

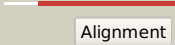
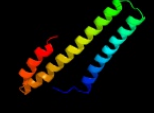
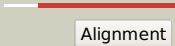

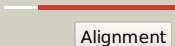

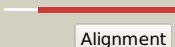
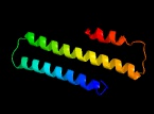




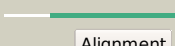

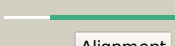

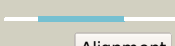
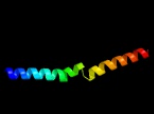

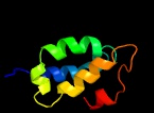
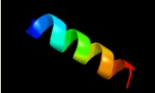
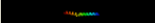

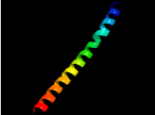


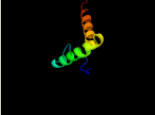




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0967_(-)_1077979_1078338
Date	Wed Jul 31 22:05:03 BST 2019
Unique Job ID	ab1bc1350dcb442c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hh7A_	 Alignment		100.0	100	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
2	c4m1pA_	 Alignment		100.0	31	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
3	c5fmnB_	 Alignment		100.0	29	PDB header: dna binding protein Chain: B; PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
4	c4adzA_	 Alignment		100.0	33	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
5	c5lbnD_	 Alignment		100.0	24	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
6	c5lcyD_	 Alignment		100.0	22	PDB header: transcription Chain: D; PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
7	c3aaiB_	 Alignment		99.9	36	PDB header: transcription Chain: B; PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
8	c1paqA_	 Alignment		49.9	6	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
9	d1paqa_	 Alignment		49.9	6	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
10	c4aj5M_	 Alignment		39.2	12	PDB header: cell cycle Chain: M; PDB Molecule: spindle and kinetochore-associated protein 2; PDBTitle: crystal structure of the ska core complex
11	c5frhA_	 Alignment		37.3	13	PDB header: transcription Chain: A; PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra

12	c2p5tA_	Alignment		24.5	56	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
13	c4u8us_	Alignment		24.4	5	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.
14	d1ivsa1	Alignment		22.2	21	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
15	c4n5bF_	Alignment		21.9	14	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the nipah virus phosphoprotein tetramerization2 domain
16	c2n5xA_	Alignment		15.9	13	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
17	c2nv2U_	Alignment		14.8	20	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	c5wuqD_	Alignment		14.6	21	PDB header: metal binding protein Chain: D: PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
19	c4fc9B_	Alignment		13.2	13	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)
20	c4n6jA_	Alignment		11.8	14	PDB header: signaling protein Chain: A: PDB Molecule: striatin-3; PDBTitle: crystal structure of human striatin-3 coiled coil domain
21	c4n6jB_	Alignment	not modelled	11.3	14	PDB header: signaling protein Chain: B: PDB Molecule: striatin-3; PDBTitle: crystal structure of human striatin-3 coiled coil domain
22	d1okkd1	Alignment	not modelled	11.0	62	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
23	c6ef3s_	Alignment	not modelled	10.6	50	PDB header: motor protein Chain: S: PDB Molecule: PDBTitle: yeast 26s proteasome bound to ubiquitinated substrate (4d motor state)
24	c5gxtA_	Alignment	not modelled	9.7	27	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pigg
25	c2gtlO_	Alignment	not modelled	9.5	7	PDB header: oxygen storage/transport Chain: O: PDB Molecule: extracellular hemoglobin linker l3 subunit; PDBTitle: lumbricus erythrocruurin at 3.5a resolution
26	c3swyB_	Alignment	not modelled	9.3	20	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated cation channel alpha-3; PDBTitle: cnga3 626-672 containing clz domain
27	c6hyeF_	Alignment	not modelled	9.1	16	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a)
28	c3zs9D_	Alignment	not modelled	8.1	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
29	d2fb5a1	Alignment	not modelled	8.1	11	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like

30	d2oa5a1	Alignment	not modelled	7.9	8	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
31	c6n6sB	Alignment	not modelled	7.5	7	PDB header: signaling protein Chain: B: PDB Molecule: tnfaip3-interacting protein 1; PDBTitle: crystal structure of abin-1 uban
32	c2ovcA	Alignment	not modelled	7.5	19	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
33	c3juia	Alignment	not modelled	7.3	10	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
34	c4vioB	Alignment	not modelled	7.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: x-ray structure of the iron/manganese cambialistic superoxide2 dismutase from streptococcus thermophilus
35	c5xbjA	Alignment	not modelled	7.1	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
36	d2i76a1	Alignment	not modelled	7.1	63	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
37	c5zbgC	Alignment	not modelled	7.0	24	PDB header: membrane protein Chain: C: PDB Molecule: short transient receptor potential channel 3; PDBTitle: cryo-em structure of human trpc3 at 4.36a resolution
38	c2q0oC	Alignment	not modelled	7.0	18	PDB header: transcription Chain: C: PDB Molecule: probable transcriptional repressor tram; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
39	c6hxoE	Alignment	not modelled	6.3	8	PDB header: plant protein Chain: E: PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate)
40	c4jqfA	Alignment	not modelled	6.3	15	PDB header: dna binding protein Chain: A: PDB Molecule: cst complex subunit stn1; PDBTitle: structure of the c-terminal domain of human telomeric stn1
41	c5vf3Z	Alignment	not modelled	6.1	31	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
42	d1zbpA1	Alignment	not modelled	5.9	29	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
43	d1o3xa	Alignment	not modelled	5.9	20	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
44	c3h09B	Alignment	not modelled	5.5	29	PDB header: hydrolase Chain: B: PDB Molecule: immunoglobulin a1 protease; PDBTitle: the structure of haemophilus influenzae iga1 protease
45	c2zbtB	Alignment	not modelled	5.5	12	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
46	c4adsF	Alignment	not modelled	5.5	24	PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex
47	c5t76A	Alignment	not modelled	5.5	19	PDB header: translation Chain: A: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: a fragment of a human trna synthetase
48	d1zq1c1	Alignment	not modelled	5.5	19	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
49	c3cveC	Alignment	not modelled	5.5	25	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
50	c2ld3A	Alignment	not modelled	5.4	18	PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: solution structure of myosin vi lever arm extension
51	c5z08A	Alignment	not modelled	5.4	10	PDB header: cell cycle Chain: A: PDB Molecule: cenp-i; PDBTitle: the crystal structure of kinetochore subunits cenp-h//k triple2 complex
52	d3mdea2	Alignment	not modelled	5.4	17	Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
53	d2db7a1	Alignment	not modelled	5.2	36	Fold: Orange domain-like Superfamily: Orange domain-like Family: Hairy Orange domain
54	c3syjA	Alignment	not modelled	5.2	53	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion and penetration protein autotransporter; PDBTitle: crystal structure of the haemophilus influenzae hap adhesin
55	c5b42A	Alignment	not modelled	5.1	27	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein muti; PDBTitle: crystal structure of the c-terminal endonuclease domain

					of aquifex2 aeolicus mutl.
56	c3o6xC_	Alignment	not modelled	5.1	14 PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
57	c3cvfA_	Alignment	not modelled	5.0	24 PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
58	c2k9yA_	Alignment	not modelled	5.0	47 PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0