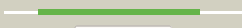
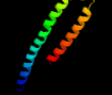

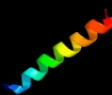



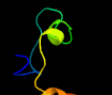



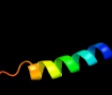











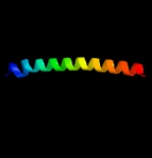
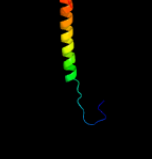
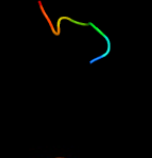

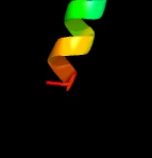
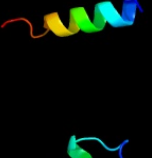

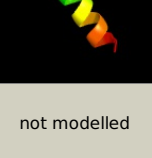


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1174c_(TB8.4)_1305674_1306006
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	ee86ad3944a52f81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4clvB_</a>	 Alignment		53.5	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
2	<a href="#">c2n2aA_</a>	 Alignment		50.5	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2; <b>PDBTitle:</b> spatial structure of her2/erbB2 dimeric transmembrane domain in the presence of cytoplasmic juxtamembrane domains
3	<a href="#">d1g7da_</a>	 Alignment		44.0	23	<b>Fold:</b> ERP29 C domain-like <b>Superfamily:</b> ERP29 C domain-like <b>Family:</b> ERP29 C domain-like
4	<a href="#">c1vw4a_</a>	 Alignment		38.4	23	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
5	<a href="#">c5k57A_</a>	 Alignment		27.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ddi1 homolog 2; <b>PDBTitle:</b> hdd domain from human ddi2
6	<a href="#">c5xnlX_</a>	 Alignment		24.9	46	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem ii reaction center protein x; <b>PDBTitle:</b> structure of stacked c2s2m2-type psii-lhcii supercomplex from pism2 sativum
7	<a href="#">d2c0ga1</a>	 Alignment		24.2	19	<b>Fold:</b> ERP29 C domain-like <b>Superfamily:</b> ERP29 C domain-like <b>Family:</b> ERP29 C domain-like
8	<a href="#">c3jcuX_</a>	 Alignment		20.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem ii reaction center x protein; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom resolution
9	<a href="#">c3jcuX_</a>	 Alignment		20.2	39	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem ii reaction center x protein; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom resolution
10	<a href="#">d1kbbB_</a>	 Alignment		17.0	33	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
11	<a href="#">c1zhcA_</a>	 Alignment		14.9	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hp1242; <b>PDBTitle:</b> solution structure of hp1242 from helicobacter pylori

12	<a href="#">c3mayE_</a>	Alignment		14.0	14	<b>PDB header:</b> heme-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> possible exported protein; <b>PDBTitle:</b> crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
13	<a href="#">c4cvoA_</a>	Alignment		13.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna excision repair protein ercc-6; <b>PDBTitle:</b> crystal structure of the n-terminal colled-coil domain of human dna2 excision repair protein ercc-6
14	<a href="#">c5frgA_</a>	Alignment		13.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
15	<a href="#">c2mnsA_</a>	Alignment		12.4	78	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane fusion protein p15; <b>PDBTitle:</b> solution nmr structure of the reovirus p15 fusion-associated small2 transmembrane (fast) protein fusion-inducing lipid packing sensor3 (flips) motif in dodecyl phosphocholine (dpc) micelles
16	<a href="#">c1tqeY_</a>	Alignment		10.0	38	<b>PDB header:</b> transcription/protein binding/dna <b>Chain:</b> Y: <b>PDB Molecule:</b> histone deacetylase 9; <b>PDBTitle:</b> mechanism of recruitment of class ii histone deacetylases by myocyte2 enhancer factor-2
17	<a href="#">c1tqeX_</a>	Alignment		10.0	38	<b>PDB header:</b> transcription/protein binding/dna <b>Chain:</b> X: <b>PDB Molecule:</b> histone deacetylase 9; <b>PDBTitle:</b> mechanism of recruitment of class ii histone deacetylases by myocyte2 enhancer factor-2
18	<a href="#">c2kaxA_</a>	Alignment		10.0	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein s100-a5; <b>PDBTitle:</b> solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states
19	<a href="#">c2l9vA_</a>	Alignment		9.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing factor 40 homolog a; <b>PDBTitle:</b> nmr structure of the ff domain l24a mutant's folding transition state
20	<a href="#">d1a4pa_</a>	Alignment		9.4	22	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
21	<a href="#">c5nr5A_</a>	Alignment	not modelled	9.2	53	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mata protein; <b>PDBTitle:</b> nmr structure and 1h, 13c and 15n signal assignments for dictyostelium2 discoideum mata protein
22	<a href="#">d1e8aa_</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
23	<a href="#">c5j1hB_</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> plectin,plectin; <b>PDBTitle:</b> structure of the spectrin repeats 5 and 6 of the plakin domain of2 plectin
24	<a href="#">c5furK_</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 6; <b>PDBTitle:</b> structure of human tfiid-iiia bound to core promoter dna
25	<a href="#">c2llvA_</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein sti1; <b>PDBTitle:</b> solution structure of the yeast sti1 dp1 domain
26	<a href="#">d1zfsa1</a>	Alignment	not modelled	7.1	28	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
27	<a href="#">d1wd3a1</a>	Alignment	not modelled	6.9	52	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Alpha-L-arabinofuranosidase B, N-terminal domain
28	<a href="#">c5nr6A_</a>	Alignment	not modelled	6.9	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> matb protein; <b>PDBTitle:</b> nmr structure and 1h, 13c and 15n signal assignments for dictyostelium2 discoidans matb protein s71a mutant
						<b>PDB header:</b> hydrolase

29	<a href="#">c2yegA</a>	Alignment	not modelled	6.8	67	<b>Chain:</b> A; <b>PDB Molecule:</b> alkaline phosphatase d; <b>PDBTitle:</b> structure of phod
30	<a href="#">d1hya1</a>	Alignment	not modelled	6.6	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Fumarylacetoacetate hydrolase, FAH, N-terminal domain <b>Family:</b> Fumarylacetoacetate hydrolase, FAH, N-terminal domain
31	<a href="#">c2f49C</a>	Alignment	not modelled	6.5	41	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> ste5 peptide; <b>PDBTitle:</b> crystal structure of fus3 in complex with a ste5 peptide
32	<a href="#">c2ke4A</a>	Alignment	not modelled	6.2	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
33	<a href="#">c3eabK</a>	Alignment	not modelled	5.9	60	<b>PDB header:</b> cell cycle <b>Chain:</b> K; <b>PDB Molecule:</b> chmp1b; <b>PDBTitle:</b> crystal structure of spastin mit in complex with escrt iii
34	<a href="#">d1ksoa</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> S100 proteins
35	<a href="#">c4uetA</a>	Alignment	not modelled	5.7	28	<b>PDB header:</b> retinol-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> nematode fatty acid retinoid binding protein; <b>PDBTitle:</b> diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
36	<a href="#">c2y5iF</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> metal-binding protein <b>Chain:</b> F; <b>PDB Molecule:</b> s100 calcium binding protein z; <b>PDBTitle:</b> s100z from zebrafish in complex with calcium
37	<a href="#">c6iczX</a>	Alignment	not modelled	5.4	44	<b>PDB header:</b> splicing <b>Chain:</b> X; <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
38	<a href="#">c2d44A</a>	Alignment	not modelled	5.4	52	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-l-arabinofuranosidase b; <b>PDBTitle:</b> crystal structure of arabinofuranosidase complexed with2 arabinofuranosyl-alpha-1,2-xylobiose
39	<a href="#">c1odpA</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
40	<a href="#">c1odqA</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
41	<a href="#">c1odrA</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40