


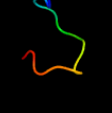

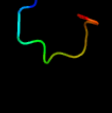
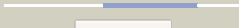



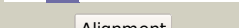
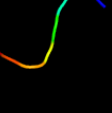
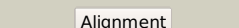

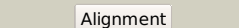
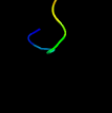
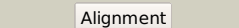
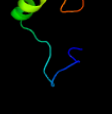









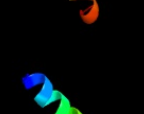


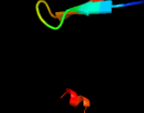


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1052_(-)_1175728_1176117
Date	Wed Jul 31 22:05:12 BST 2019
Unique Job ID	44471d4e32449842

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3nw0B_</a>	 Alignment		23.0	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> melanoma-associated antigen g1; <b>PDBTitle:</b> crystal structure of mageg1 and nse1 complex
2	<a href="#">c1dmeA_</a>	 Alignment		21.7	57	<b>PDB header:</b> metallothionein <b>Chain:</b> A: <b>PDB Molecule:</b> cd6 metallothionein-1; <b>PDBTitle:</b> the three-dimensional solution structure of callinectes2 sapidus metallothionein-i determined by homonuclear and3 heteronuclear magnetic resonance spectroscopy
3	<a href="#">c1dmfA_</a>	 Alignment		20.7	57	<b>PDB header:</b> metallothionein <b>Chain:</b> A: <b>PDB Molecule:</b> cd6 metallothionein-1; <b>PDBTitle:</b> the three-dimensional solution structure of callinectes2 sapidus metallothionein-i determined by homonuclear and3 heteronuclear magnetic resonance spectroscopy
4	<a href="#">c2wa0A_</a>	 Alignment		20.3	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> melanoma-associated antigen 4; <b>PDBTitle:</b> crystal structure of the human magea4
5	<a href="#">c6c62D_</a>	 Alignment		19.6	41	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atzg; <b>PDBTitle:</b> an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme.
6	<a href="#">c1xdyC_</a>	 Alignment		17.4	75	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> bacterial sulfite oxidase; <b>PDBTitle:</b> structural and biochemical identification of a novel2 bacterial oxidoreductase, w-containing cofactor
7	<a href="#">d1xdya_</a>	 Alignment		17.3	100	<b>Fold:</b> Oxidoreductase molybdopterin-binding domain <b>Superfamily:</b> Oxidoreductase molybdopterin-binding domain <b>Family:</b> Oxidoreductase molybdopterin-binding domain
8	<a href="#">d1jmab2</a>	 Alignment		15.6	58	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
9	<a href="#">c3ulxA_</a>	 Alignment		13.1	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> stress-induced transcription factor nac1; <b>PDBTitle:</b> crystal structural of the conserved domain of rice stress-responsive2 nac1
10	<a href="#">c6dmxE_</a>	 Alignment		12.7	52	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> bzip factor; <b>PDBTitle:</b> hbz56 in complex with kix and c-myb
11	<a href="#">c6mzIS_</a>	 Alignment		12.1	30	<b>PDB header:</b> transcription <b>Chain:</b> S: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 13; <b>PDBTitle:</b> human tfiid canonical state

12	<a href="#">d1bh9a_</a>	Alignment		12.1	30	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
13	<a href="#">d1dpua_</a>	Alignment		11.9	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of RPA32
14	<a href="#">c1dpuA_</a>	Alignment		11.9	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
15	<a href="#">c6dnqE_</a>	Alignment		11.8	52	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> bzip factor; <b>PDBTitle:</b> hbz77 in complex with kix and c-myb
16	<a href="#">c6n7xH_</a>	Alignment		11.5	28	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> H: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein component snu71; <b>PDBTitle:</b> s. cerevisiae u1 snrnp
17	<a href="#">c6dmxj_</a>	Alignment		11.0	52	<b>PDB header:</b> transcription <b>Chain:</b> J: <b>PDB Molecule:</b> bzip factor; <b>PDBTitle:</b> hbz56 in complex with kix and c-myb
18	<a href="#">d1xwdb1</a>	Alignment		10.6	30	<b>Fold:</b> Cystine-knot cytokines <b>Superfamily:</b> Cystine-knot cytokines <b>Family:</b> Gonadotropin/Follitropin
19	<a href="#">d1cta1</a>	Alignment		9.7	67	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
20	<a href="#">c4d9gA_</a>	Alignment		9.3	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diaminopropionate ammonia-lyase; <b>PDBTitle:</b> crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
21	<a href="#">c1dgiA_</a>	Alignment	not modelled	9.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidoreductase; <b>PDBTitle:</b> crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
22	<a href="#">d1rp3a1</a>	Alignment	not modelled	8.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma3 domain
23	<a href="#">c6et6A_</a>	Alignment	not modelled	8.6	19	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> crystal structure of muramidase from acinetobacter baumannii ab 5075uw2 prophage
24	<a href="#">d176la_</a>	Alignment	not modelled	8.3	27	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage lysozyme
25	<a href="#">c3h36A_</a>	Alignment	not modelled	8.2	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> structure of an uncharacterized domain in polyribonucleotide2 nucleotidyltransferase from streptococcus mutans ua159
26	<a href="#">c1qfwB_</a>	Alignment	not modelled	8.1	36	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> gonadotrophin beta subunit; <b>PDBTitle:</b> ternary complex of human chorionic gonadotropin with fv anti alpha2 subunit and fv anti beta subunit
27	<a href="#">d1zxia1</a>	Alignment	not modelled	8.0	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
28	<a href="#">d1hcnb_</a>	Alignment	not modelled	8.0	36	<b>Fold:</b> Cystine-knot cytokines <b>Superfamily:</b> Cystine-knot cytokines <b>Family:</b> Gonadotropin/Follitropin

29	<a href="#">d2h7aa1</a>	Alignment	not modelled	7.8	30	<b>Fold:</b> Ycgl-like <b>Superfamily:</b> Ycgl-like <b>Family:</b> Ycgl-like
30	<a href="#">c2xl1A</a>	Alignment	not modelled	7.8	44	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> arginine attenuator peptide; <b>PDBTitle:</b> structural basis of translational stalling by human cytomegalovirus2 (hcmv) and fungal arginine attenuator peptide (aap)
31	<a href="#">c6g90J</a>	Alignment	not modelled	7.7	29	<b>PDB header:</b> splicing <b>Chain:</b> J: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein component snu71; <b>PDBTitle:</b> prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
32	<a href="#">c3hdfA</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> crystal structure of truncated endolysin r21 from phage 21
33	<a href="#">c2k9oA</a>	Alignment	not modelled	6.9	42	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> vm24 scorpion toxin; <b>PDBTitle:</b> solution structure of vm24 synthetic scorpion toxin
34	<a href="#">c3ebnD</a>	Alignment	not modelled	6.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
35	<a href="#">c2ewtA</a>	Alignment	not modelled	6.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of the dna-binding domain of bldd
36	<a href="#">d1jroa1</a>	Alignment	not modelled	6.7	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
37	<a href="#">c2lo9A</a>	Alignment	not modelled	6.6	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> mu-conotoxin buiiib; <b>PDBTitle:</b> nmr solution structure of mu-conotoxin buiiib
38	<a href="#">d1ffva1</a>	Alignment	not modelled	6.6	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
39	<a href="#">c2locA</a>	Alignment	not modelled	6.5	37	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> mu-conotoxin buiiib; <b>PDBTitle:</b> conotoxin analogue [d-ala2]buiiib
40	<a href="#">d1lxja</a>	Alignment	not modelled	6.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
41	<a href="#">c2y35A</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ld22664p; <b>PDBTitle:</b> crystal structure of xrn1-substrate complex
42	<a href="#">c2ef8A</a>	Alignment	not modelled	6.3	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
43	<a href="#">d1vlba1</a>	Alignment	not modelled	6.2	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
44	<a href="#">c2pl9D</a>	Alignment	not modelled	6.1	88	<b>PDB header:</b> signaling protien <b>Chain:</b> D: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
45	<a href="#">c2pl9F</a>	Alignment	not modelled	6.0	88	<b>PDB header:</b> signaling protien <b>Chain:</b> F: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
46	<a href="#">c2pl9E</a>	Alignment	not modelled	6.0	88	<b>PDB header:</b> signaling protien <b>Chain:</b> E: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
47	<a href="#">d1n62a1</a>	Alignment	not modelled	6.0	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
48	<a href="#">d1rm6c1</a>	Alignment	not modelled	6.0	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
49	<a href="#">c5u1dX</a>	Alignment	not modelled	5.9	64	<b>PDB header:</b> transport protein <b>Chain:</b> X: <b>PDB Molecule:</b> tap transporter inhibitor icp47; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
50	<a href="#">c3pifD</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'->3' exoribonuclease (xrn1); <b>PDBTitle:</b> crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
51	<a href="#">d1dgja1</a>	Alignment	not modelled	5.5	57	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
52	<a href="#">c1jleC</a>	Alignment	not modelled	5.4	24	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> troponin i; <b>PDBTitle:</b> crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
53	<a href="#">c2fhoA</a>	Alignment	not modelled	5.4	48	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> spliceosomal protein sf3b155; <b>PDBTitle:</b> nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
54	<a href="#">c1ytzl</a>	Alignment	not modelled	5.4	32	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> troponin i; <b>PDBTitle:</b> crystal structure of skeletal muscle troponin in the ca2+2 activated state
						<b>Fold:</b> CO dehydrogenase ISP C-domain like

55	<a href="#">d1v97a1</a>	Alignment	not modelled	5.3	71	<b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
56	<a href="#">c2i3tf_</a>	Alignment	not modelled	5.2	41	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> spindle assembly checkpoint component; <b>PDBTitle:</b> bub3 complex with mad3 (bubr1) glebs motif