

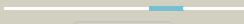
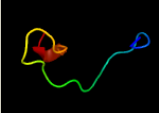

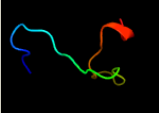









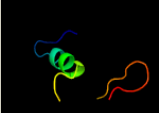

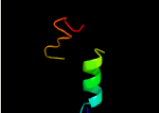

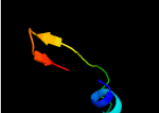




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1097c_(-)_1225268_1226149
Date	Wed Jul 31 22:05:17 BST 2019
Unique Job ID	043fbb0e9eba65b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nl6C_	 Alignment		86.1	22	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
2	c3d9xA_	 Alignment		39.6	8	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin a; PDBTitle: structure of the head of the bartonella adhesin bada
3	c4lgoC_	 Alignment		37.4	4	PDB header: cell adhesion Chain: C: PDB Molecule: vompd; PDBTitle: crystal structure of n-terminal domain 1 of vompd from bartonella2 quintana
4	c5do7B_	 Alignment		31.1	15	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
5	d2vnud3	 Alignment		30.1	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
6	d1xhja_	 Alignment		20.7	26	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
7	c4ol4A_	 Alignment		20.3	13	PDB header: lipid binding protein Chain: A: PDB Molecule: proline-rich 28 kda antigen; PDBTitle: crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
8	c5do7A_	 Alignment		20.0	13	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
9	c5nj3B_	 Alignment		16.9	34	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
10	c1qysA_	 Alignment		16.8	30	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
11	c2jvfA_	 Alignment		16.4	28	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein

12	c4wyqB_	Alignment		15.5	22	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: crystal structure of the dicer-trbp interface
13	c2mbIA_	Alignment		15.4	36	PDB header: de novo protein Chain: A: PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
14	d1trra_	Alignment		15.0	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
15	d1jhga_	Alignment		12.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
16	c2yo1A_	Alignment		12.5	0	PDB header: membrane protein Chain: A: PDB Molecule: general control protein gcn4, putative inner membrane PDBTitle: salmonella enterica sada 1049-1304 fused to gcn4 adaptors (sadaK9-2 cfii)
17	c3wprA_	Alignment		12.1	4	PDB header: cell adhesion Chain: A: PDB Molecule: trimeric autotransporter adhesin; PDBTitle: acinetobacter sp. tol 5 ataa n-terminal half of c-terminal stalk fused2 to gcn4 adaptors (cstalkn)
18	c2qjIA_	Alignment		11.5	32	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
19	c3pr7A_	Alignment		10.8	4	PDB header: membrane protein Chain: A: PDB Molecule: uspa1; PDBTitle: multi-functional and mechanosensitive receptor binding activity of the2 moraxella catarrhalis adhesin uspa1
20	c3ah9C_	Alignment		10.4	56	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
21	c3ah9B_	Alignment	not modelled	10.4	56	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
22	c3ah9E_	Alignment	not modelled	10.4	56	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
23	c4usxB_	Alignment	not modelled	9.6	5	PDB header: transport protein Chain: B: PDB Molecule: trimeric autotransporter adhesin; PDBTitle: the structure of the c-terminal yada-like domain of2 bpsl2063 from burkholderia pseudomallei
24	c3wp8A_	Alignment	not modelled	9.5	0	PDB header: cell adhesion Chain: A: PDB Molecule: trimeric autotransporter adhesin; PDBTitle: acinetobacter sp. tol 5 ataa c-terminal yhead fused to gcn4 adaptors2 (thead)
25	d1veha_	Alignment	not modelled	8.3	18	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: Nifu C-terminal domain-like
26	c2cuoA_	Alignment	not modelled	8.1	54	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
27	c2cuoD_	Alignment	not modelled	8.1	54	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
28	c2cuoB_	Alignment	not modelled	8.1	54	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
29	c2cuoE_	Alignment	not modelled	8.1	54	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9;

						PDBTitle: collagen model peptide (pro-pro-gly)9
30	c4fasD	Alignment	not modelled	7.5	22	PDB header: oxidoreductase Chain: D: PDB Molecule: ne1300; PDBTitle: complex crystal structure of hydroxylamine oxidoreductase and ne13002 from nitrosomonas europaea
31	c3frwF	Alignment	not modelled	7.4	43	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
32	c2cuoC	Alignment	not modelled	7.2	54	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
33	c2cuoF	Alignment	not modelled	7.2	54	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
34	c1p9hA	Alignment	not modelled	7.1	0	PDB header: cell adhesion Chain: A: PDB Molecule: invasin; PDBTitle: crystal structure of the collagen-binding domain of yersinia adhesin2 yada
35	d1p9ha	Alignment	not modelled	7.1	0	Fold: Single-stranded left-handed beta-helix Superfamily: Adhesin YadA, collagen-binding domain Family: Adhesin YadA, collagen-binding domain
36	c5u59A	Alignment	not modelled	7.0	45	PDB header: de novo protein Chain: A: PDB Molecule: designed dimeric coiled coil peptide with two terpyridine PDBTitle: coiled coil peptide metal coordination framework: dimer fold grown2 with citrate
37	c5u5aA	Alignment	not modelled	6.9	45	PDB header: de novo protein Chain: A: PDB Molecule: designed dimeric coiled coil peptide with two terpyridine PDBTitle: coiled coil peptide metal coordination framework: dimer fold
38	c3ah9A	Alignment	not modelled	6.9	54	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
39	d2pi2e1	Alignment	not modelled	6.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
40	c4dznC	Alignment	not modelled	6.4	45	PDB header: de novo protein Chain: C: PDB Molecule: coiled-coil peptide cc-pil; PDBTitle: a de novo designed coiled coil cc-pil
41	c4dznA	Alignment	not modelled	6.4	45	PDB header: de novo protein Chain: A: PDB Molecule: coiled-coil peptide cc-pil; PDBTitle: a de novo designed coiled coil cc-pil
42	c4dznB	Alignment	not modelled	6.4	45	PDB header: de novo protein Chain: B: PDB Molecule: coiled-coil peptide cc-pil; PDBTitle: a de novo designed coiled coil cc-pil
43	c3ah9F	Alignment	not modelled	6.2	54	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	c3korD	Alignment	not modelled	6.0	43	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
45	c2pqaB	Alignment	not modelled	5.9	18	PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
46	c5ol2D	Alignment	not modelled	5.6	22	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
47	c2jnvA	Alignment	not modelled	5.5	23	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
48	c3la9A	Alignment	not modelled	5.5	13	PDB header: transport protein Chain: A: PDB Molecule: haemagglutinin family protein; PDBTitle: crystal structure of the trimeric autotransporter adhesin head domain2 bpa from burkholderia pseudomallei, iodide phased
49	d1q0qa1	Alignment	not modelled	5.3	20	Fold: Left-handed superhelix Superfamily: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain Family: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
50	c4x8wE	Alignment	not modelled	5.3	23	PDB header: gene regulation Chain: E: PDB Molecule: loquacious, isoform b; PDBTitle: dsrbd3 of loquacious
51	c2z51A	Alignment	not modelled	5.1	26	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 2, chloroplast; PDBTitle: crystal structure of arabidopsis cnfu involved in iron-sulfur cluster2 biosynthesis