxin maze4; <b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
3	<a href="#">c6f0kH_</a>	 Alignment		87.6	50	<b>PDB header:</b> membrane protein <b>Chain:</b> H; <b>PDB Molecule:</b> acth; <b>PDBTitle:</b> alternative complex iii
4	<a href="#">d1mnta_</a>	 Alignment		77.8	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
5	<a href="#">c6iyaD_</a>	 Alignment		76.4	25	<b>PDB header:</b> antitoxin <b>Chain:</b> D; <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
6	<a href="#">c5cegC_</a>	 Alignment		75.1	23	<b>PDB header:</b> toxin <b>Chain:</b> C; <b>PDB Molecule:</b> addiction module antidote protein, copg/arc/metj family; <b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
7	<a href="#">c2rbfB_</a>	 Alignment		58.1	34	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
8	<a href="#">c3kxeD_</a>	 Alignment		56.7	22	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
9	<a href="#">c3qoqC_</a>	 Alignment		44.3	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> C; <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
10	<a href="#">c6db1A_</a>	 Alignment		37.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative methyl-accepting chemotaxis protein; <b>PDBTitle:</b> 2.0 angstrom resolution crystal structure of n-terminal ligand-binding2 domain of putative methyl-accepting chemotaxis protein from3 salmonella enterica
11	<a href="#">d2ay0a1</a>	 Alignment		35.0	34	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like

12	<a href="#">d2hzaa1</a>	Alignment		27.0	26	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
13	<a href="#">c1u9pA</a>	Alignment		21.6	12	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
14	<a href="#">d2bj7a1</a>	Alignment		19.0	21	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
15	<a href="#">c3izoG</a>	Alignment		17.0	63	<b>PDB header:</b> viral protein <b>Chain:</b> G; <b>PDB Molecule:</b> fiber; <b>PDBTitle:</b> model of the fiber tail and its interactions with the penton base of 2 human adenovirus by cryo-electron microscopy
16	<a href="#">c1zllE</a>	Alignment		16.4	47	<b>PDB header:</b> membrane protein/signaling protein <b>Chain:</b> E; <b>PDB Molecule:</b> cardiac phospholamban; <b>PDBTitle:</b> nmr structure of unphosphorylated human phospholamban2 pentamer
17	<a href="#">c3fozB</a>	Alignment		13.1	36	<b>PDB header:</b> transferase/rna <b>Chain:</b> B; <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
18	<a href="#">c6nhwE</a>	Alignment		12.6	88	<b>PDB header:</b> immune system <b>Chain:</b> E; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
19	<a href="#">c6nhwF</a>	Alignment		12.6	88	<b>PDB header:</b> immune system <b>Chain:</b> F; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
20	<a href="#">c6nhwD</a>	Alignment		12.6	88	<b>PDB header:</b> immune system <b>Chain:</b> D; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
21	<a href="#">c6nhwA</a>	Alignment	not modelled	11.9	88	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
22	<a href="#">c6nhwB</a>	Alignment	not modelled	11.9	88	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
23	<a href="#">c4xhpA</a>	Alignment	not modelled	11.6	25	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> parm hybrid fusion protein; <b>PDBTitle:</b> bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
24	<a href="#">c6nhwC</a>	Alignment	not modelled	10.7	88	<b>PDB header:</b> immune system <b>Chain:</b> C; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
25	<a href="#">c1wixA</a>	Alignment	not modelled	10.0	31	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-actinin 4; <b>PDBTitle:</b> solution structure of the third spectrin repeat of alpha-2 actinin-4
26	<a href="#">c2p06A</a>	Alignment	not modelled	9.9	67	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein af_0060; <b>PDBTitle:</b> crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
27	<a href="#">d2p06a1</a>	Alignment	not modelled	9.9	67	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> AF0060-like
						<b>PDB header:</b> transcription

28	<a href="#">c2bj3D_</a>	Alignment	not modelled	9.8	21	<b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
29	<a href="#">d2hzab1</a>	Alignment	not modelled	9.6	26	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
30	<a href="#">d1lwma_</a>	Alignment	not modelled	9.5	12	<b>Fold:</b> HMG-box <b>Superfamily:</b> HMG-box <b>Family:</b> HMG-box
31	<a href="#">c1q5vB_</a>	Alignment	not modelled	8.6	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
32	<a href="#">c4mt0A_</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> membrane protein, tranport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mtre protein; <b>PDBTitle:</b> crystal structure of the open state of the neisseria gonorrhoeae mtre2 outer membrane channel
33	<a href="#">c3s32A_</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> set1/ash2 histone methyltransferase complex subunit ash2; <b>PDBTitle:</b> crystal structure of ash2l n-terminal domain
34	<a href="#">c6a6xC_</a>	Alignment	not modelled	7.9	57	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
35	<a href="#">c6fjwA_</a>	Alignment	not modelled	7.4	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cas6 protein; <b>PDBTitle:</b> streptococcus thermophilus cas6
36	<a href="#">c1yodA_</a>	Alignment	not modelled	7.4	60	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> water-solublized phospholamban; <b>PDBTitle:</b> crystal structure of a water soluble analog of phospholamban
37	<a href="#">c4l0kC_</a>	Alignment	not modelled	7.3	58	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> draiii; <b>PDBTitle:</b> crystal structure of a type ii restriction endonuclease
38	<a href="#">d1ryla_</a>	Alignment	not modelled	7.1	67	<b>Fold:</b> Hypothetical protein yfbM <b>Superfamily:</b> Hypothetical protein yfbM <b>Family:</b> Hypothetical protein yfbM
39	<a href="#">c6humQ_</a>	Alignment	not modelled	6.8	30	<b>PDB header:</b> proton transport <b>Chain:</b> Q: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
40	<a href="#">c2jrdA_</a>	Alignment	not modelled	6.7	47	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> influenza hemagglutinin fusion domain mutant f9a
41	<a href="#">c5ij7B_</a>	Alignment	not modelled	6.7	32	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> enhancer of zeste homolog 2 (ezh2),histone-lysine n- <b>PDBTitle:</b> structure of hs/acprc2 in complex with a pyridone inhibitor
42	<a href="#">c2ca9B_</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
43	<a href="#">c4y3uB_</a>	Alignment	not modelled	6.5	60	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cardiac phospholamban; <b>PDBTitle:</b> the structure of phospholamban bound to the calcium pump serca1a
44	<a href="#">d1i11a_</a>	Alignment	not modelled	6.5	18	<b>Fold:</b> HMG-box <b>Superfamily:</b> HMG-box <b>Family:</b> HMG-box
45	<a href="#">c2yulA_</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sox-17; <b>PDBTitle:</b> solution structure of the hmg box of human transcription2 factor sox-17
46	<a href="#">d1nz6a_</a>	Alignment	not modelled	5.9	18	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
47	<a href="#">c2cosA_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine protein kinase lats2; <b>PDBTitle:</b> solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
48	<a href="#">d2clyb1</a>	Alignment	not modelled	5.4	41	<b>Fold:</b> ATP synthase D chain-like <b>Superfamily:</b> ATP synthase D chain-like <b>Family:</b> ATP synthase D chain-like
49	<a href="#">d2cosa1</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
50	<a href="#">c2clyE_</a>	Alignment	not modelled	5.2	41	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> atp synthase d chain, mitochondrial; <b>PDBTitle:</b> subcomplex of the stator of bovine mitochondrial atp synthase