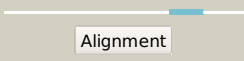

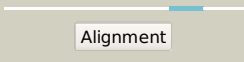

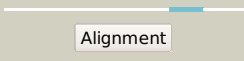

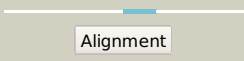
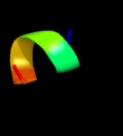
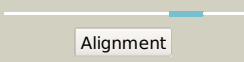

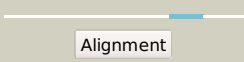

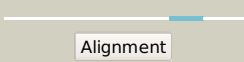
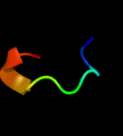
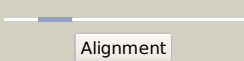

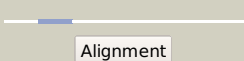

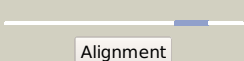
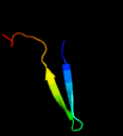
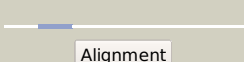
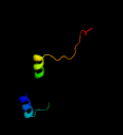











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0311 (-) _379172_380401
Date	Tue Jul 23 14:50:37 BST 2019
Unique Job ID	ed270a2e4e77ec5f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2is9A_	 Alignment		38.6	18	PDB header: transcription Chain: A; PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
2	c5v89A_	 Alignment		37.1	45	PDB header: ligase / protein binding Chain: A; PDB Molecule: dcn1-like protein 4; PDBTitle: structure of dcn4 pony domain bound to cul1 whb
3	c4gbaA_	 Alignment		36.4	45	PDB header: ligase/peptide Chain: A; PDB Molecule: dcn1-like protein 3; PDBTitle: dcn1 complex with n-terminally acetylated nedd8 e2 peptide
4	c1wqeA_	 Alignment		34.4	57	PDB header: toxin Chain: A; PDB Molecule: omtx3; PDBTitle: an unusual fold for potassium channel blockers: nmr structure of three toxins from the scorpion opisthacanthus3 madagascariensis
5	c4gaoA_	 Alignment		33.9	36	PDB header: ligase/peptide Chain: A; PDB Molecule: dcn1-like protein 2; PDBTitle: dcn1 complex with n-terminally acetylated nedd8 e2 peptide
6	c3bq3A_	 Alignment		33.7	18	PDB header: cell cycle, ligase Chain: A; PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
7	c5v88A_	 Alignment		33.0	36	PDB header: ligase / protein binding Chain: A; PDB Molecule: lysozyme,dcn1-like protein 1; PDBTitle: structure of dcn1 bound to nacm-cov
8	d2cb5a_	 Alignment		26.7	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Papain-like
9	c2pjpA_	 Alignment		26.5	13	PDB header: translation/rna Chain: A; PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
10	c4l6tB_	 Alignment		24.9	35	PDB header: hydrolase Chain: B; PDB Molecule: ecxb; PDBTitle: gm1 bound form of the ecx ab5 holotoxin
11	c4k7cA_	 Alignment		24.8	21	PDB header: hydrolase Chain: A; PDB Molecule: aminopeptidase c; PDBTitle: crystal structure of pepw from lactobacillus rhamnosis hn001 (dr20)2 determined as the selenomet derivative

12	c1gngY	Alignment		24.6	58	PDB header: transferase Chain: Y; PDB Molecule: frattide; PDBTitle: glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
13	c1gngX	Alignment		24.6	58	PDB header: transferase Chain: X; PDB Molecule: frattide; PDBTitle: glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
14	c3bwwA	Alignment		24.3	37	PDB header: metal binding protein Chain: A; PDB Molecule: protein of unknown function duf692/cog3220; PDBTitle: crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
15	c3zrmX	Alignment		23.0	58	PDB header: transferase/peptide Chain: X; PDB Molecule: proto-oncogene frat1; PDBTitle: identification of 2-(4-pyridyl)thienopyridinones as gsk-2 3beta inhibitors
16	c3zrlX	Alignment		23.0	58	PDB header: transferase/peptide Chain: X; PDB Molecule: proto-oncogene frat1; PDBTitle: identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
17	c5oy4Y	Alignment		22.8	58	PDB header: transferase Chain: Y; PDB Molecule: proto-oncogene frat1; PDBTitle: gsk3beta complex with n-(6-(3,4-dihydroxyphenyl)-1h-pyrazolo[3,4-2 b]pyridin-3-yl)acetamide
18	c3zrkX	Alignment		22.8	58	PDB header: transferase/peptide Chain: X; PDB Molecule: proto-oncogene frat1; PDBTitle: identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
19	c1wx4B	Alignment		21.9	55	PDB header: oxidoreductase/metal transport Chain: B; PDB Molecule: melc; PDBTitle: crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a cddie protein3 prepared by the addition of dithiothreitol
20	c3o0lB	Alignment		20.9	20	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
21	c1wqcA	Alignment	not modelled	20.3	86	PDB header: toxin Chain: A; PDB Molecule: omtx1; PDBTitle: an unusual fold for potassium channel blockers : nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
22	d1ukfa	Alignment	not modelled	20.0	45	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Avirulence protein Avrpph3
23	d1v1ha1	Alignment	not modelled	19.1	78	Fold: Triple beta-spiral Superfamily: Fibre shaft of virus attachment proteins Family: Adenovirus
24	c3uuuA	Alignment	not modelled	18.3	9	PDB header: hydrolase Chain: A; PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
25	c1lrjG	Alignment	not modelled	17.8	17	PDB header: metal binding protein Chain: G; PDB Molecule: migration inhibitory factor-related protein 14; PDBTitle: crystal structure of the mrp14 complexed with chaps
26	c5lslF	Alignment	not modelled	16.9	19	PDB header: rna binding domain Chain: F; PDB Molecule: cold sensitive u2 snrna suppressor 1; PDBTitle: crystal structure of yeast hsh49p in complex with cus1p binding2 domain.
27	c1wqdA	Alignment	not modelled	16.1	86	PDB header: toxin Chain: A; PDB Molecule: omtx2; PDBTitle: an unusual fold for potassium channel blockers: nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
28	c1fuiB	Alignment	not modelled	15.9	29	PDB header: isomerase Chain: B; PDB Molecule: l-fucose isomerase; PDBTitle: l-fucose isomerase from escherichia coli

29	c2kdkA_	Alignment	not modelled	15.3	9	PDB header: transcription regulator Chain: A: PDB Molecule: aryl hydrocarbon receptor nuclear translocator-like protein PDBTitle: structure of human circadian clock protein bmal2 c-terminal pas domain
30	c4wiuA_	Alignment	not modelled	14.7	25	PDB header: lyase,transferase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase [gtp]; PDBTitle: crystal structure of pepck (rv0211) from mycobacterium tuberculosis in2 complex with oxalate and mn2+
31	c4xb6E_	Alignment	not modelled	14.6	9	PDB header: transferase Chain: E: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-triphosphate synthase PDBTitle: structure of the e. coli c-p lyase core complex
32	c2dqbB_	Alignment	not modelled	14.6	32	PDB header: hydrolase, dna binding protein Chain: B: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase, putative; PDBTitle: crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dtgp triphosphohydrolase
33	d1k8ua_	Alignment	not modelled	14.5	21	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
34	d1olza3	Alignment	not modelled	14.5	71	Fold: Trefoil/Plexin domain-like Superfamily: Plexin repeat Family: Plexin repeat
35	c4gioA_	Alignment	not modelled	14.0	19	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of campylobacter jejuni cj0090
36	c5lxyH_	Alignment	not modelled	13.6	19	PDB header: rna binding protein Chain: H: PDB Molecule: zinc finger cchc domain-containing protein 8; PDBTitle: structure of the minimal rbm7 - zcchc8 complex
37	d1pjqa3	Alignment	not modelled	13.1	24	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
38	c5e97B_	Alignment	not modelled	12.5	35	PDB header: hydrolase Chain: B: PDB Molecule: heparanase; PDBTitle: glycoside hydrolase ligand structure 1
39	c5b7wB_	Alignment	not modelled	12.1	43	PDB header: unknown function Chain: B: PDB Molecule: upf0234 protein xc_3703; PDBTitle: crystal structure of the yajq-family protein xc_3703 from xanthomonas2 campestris pv.campestris
40	c3c0vC_	Alignment	not modelled	12.0	13	PDB header: plant protein Chain: C: PDB Molecule: cytokinin-specific binding protein; PDBTitle: crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12
41	d1in0a2	Alignment	not modelled	12.0	50	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
42	d1tgoa2	Alignment	not modelled	11.9	36	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
43	c3kf6B_	Alignment	not modelled	11.8	21	PDB header: structural protein Chain: B: PDB Molecule: protein ten1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex
44	c2i7xA_	Alignment	not modelled	11.8	22	PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p)
45	d2i7xa1	Alignment	not modelled	11.8	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
46	c3kevA_	Alignment	not modelled	11.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galieria sulfuraria dcun1 domain-containing protein; PDBTitle: x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria
47	d3chbd_	Alignment	not modelled	11.2	30	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
48	c5syrA_	Alignment	not modelled	11.2	20	PDB header: hydrolase Chain: A: PDB Molecule: probable atp synthase spa1/mxib; PDBTitle: crystal structure of atpase delta1-79 spa47 r350a
49	c6qppA_	Alignment	not modelled	11.0	33	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
50	c5sy5B_	Alignment	not modelled	11.0	13	PDB header: transcription Chain: B: PDB Molecule: neuronal pas domain-containing protein 1; PDBTitle: crystal structure of the heterodimeric npas1-arnt complex
51	c5mntD_	Alignment	not modelled	10.7	19	PDB header: rna binding protein Chain: D: PDB Molecule: aa2 maturation protein; PDBTitle: bacteriophage qbeta maturation protein
52	c4c22B_	Alignment	not modelled	10.7	11	PDB header: isomerase Chain: B: PDB Molecule: l-fucose isomerase; PDBTitle: l-fucose isomerase in complex with fucose
53	d1xk4a1	Alignment	not modelled	10.5	17	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
54	c3zdkA_	Alignment	not modelled	10.5	44	PDB header: hydrolase Chain: A: PDB Molecule: 5' exonuclease apollo; PDBTitle: crystal structure of human 5' exonuclease apollo

55	d1ltrd_	Alignment	not modelled	10.1	30	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
56	c1v1cA_	Alignment	not modelled	10.0	29	PDB header: sh3-domain Chain: A: PDB Molecule: obscurin; PDBTitle: solution structure of the sh3 domain of obscurin
57	d2es7a1	Alignment	not modelled	9.6	40	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like
58	c1in0B_	Alignment	not modelled	9.6	50	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
59	c1i3aA_	Alignment	not modelled	9.4	50	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: rnase hii from archaeoglobus fulgidus with cobalt hexamine2 chloride
60	d1i39a_	Alignment	not modelled	9.4	50	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
61	d2ctsa_	Alignment	not modelled	9.3	27	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
62	d1khba1	Alignment	not modelled	9.2	25	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: PEP carboxykinase C-terminal domain
63	c2ycbA_	Alignment	not modelled	9.1	67	PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor; PDBTitle: structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermotrophicus
64	c4zyeA_	Alignment	not modelled	9.1	35	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfobolus solfataricus o6-methylguanine2 methyltransferase
65	c2apoA_	Alignment	not modelled	8.9	19	PDB header: isomerase/rna binding protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of the methanococcus jannaschii cbf52 nop10 complex
66	c1t39A_	Alignment	not modelled	8.9	35	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
67	c2vwkA_	Alignment	not modelled	8.8	36	PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
68	c2xr1B_	Alignment	not modelled	8.8	56	PDB header: hydrolase Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
69	c5gw8A_	Alignment	not modelled	8.7	9	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
70	c2fe3B_	Alignment	not modelled	8.7	24	PDB header: dna binding protein Chain: B: PDB Molecule: peroxide operon regulator; PDBTitle: the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
71	c3eerA_	Alignment	not modelled	8.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein, putative; PDBTitle: high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
72	d1vsra_	Alignment	not modelled	8.4	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
73	d1csca_	Alignment	not modelled	8.3	28	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
74	c3vn5A_	Alignment	not modelled	8.3	50	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hiii; PDBTitle: crystal structure of aquifex aeolicus rnase h3
75	c4py5A_	Alignment	not modelled	8.2	50	PDB header: hydrolase/dna/rna Chain: A: PDB Molecule: ribonuclease; PDBTitle: thermovibrio ammonificans rnase h3 in complex with 19-mer rna/dna
76	c3qacA_	Alignment	not modelled	8.2	10	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin seed storage protein; PDBTitle: structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
77	c5mjrA_	Alignment	not modelled	8.2	33	PDB header: photosynthesis Chain: A: PDB Molecule: protein thf1; PDBTitle: structure of psb29 at 1.55a
78	d1y6da_	Alignment	not modelled	8.2	7	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Phosphorelay protein luxU
79	c4lb6B_	Alignment	not modelled	8.2	50	PDB header: transferase/dna Chain: B: PDB Molecule: protein kinase containing z-dna binding domains; PDBTitle: crystal structure of pkz alpha in complex with ds(cg)6

						(tetragonal2 form)
80	c3afcB	Alignment	not modelled	7.9	43	PDB header: signaling protein Chain: B; PDB Molecule: semaphorin-6a; PDBTitle: mouse semaphorin 6a extracellular domain
81	d2apoa2	Alignment	not modelled	7.9	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
82	c5ua7A	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb2; PDBTitle: ocellatin-lb2, solution structure in sds micelle by nmr spectroscopy
83	c5u9rA	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb2; PDBTitle: ocellatin-lb2, solution structure in tfe by nmr spectroscopy
84	c5u9xA	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-k1; PDBTitle: ocellatin-lb2
85	c5u9qA	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1
86	c5u9vA	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1, solution structure in dpc micelle by nmr spectroscopy
87	c5ua6A	Alignment	not modelled	7.8	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1, solution structure in sds micelle by nmr spectroscopy
88	c5ua8A	Alignment	not modelled	7.7	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-f1; PDBTitle: ocellatin-f1, solution structure in sds micelle by nmr spectroscopy
89	c5u9yA	Alignment	not modelled	7.7	46	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-k1; PDBTitle: ocellatin-f1
90	c3kscD	Alignment	not modelled	7.7	12	PDB header: plant protein Chain: D; PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
91	c4bhCA	Alignment	not modelled	7.7	41	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r37l variant
92	c3qsqA	Alignment	not modelled	7.7	22	PDB header: viral protein Chain: A; PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the human astrovirus2 capsid protein
93	c2p3fN	Alignment	not modelled	7.6	67	PDB header: hydrolase Chain: N; PDB Molecule: anti-coagulant protein 5; PDBTitle: crystal structure of the factor xa/nap5 complex
94	c2qnfB	Alignment	not modelled	7.5	18	PDB header: hydrolase/dna Chain: B; PDB Molecule: recombination endonuclease vii; PDBTitle: crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
95	c2o8hA	Alignment	not modelled	7.5	15	PDB header: hydrolase Chain: A; PDB Molecule: phosphodiesterase-10a; PDBTitle: crystal structure of the catalytic domain of rat phosphodiesterase 10a
96	d1e8aa	Alignment	not modelled	7.4	25	Fold: EF Hand-like Superfamily: EF-hand Family: S100 proteins
97	c1ye9E	Alignment	not modelled	7.4	14	PDB header: oxidoreductase Chain: E; PDB Molecule: catalase hpII; PDBTitle: crystal structure of proteolytically truncated catalase2 hpII from e. coli
98	d2aega1	Alignment	not modelled	7.3	35	Fold: BB1717-like Superfamily: BB1717-like Family: BB1717-like
99	c2aegA	Alignment	not modelled	7.3	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein agr_pat_140; PDBTitle: x-ray crystal structure of protein atu5096 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr63.