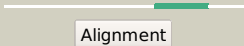

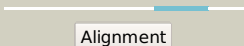


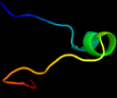
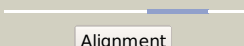

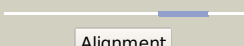

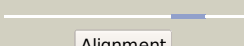

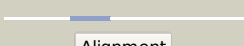
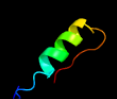



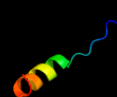






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2645 (-) _2970133_2970564
Date	Wed Aug 7 12:50:29 BST 2019
Unique Job ID	18d81eba081920b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bcqa2	 Alignment		41.4	27	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
2	d1jmsa3	 Alignment		37.5	27	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
3	c6j7jA_	 Alignment		28.8	48	PDB header: transferase Chain: A: PDB Molecule: pseudomonas aeruginosa earp; PDBTitle: crystal structure of pseudomonas aeruginosa earp
4	d1a77a1	 Alignment		28.3	29	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
5	d2fmpa2	 Alignment		27.3	50	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
6	d1mc8a1	 Alignment		23.7	35	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
7	c3qdnA_	 Alignment		23.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
8	c5e37A_	 Alignment		23.2	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ef-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
9	d1nhoa_	 Alignment		21.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
10	d2vana1	 Alignment		20.8	53	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
11	c5zvqA_	 Alignment		20.5	32	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr

12	c2in3A_	Alignment		19.0	32	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative protein disulfide isomerase from <i>Nitrosomonas europaea</i>
13	c5ganD_	Alignment		18.9	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 2.37 Å
14	c2dj0A_	Alignment		17.1	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-related transmembrane protein 2; PDBTitle: the solution structure of the thioredoxin domain of human 2 thioredoxin-related transmembrane protein 2
15	d2c0ga2	Alignment		17.1	0	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ERP29 N domain-like
16	d1b43a1	Alignment		16.2	25	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
17	c3fm2A_	Alignment		15.3	50	PDB header: heme-binding protein Chain: A: PDB Molecule: uncharacterized protein, distantly related to a heme PDBTitle: crystal structure of a putative heme-binding protein (ava_4353) from <i>Anabaena variabilis</i> ATCC 29413 at 1.80 Å resolution
18	c3p2aB_	Alignment		15.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from <i>Yersinia pestis</i>
19	d1wija_	Alignment		14.7	47	Fold: LEM/SAP HeH motif Superfamily: DNA-binding domain of E1N3-like Family: DNA-binding domain of E1N3-like
20	c2i9ha_	Alignment		14.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (Trx1)
21	c4euyA_	Alignment	not modelled	14.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of thioredoxin-like protein bce_0499 from <i>Bacillus cereus</i> ATCC 10987
22	c2l6dA_	Alignment	not modelled	14.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of desulfothioredoxin from <i>Desulfovibrio vulgaris</i> Hildenborough in its reduced form
23	c4tq1B_	Alignment	not modelled	14.6	75	PDB header: protein binding Chain: B: PDB Molecule: tectonin beta-propeller repeat-containing protein 1; PDBTitle: crystal structure of human Atg5-tecA
24	c2dbcA_	Alignment	not modelled	14.6	4	PDB header: signaling protein Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of the thioredoxin-like domain of 2-phospho-tyrosine phosphatase 2 (Pdp2)
25	c2qc7A_	Alignment	not modelled	14.5	10	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic reticulum protein erp29; PDBTitle: crystal structure of the protein-disulfide isomerase related chaperone 2 erp29
26	c3mhaB_	Alignment	not modelled	14.3	26	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from <i>Mycobacterium tuberculosis</i> bound to Pim
27	d1ti3a_	Alignment	not modelled	14.1	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
28	d1w6va1	Alignment	not modelled	13.9	28	Fold: DUSP-like Superfamily: DUSP-like Family: DUSP, domain in ubiquitin-specific proteases
						Fold: Thioredoxin fold

29	d1qgva_	Alignment	not modelled	12.7	10	Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
30	c3k8aA_	Alignment	not modelled	12.5	27	PDB header: dna binding protein Chain: A: PDB Molecule: putative primosomal replication protein; PDBTitle: neisseria gonorrhoeae prib
31	c1yvlB_	Alignment	not modelled	11.9	27	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
32	d1j08a1	Alignment	not modelled	11.8	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
33	d1vdda_	Alignment	not modelled	11.8	56	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
34	c1vddC_	Alignment	not modelled	11.2	56	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
35	c3p2aA_	Alignment	not modelled	11.2	35	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
36	c6f8sD_	Alignment	not modelled	11.0	48	PDB header: toxin Chain: D: PDB Molecule: putative killer protein; PDBTitle: toxin-antitoxin complex grata
37	c2odxA_	Alignment	not modelled	10.1	42	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4
38	c6ilcB_	Alignment	not modelled	9.7	25	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin f2; PDBTitle: crystal structure of chlamydomonas reinhardtii thioredoxin f2
39	c3en2A_	Alignment	not modelled	9.7	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable primosomal replication protein n; PDBTitle: three-dimensional structure of the protein prib from ralstonia2 solanacearum at the resolution 2.3a. northeast structural genomics3 consortium target rsr213c.
40	c6c04J_	Alignment	not modelled	9.1	24	PDB header: transcription/dna Chain: J: PDB Molecule: rna polymerase-binding protein rbpa; PDBTitle: mtb rnap holo/rbpa/double fork dna -closed clamp
41	c5kkmA_	Alignment	not modelled	9.1	80	PDB header: unknown function Chain: A: PDB Molecule: o2_contryphan_vc1 prepropeptide; PDBTitle: con-vc11-22
42	d1cuka2	Alignment	not modelled	9.1	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
43	d1q23a_	Alignment	not modelled	8.9	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
44	c3fhwB_	Alignment	not modelled	8.8	29	PDB header: dna binding protein Chain: B: PDB Molecule: primosomal replication protein n; PDBTitle: crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
45	c6ibIB_	Alignment	not modelled	8.8	30	PDB header: immune system Chain: B: PDB Molecule: thioredoxin 1,beta-1 adrenergic receptor; PDBTitle: activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80
46	d1i36a1	Alignment	not modelled	8.7	33	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Conserved hypothetical protein MTH1747
47	d1ci4a_	Alignment	not modelled	8.6	22	Fold: SAM domain-like Superfamily: Barrier-to-autointegration factor, BAF Family: Barrier-to-autointegration factor, BAF
48	d1xf1a_	Alignment	not modelled	8.6	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
49	c1ixrA_	Alignment	not modelled	8.6	50	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
50	d1bvsa2	Alignment	not modelled	8.5	50	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
51	d1ixra1	Alignment	not modelled	8.4	44	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
52	c2n24A_	Alignment	not modelled	8.3	80	PDB header: toxin Chain: A: PDB Molecule: o2_contryphan_vc1; PDBTitle: solution nmr structure of contryphan-vc1
53	c5wxkA_	Alignment	not modelled	8.3	20	PDB header: transferase Chain: A: PDB Molecule: earp; PDBTitle: earp bound with domain i of ef-p
54	c1d8IA_	Alignment	not modelled	8.2	50	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
55	c1kftA_	Alignment	not modelled	8.1	14	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrc from

					e-2 coli	
56	d1kfta	Alignment	not modelled	8.1	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
57	d1f46a	Alignment	not modelled	8.0	33	Fold: TBP-like Superfamily: Cell-division protein ZipA, C-terminal domain Family: Cell-division protein ZipA, C-terminal domain
58	c3zzxB	Alignment	not modelled	7.8	29	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystallographic structure of thioredoxin from litopenaues vannamei
59	c2wz9A	Alignment	not modelled	7.7	16	PDB header: protein binding Chain: A: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the thioredoxin domain of human txn12
60	c4kndA	Alignment	not modelled	7.7	40	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: thioredoxin from anaeromyxobacter dehalogenans.
61	c1ciiA	Alignment	not modelled	7.7	43	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
62	c2qsiB	Alignment	not modelled	7.6	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
63	c6drmA	Alignment	not modelled	7.5	23	PDB header: hydrolase Chain: A: PDB Molecule: inactive ubiquitin thioesterase fam105a; PDBTitle: otu domain of fam105a
64	c2i9dC	Alignment	not modelled	7.4	6	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
65	c5xknF	Alignment	not modelled	7.3	63	PDB header: transferase/signaling protein Chain: F: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epfl4
66	c5xknE	Alignment	not modelled	7.3	63	PDB header: transferase/signaling protein Chain: E: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epfl4
67	c2i4aA	Alignment	not modelled	7.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti
68	d2paja1	Alignment	not modelled	7.2	30	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
69	c2wy3B	Alignment	not modelled	7.1	39	PDB header: immune system/viral protein Chain: B: PDB Molecule: uncharacterized protein ul16; PDBTitle: structure of the hcmv ul16-micb complex elucidates select2 binding of a viral immunoevasin to diverse nkg2d ligands
70	c2y69S	Alignment	not modelled	7.1	45	PDB header: electron transport Chain: S: PDB Molecule: cytochrome c oxidase subunit 5b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
71	c2lrcA	Alignment	not modelled	7.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
72	d1enf1	Alignment	not modelled	7.0	67	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
73	d1bxta1	Alignment	not modelled	7.0	83	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
74	d1ck1a1	Alignment	not modelled	6.9	67	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
75	c2diyA	Alignment	not modelled	6.8	17	PDB header: protein binding Chain: A: PDB Molecule: thioredoxin-like protein 2; PDBTitle: the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
76	d3seba1	Alignment	not modelled	6.7	83	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
77	d1b6aa1	Alignment	not modelled	6.7	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
78	c3dxbE	Alignment	not modelled	6.7	35	PDB header: splicing, transcription Chain: E: PDB Molecule: thioredoxin n-terminally fused to puf60(uhm); PDBTitle: structure of the uhm domain of puf60 fused to thioredoxin
79	d1klud1	Alignment	not modelled	6.7	67	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
80	d2ifqa1	Alignment	not modelled	6.5	35	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
81	c4i14B	Alignment	not modelled	6.4	60	PDB header: hydrolase, lyase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: crystal structure of mtb-riba2 (rv1415)

82	d2ilqa1	Alignment	not modelled	6.4	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
83	c1xbsA	Alignment	not modelled	6.4	4	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
84	d2bz1a1	Alignment	not modelled	6.3	40	Fold: RibA-like Superfamily: RibA-like Family: RibA-like
85	d1v54f	Alignment	not modelled	6.3	50	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Cytochrome c oxidase Subunit F
86	c4rl4B	Alignment	not modelled	6.3	40	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase-2; PDBTitle: crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
87	c2pptA	Alignment	not modelled	6.2	30	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
88	d1fnua1	Alignment	not modelled	6.2	83	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
89	d1i4pa1	Alignment	not modelled	6.2	67	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
90	c4ruvA	Alignment	not modelled	6.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
91	d1rr7a	Alignment	not modelled	6.1	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
92	c1rr7A	Alignment	not modelled	6.1	30	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
93	d1wj9a1	Alignment	not modelled	6.1	42	Fold: Ferredoxin-like Superfamily: CRISPR-associated protein Family: CRISPR-associated protein
94	c2ihmA	Alignment	not modelled	6.0	36	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
95	d2aq2b1	Alignment	not modelled	5.9	67	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
96	c2i5IA	Alignment	not modelled	5.9	40	PDB header: transport protein Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution structure of thioredoxin from bacteroides vulgatus
97	d1kf6a3	Alignment	not modelled	5.9	67	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
98	c3pfnB	Alignment	not modelled	5.9	29	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
99	d1rutx2	Alignment	not modelled	5.9	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain