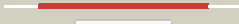
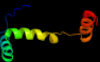



















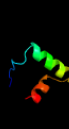

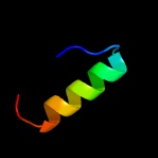




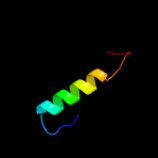
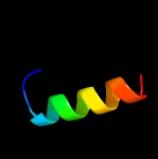
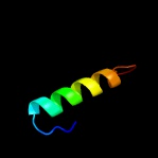


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0064A\_(RVBD0064A)\_71586\_71825  
 Date Tue Jul 23 14:50:09 BST 2019  
 Unique Job ID 9c71d2c7b408b9af

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2h1oH_</a>	 Alignment		95.1	30	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H: <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
2	<a href="#">d2bsqe1</a>	 Alignment		95.0	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Trafficking protein A-like
3	<a href="#">c3h87D_</a>	 Alignment		57.6	35	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	<a href="#">c5z1nA_</a>	 Alignment		20.7	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> g-protein interacting protein 1; <b>PDBTitle:</b> crystal structure of c terminal region of g-protein interacting2 protein 1 (gip1) from dictyostelium discoideum
5	<a href="#">c4gehB_</a>	 Alignment		16.8	61	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mst4; <b>PDBTitle:</b> crystal structure of mst4 dimerization domain complex with pdcd10
6	<a href="#">c3w8hB_</a>	 Alignment		15.5	61	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 25; <b>PDBTitle:</b> crystal structure of ccm3 in complex with the c-terminal regulatory2 domain of stk25
7	<a href="#">d1mgra_</a>	 Alignment		14.9	16	<b>Fold:</b> Microbial ribonucleases <b>Superfamily:</b> Microbial ribonucleases <b>Family:</b> Bacterial ribonucleases
8	<a href="#">d1pyla_</a>	 Alignment		14.5	21	<b>Fold:</b> Microbial ribonucleases <b>Superfamily:</b> Microbial ribonucleases <b>Family:</b> Bacterial ribonucleases
9	<a href="#">c1b9qA_</a>	 Alignment		12.1	41	<b>PDB header:</b> collagen facit xiv <b>Chain:</b> A: <b>PDB Molecule:</b> protein (collagen alpha 1); <b>PDBTitle:</b> nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
10	<a href="#">c1b9pA_</a>	 Alignment		12.0	41	<b>PDB header:</b> collagen facit xiv <b>Chain:</b> A: <b>PDB Molecule:</b> protein (collagen alpha 1); <b>PDBTitle:</b> nmr structure of heparin binding site of non collagenous2 domain i (nc1) of collagen facit xiv
11	<a href="#">c2k5jB_</a>	 Alignment		11.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1

12	<a href="#">c2wttL_</a>	Alignment		11.5	41	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> tumor protein p73; <b>PDBTitle:</b> structure of the human p73 tetramerization domain (crystal form ii)
13	<a href="#">d1ofux_</a>	Alignment		8.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Bacterial cell division inhibitor SulA
14	<a href="#">c1oftC_</a>	Alignment		8.6	27	<b>PDB header:</b> bacterial cell division inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein pa3008; <b>PDBTitle:</b> crystal structure of sula from pseudomonas aeruginosa
15	<a href="#">c3zy1A_</a>	Alignment		8.2	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tumor protein 63; <b>PDBTitle:</b> crystal structure of the human p63 tetramerization domain
16	<a href="#">c4d1mE_</a>	Alignment		8.2	41	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> tetramerization domain of zebrafish p53 (crystal form ii)
17	<a href="#">c4a9zD_</a>	Alignment		7.7	35	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> tumor protein 63; <b>PDBTitle:</b> crystal structure of human p63 tetramerization domain
18	<a href="#">d1ulza1</a>	Alignment		7.4	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
19	<a href="#">c5hobB_</a>	Alignment		7.4	41	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tumor protein p73; <b>PDBTitle:</b> p73 homo-tetramerization domain mutant i
20	<a href="#">d1w96c1</a>	Alignment		7.3	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
21	<a href="#">c1kjkA_</a>	Alignment	not modelled	7.0	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution structure of the lambda integrase amino-terminal2 domain
22	<a href="#">d1z1ba1</a>	Alignment	not modelled	7.0	50	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> lambda integrase N-terminal domain
23	<a href="#">c2bw2A_</a>	Alignment	not modelled	6.8	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bypass of forespore c; <b>PDBTitle:</b> bofc from bacillus subtilis
24	<a href="#">c3kwvF_</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> toxin/protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> lethal factor; <b>PDBTitle:</b> structural basis for the unfolding of anthrax lethal factor by2 protective antigen oligomers
25	<a href="#">c4a9zC_</a>	Alignment	not modelled	6.3	35	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> tumor protein 63; <b>PDBTitle:</b> crystal structure of human p63 tetramerization domain
26	<a href="#">d1j7na1</a>	Alignment	not modelled	5.7	36	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Anthrax toxin lethal factor, N- and C-terminal domains
27	<a href="#">d1zl8a1</a>	Alignment	not modelled	5.5	20	<b>Fold:</b> L27 domain <b>Superfamily:</b> L27 domain <b>Family:</b> L27 domain
28	<a href="#">c4uzxA_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein tho1; <b>PDBTitle:</b> high-resolution nmr structures of the domains of saccharomyces2 cerevisiae tho1