
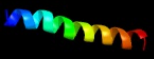

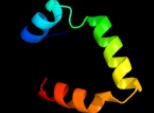



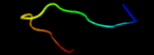









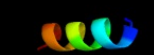

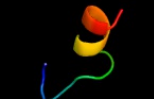

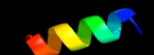


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2049c_(-)_2307301_2307525
Date	Mon Aug 5 13:25:16 BST 2019
Unique Job ID	6be33edaef7d2e81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1st6a3	 Alignment		31.4	21	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
2	c5ytpA	 Alignment		30.7	44	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 l34a from thermus thermophilus hb8
3	d2a6qb1	 Alignment		19.7	21	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
4	d1n26a1	 Alignment		16.7	41	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: ! set domains
5	d1st6a5	 Alignment		16.0	20	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
6	c3g5rA	 Alignment		15.0	41	PDB header: transferase Chain: A: PDB Molecule: methylenetetrahydrofolate--trna-(uracil-5-)- PDBTitle: crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
7	d1st6a4	 Alignment		13.6	18	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
8	c3g5oA	 Alignment		13.4	24	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
9	c3tweA	 Alignment		12.6	29	PDB header: unknown function Chain: A: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
10	c2le7A	 Alignment		12.3	44	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: solution nmr structure of the s4s5 linker of herg potassium channel
11	c3tweB	 Alignment		12.3	29	PDB header: unknown function Chain: B: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h

12	c6q5sB_	Alignment		11.9	32	PDB header: de novo protein Chain: B: PDB Molecule: apcc-tet; PDBTitle: crystal structure of a de novo designed antiparallel four-helix coiled2 coil apcc-tet
13	c6q5sC_	Alignment		11.9	32	PDB header: de novo protein Chain: C: PDB Molecule: apcc-tet; PDBTitle: crystal structure of a de novo designed antiparallel four-helix coiled2 coil apcc-tet
14	c6q5sD_	Alignment		11.9	32	PDB header: de novo protein Chain: D: PDB Molecule: apcc-tet; PDBTitle: crystal structure of a de novo designed antiparallel four-helix coiled2 coil apcc-tet
15	c6q5sA_	Alignment		11.9	32	PDB header: de novo protein Chain: A: PDB Molecule: apcc-tet; PDBTitle: crystal structure of a de novo designed antiparallel four-helix coiled2 coil apcc-tet
16	c3d55A_	Alignment		9.6	35	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
17	c3oeiB_	Alignment		9.1	48	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
18	c2vs0B_	Alignment		8.9	8	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
19	d2a6qa1	Alignment		8.1	23	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
20	c2lq0A_	Alignment		8.0	63	PDB header: antifreeze protein Chain: A: PDB Molecule: de novo designed antifreeze peptide 1m; PDBTitle: solution structure of de novo designed antifreeze peptide 1m
21	c6g1qA_	Alignment	not modelled	7.5	7	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribosylhydrolase like 2; PDBTitle: adp-ribosylserine hydrolase arh3 of latimeria chalumnae in complex2 with adp-ribose
22	c1aq5C_	Alignment	not modelled	7.1	15	PDB header: coiled-coil Chain: C: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
23	c1aq5B_	Alignment	not modelled	7.1	15	PDB header: coiled-coil Chain: B: PDB Molecule: cartilage matrix protein; PDBTitle: high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
24	c5y02D_	Alignment	not modelled	6.8	4	PDB header: lyase Chain: D: PDB Molecule: hydroxynitrile lyase; PDBTitle: c-terminal peptide depleted mutant of hydroxynitrile lyase from2 passiflora edulis (pehnl) bound with (r)-mandelonitrile
25	c1dmIH_	Alignment	not modelled	6.7	40	PDB header: dna binding protein/transferase Chain: H: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
26	c1dmIF_	Alignment	not modelled	6.7	40	PDB header: dna binding protein/transferase Chain: F: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
27	c1dmID_	Alignment	not modelled	6.6	40	PDB header: dna binding protein/transferase Chain: D: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
28	c1dmIB_	Alignment	not modelled	6.6	40	PDB header: dna binding protein/transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol

29	c3kdqB_	Alignment	not modelled	6.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of a functionally unknown conserved2 protein from corynebacterium diphtheriae.
30	c5j0hA_	Alignment	not modelled	6.0	38	PDB header: de novo protein Chain: A: PDB Molecule: design construct 2l6hc3_13; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
31	c5vr2A_	Alignment	not modelled	5.9	32	PDB header: signaling protein Chain: A: PDB Molecule: myocilin; PDBTitle: mouse myocilin leucine zipper c-terminal 7 heptad repeat
32	c5uupB_	Alignment	not modelled	5.9	55	PDB header: apoptosis Chain: B: PDB Molecule: bfl-1-specific selected peptide; PDBTitle: human bfl-1 covalently cross-linked to an electrophilic variant of a2 bfl-1-specific selected peptide
33	d1rutx3	Alignment	not modelled	5.9	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
34	c4rirA_	Alignment	not modelled	5.8	50	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c, 1 heme-binding site; PDBTitle: structure of monoheme cytochrome pcch from geobacter sulfurreducens
35	d1u61a_	Alignment	not modelled	5.8	31	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: RNase III catalytic domain-like
36	d1yaro1	Alignment	not modelled	5.6	30	Fold: Four-helical up-and-down bundle Superfamily: Proteasome activator Family: Proteasome activator
37	c3zbhC_	Alignment	not modelled	5.5	12	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
38	d1e52a_	Alignment	not modelled	5.2	36	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
39	c2hw2A_	Alignment	not modelled	5.1	20	PDB header: transferase Chain: A: PDB Molecule: rifampin adp-ribosyl transferase; PDBTitle: crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin