
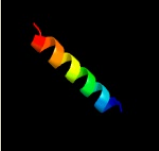

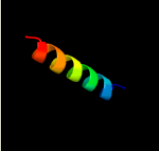
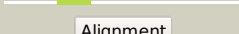



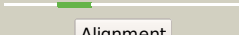



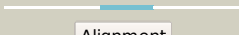
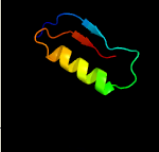





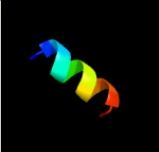


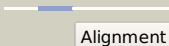
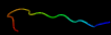
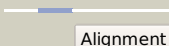


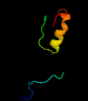

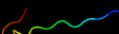
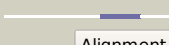

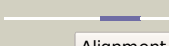

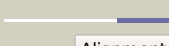


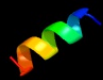


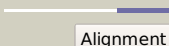

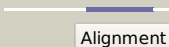




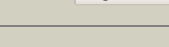


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1507A (-) _1697362_1697865
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	81422cb17b404f40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j8bA_	 Alignment		60.5	35	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
2	c3j7jA_	 Alignment		60.5	35	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
3	c3j7kA_	 Alignment		60.5	35	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
4	c3j8cA_	 Alignment		60.5	35	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
5	c5a5tA_	 Alignment		58.4	35	PDB header: hydrolase Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: structure of mammalian eif3 in the context of the 43s preinitiation2 complex
6	c4u1dA_	 Alignment		44.1	37	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: structure of the pci domain of translation initiation factor eif3a
7	d2dw4a2	 Alignment		37.4	38	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
8	c2n5lA_	 Alignment		34.8	26	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
9	c3lovA_	 Alignment		27.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
10	c3zqpB_	 Alignment		25.6	33	PDB header: dna-binding protein Chain: B: PDB Molecule: terminase small subunit; PDBTitle: crystal structure of the small terminase oligomerization2 domain from a spp1-like bacteriophage
11	c6fxsA_	 Alignment		24.2	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase

12	d1p7ba1	 Alignment		20.5	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
13	d1xl4a1	 Alignment		20.3	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
14	c5fjnB_	 Alignment		16.3	37	PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase; PDBTitle: structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate
15	c1u4fD_	 Alignment		16.3	43	PDB header: allergen Chain: D: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: crystal structure of cytoplasmic domains of irk1 (kir2.1) channel
16	c2v1dA_	 Alignment		15.2	41	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
17	c2xagA_	 Alignment		15.2	41	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
18	c3k7pA_	 Alignment		13.8	17	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
19	d1dxja_	 Alignment		12.3	38	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Family 19 glycosidase
20	c4yk8B_	 Alignment		11.9	25	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 13; PDBTitle: crystal structure of the atg101-atg13 complex from fission yeast
21	c3m1pA_	 Alignment	not modelled	11.8	17	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
22	d1d5ta1	 Alignment	not modelled	11.8	9	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
23	c1ps9A_	 Alignment	not modelled	10.9	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
24	c2bpa3_	 Alignment	not modelled	10.8	67	PDB header: virus/dna Chain: 3: PDB Molecule: protein (subunit of bacteriophage phix174); PDBTitle: atomic structure of single-stranded dna bacteriophage2 phix174 and its functional implications
25	c2gixC_	 Alignment	not modelled	10.4	33	PDB header: metal transport Chain: C: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: cytoplasmic domain structure of kir2.1 containing andersen's mutation2 r218q and rescue mutation t309k
26	c2hkoA_	 Alignment	not modelled	10.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1
27	d1n9pa_	 Alignment	not modelled	9.9	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
28	c3ka7A_	 Alignment	not modelled	9.7	36	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazeri. northeast structural genomics consortium

						target id3 mar208
29	c2lm0A_	Alignment	not modelled	9.4	48	PDB header: nuclear protein Chain: A: PDB Molecule: af4/fmr2 family member 1/protein af-9 chimera; PDBTitle: solution structure of the af4-af9 complex
30	c6cglA_	Alignment	not modelled	9.3	44	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
31	c4rdmB_	Alignment	not modelled	9.2	25	PDB header: hydrolase/dna Chain: B: PDB Molecule: restriction endonuclease r.ngovii; PDBTitle: crystal structure of r.ngoavii restriction endonuclease b3 domain with2 cognate dna
32	c6mquC_	Alignment	not modelled	9.0	48	PDB header: de novo protein Chain: C: PDB Molecule: p15, designed tm pentamer; PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban
33	d2bcgg1	Alignment	not modelled	8.8	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
34	d1vg0a1	Alignment	not modelled	7.8	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
35	d1ps9a3	Alignment	not modelled	7.7	26	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
36	c4o4aD_	Alignment	not modelled	7.4	15	PDB header: lipid binding protein Chain: D: PDB Molecule: lipoprotein, putative; PDBTitle: 2.75 angstrom crystal structure of putative lipoprotein from bacillus2 anthracis.
37	d2baaa_	Alignment	not modelled	7.4	46	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Family 19 glycosidase
38	c2z39A_	Alignment	not modelled	7.2	38	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of brassica juncea chitinase catalytic2 module glu234ala mutant (bjchi3-e234a)
39	c5nhul_	Alignment	not modelled	7.1	54	PDB header: hydrolase Chain: I: PDB Molecule: agap008004-pa; PDBTitle: human alpha thrombin complexed with anopheles gambiae ce52 anticoagulant
40	c1txR_	Alignment	not modelled	7.1	18	PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
41	c6dnoB_	Alignment	not modelled	7.0	63	PDB header: signaling protein Chain: B: PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: crystal structure of protein phosphatase 1 (pp1) bound to the muscle2 glycogen-targeting subunit (gm)
42	d1wxsa1	Alignment	not modelled	7.0	54	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
43	c5twvG_	Alignment	not modelled	6.7	20	PDB header: transport protein Chain: G: PDB Molecule: atp-sensitive inward rectifier potassium channel 11; PDBTitle: cryo-em structure of the pancreatic atp-sensitive k+ channel2 sur1/kir6.2 in the presence of atp and glibenclamide
44	d1j0ga_	Alignment	not modelled	6.7	54	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
45	c2jg6A_	Alignment	not modelled	6.6	28	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
46	d1etea_	Alignment	not modelled	6.6	35	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
47	c2k2ba_	Alignment	not modelled	6.5	37	PDB header: transport protein Chain: A: PDB Molecule: degenerin mec-4; PDBTitle: sparse-constraint solution nmr structure of micelle-2 solubilized cytosolic amino terminal domain of c. elegans3 mechanosensory ion channel subunit mec-4. new york4 consortium on membrane protein structure (nycomps) (casp5 target)
48	c4ue9B_	Alignment	not modelled	6.3	44	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 4e transporter; PDBTitle: complex of d. melanogaster eif4e with the 4e-binding protein 4e-t
49	c1gndA_	Alignment	not modelled	6.2	9	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
50	c5hs5A_	Alignment	not modelled	6.2	41	PDB header: transcriptional regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarx; PDBTitle: crystal structure of staphylococcus aureus sarx
51	d1w1za1	Alignment	not modelled	6.0	19	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
52	c1wvvB_	Alignment	not modelled	6.0	33	PDB header: hydrolase Chain: B: PDB Molecule: chitinase c; PDBTitle: crystal structure of chitinase c mutant e147q
53	c1f8sa_	Alignment	not modelled	5.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-

						aminobenzoate.
54	c2dbtA_	Alignment	not modelled	5.8	29	PDB header: hydrolase Chain: A: PDB Molecule: chitinase c; PDBTitle: crystal structure of chitinase c from streptomyces griseus2 hut6037
55	c1w1zD_	Alignment	not modelled	5.7	19	PDB header: unknown function Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
56	c1z8yP_	Alignment	not modelled	5.6	58	PDB header: virus Chain: P: PDB Molecule: spike glycoprotein e2; PDBTitle: mapping the e2 glycoprotein of alphaviruses
57	c1z8yL_	Alignment	not modelled	5.6	58	PDB header: virus Chain: L: PDB Molecule: spike glycoprotein e2; PDBTitle: mapping the e2 glycoprotein of alphaviruses
58	c1z8yJ_	Alignment	not modelled	5.6	58	PDB header: virus Chain: J: PDB Molecule: spike glycoprotein e2; PDBTitle: mapping the e2 glycoprotein of alphaviruses
59	c1z8yN_	Alignment	not modelled	5.6	58	PDB header: virus Chain: N: PDB Molecule: spike glycoprotein e2; PDBTitle: mapping the e2 glycoprotein of alphaviruses
60	c2jrfA_	Alignment	not modelled	5.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tubulin polymerization-promoting protein family PDBTitle: solution nmr structure of tubulin polymerization-promoting2 protein family member 3 from homo sapiens. northeast3 structural genomics target hr387.
61	c3i6dA_	Alignment	not modelled	5.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
62	c2e3eA_	Alignment	not modelled	5.5	64	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin, mutant def-bbb; PDBTitle: nmr structure of def-bbb, a mutant of anopheles defensin2 def-aaa
63	c6fxwA_	Alignment	not modelled	5.5	17	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase
64	d1nkua_	Alignment	not modelled	5.4	25	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
65	c2dkvA_	Alignment	not modelled	5.3	31	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of class i chitinase from oryza sativa l.2 japonica
66	d2diga1	Alignment	not modelled	5.3	35	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
67	c3qzrC_	Alignment	not modelled	5.2	31	PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
68	c1djnB_	Alignment	not modelled	5.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylphilus methylotrophus (sp.3 w3a1)
69	d2pa2a1	Alignment	not modelled	5.2	30	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e
70	d2fnaa1	Alignment	not modelled	5.1	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
71	c2lrba_	Alignment	not modelled	5.1	21	PDB header: protein binding Chain: A: PDB Molecule: actin-depolymerizing factor 1, isoforms a; PDBTitle: solution structure of adf like unc-60a protein of caenorhabditis2 elegans
72	d1r4xa1	Alignment	not modelled	5.0	43	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Coatomer appendage domain
73	c3p1wA_	Alignment	not modelled	5.0	18	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c