
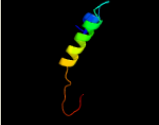
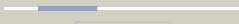
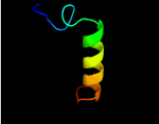








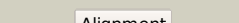







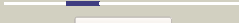
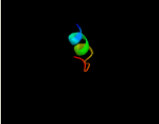
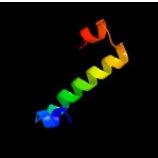
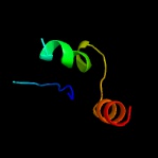

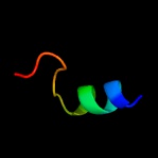

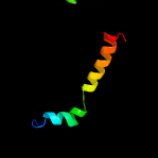

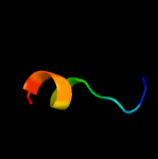
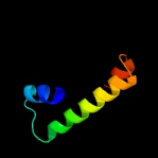


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1804c (-) _2047030_2047356
Date	Fri Aug 2 13:30:41 BST 2019
Unique Job ID	d38c30233cab12da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c3rB_	 Alignment		61.7	14	PDB header: viral protein Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
2	c4rl6A_	 Alignment		22.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
3	c3pvsA_	 Alignment		21.3	16	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
4	d2csua3	 Alignment		20.4	25	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
5	d1mkea1	 Alignment		15.0	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
6	c4inaA_	 Alignment		14.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinnella2 succinogenes. northeast structural genomics consortium target wsr35
7	c5k9xA_	 Alignment		14.2	21	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
8	c2ekcA_	 Alignment		13.3	21	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
9	c5uqdA_	 Alignment		11.8	38	PDB header: oxidoreductase Chain: A: PDB Molecule: dumpy; shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
10	c5kinC_	 Alignment		10.5	20	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
11	c2lweA_	 Alignment		9.5	20	PDB header: signaling protein Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: solution structure of mutant (t170e) second card of human rig-i

12	c3j9xj_	Alignment		9.0	28	PDB header: virus Chain: J: PDB Molecule: coat protein; PDBTitle: a virus that infects a hyperthermophile encapsidates a-form dna
13	c5tchG_	Alignment		9.0	24	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
14	c5l78A_	Alignment		8.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
15	c3ss4C_	Alignment		8.5	31	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
16	d2j9ga2	Alignment		8.3	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
17	d1zsqaz	Alignment		7.8	25	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myotubularin-like phosphatases
18	d1ulza2	Alignment		7.7	33	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
19	c2mulA_	Alignment		7.1	58	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: solution structure of the ubm1 domain of human huwe1/arf-bp1
20	c3f2eA_	Alignment		6.6	23	PDB header: viral protein Chain: A: PDB Molecule: sirv coat protein; PDBTitle: crystal structure of yellowstone sirv coat protein c-terminus
21	d1axib1	Alignment	not modelled	6.4	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
22	c1vjqB_	Alignment	not modelled	6.4	37	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
23	d1xoda1	Alignment	not modelled	6.1	27	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
24	c2gacD_	Alignment	not modelled	6.0	24	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
25	c5us3A_	Alignment	not modelled	6.0	75	PDB header: de novo protein Chain: A: PDB Molecule: heterogeneous-backbone variant of the sp1-3 zinc finger: n- PDBTitle: heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger
26	c4y7iB_	Alignment	not modelled	5.9	22	PDB header: hydrolase Chain: B: PDB Molecule: myotubularin-related protein 8; PDBTitle: crystal structure of mtmr8
27	c2ifsA_	Alignment	not modelled	5.6	19	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
28	c1anzB_	Alignment	not modelled	5.5	12	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase;

28	c1gpzB_	Alignment	not modelled	5.3	42	PDBTitle: human aspartylglucosaminidase complex with reaction product PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
29	c3uo9B_	Alignment	not modelled	5.4	31	PDB header: signaling protein Chain: A; PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
30	c2l5yA_	Alignment	not modelled	5.3	5	PDB header: toxin Chain: A; PDB Molecule: cholix toxin; PDBTitle: full-length cholix toxin from vibrio cholerae
31	c2q5tA_	Alignment	not modelled	5.3	26	PDB header: hydrolase Chain: B; PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: multidomain structure of human kidney-type glutaminase(kga/gls)
32	c5uqeB_	Alignment	not modelled	5.2	31	PDB header: protein transport Chain: B; PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: nmr structure of atg8-atg7c30 complex
33	c2li5B_	Alignment	not modelled	5.2	56	PDB header: transferase Chain: A; PDB Molecule: heptaprenylglyceryl phosphate synthase; PDBTitle: pcrb from geobacillus kaustophilus, with bound g1p
34	c4naeA_	Alignment	not modelled	5.1	28	