


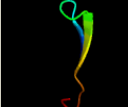
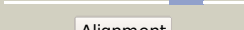
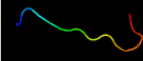



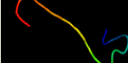



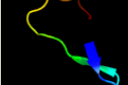

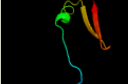
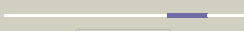
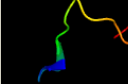
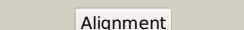

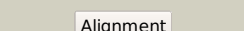
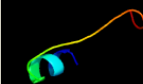
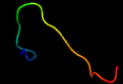
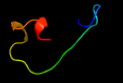


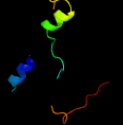
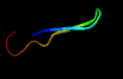





Phyre2

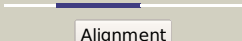

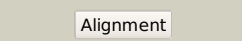
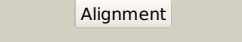
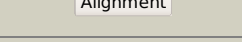
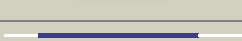
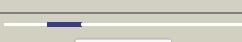
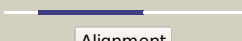
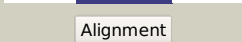
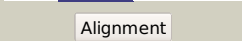
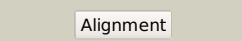

Email	mdejesus@rockefeller.edu
Description	RVBD0572c_(-)_665045_665386
Date	Fri Jul 26 01:50:12 BST 2019
Unique Job ID	f12098ac8d6336c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sr3a_	 Alignment		35.2	25	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
2	c3k8rA_	 Alignment		27.0	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
3	c2gj2A_	 Alignment		26.4	50	PDB header: metal binding protein Chain: A: PDB Molecule: wsv230; PDBTitle: crystal structure of vp9 from white spot syndrome virus
4	d1lizna_	 Alignment		20.0	44	Fold: Subunits of heterodimeric actin filament capping protein Capz Superfamily: Subunits of heterodimeric actin filament capping protein Capz Family: Capz alpha-1 subunit
5	c4j43A_	 Alignment		19.9	38	PDB header: oxidoreductase Chain: A: PDB Molecule: pyld; PDBTitle: pyld holoenzyme
6	d2f69a1	 Alignment		18.6	47	Fold: open-sided beta-meander Superfamily: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain Family: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
7	c5nz7A_	 Alignment		18.6	19	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
8	c4m6tA_	 Alignment		18.4	29	PDB header: transcription regulator Chain: A: PDB Molecule: rna polymerase ii-associated factor 1 homolog, linker, rna PDBTitle: structure of human paf1 and leo1 complex
9	c5nz8A_	 Alignment		18.3	19	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
10	c4akrC_	 Alignment		18.2	67	PDB header: actin-binding protein Chain: C: PDB Molecule: f-actin-capping protein subunit alpha; PDBTitle: crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
11	c4c9vA_	 Alignment		14.2	47	PDB header: signaling protein Chain: A: PDB Molecule: rnf43; PDBTitle: xenopus rnf43 ectodomain in complex with xenopus rspo2 fu1-fu2

12	d2es7a1	Alignment		14.1	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like
13	d2fd6u2	Alignment		13.6	31	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
14	d1pzqa2	Alignment		12.9	63	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
15	c4c84B_	Alignment		12.8	37	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase znr3; PDBTitle: zebrafish znr3 ectodomain crystal form i
16	c3ddsB_	Alignment		12.6	29	PDB header: transferase Chain: B: PDB Molecule: glycogen phosphorylase, liver form; PDBTitle: crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
17	c3hwuA_	Alignment		12.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of putative dna-binding protein (yp_299413.1) from2 ralstonia eutropha jmp134 at 1.30 a resolution
18	c3t69A_	Alignment		11.2	38	PDB header: transferase Chain: A: PDB Molecule: putative 2-dehydro-3-deoxygalactonokinase; PDBTitle: crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
19	c2vx8D_	Alignment		11.2	23	PDB header: endocytosis,exocytosis Chain: D: PDB Molecule: nucleoporin-like protein rip, vesicle-associated membrane PDBTitle: vamp7 longin domain hrb peptide complex
20	c2glijR_	Alignment		11.2	23	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
21	d1x92a_	Alignment	not modelled	11.2	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
22	c3trjC_	Alignment	not modelled	11.2	12	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
23	d2atia1	Alignment	not modelled	11.1	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
24	c2yvaB_	Alignment	not modelled	11.1	24	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
25	c1qqgA_	Alignment	not modelled	10.6	8	PDB header: signal transduction Chain: A: PDB Molecule: insulin receptor substrate 1; PDBTitle: crystal structure of the ph-ptb targeting region of irs-1
26	d1tk9a_	Alignment	not modelled	10.4	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
27	c2x8nA_	Alignment	not modelled	10.1	26	PDB header: structural genomics Chain: A: PDB Molecule: cv0863; PDBTitle: solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. ocsb target cv0863.
28	d1wdia_	Alignment	not modelled	10.0	18	Fold: QueA-like Superfamily: QueA-like Family: QueA-like
						PDB header: transcription regulator

29	c3shoA	Alignment	not modelled	9.6	31	Chain: A; PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
30	c2ys5A	Alignment	not modelled	9.3	23	PDB header: signaling protein Chain: A; PDB Molecule: fibroblast growth factor receptor substrate 3; PDBTitle: solution structure of the complex of the ptb domain of snt-2 and 19-2 residue peptide (aa 1571-1589) of halk
31	c2kctA	Alignment	not modelled	9.1	13	PDB header: chaperone Chain: A; PDB Molecule: cytochrome c-type biogenesis protein ccme; PDBTitle: solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g.
32	c2lcdA	Alignment	not modelled	8.9	25	PDB header: transcription Chain: A; PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 tudor domain
33	c2qvoA	Alignment	not modelled	8.8	39	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein af_1382; PDBTitle: crystal structure of af1382 from archaeoglobus fulgidus
34	c5by2A	Alignment	not modelled	8.8	24	PDB header: isomerase Chain: A; PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
35	c1j6qA	Alignment	not modelled	8.7	18	PDB header: chaperone Chain: A; PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme2 chaperone ccme
36	d1j6qa	Alignment	not modelled	8.7	18	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
37	c2x3yA	Alignment	not modelled	8.6	25	PDB header: isomerase Chain: A; PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
38	d1x94a	Alignment	not modelled	8.5	19	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
39	c1h0hA	Alignment	not modelled	8.2	38	PDB header: electron transport Chain: A; PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
40	c2kc2A	Alignment	not modelled	7.9	29	PDB header: structural protein Chain: A; PDB Molecule: talin-1; PDBTitle: nmr structure of the f1 domain (residues 86-202) of the2 talin
41	c4l7zC	Alignment	not modelled	7.9	26	PDB header: lyase Chain: C; PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase
42	d1pfsa	Alignment	not modelled	7.8	53	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
43	c3htnA	Alignment	not modelled	7.6	18	PDB header: metal binding protein Chain: A; PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
44	c2mr6A	Alignment	not modelled	7.4	58	PDB header: de novo protein Chain: A; PDB Molecule: de novo designed protein or462; PDBTitle: solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or462
45	c6b4sB	Alignment	not modelled	7.2	21	PDB header: allergen Chain: B; PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
46	d1qqqa2	Alignment	not modelled	7.2	8	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
47	d1jeoa	Alignment	not modelled	7.1	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
48	c3ml4D	Alignment	not modelled	6.8	17	PDB header: signaling protein Chain: D; PDB Molecule: protein dok-7; PDBTitle: crystal structure of a complex between dok7 ph-ptb and the musk2 juxtamembrane region
49	c1h5nC	Alignment	not modelled	6.7	31	PDB header: oxidoreductase Chain: C; PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
50	d2nn6g2	Alignment	not modelled	6.3	60	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
51	d1vima	Alignment	not modelled	6.3	20	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
52	d2afwa1	Alignment	not modelled	6.2	32	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminyl-peptide cyclotransferase-like
53	d1xgsa1	Alignment	not modelled	6.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
54	c3h8tA	Alignment	not modelled	6.2	28	PDB header: heme-binding protein Chain: A; PDB Molecule: hmuy; PDBTitle: structure of porphyromonas gingivalis heme-binding protein hmuy in2 complex with heme

55	c5uqzA_	 Alignment	not modelled	6.2	17	PDB header: sugar binding protein Chain: A: PDB Molecule: glucan-binding protein c, gbpc; PDBTitle: structural analysis of the glucan binding protein c of streptococcus2 mutans provides evidence that it mediates both sucrose-independent3 and -dependent adherence
56	c4gwpB_	 Alignment	not modelled	6.1	22	PDB header: transcription Chain: B: PDB Molecule: mediator of rna polymerase ii transcription subunit 17; PDBTitle: structure of the mediator head module from s. cerevisiae
57	c2l8bA_	 Alignment	not modelled	5.7	24	PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: trai (381-569)
58	d1vlfm2	 Alignment	not modelled	5.7	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
59	c5y59B_	 Alignment	not modelled	5.6	55	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
60	c3s6kA_	 Alignment	not modelled	5.6	22	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of xcnags
61	c6b9rD_	 Alignment	not modelled	5.6	17	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
62	c2e7zA_	 Alignment	not modelled	5.4	56	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
63	c4mhza_	 Alignment	not modelled	5.4	19	PDB header: transferase Chain: A: PDB Molecule: glutaminy cyclase, putative; PDBTitle: crystal structure of apo-form glutaminy cyclase from ixodes2 scapularis in complex with pbd150
64	d1e6vc_	 Alignment	not modelled	5.3	23	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase gamma chain
65	c2vt2A_	 Alignment	not modelled	5.2	25	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor receptor substrate 3 and alk PDBTitle: solution structure of the chimera of the ptb domain of snt-2 and 19-2 residue peptide (aa 1571-1589) of halk
66	c5uqiA_	 Alignment	not modelled	5.1	24	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p