
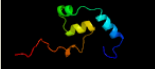
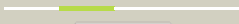




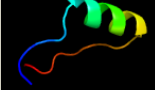

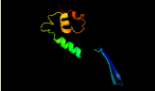












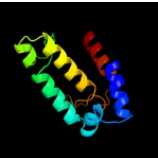
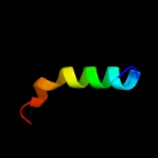



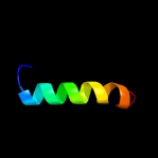
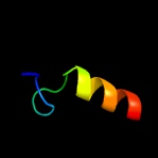




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2102_(-)_2363399_2364115
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	3182d48f40c1016a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vzyA_	 Alignment		82.2	17	PDB header: chaperone Chain: A: PDB Molecule: 33 kda chaperonin; PDBTitle: crystal structure of the bacillus subtilis hsp33
2	c1vq0A_	 Alignment		67.8	13	PDB header: chaperone Chain: A: PDB Molecule: 33 kda chaperonin; PDBTitle: crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
3	c3h7hA_	 Alignment		60.4	15	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
4	c5xonV_	 Alignment		59.6	24	PDB header: transcription/rna Chain: V: PDB Molecule: transcription elongation factor spt4; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
5	d1hw7a_	 Alignment		57.1	9	Fold: Hsp33 domain Superfamily: Hsp33 domain Family: Hsp33 domain
6	c1hw7A_	 Alignment		57.1	9	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp33; PDBTitle: hsp33, heat shock protein with redox-regulated chaperone activity
7	d3c7bb2	 Alignment		26.2	18	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
8	d1wfra_	 Alignment		24.7	18	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
9	c5e37A_	 Alignment		24.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
10	c5nymA_	 Alignment		19.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein 2.1; PDBTitle: crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state
11	d1yvwa1	 Alignment		19.0	20	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)

12	c1yvwd_	Alignment		19.0	20	PDB header: hydrolase Chain: D: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
13	d1qgva_	Alignment		17.4	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
14	c2muyA_	Alignment		14.7	15	PDB header: nucleotide binding protein Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsH; PDBTitle: the solution structure of the ftsH periplasmic n-domain
15	c2ashB_	Alignment		14.3	12	PDB header: transferase Chain: B: PDB Molecule: queuine trna-ribosyltransferase; PDBTitle: crystal structure of queuine trna-ribosyltransferase (ec 2.4.2.29)2 (trna-guanine (tm1561) from thermotoga maritima at 1.90 a resolution
16	c2yukA_	Alignment		14.2	36	PDB header: transferase Chain: A: PDB Molecule: myeloid/lymphoid or mixed-lineage leukemia PDBTitle: solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
17	c5ganD_	Alignment		14.1	13	PDB header: transcription Chain: D: PDB Molecule: spliceosomal protein dib1; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snRNP at 2 3.7 angstrom
18	c5bniA_	Alignment		13.9	33	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: porcine cd38 complexed with a covalent intermediate,2 ribo-f-ribose-5'-phosphate
19	c6iedA_	Alignment		13.3	25	PDB header: membrane protein Chain: A: PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
20	c2xzmS_	Alignment		12.3	38	PDB header: ribosome Chain: S: PDB Molecule: rps15e; 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
21	c1k48A_	Alignment	not modelled	11.9	38	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
22	c1jza_	Alignment	not modelled	11.9	38	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
23	d1vaza_	Alignment	not modelled	11.9	24	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
24	c1xbsA_	Alignment	not modelled	11.2	15	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
25	c5xyiP_	Alignment	not modelled	11.1	38	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
26	c6dy3G_	Alignment	not modelled	10.9	15	PDB header: hydrolase Chain: G: PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
27	c3k1tA_	Alignment	not modelled	10.8	24	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase gsha; PDBTitle: crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
28	d2ifqa1	Alignment	not modelled	10.7	27	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

29	c3j20T_	Alignment	not modelled	10.7	31	PDB header: ribosome Chain: T; PDB Molecule: 30s ribosomal protein s19p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
30	d1ss6a_	Alignment	not modelled	10.1	24	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
31	c5fa0B_	Alignment	not modelled	9.8	13	PDB header: transferase Chain: B; PDB Molecule: putative n-acetyl glucosaminyl transferase; PDBTitle: the structure of the beta-3-deoxy-d-manno-oct-2-ulosonic acid2 transferase domain from wbbb
32	c4u4cB_	Alignment	not modelled	9.7	33	PDB header: hydrolase Chain: B; PDB Molecule: protein air2,poly(a) rna polymerase protein 2; PDBTitle: the molecular architecture of the tramp complex reveals the2 organization and interplay of its two catalytic activities
33	c4v0bA_	Alignment	not modelled	9.5	15	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: escherichia coli ftsh hexameric n-domain
34	c1vyuB_	Alignment	not modelled	9.3	15	PDB header: ion transport Chain: B; PDB Molecule: calcium channel beta-3 subunit; PDBTitle: beta3 subunit of voltage-gated ca2+-channel
35	c2exuA_	Alignment	not modelled	9.2	18	PDB header: transcription Chain: A; PDB Molecule: transcription initiation protein spt4/spt5; PDBTitle: crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
36	c4kmhB_	Alignment	not modelled	9.0	20	PDB header: protein binding Chain: B; PDB Molecule: suppressor of fused homolog; PDBTitle: crystal structure of suppressor of fused d20
37	d2hfa1	Alignment	not modelled	8.7	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like
38	c5td6A_	Alignment	not modelled	8.6	17	PDB header: rna binding protein Chain: A; PDB Molecule: fog-3 protein; PDBTitle: c. elegans fog-3 btg/tob domain - h47n, c117a
39	c5yixB_	Alignment	not modelled	8.6	22	PDB header: dna binding protein Chain: B; PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
40	c2a7wF_	Alignment	not modelled	8.3	17	PDB header: hydrolase Chain: F; PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
41	d2a7wa1	Alignment	not modelled	8.3	17	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
42	c3ghhA_	Alignment	not modelled	8.1	27	PDB header: hydrolase Chain: A; PDB Molecule: ecto-nad+ glycohydrolase (cd38 molecule); PDBTitle: structural insights into the catalytic mechanism of cd38: evidence for2 a conformationally flexible covalent enzyme-substrate complex.
43	c3j38P_	Alignment	not modelled	8.1	31	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
44	c1rjuV_	Alignment	not modelled	7.9	80	PDB header: metal binding protein Chain: V; PDB Molecule: metallothionein; PDBTitle: crystal structure of a truncated form of yeast copper2 thionein
45	c1aqsA_	Alignment	not modelled	7.9	80	PDB header: metallothionein Chain: A; PDB Molecule: cu-metallothionein; PDBTitle: cu-metallothionein from saccharomyces cerevisiae, nmr, 102 structures
46	c4cvuA_	Alignment	not modelled	7.9	12	PDB header: hydrolase Chain: A; PDB Molecule: beta-mannosidase; PDBTitle: structure of fungal beta-mannosidase from glycoside hydrolase family 22 of trichoderma harzianum
47	c4lhdB_	Alignment	not modelled	7.7	18	PDB header: oxidoreductase Chain: B; PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
48	c6fv5B_	Alignment	not modelled	7.7	24	PDB header: transferase Chain: B; PDB Molecule: queuine trna-ribosyltransferase accessory subunit 2; PDBTitle: qtrt2, the non-catalytic subunit of murine trna-guanine2 transglycosylase
49	c4d18G_	Alignment	not modelled	7.4	19	PDB header: signaling protein Chain: G; PDB Molecule: cop9 signalosome complex subunit 7a; PDBTitle: crystal structure of the cop9 signalosome
50	d1xjha_	Alignment	not modelled	7.4	25	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
51	d1bwva2	Alignment	not modelled	7.4	15	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
52	c4ttnA_	Alignment	not modelled	7.2	38	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
53	c3zeyl_	Alignment	not modelled	7.2	46	PDB header: ribosome Chain: I; PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

54	c4ttmA	Alignment	not modelled	7.1	38	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
55	c2khaA	Alignment	not modelled	7.1	38	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
56	d1gyxA	Alignment	not modelled	7.1	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
57	d1b5ta	Alignment	not modelled	7.0	6	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Methylenetetrahydrofolate reductase
58	c5xxuP	Alignment	not modelled	6.9	38	PDB header: ribosome Chain: P; PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
59	c2k2wA	Alignment	not modelled	6.8	29	PDB header: cell cycle Chain: A; PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
60	d1ijwc	Alignment	not modelled	6.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
61	c2dj0A	Alignment	not modelled	6.7	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: thioredoxin-related transmembrane protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
62	c4ttoA	Alignment	not modelled	6.6	38	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
63	d2z15a1	Alignment	not modelled	6.6	10	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
64	c2v1wA	Alignment	not modelled	6.5	44	PDB header: toxin Chain: A; PDB Molecule: muscarinic m1-toxin1; PDBTitle: crystal structure of the muscarinic toxin mt7 diiodotyrosine derivative.
65	c5husA	Alignment	not modelled	6.3	16	PDB header: transferase Chain: A; PDB Molecule: trehalose synthase regulatory protein; PDBTitle: structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
66	c6mwcN	Alignment	not modelled	6.3	16	PDB header: virus/immune system Chain: N; PDB Molecule: e2; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus with2 fab of eeev-5 antibody
67	c2kukA	Alignment	not modelled	6.2	33	PDB header: antiviral protein Chain: A; PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
68	c3phfX	Alignment	not modelled	5.9	50	PDB header: viral protein Chain: X; PDB Molecule: envelope glycoprotein I; PDBTitle: crystal structure of the epstein-barr virus gh and gl complex
69	d1hcra	Alignment	not modelled	5.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
70	c3hypB	Alignment	not modelled	5.8	26	PDB header: electron transport Chain: B; PDB Molecule: thioredoxin; PDBTitle: crystal structure of bacteroides fragilis trxp_s105g mutant
71	d1nt0a3	Alignment	not modelled	5.7	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
72	d1yh5a1	Alignment	not modelled	5.6	16	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
73	c6ckdA	Alignment	not modelled	5.6	27	PDB header: toxin Chain: A; PDB Molecule: osptx2a-p1; PDBTitle: structure of a new shkt peptide from the sea anemone oulactis sp:2 osptx2a-p1
74	d1j08a1	Alignment	not modelled	5.5	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
75	c2pptA	Alignment	not modelled	5.3	22	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
76	d1w2za3	Alignment	not modelled	5.2	3	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
77	d1w6ga3	Alignment	not modelled	5.2	15	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
78	c4z45A	Alignment	not modelled	5.2	13	PDB header: odorant binding protein Chain: A; PDB Molecule: odorant-binding protein nr1b3p3; PDBTitle: structure of obp3 from the currant-lettuce aphid nasonovia ribisnigri
79	c1i7fA	Alignment	not modelled	5.1	8	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 33; PDBTitle: crystal structure of the hsp33 domain with constitutive chaperone2 activity
80	d1m7xa2	Alignment	not modelled	5.1	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain

81	d1fcdc1	Alignment	not modelled	5.1	0	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
82	d1vqqa2	Alignment	not modelled	5.1	20	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
83	d2i9aa1	Alignment	not modelled	5.1	60	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module