

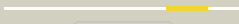










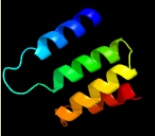





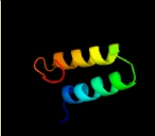


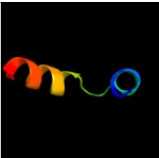
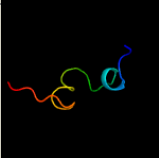
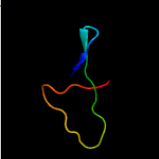

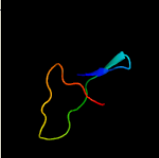
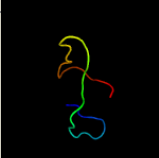
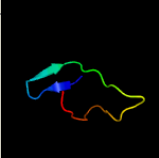
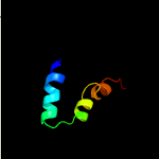
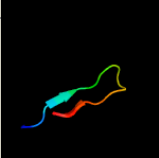


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2712c (-)_3024280_3025338
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	e2541932a9c30099

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pqrbl	 Alignment		85.8	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
2	d1nzna_	 Alignment		79.7	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
3	c2qlcC_	 Alignment		77.7	10	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
4	d1y8ma1	 Alignment		70.5	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
5	d1iyga_	 Alignment		59.0	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
6	c4f3vB_	 Alignment		48.0	17	PDB header: protein transport Chain: B: PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
7	c4ui9K_	 Alignment		47.4	13	PDB header: cell cycle Chain: K: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
8	c2xpiA_	 Alignment		38.7	19	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
9	d1pc2a_	 Alignment		32.8	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
10	d1tjca_	 Alignment		30.9	26	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
11	c3beeB_	 Alignment		30.5	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 paraaerolyticus

12	c5tmxA	Alignment		30.1	22	PDB header: transcription regulator Chain: A: PDB Molecule: protein sini; PDBTitle: solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
13	c4fm4C	Alignment		28.3	22	PDB header: lyase Chain: C: PDB Molecule: nitrile hydratase alpha subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
14	d1i94l	Alignment		27.4	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
15	d2icsa2	Alignment		26.5	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
16	d2uubl1	Alignment		22.4	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
17	c3j6vL	Alignment		19.6	21	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
18	c1zn1L	Alignment		19.4	14	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
19	d1i0da	Alignment		16.5	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
20	d1g5aa1	Alignment		15.8	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
21	c6evoA	Alignment	not modelled	14.4	18	PDB header: hydrolase Chain: A: PDB Molecule: prolyl 4-hydroxylase subunit alpha-2; PDBTitle: crystal structure the peptide-substrate-binding domain of human type2 ii collagen prolyl 4-hydroxylase complexed with pro-pro-gly-pro-arg-3 gly-pro-pro-gly.
22	c3j20N	Alignment	not modelled	14.0	19	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal protein s12p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
23	d1kcx2	Alignment	not modelled	13.8	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
24	c2k2uB	Alignment	not modelled	13.7	50	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16
25	c4bt8B	Alignment	not modelled	13.6	28	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase subunit alpha-1; PDBTitle: crystal structure of the apo form of n-terminal domain and2 peptide substrate binding domain of prolyl-4 hydroxylase3 type i from human
26	d2qa1l1	Alignment	not modelled	13.3	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
27	d1iioa	Alignment	not modelled	13.0	58	Fold: EF Hand-like Superfamily: Hypothetical protein MTH865 Family: Hypothetical protein MTH865
28	d1e12a2	Alignment	not modelled	12.5	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

28	v1012aZ	Alignment	not modelled	12.5	11	Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
29	c3mixA	Alignment	not modelled	12.2	30	PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthesis protein flha; PDBTitle: crystal structure of the cytosolic domain of b. subtilis flha
30	c4xvnC	Alignment	not modelled	11.9	44	PDB header: viral protein Chain: C: PDB Molecule: small terminase; PDBTitle: crystal structure of the small terminase from thermophilic phage g20c
31	c4u0zH	Alignment	not modelled	11.8	23	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
32	c3hymB	Alignment	not modelled	11.7	10	PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
33	c4jx0A	Alignment	not modelled	11.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a two domain protein with unknown function2 (bf3416) from bacteroides fragilis nctc 9343 at 2.90 a resolution
34	c6q8jA	Alignment	not modelled	10.9	33	PDB header: splicing Chain: A: PDB Molecule: wd40 repeat-containing protein smu1; PDBTitle: nterminal domain of human smu1 in complex with lsp641
35	c6h82b	Alignment	not modelled	10.8	44	PDB header: virus Chain: B: PDB Molecule: vp4; PDBTitle: cryo-em structure of the archaeal extremophilic internal membrane2 containing haloarcula hispanica icosahedral virus 2 (hhv-2) at 3.783 angstroms resolution.
36	c3msrA	Alignment	not modelled	10.1	24	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
37	d2gs5a1	Alignment	not modelled	9.8	14	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
38	d1onwa2	Alignment	not modelled	9.5	8	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
39	d2q0ta1	Alignment	not modelled	9.2	17	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
40	c1n0wB	Alignment	not modelled	9.2	57	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: crystal structure of a rad51-brca2 brc repeat complex
41	c5y10C	Alignment	not modelled	9.2	44	PDB header: viral protein Chain: C: PDB Molecule: membrane glycoprotein polyprotein; PDBTitle: sftsv gn head domain
42	c5a1sB	Alignment	not modelled	9.2	36	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate symporter seci2s2 form salmonella enterica.
43	c2iykB	Alignment	not modelled	9.1	33	PDB header: hydrolase Chain: B: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the upf2-interacting domain of 2 nonsense mediated mrna decay factor upf1
44	c2xzmL	Alignment	not modelled	9.1	31	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s12; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
45	c3eebB	Alignment	not modelled	8.9	19	PDB header: toxin Chain: B: PDB Molecule: rtx toxin rtxa; PDBTitle: structure of the v. cholerae rtx cysteine protease domain
46	c4rg9S	Alignment	not modelled	8.8	44	PDB header: protein binding Chain: S: PDB Molecule: anaphase-promoting complex subunit 16; PDBTitle: crystal structure of apc3-apc16 complex (selenomethionine derivative)
47	c4rg6S	Alignment	not modelled	8.8	44	PDB header: protein binding Chain: S: PDB Molecule: anaphase-promoting complex subunit 16; PDBTitle: crystal structure of apc3-apc16 complex
48	d2puza2	Alignment	not modelled	8.3	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
49	c3mydA	Alignment	not modelled	8.2	30	PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthesis protein flha; PDBTitle: structure of the cytoplasmic domain of flha from helicobacter pylori
50	c1s1hL	Alignment	not modelled	8.0	31	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s23; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
51	c3u4tA	Alignment	not modelled	7.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tpr repeat-containing protein; PDBTitle: crystal structure of the c-terminal part of the tpr repeat-containing2 protein q11t6_cyth3 from cytophaga hutchinsonii. northeast3 structural genomics consortium target chr11b.
52	c2q7fA	Alignment	not modelled	7.6	20	PDB header: protein binding Chain: A: PDB Molecule: yrrb protein; PDBTitle: crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
						Fold: Phosphorylase/hydrolase-like

53	d1de4c3	Alignment	not modelled	7.5	30	Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
54	d1hxia	Alignment	not modelled	7.4	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
55	c3zeyS	Alignment	not modelled	7.0	34	PDB header: ribosome Chain: S; PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
56	c2muiA	Alignment	not modelled	6.8	16	PDB header: unknown function Chain: A; PDB Molecule: upf0301 protein algh; PDBTitle: solution structure of the algh protein from pseudomonas aeruginosa,2 pa0405, upf0301
57	c2kztA	Alignment	not modelled	6.5	14	PDB header: apoptosis Chain: A; PDB Molecule: programmed cell death protein 4; PDBTitle: structure of the tandem ma-3 region of pdcd4
58	c3u5gX	Alignment	not modelled	6.5	31	PDB header: ribosome Chain: X; PDB Molecule: 40s ribosomal protein s23-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
59	c4g9qA	Alignment	not modelled	6.5	22	PDB header: lyase Chain: A; PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
60	c1cx8F	Alignment	not modelled	6.4	30	PDB header: metal transport Chain: F; PDB Molecule: transferrin receptor protein; PDBTitle: crystal structure of the ectodomain of human transferrin receptor
61	c5f3xB	Alignment	not modelled	6.3	13	PDB header: structural protein/protein binding Chain: B; PDB Molecule: ankyrin repeat and sam domain-containing protein 4b; PDBTitle: crystal structure of harmonin npdz1 in complex with anks4b sam-pbm
62	c3k9iA	Alignment	not modelled	6.0	16	PDB header: protein binding Chain: A; PDB Molecule: bh0479 protein; PDBTitle: crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
63	c5en7A	Alignment	not modelled	5.9	20	PDB header: splicing Chain: A; PDB Molecule: smu-1; PDBTitle: crystal structure of the smu1-red complex (native) of caenorhabditis2 elegans.
64	c3pa8A	Alignment	not modelled	5.8	17	PDB header: toxin/peptide inhibitor Chain: A; PDB Molecule: toxin b; PDBTitle: structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
65	d2ezha	Alignment	not modelled	5.6	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
66	c2l3vA	Alignment	not modelled	5.6	25	PDB header: lipid binding protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: nmr structure of acyl carrier protein from brucella melitensis
67	c3nqbB	Alignment	not modelled	5.5	26	PDB header: hydrolase Chain: B; PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
68	d3be7a2	Alignment	not modelled	5.5	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
69	c2wvpvH	Alignment	not modelled	5.3	57	PDB header: protein binding Chain: H; PDB Molecule: ubiquitin-like protein mdy2; PDBTitle: crystal structure of s. cerevisiae get4-get5 complex
70	c2wvpvF	Alignment	not modelled	5.3	57	PDB header: protein binding Chain: F; PDB Molecule: ubiquitin-like protein mdy2; PDBTitle: crystal structure of s. cerevisiae get4-get5 complex
71	d2ftwa2	Alignment	not modelled	5.3	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
72	d1wf9a1	Alignment	not modelled	5.2	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
73	c3as5A	Alignment	not modelled	5.2	20	PDB header: protein binding Chain: A; PDB Molecule: mama; PDBTitle: mama amb-1 p212121
74	c3aiiA	Alignment	not modelled	5.2	22	PDB header: ligase Chain: A; PDB Molecule: glutamyl-trna synthetase; PDBTitle: archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
75	c1pscA	Alignment	not modelled	5.1	18	PDB header: hydrolase Chain: A; PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
76	c2kckA	Alignment	not modelled	5.1	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: tpr repeat; PDBTitle: nmr solution structure of the northeast structural genomics consortium2 (nesg) target mrr121a
77	d2bb0a2	Alignment	not modelled	5.1	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
78	c2xevB	Alignment	not modelled	5.1	24	PDB header: metal binding Chain: B; PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
79	c4u9E	Alignment	not modelled	5.0	44	PDB header: cell cycle Chain: E; PDB Molecule: anaphase-promoting complex subunit 16;

