
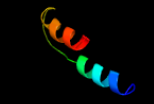

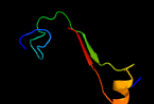













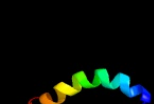



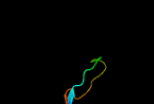
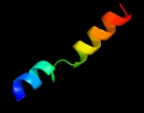

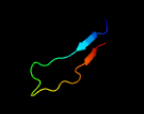
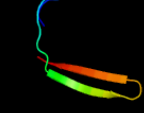


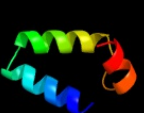




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2297 (-) _2568448_2568900
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	28f0802a899e5bc3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5sv0C_	 Alignment		70.2	35	PDB header: transport protein Chain: C; PDB Molecule: biopolymer transport protein exbb; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 7.0
2	c4n2oD_	 Alignment		54.8	42	PDB header: structural protein Chain: D; PDB Molecule: autonomous cohesin; PDBTitle: structure of a novel autonomous cohesin protein from ruminococcus2 flavefaciens
3	c1v0dA_	 Alignment		43.6	28	PDB header: hydrolase Chain: A; PDB Molecule: dna fragmentation factor 40 kda subunit; PDBTitle: crystal structure of caspase-activated dnase (cad)
4	d1v0da_	 Alignment		43.6	28	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Caspase-activated DNase, CAD (DffB, DFF40)
5	c2mltB_	 Alignment		18.4	31	PDB header: toxin (hemolytic polypeptide) Chain: B; PDB Molecule: melittin; PDBTitle: melittin
6	c6o4mB_	 Alignment		18.4	31	PDB header: toxin Chain: B; PDB Molecule: melittin; PDBTitle: racemic melittin
7	c6o4mA_	 Alignment		17.9	31	PDB header: toxin Chain: A; PDB Molecule: melittin; PDBTitle: racemic melittin
8	c2mltA_	 Alignment		17.6	31	PDB header: toxin (hemolytic polypeptide) Chain: A; PDB Molecule: melittin; PDBTitle: melittin
9	c6dstA_	 Alignment		17.1	31	PDB header: toxin Chain: A; PDB Molecule: melittin; PDBTitle: recombinant melittin
10	c2juia_	 Alignment		13.0	67	PDB header: toxin Chain: A; PDB Molecule: plne; PDBTitle: three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
11	d1m1sa_	 Alignment		12.8	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like

12	c2mw6A	Alignment		12.4	31	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: structure of the bee venom toxin melittin with [(c5h5)ru]+ fragment2 attached to the tryptophan residue
13	c1bh1A	Alignment		11.7	31	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: structural studies of d-pro melittin, nmr, 20 structures
14	d1rowa	Alignment		11.0	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
15	d1cuka3	Alignment		10.6	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
16	d2bnma1	Alignment		10.3	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
17	d1yqea1	Alignment		8.8	30	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
18	c4gr2A	Alignment		8.4	27	PDB header: chaperone Chain: A: PDB Molecule: atrbcx1; PDBTitle: structure of atrbcx1 from arabidopsis thaliana.
19	d1s4ka	Alignment		8.2	38	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Ydil-like
20	c4pnbC	Alignment		7.9	56	PDB header: de novo protein Chain: C: PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
21	c4pnbD	Alignment	not modelled	7.6	56	PDB header: de novo protein Chain: D: PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
22	c4pnbA	Alignment	not modelled	7.6	56	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
23	d1q8da	Alignment	not modelled	7.5	55	Fold: GDNF receptor-like Superfamily: GDNF receptor-like Family: GDNF receptor-like
24	d1txga2	Alignment	not modelled	7.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
25	c1qqp4	Alignment	not modelled	7.3	43	PDB header: virus Chain: 4: PDB Molecule: protein (genome polyprotein); PDBTitle: foot-and-mouth disease virus/ oligosaccharide receptor complex.
26	c4pnbB	Alignment	not modelled	7.3	56	PDB header: de novo protein Chain: B: PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
27	c4cmrB	Alignment	not modelled	7.1	46	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase/deacetylase family protein; PDBTitle: the crystal structure of novel exo-type maltose-forming2 amylase(py04_0872) from pyrococcus sp. st04
28	d2gfga1	Alignment	not modelled	7.1	36	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
						Fold: Glycosyl hydrolase domain

29	d1gcya1	Alignment	not modelled	7.0	100	Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
30	c1y7xA	Alignment	not modelled	7.0	28	PDB header: structural protein, protein binding Chain: A: PDB Molecule: major vault protein; PDBTitle: solution structure of a two-repeat fragment of major vault2 protein
31	c3trkA	Alignment	not modelled	6.8	24	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
32	c6jifA	Alignment	not modelled	6.7	22	PDB header: antitoxin Chain: A: PDB Molecule: tai4; PDBTitle: crystal structure of the type vi effector-immunity complex (tae4-tai4)2 from agrobacterium tumefaciens
33	c1xnlA	Alignment	not modelled	6.7	43	PDB header: viral protein Chain: A: PDB Molecule: membrane protein gp37; PDBTitle: aslv fusion peptide
34	c6e5hA	Alignment	not modelled	6.5	64	PDB header: de novo protein Chain: A: PDB Molecule: designed peptide nc_hee_d1: aib turn mutant; PDBTitle: heterogeneous-backbone mimics of a designed disulfide-rich protein:2 aib turn
35	d2py8a1	Alignment	not modelled	6.3	22	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
36	c2auvA	Alignment	not modelled	6.2	35	PDB header: oxidoreductase Chain: A: PDB Molecule: potential nad-reducing hydrogenase subunit; PDBTitle: solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
37	d1yuaa1	Alignment	not modelled	6.1	41	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
38	c4bqdD	Alignment	not modelled	6.0	58	PDB header: blood clotting Chain: D: PDB Molecule: peptide; PDBTitle: kd1 of human tfpi in complex with a synthetic peptide
39	c4bqdC	Alignment	not modelled	6.0	58	PDB header: blood clotting Chain: C: PDB Molecule: peptide; PDBTitle: kd1 of human tfpi in complex with a synthetic peptide
40	c4gr6B	Alignment	not modelled	6.0	24	PDB header: chaperone Chain: B: PDB Molecule: atrbcx2; PDBTitle: crystal structure of atrbcx2 from arabidopsis thaliana
41	c2gfgC	Alignment	not modelled	5.9	36	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
42	c2penE	Alignment	not modelled	5.9	22	PDB header: chaperone Chain: E: PDB Molecule: orf134; PDBTitle: crystal structure of rbcx, crystal form i
43	c2py8B	Alignment	not modelled	5.5	22	PDB header: chaperone Chain: B: PDB Molecule: hypothetical protein rbcx; PDBTitle: rbcx
44	c5kvnA	Alignment	not modelled	5.4	100	PDB header: de novo protein Chain: A: PDB Molecule: designed peptide nc_hee_d1; PDBTitle: nmr solution structure of designed peptide nc_hee_d1
45	c6j5ib	Alignment	not modelled	5.4	33	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
46	c6igz0	Alignment	not modelled	5.3	23	PDB header: plant protein Chain: 0: PDB Molecule: lhca-;; PDBTitle: structure of psi-lhci
47	c1d8IA	Alignment	not modelled	5.3	28	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
48	c6e5IA	Alignment	not modelled	5.3	100	PDB header: de novo protein Chain: A: PDB Molecule: designed peptide nc_hee_d1: orn turn mutant; PDBTitle: heterogeneous-backbone mimics of a designed disulfide-rich protein:2 orn turn
49	d2fg1a1	Alignment	not modelled	5.1	15	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain