

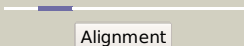
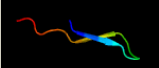
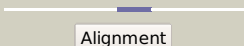

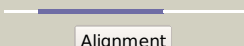
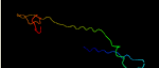
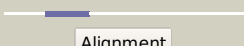
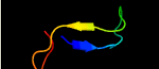
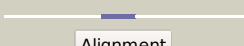
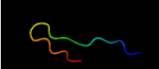
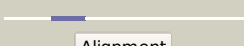


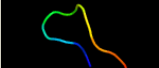

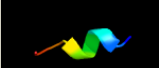



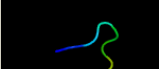


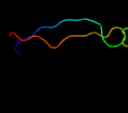








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2658c (-) _2979336_2979698
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	b4e38f24ef912a78

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wkta_	 Alignment		17.3	58	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Yeast killer toxin
2	c2v1nA_	 Alignment		17.0	33	PDB header: nuclear protein Chain: A: PDB Molecule: protein kin homolog; PDBTitle: solution structure of the region 51-160 of human kin172 reveals a winged helix fold
3	c2ro5B_	 Alignment		16.7	67	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
4	c4g0rA_	 Alignment		14.5	16	PDB header: virus/dna Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: structural characterization of h-1 parvovirus: comparison of2 infectious virions to replication defective particles
5	c4hffA_	 Alignment		12.2	21	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of the type vi effector-immunity complex tae4-tai42 from salmonella typhimurium
6	c6g5iy_	 Alignment		11.9	24	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
7	c5yhkB_	 Alignment		11.2	50	PDB header: metal binding protein Chain: B: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 aerogenes
8	c5yhoA_	 Alignment		10.2	50	PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
9	c3kyzA_	 Alignment		9.6	20	PDB header: transferase Chain: A: PDB Molecule: sensor protein pfes; PDBTitle: the crystal structure of the sensor domain of two-component2 sensor pfes from pseudomonas aeruginosa pa01
10	d1rooa_	 Alignment		9.6	43	Fold: Crisp domain-like Superfamily: Crisp domain-like Family: Sea anemone toxin k
11	c4bt7A_	 Alignment		9.4	33	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: acetolactate decarboxylase with a bound phosphate ion

12	c2lcqA_	Alignment		9.1	23	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
13	d2oola2	Alignment		8.4	67	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
14	d1bg1a3	Alignment		8.4	21	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
15	c6ig0B_	Alignment		8.4	46	PDB header: rna binding protein Chain: B: PDB Molecule: type iii-a crispr-associated ramp protein csm4; PDBTitle: type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound
16	c4ghjA_	Alignment		8.0	37	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator from2 vibrio vulnificus.
17	c3kieF_	Alignment		7.7	27	PDB header: virus Chain: F: PDB Molecule: capsid protein vp1; PDBTitle: crystal structure of adeno-associated virus serotype 3b
18	c2w1tB_	Alignment		7.3	54	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
19	c5xneA_	Alignment		7.3	50	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: x-ray crystal structure of alpha-acetolactate decarboxylase from2 bacillus subtilis strain 168
20	c5zkeA_	Alignment		7.2	58	PDB header: ligase Chain: A: PDB Molecule: aminoacyl trna synthetase complex-interacting PDBTitle: crystal structure of n-terminal domain of plasmodium vivax p43 in2 space group p212121
21	c3nttA_	Alignment	not modelled	7.1	17	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
22	c2n6bA_	Alignment	not modelled	6.9	58	PDB header: toxin Chain: A: PDB Molecule: hui1; PDBTitle: nmr structure of the de-novo toxin hui1
23	c4bi3B_	Alignment	not modelled	6.6	24	PDB header: toxin Chain: B: PDB Molecule: ssp1; PDBTitle: structure and function of amidase toxin - antitoxin2 combinations associated with the type vi secretion system3 of serratia marcescens.
24	d2cona1	Alignment	not modelled	6.6	31	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
25	c1l2yA_	Alignment	not modelled	6.4	43	PDB header: de novo protein Chain: A: PDB Molecule: tc5b; PDBTitle: nmr structure of trp-cage miniprotein construct tc5b
26	d1lp3a_	Alignment	not modelled	6.3	27	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Parvoviridae-like VP
27	d1xv2a_	Alignment	not modelled	6.2	57	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
28	d1lqsl_	Alignment	not modelled	6.0	26	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
						PDB header: immune system

29	c5xvnM_	Alignment	not modelled	5.9	44	Chain: M: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: e. far cas1-cas2/prespacer binary complex
30	c3ro2B_	Alignment	not modelled	5.9	55	PDB header: protein binding Chain: B: PDB Molecule: peptide of nuclear mitotic apparatus protein 1; PDBTitle: structures of the lgn/numa complex
31	c4gxbA_	Alignment	not modelled	5.9	21	PDB header: protein transport/cell adhesion Chain: A: PDB Molecule: sorting nexin-17; PDBTitle: structure of the snx17 atypical ferm domain bound to the npxy motif of 2 p-selectin
32	c3wtfB_	Alignment	not modelled	5.8	15	PDB header: immune system Chain: B: PDB Molecule: uncharacterized protein c9orf142; PDBTitle: structure of paxx
33	d2o9ca2	Alignment	not modelled	5.7	67	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
34	c4qc8A_	Alignment	not modelled	5.7	23	PDB header: virus Chain: A: PDB Molecule: vp2; PDBTitle: structural annotation of pathogenic bovine parvovirus-1
35	c1puoA_	Alignment	not modelled	5.5	20	PDB header: allergen Chain: A: PDB Molecule: major allergen i polypeptide, fused chain 2, chain 1; PDBTitle: crystal structure of fel d 1- the major cat allergen
36	c3jvfC_	Alignment	not modelled	5.5	37	PDB header: signaling protein / cytokine Chain: C: PDB Molecule: interleukin-17 receptor a; PDBTitle: crystal structure of an interleukin-17 receptor complex
37	d1foea2	Alignment	not modelled	5.4	24	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
38	c5vgbA_	Alignment	not modelled	5.2	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of nmecas9 hnh domain bound to anti-crispr acriic1
39	c5zmmD_	Alignment	not modelled	5.2	48	PDB header: dna binding protein Chain: D: PDB Molecule: uncharacterized protein mcra; PDBTitle: structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
40	c2v4xA_	Alignment	not modelled	5.1	29	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain