



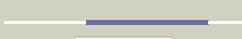
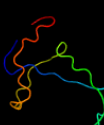

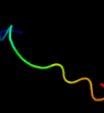

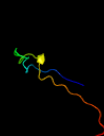





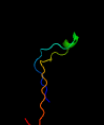



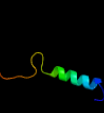



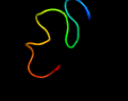
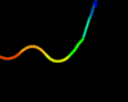



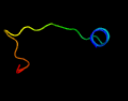



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2662_(-)_2981492_2981764
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	9eb8ce27f5d02e82

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2co5a1</a>	 Alignment		18.3	67	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> F93-like
2	<a href="#">c1z2iA_</a>	 Alignment		14.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
3	<a href="#">c2lnuA_</a>	 Alignment		13.3	29	<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 uncharacterized protein from gene locus2 rrnac0354 of haloarcula marismortui, northeast structural genomics3 consortium target hmr11
4	<a href="#">c5m0jl_</a>	 Alignment		11.2	64	<b>PDB header:</b> rna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> swi5-dependent ho expression protein 2,swi5-dependent ho <b>PDBTitle:</b> crystal structure of the cytoplasmic complex with she2p, she3p, and2 the ash1 mrna e3-localization element
5	<a href="#">c3i0pA_</a>	 Alignment		10.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from entamoeba histolytica
6	<a href="#">d2eyqa6</a>	 Alignment		10.3	43	<b>Fold:</b> TRCF domain-like <b>Superfamily:</b> TRCF domain-like <b>Family:</b> TRCF domain
7	<a href="#">c2mrba_</a>	 Alignment		9.1	43	<b>PDB header:</b> metallothionein <b>Chain:</b> A: <b>PDB Molecule:</b> cd7 metallothionein-2a; <b>PDBTitle:</b> three-dimensional structure of rabbit liver cd-72 metallothionein-2a in aqueous solution determined by3 nuclear magnetic resonance
8	<a href="#">c1wtjB_</a>	 Alignment		8.5	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ureidoglycolate dehydrogenase; <b>PDBTitle:</b> crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
9	<a href="#">d1sxma_</a>	 Alignment		7.4	50	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
10	<a href="#">c2l3oA_</a>	 Alignment		7.0	29	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin 3; <b>PDBTitle:</b> solution structure of murine interleukin 3
11	<a href="#">c1tz5A_</a>	 Alignment		6.9	56	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of pancreatic hormone and neuropeptide y; <b>PDBTitle:</b> [pnpy19-23]-hpp bound to dpc micelles

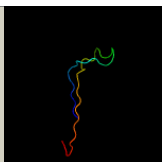
12	<a href="#">d1mtxa_</a>	Alignment		6.4	60	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
13	<a href="#">d2fyuk1</a>	Alignment		6.4	47	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
14	<a href="#">c2dezA_</a>	Alignment		6.3	50	<b>PDB header:</b> neuropeptide <b>Chain:</b> A; <b>PDB Molecule:</b> peptide yy; <b>PDBTitle:</b> structure of human pyy
15	<a href="#">c5b52B_</a>	Alignment		5.9	64	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> h-ns family protein mvat; <b>PDBTitle:</b> crystal structure of the n-terminal domain of h-ns family protein turb
16	<a href="#">c2qsrA_</a>	Alignment		5.8	30	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of c-terminal domain of transcription-repair2 coupling factor
17	<a href="#">c2bt7A_</a>	Alignment		5.8	45	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> sigma c; <b>PDBTitle:</b> structure of the c-terminal receptor-binding domain of avian reovirus2 fibre sigmac, cd crystal form
18	<a href="#">c4ol4A_</a>	Alignment		5.5	7	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
19	<a href="#">d1hlva_</a>	Alignment		5.5	60	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins

20

[c1vbiA\\_](#)



Alignment



5.5

41

**PDB header:** oxidoreductase  
**Chain:** A: **PDB Molecule:** type 2 malate/lactate dehydrogenase;  
**PDB Title:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8