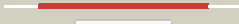
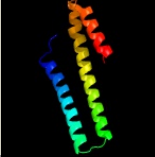


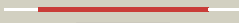














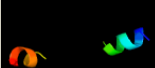




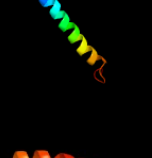
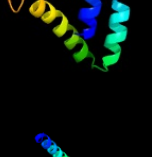
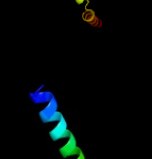

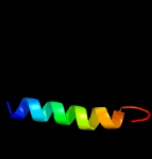

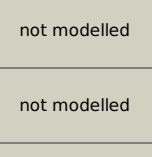


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1766 (-) _1999744_2000013
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	a1ac11495e791a59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4m1pA_	 Alignment		100.0	28	PDB header: transcription repressor Chain: A: PDB Molecule: copper-sensitive operon repressor (csor); PDBTitle: crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
2	c5lbnD_	 Alignment		100.0	22	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor frmr; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
3	c5fmnB_	 Alignment		100.0	35	PDB header: dna binding protein Chain: B: PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
4	c5lcyD_	 Alignment		100.0	24	PDB header: transcription Chain: D: PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
5	c4adzA_	 Alignment		99.9	29	PDB header: transcription Chain: A: PDB Molecule: csor; PDBTitle: crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
6	c2hh7A_	 Alignment		99.9	32	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
7	c3aaiB_	 Alignment		99.9	34	PDB header: transcription Chain: B: PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
8	c2p5tA_	 Alignment		36.2	38	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator peza; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
9	c4aj5M_	 Alignment		34.0	15	PDB header: cell cycle Chain: M: PDB Molecule: spindle and kinetochore-associated protein 2; PDBTitle: crystal structure of the ska core complex
10	c3zs9D_	 Alignment		31.5	33	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
11	c5frhA_	 Alignment		31.4	12	PDB header: transcription Chain: A: PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra

12	c1paqA	Alignment		29.7	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
13	d1paqa	Alignment		29.7	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
14	d1ivsa1	Alignment		19.9	6	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
15	c3juia	Alignment		19.1	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
16	c4u8us	Alignment		18.8	4	PDB header: oxygen storage/transport Chain: S: PDB Molecule: globin d chain; PDBTitle: the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
17	c2nv2U	Alignment		18.5	18	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
18	c4fc9B	Alignment		18.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of the c-terminal domain of the type iii effector xcv32202 (xopl)
19	c2qycA	Alignment		17.4	18	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
20	d1kkga	Alignment		14.8	27	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
21	c4n6jA	Alignment	not modelled	14.3	21	PDB header: signaling protein Chain: A: PDB Molecule: striatin-3; PDBTitle: crystal structure of human striatin-3 coiled coil domain
22	c4n6jB	Alignment	not modelled	13.9	21	PDB header: signaling protein Chain: B: PDB Molecule: striatin-3; PDBTitle: crystal structure of human striatin-3 coiled coil domain
23	c5vf3Z	Alignment	not modelled	12.8	31	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
24	c5an5J	Alignment	not modelled	12.6	27	PDB header: cell cycle Chain: J: PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb c-terminal domain
25	c2n5xA	Alignment	not modelled	12.2	8	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
26	d1josa	Alignment	not modelled	11.9	18	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
27	c4lh9A	Alignment	not modelled	11.5	14	PDB header: transcription Chain: A: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the refolded hood domain (asp256-gly295) of hetr
28	c4n5bF	Alignment	not modelled	10.3	10	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the nipah virus phosphoprotein tetramerization2 domain
29	c2gtlO	Alignment	not modelled	9.6	10	PDB header: oxygen storage/transport Chain: O: PDB Molecule: extracellular hemoglobin linker I3 subunit;

						PDBTitle: lumbricus erythrocrucorin at 3.5a resolution
30	d2igsA1	Alignment	not modelled	9.2	27	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PA2222-like
31	c2mhwA_	Alignment	not modelled	8.4	21	PDB header: antimicrobial protein, membrane protein Chain: A: PDB Molecule: antimicrobial peptide; PDBTitle: the solution nmr structure of maximin-4 in sds micelles
32	c3femB_	Alignment	not modelled	8.2	9	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
33	c6hyeF_	Alignment	not modelled	8.1	18	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a)
34	c2ovcA_	Alignment	not modelled	8.1	10	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
35	d1q4ra_	Alignment	not modelled	8.0	5	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
36	c4p3gC_	Alignment	not modelled	8.0	12	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: structure of the srp68-rbd from chaetomium thermophilum
37	c2i9iA_	Alignment	not modelled	7.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of helicobacter pylori protein hp0492
38	d2i9ia1	Alignment	not modelled	7.4	11	Fold: Anticodon-binding domain-like Superfamily: XCC0632-like Family: NLBH-like
39	c2kzfA_	Alignment	not modelled	6.9	23	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome-binding factor a; PDBTitle: solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
40	d1tr0a_	Alignment	not modelled	6.8	9	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
41	c3cveC_	Alignment	not modelled	6.8	21	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
42	c5y02D_	Alignment	not modelled	6.7	14	PDB header: lyase Chain: D: PDB Molecule: hydroxynitrile lyase; PDBTitle: c-terminal peptide depleted mutant of hydroxynitrile lyase from2 passiflora edulis (pehnl) bound with (r)-mandelonitrile
43	c1cffB_	Alignment	not modelled	6.6	40	PDB header: calmodulin Chain: B: PDB Molecule: calcium pump; PDBTitle: nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
44	c6hxgE_	Alignment	not modelled	6.3	18	PDB header: plant protein Chain: E: PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate)
45	c3ibwA_	Alignment	not modelled	6.1	26	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
46	c4yioB_	Alignment	not modelled	6.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: x-ray structure of the iron/manganese cambialistic superoxide2 dismutase from streptococcus thermophilus
47	c3vdoB_	Alignment	not modelled	6.1	6	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rska; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
48	d1tiza_	Alignment	not modelled	6.0	9	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
49	c5b0aA_	Alignment	not modelled	5.9	0	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
50	c3rkgA_	Alignment	not modelled	5.7	4	PDB header: metal transport Chain: A: PDB Molecule: magnesium transporter mrs2, mitochondrial; PDBTitle: structural and functional characterization of the yeast mg2+ channel2 mrs2
51	c6bp6A_	Alignment	not modelled	5.5	30	PDB header: endocytosis Chain: A: PDB Molecule: comm domain-containing protein 9; PDBTitle: crystal structure of commd9 comm domain
52	c3nepX_	Alignment	not modelled	5.5	17	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
53	d1pa4a_	Alignment	not modelled	5.3	17	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
54	d1gtda_	Alignment	not modelled	5.3	17	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
						Fold: Spectrin repeat-like

55	d1j2b_	Alignment	not modelled	5.3	16	Superfamily: GAT-like domain Family: GAT domain
56	c2xa0C_	Alignment	not modelled	5.3	26	PDB header: apoptosis Chain: C: PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
57	c4oe8C_	Alignment	not modelled	5.1	19	PDB header: immune system Chain: C: PDB Molecule: alphabody ma12; PDBTitle: interleukin-23 complex with an antagonistic alphabody, crystal form 1