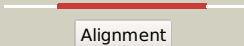

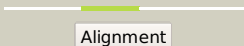

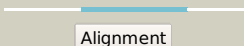

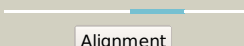
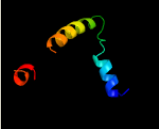
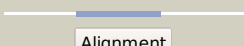
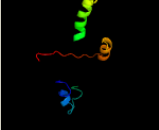
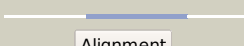

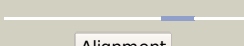










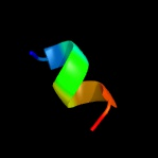
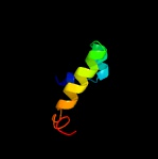
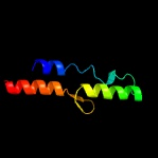
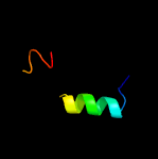

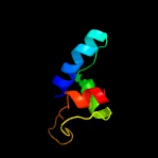
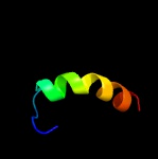



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3780_(-)_4227167_4227703
Date	Fri Aug 9 18:20:48 BST 2019
Unique Job ID	d57d29f106d24bc6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ietA_	 Alignment		100.0	97	PDB header: gene regulation Chain: A: PDB Molecule: bacterial proteasome activator; PDBTitle: crystal structure of mycobacterium tuberculosis atp-independent2 proteasome activator
2	c2lseA_	 Alignment		69.8	32	PDB header: de novo protein Chain: A: PDB Molecule: four helix bundle protein; PDBTitle: solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nesg) target or188
3	c2veeC_	 Alignment		36.9	16	PDB header: transport protein Chain: C: PDB Molecule: protoglobin; PDBTitle: structure of protoglobin from methanosarcina acetivorans2 c2a
4	d2bmob1	 Alignment		31.8	31	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
5	c2l6fA_	 Alignment		28.6	27	PDB header: transferase,cell adhesion Chain: A: PDB Molecule: focal adhesion kinase 1, linker1, paxillin, linker2, PDBTitle: nmr solution structure of fat domain of fak complexed with ld2 and ld42 motifs of paxillin
6	c5oheA_	 Alignment		24.3	16	PDB header: transferase Chain: A: PDB Molecule: globin-coupled histidine kinase; PDBTitle: globin sensor domain of afgchk (feiii form) in complex with cyanide
7	d2qjxa2	 Alignment		21.1	38	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: beta-N-acetylhexosaminidase domain
8	d1qbaa4	 Alignment		17.8	44	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: beta-N-acetylhexosaminidase domain
9	d2csba1	 Alignment		17.7	50	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
10	d2cbia3	 Alignment		15.3	45	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: Hyaluronidase N-terminal domain-like
11	c4tzoC_	 Alignment		14.6	14	PDB header: peptide binding protein Chain: C: PDB Molecule: protein htp-1; PDBTitle: structure of c. elegans htp-1 bound to him-3 closure motif

12	d1m98a1	Alignment		12.8	33	Fold: Orange carotenoid protein, N-terminal domain Superfamily: Orange carotenoid protein, N-terminal domain Family: Orange carotenoid protein, N-terminal domain
13	d1nowa2	Alignment		12.6	38	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: beta-N-acetylhexosaminidase domain
14	d2aq0a1	Alignment		12.2	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
15	c4xy3A_	Alignment		12.1	20	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
16	c2gbxF_	Alignment		10.5	23	PDB header: oxidoreductase Chain: F: PDB Molecule: biphenyl 2,3-dioxygenase beta subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
17	d1jaka2	Alignment		10.1	88	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: beta-N-acetylhexosaminidase domain
18	d1j9ia_	Alignment		9.3	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
19	c1o8tA_	Alignment		9.3	26	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein c-ii; PDBTitle: global structure and dynamics of human apolipoprotein ci2 in complex with micelles: evidence for increased mobility3 of the helix involved in the activation of lipoprotein4 lipase.
20	d2choa3	Alignment		9.2	33	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: Hyaluronidase N-terminal domain-like
21	c4wj2A_	Alignment	not modelled	9.1	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
22	d1ha9a_	Alignment	not modelled	9.1	39	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant inhibitors of proteinases and amylases Family: Plant inhibitors of proteinases and amylases
23	c2xcqA_	Alignment	not modelled	8.6	34	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit b, dna gyrase subunit a; PDBTitle: the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
24	d2paga1	Alignment	not modelled	8.6	26	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
25	d2eifa1	Alignment	not modelled	8.6	57	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
26	c2wssT_	Alignment	not modelled	8.4	18	PDB header: hydrolase Chain: T: PDB Molecule: atp synthase subunit b, mitochondrial; PDBTitle: the structure of the membrane extrinsic region of bovine atp synthase
27	c3kogA_	Alignment	not modelled	8.4	58	PDB header: membrane protein Chain: A: PDB Molecule: putative pore-forming toxin; PDBTitle: crystal structure of putative pore-forming toxin (yp_001301288.1) from2 bacteroides vulgatus atcc 8482 at 1.85 a resolution
28	c5wowA_	Alignment	not modelled	8.1	39	PDB header: de novo protein Chain: A: PDB Molecule: two inhibitor peptide topologies 2; PDBTitle: solution nmr structure of cyclotide mctoi-i

29	c6mcjA	Alignment	not modelled	7.9	27	PDB header: protein binding Chain: A: PDB Molecule: orange carotenoid-binding protein; PDBTitle: structure of helical carotenoid protein 2 from fremyella diplosiphon
30	d1bkba1	Alignment	not modelled	7.9	57	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
31	d1iz6a1	Alignment	not modelled	7.8	43	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
32	c2m86A	Alignment	not modelled	7.7	39	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: mco-pmi; PDBTitle: solution structure of hdm2 with engineered cyclotide
33	c1abzA	Alignment	not modelled	7.3	47	PDB header: de novo design Chain: A: PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
34	d1t8sa	Alignment	not modelled	7.2	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
35	d1t3ta1	Alignment	not modelled	7.2	34	Fold: RuvA C-terminal domain-like Superfamily: FGAM synthase PurL, linker domain Family: FGAM synthase PurL, linker domain
36	c3odmE	Alignment	not modelled	7.2	29	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
37	c1bdgA	Alignment	not modelled	6.9	20	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
38	d2acva1	Alignment	not modelled	6.8	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
39	d1v4sa1	Alignment	not modelled	6.6	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
40	c6db1A	Alignment	not modelled	6.6	26	PDB header: transferase Chain: A: PDB Molecule: putative methyl-accepting chemotaxis protein; PDBTitle: 2.0 angstrom resolution crystal structure of n-terminal ligand-binding2 domain of putative methyl-accepting chemotaxis protein from3 salmonella enterica
41	d2fug71	Alignment	not modelled	6.5	35	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Nqo15-like
42	c3a0mB	Alignment	not modelled	6.5	64	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
43	c3a0mD	Alignment	not modelled	6.5	64	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
44	c1t3tA	Alignment	not modelled	6.4	34	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
45	c4z2cA	Alignment	not modelled	6.2	27	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
46	c1m98A	Alignment	not modelled	6.2	33	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
47	c2h1yA	Alignment	not modelled	6.2	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coenzyme a-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
48	c6b9rD	Alignment	not modelled	6.1	7	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
49	c3a0mC	Alignment	not modelled	6.0	64	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
50	c3a0mE	Alignment	not modelled	5.9	64	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
51	d1bdga1	Alignment	not modelled	5.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
52	c6n0wA	Alignment	not modelled	5.9	18	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
53	d2je6i3	Alignment	not modelled	5.7	47	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
54	c5zqtA	Alignment	not modelled	5.7	29	PDB header: transferase Chain: A: PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6

55	c1dlyA_	Alignment	not modelled	5.7	13	PDB header: oxygen storage/transport Chain: A: PDB Molecule: hemoglobin; PDBTitle: x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
56	d1dlya_	Alignment	not modelled	5.7	13	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
57	d2cs7a1	Alignment	not modelled	5.6	50	Fold: IL8-like Superfamily: PhtA domain-like Family: PhtA domain-like
58	c3wqyB_	Alignment	not modelled	5.6	29	PDB header: ligase/rna Chain: B: PDB Molecule: alanine--trna ligase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna synthetase in2 complex with wild-type trna(ala) having g3.u70
59	d1xbta2	Alignment	not modelled	5.6	54	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
60	d1k1ga_	Alignment	not modelled	5.6	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
61	c4lgiD_	Alignment	not modelled	5.4	50	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: n-terminal truncated nlec structure
62	c4bxoB_	Alignment	not modelled	5.4	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
63	c3a0mA_	Alignment	not modelled	5.4	64	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
64	c3k7dA_	Alignment	not modelled	5.3	11	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenyllyltransferase; PDBTitle: c-terminal (adenylation) domain of e.coli glutamine synthetase2 adenyllyltransferase
65	c6fpeG_	Alignment	not modelled	5.2	28	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
66	d2ebfx3	Alignment	not modelled	5.1	54	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: PMT C-terminal domain like
67	d2cfua2	Alignment	not modelled	5.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
68	d1bg3a1	Alignment	not modelled	5.0	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase