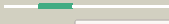
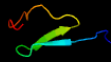
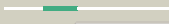














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0090 (-)_98477_99247
Date	Tue Jul 23 14:50:12 BST 2019
Unique Job ID	1494ffdd3687c3fa

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hr5B_	 Alignment		42.4	23	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
2	c5xknF_	 Alignment		40.0	67	PDB header: transferase/signaling protein Chain: F: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
3	c5xknE_	 Alignment		40.0	67	PDB header: transferase/signaling protein Chain: E: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
4	c6btmD_	 Alignment		38.4	24	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
5	d2dipa1	 Alignment		35.5	29	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
6	c2e5rA_	 Alignment		33.2	33	PDB header: dna binding protein Chain: A: PDB Molecule: dystrobrevin alpha; PDBTitle: solution structure of the zz domain of dystrobrevin alpha2 (dystrobrevin-alpha)
7	c6mj7A_	 Alignment		30.6	36	PDB header: signaling protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: crystal structure of p62 zz domain in complex with free arginine
8	c2lvhA_	 Alignment		28.6	75	PDB header: metal binding protein Chain: A: PDB Molecule: putative zinc finger protein orf59a; PDBTitle: solution structure of the zinc finger afv1p06 protein from the2 hyperthermophilic archaeal virus afv1
9	c5ypeD_	 Alignment		27.4	36	PDB header: signaling protein Chain: D: PDB Molecule: 78 kda glucose-regulated protein,sequestosome-1; PDBTitle: p62/sqstm1 zz domain with tyr-peptide
10	d2d8xa2	 Alignment		25.8	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
11	d1gtea1	 Alignment		25.8	60	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain

12	c1yuzB_	Alignment		24.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
13	d1f16a_	Alignment		23.0	16	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
14	d1tota1	Alignment		22.3	36	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
15	c1totA_	Alignment		22.3	36	PDB header: transferase Chain: A: PDB Molecule: creb-binding protein; PDBTitle: zz domain of cbp- a novel fold for a protein interaction2 module
16	c2jd3B_	Alignment		22.0	23	PDB header: dna binding protein Chain: B: PDB Molecule: stbb protein; PDBTitle: parr from plasmid pb171
17	c6cw3G_	Alignment		21.8	21	PDB header: gene regulation Chain: G: PDB Molecule: transcriptional adapter 2; PDBTitle: crystal structure of a yeast saga transcriptional coactivator2 ada2/gcn5 hat subcomplex, crystal form 2
18	d1dxga_	Alignment		18.7	32	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
19	d1a6ca3	Alignment		17.4	29	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
20	d1yua2	Alignment		17.3	18	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
21	d2fc7a1	Alignment	not modelled	17.1	33	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
22	d3e9va1	Alignment	not modelled	16.7	36	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
23	d2z15a1	Alignment	not modelled	14.9	36	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
24	c1dvbA_	Alignment	not modelled	14.9	30	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
25	d1e5qa2	Alignment	not modelled	14.2	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
26	d2idaa1	Alignment	not modelled	13.9	14	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
27	c4xi7A_	Alignment	not modelled	13.9	33	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
28	d1p1da1	Alignment	not modelled	13.3	29	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
29	c3rv2B_	Alignment	not modelled	13.0	64	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase;

29	c1vzb_	Alignment	not modelled	13.0	04	PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
30	d2h3la1	Alignment	not modelled	12.9	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
31	c6cfwl_	Alignment	not modelled	12.5	32	PDB header: membrane protein Chain: I; PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
32	c2m6oA_	Alignment	not modelled	11.4	44	PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpA binds to the principal2 sigma subunit of rna polymerase
33	d1ej5a_	Alignment	not modelled	11.4	10	Fold: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Superfamily: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Family: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
34	d1lkoa2	Alignment	not modelled	11.3	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
35	c3admC_	Alignment	not modelled	11.2	56	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
36	c2i50A_	Alignment	not modelled	11.1	30	PDB header: hydrolase Chain: A; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 16; PDBTitle: solution structure of ubp-m znf-ubp domain
37	c3admD_	Alignment	not modelled	11.1	56	PDB header: structural protein Chain: D; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
38	c4le5A_	Alignment	not modelled	10.9	9	PDB header: transferase Chain: A; PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni
39	c3eggC_	Alignment	not modelled	10.9	24	PDB header: hydrolase Chain: C; PDB Molecule: spinophilin; PDBTitle: crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
40	c1fi8F_	Alignment	not modelled	10.7	36	PDB header: hydrolase/hydrolase inhibitor Chain: F; PDB Molecule: ecotin; PDBTitle: rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
41	c6c04J_	Alignment	not modelled	10.7	50	PDB header: transcription/dna Chain: J; PDB Molecule: rna polymerase-binding protein rbpA; PDBTitle: mtb rnap holo/rbpA/double fork dna -closed clamp
42	c2n1pA_	Alignment	not modelled	10.5	14	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
43	c3admF_	Alignment	not modelled	10.5	56	PDB header: structural protein Chain: F; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
44	c3admA_	Alignment	not modelled	10.5	56	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
45	c3admE_	Alignment	not modelled	10.5	56	PDB header: structural protein Chain: E; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
46	c3admB_	Alignment	not modelled	10.5	56	PDB header: structural protein Chain: B; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
47	c3so4C_	Alignment	not modelled	10.1	55	PDB header: transferase Chain: C; PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica
48	c2l9za_	Alignment	not modelled	10.0	43	PDB header: transcription Chain: A; PDB Molecule: pr domain zinc finger protein 4; PDBTitle: zinc knuckle in prdm4
49	d1libia1	Alignment	not modelled	9.8	56	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
50	c5h67C_	Alignment	not modelled	9.7	19	PDB header: dna binding protein/cell cycle Chain: C; PDB Molecule: segregation and condensation protein a; PDBTitle: crystal structure of the bacillus subtilis smc head domain complexed2 with the cognate scpa c-terminal domain and soaked atp
51	c5tw1J_	Alignment	not modelled	9.5	50	PDB header: transcription activator/transferase/dna Chain: J; PDB Molecule: rna polymerase-binding protein rbpA; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
52	c2m4vA_	Alignment	not modelled	9.4	50	PDB header: transcription Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: mycobacterium tuberculosis rna polymerase binding protein a (rbpa) and2 its interactions with sigma factors
53	c5kzoA_	Alignment	not modelled	9.3	30	PDB header: transcription Chain: A; PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated jxtamembrane segment
54	d1nnqa2	Alignment	not modelled	9.3	26	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
						PDB header: structural genomics, unknown function

55	c3upsA_	Alignment	not modelled	9.1	19	Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
56	c2jr7A_	Alignment	not modelled	9.0	44	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
57	c3zf7o_	Alignment	not modelled	9.0	26	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
58	c3imlB_	Alignment	not modelled	8.9	64	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
59	d2g45a1	Alignment	not modelled	8.9	25	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
60	d1vaea_	Alignment	not modelled	8.7	12	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
61	d1x45a1	Alignment	not modelled	8.6	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
62	d1ny722	Alignment	not modelled	8.5	71	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
63	c1gthD_	Alignment	not modelled	8.5	60	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
64	d1dfxa2	Alignment	not modelled	8.4	29	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
65	c5ejcD_	Alignment	not modelled	8.4	36	PDB header: signaling protein Chain: D: PDB Molecule: hamartin; PDBTitle: crystal structural of the tsc1-tbc1d7 complex
66	d2uzga1	Alignment	not modelled	8.2	22	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
67	c3izrm_	Alignment	not modelled	8.2	29	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
68	d2o5aa1	Alignment	not modelled	8.2	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
69	d1pgl22	Alignment	not modelled	8.0	57	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
70	c5uz4Z_	Alignment	not modelled	7.9	29	PDB header: ribosome/hydrolase Chain: Z: PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
71	c5h9uC_	Alignment	not modelled	7.9	55	PDB header: transferase Chain: C: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a thermostable methionine adenosyltransferase
72	c2obvA_	Alignment	not modelled	7.9	64	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
73	d1xera_	Alignment	not modelled	7.8	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
74	c4odjA_	Alignment	not modelled	7.8	45	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine
75	c6fb3A_	Alignment	not modelled	7.7	45	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
76	c2k2jA_	Alignment	not modelled	7.7	14	PDB header: hydrolase, signaling protein Chain: A: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate PDBTitle: nmr solution structure of the split ph domain from2 phospholipase c gamma 2
77	d6rxna_	Alignment	not modelled	7.6	29	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
78	d1wifa_	Alignment	not modelled	7.5	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
79	c5oomu_	Alignment	not modelled	7.4	14	PDB header: ribosome Chain: U: PDB Molecule: 39s ribosomal protein l23, mitochondrial; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rrna
80	c4b6ap_	Alignment	not modelled	7.3	26	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1

81	c5lrva_	Alignment	not modelled	7.3	67	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 7b; PDBTitle: structure of cezanne/otud7b otu domain bound to lys11-linked2 diubiquitin
82	c6fkip_	Alignment	not modelled	7.2	6	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
83	c2yt7A_	Alignment	not modelled	7.2	29	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3
84	d1b8qa_	Alignment	not modelled	7.2	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
85	c3ziaT_	Alignment	not modelled	7.1	24	PDB header: hydrolase Chain: T: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae inhibited by2 its regulatory protein if1
86	c3ziaJ_	Alignment	not modelled	7.1	24	PDB header: hydrolase Chain: J: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae inhibited by2 its regulatory protein if1
87	c2qneA_	Alignment	not modelled	7.0	8	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
88	d1btna_	Alignment	not modelled	6.9	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
89	d1n7ea_	Alignment	not modelled	6.9	35	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
90	c2vsvB_	Alignment	not modelled	6.9	18	PDB header: protein binding Chain: B: PDB Molecule: rhophilin-2; PDBTitle: crystal structure of the pdz domain of human rhophilin-2
91	c2qbwA_	Alignment	not modelled	6.8	24	PDB header: unknown function Chain: A: PDB Molecule: pdz-fibronectin fusion protein; PDBTitle: the crystal structure of pdz-fibronectin fusion protein
92	c6k0bH_	Alignment	not modelled	6.8	33	PDB header: rna binding protein/rna Chain: H: PDB Molecule: ribonuclease p protein component 4; PDBTitle: cryo-em structure of archaeal ribonuclease p with mature trna
93	c2hqlB_	Alignment	not modelled	6.7	44	PDB header: dna binding protein Chain: B: PDB Molecule: hypothetical protein mg376 homolog; PDBTitle: crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
94	d1zaka2	Alignment	not modelled	6.7	40	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
95	d2ijqa1	Alignment	not modelled	6.7	16	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
96	c3ggeA_	Alignment	not modelled	6.6	18	PDB header: protein binding Chain: A: PDB Molecule: pdz domain-containing protein gipc2; PDBTitle: crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
97	c2vwrA_	Alignment	not modelled	6.5	24	PDB header: protein binding Chain: A: PDB Molecule: ligand of numb protein x 2; PDBTitle: crystal structure of the second pdz domain of numb-binding protein 2
98	c1u39A_	Alignment	not modelled	6.5	24	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding, PDBTitle: auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
99	c4wcwB_	Alignment	not modelled	6.4	19	PDB header: translation Chain: B: PDB Molecule: ribosomal silencing factor rsfs; PDBTitle: ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis