
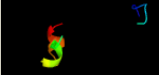


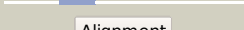

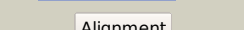

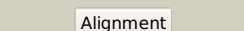





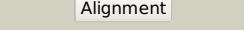

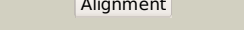

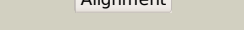

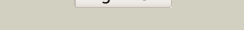



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2142A_(RVBD2142A)_2402515_2402730
Date	Mon Aug 5 13:25:26 BST 2019
Unique Job ID	3bf073104d2b65f6

Detailed template information

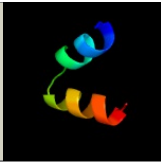
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2icya1</a>	 Alignment		33.1	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
2	<a href="#">c3terA_</a>	 Alignment		28.8	40	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mammalian stromal interaction molecule-1; <b>PDBTitle:</b> crystal structure of soar domain with inhibition helix from c. elegans
3	<a href="#">d2glia1</a>	 Alignment		26.2	58	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
4	<a href="#">d1nкта1</a>	 Alignment		21.0	32	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA <b>Family:</b> Pre-protein crosslinking domain of SecA
5	<a href="#">c3teqB_</a>	 Alignment		14.7	47	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stromal interaction molecule 1; <b>PDBTitle:</b> crystal structure of soar domain
6	<a href="#">c3ajbB_</a>	 Alignment		14.5	75	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 19; <b>PDBTitle:</b> crystal structure of human pex3p in complex with n-terminal pex19p2 peptide
7	<a href="#">d1tf5a1</a>	 Alignment		14.4	33	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA <b>Family:</b> Pre-protein crosslinking domain of SecA
8	<a href="#">d1r1ra1</a>	 Alignment		12.7	16	<b>Fold:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Superfamily:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Family:</b> R1 subunit of ribonucleotide reductase, N-terminal domain
9	<a href="#">d3ci0k1</a>	 Alignment		8.6	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like
10	<a href="#">c5w21A_</a>	 Alignment		8.3	30	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> klotho; <b>PDBTitle:</b> crystal structure of a 1:1:1 fgf23-fgfr1c-aklotho ternary complex
11	<a href="#">c2kp6A_</a>	 Alignment		6.9	19	<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 protein cv0237 from chromobacterium2 violaceum. northeast structural genomics consortium (nesg) target3 cvt1

12	<a href="#">c5ld1D_</a>	Alignment		6.1	24	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> polyphosphate:amp phosphotransferase; <b>PDBTitle:</b> crystal structure of polyphosphate kinase from meiothermus ruber bound2 to atp
13	<a href="#">c3hgkE_</a>	Alignment		6.1	35	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> effector protein hopab2; <b>PDBTitle:</b> crystal structure of effect protein avrptob complexed with2 kinase pto
14	<a href="#">d1h3na2</a>	Alignment		5.7	19	<b>Fold:</b> ValRS/IleRS/LeuRS editing domain <b>Superfamily:</b> ValRS/IleRS/LeuRS editing domain <b>Family:</b> ValRS/IleRS/LeuRS editing domain
15	<a href="#">c5aj8B_</a>	Alignment		5.5	18	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> tubulin binding cofactor c; <b>PDBTitle:</b> tubulin binding cofactor c from leishmania major
16	<a href="#">c3miwE_</a>	Alignment		5.5	57	<b>PDB header:</b> viral protein <b>Chain:</b> E; <b>PDB Molecule:</b> non-structural glycoprotein 4; <b>PDBTitle:</b> crystal structure of rotavirus nsp4
17	<a href="#">c6aqeB_</a>	Alignment		5.4	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> molecule a; <b>PDBTitle:</b> crystal structure of ppk2 in complex with mg atp
18	<a href="#">c3r1rB_</a>	Alignment		5.3	14	<b>PDB header:</b> complex (oxidoreductase/peptide) <b>Chain:</b> B; <b>PDB Molecule:</b> ribonucleotide reductase r1 protein; <b>PDBTitle:</b> ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli

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[c6mcjA](#)

Alignment



5.3

27

**PDB header:**protein binding

**Chain:** A: **PDB Molecule:**orange carotenoid-binding protein;  
**PDB Title:** structure of helical carotenoid protein 2 from fremyella diplosiphon