
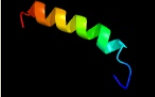
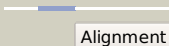
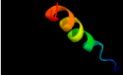
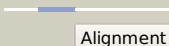
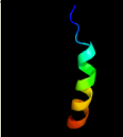
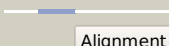
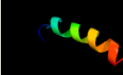
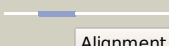
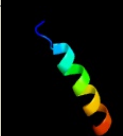
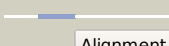
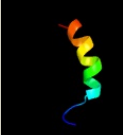
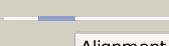
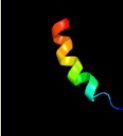

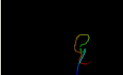

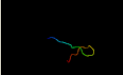

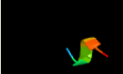

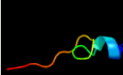
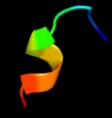
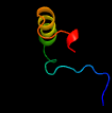

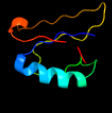


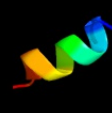




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0559c (-) _650410_650748
Date	Fri Jul 26 01:50:11 BST 2019
Unique Job ID	1ee5c69d805f9c38

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ismC_	 Alignment		90.7	42	PDB header: hydrolase inhibitor/hydrolase Chain: C: PDB Molecule: cg4930; PDBTitle: crystal structure of the endog/endogi complex: mechanism of endog2 inhibition
2	c6nhwA_	 Alignment		28.6	47	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
3	c6nhwB_	 Alignment		28.5	47	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
4	c6nhwC_	 Alignment		27.5	47	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
5	c6nhwD_	 Alignment		26.7	47	PDB header: immune system Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
6	c6nhwF_	 Alignment		26.6	47	PDB header: immune system Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
7	c6nhwE_	 Alignment		26.6	47	PDB header: immune system Chain: E: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
8	d1mg7a1	 Alignment		23.3	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Early switch protein XOL-1, N-terminal domain
9	c1mg7B_	 Alignment		20.5	33	PDB header: gene regulation Chain: B: PDB Molecule: early switch protein xol-1 2.2k splice form; PDBTitle: crystal structure of xol-1
10	d2euca1	 Alignment		19.4	71	Fold: YfmB-like Superfamily: YfmB-like Family: YfmB-like
11	c6c3rB_	 Alignment		18.1	47	PDB header: viral protein Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a

12	c3v46A	Alignment		16.6	40	PDB header: transcription Chain: A: PDB Molecule: cell division control protein 73; PDBTitle: crystal structure of yeast cdc73 c-terminal domain
13	d1afra	Alignment		15.9	26	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
14	d1qhka	Alignment		15.7	42	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: N-terminal domain of RNase HI
15	d1joia	Alignment		11.8	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
16	d1nyed	Alignment		11.1	31	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
17	c3ts9A	Alignment		11.1	31	PDB header: antiviral protein, hydrolase Chain: A: PDB Molecule: interferon-induced helicase c domain-containing protein 1; PDBTitle: crystal structure of the mda5 helicase insert domain
18	c6f46A	Alignment		10.4	64	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
19	c5wodA	Alignment		9.4	36	PDB header: de novo protein Chain: A: PDB Molecule: 38-mer peptide; PDBTitle: de novo design of covalently constrained meso-size protein scaffolds2 with unique tertiary structures
20	d1rkra	Alignment		8.6	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
21	c2n0pA	Alignment	not modelled	7.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein aq_1974; PDBTitle: solution structure of aqifex aeolicus aq1974
22	c4wwrD	Alignment	not modelled	7.3	22	PDB header: transport protein Chain: D: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
23	d1jzga	Alignment	not modelled	7.2	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
24	d2bcqa3	Alignment	not modelled	7.0	17	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
25	c1v55B	Alignment	not modelled	6.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: bovine heart cytochrome c oxidase at the fully reduced state
26	d1za0a1	Alignment	not modelled	6.9	10	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
27	c3r79B	Alignment	not modelled	6.7	27	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
28	c5xtbW	Alignment	not modelled	6.6	75	PDB header: oxidoreductase/electron transport Chain: W: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i matrix arm PDB header: transcription repressor

29	c2kelB_	Alignment	not modelled	6.4	47	Chain: B; PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
30	c4cyyA_	Alignment	not modelled	6.3	15	PDB header: hydrolase Chain: A; PDB Molecule: pantetheinase; PDBTitle: the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
31	d1k1ga_	Alignment	not modelled	5.7	30	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)
32	c4tkrB_	Alignment	not modelled	5.7	38	PDB header: membrane protein Chain: B; PDB Molecule: thiamine transporter thia; PDBTitle: native-sad phasing for thit from listeria monocytogenes serovar.
33	c2kw6A_	Alignment	not modelled	5.5	55	PDB header: cell cycle Chain: A; PDB Molecule: cyclin-dependent kinase 2-associated protein 1; PDBTitle: solution nmr structure of cyclin-dependent kinase 2-associated protein2 1 (cdk2-associated protein 1; oral cancer suppressor deleted in oral3 cancer 1, doc-1) from h.sapiens, northeast structural genomics4 consortium target target hr3057h
34	c6gcsA_	Alignment	not modelled	5.3	26	PDB header: oxidoreductase Chain: A; PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
35	c1i7wB_	Alignment	not modelled	5.3	37	PDB header: cell adhesion Chain: B; PDB Molecule: epithelial-cadherin; PDBTitle: beta-catenin/phosphorylated e-cadherin complex
36	c2ltaA_	Alignment	not modelled	5.3	46	PDB header: de novo protein Chain: A; PDB Molecule: de novo designed protein; PDBTitle: solution nmr structure of de novo designed protein, rossmann 3x1 fold,2 northeast structural genomics consortium target or157
37	d1l1aa2	Alignment	not modelled	5.2	47	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain
38	c6fxfA_	Alignment	not modelled	5.2	19	PDB header: signaling protein Chain: A; PDB Molecule: sam and sh3 domain-containing protein 3; PDBTitle: crystal structure of the sam domain of murine sly1
39	c3ahpA_	Alignment	not modelled	5.1	28	PDB header: electron transport Chain: A; PDB Molecule: cuta1; PDBTitle: crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
40	c6c41A_	Alignment	not modelled	5.1	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: clavamin-a; PDBTitle: the clavamin peptide in the presence of tfe (2,2,2-trifluoroethanol),2 presented a amphipathic alpha-helices from phe-2 to val-22 residues
41	c4walaA_	Alignment	not modelled	5.0	30	PDB header: protein binding/rna Chain: A; PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
42	c1m57H_	Alignment	not modelled	5.0	40	PDB header: oxidoreductase Chain: H; PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
43	d1lukua_	Alignment	not modelled	5.0	36	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)