

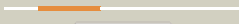




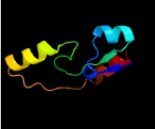

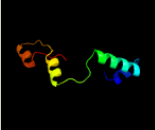
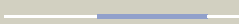
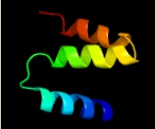

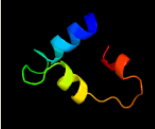







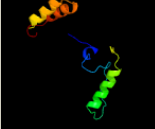

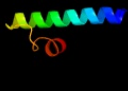






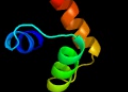


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3749c_(-)_4197806_4198096
Date	Fri Aug 9 18:20:45 BST 2019
Unique Job ID	73827dc0c8bb58c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y82a1	 Alignment		94.4	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
2	d1v96a1	 Alignment		89.2	19	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	d1t06a_	 Alignment		65.9	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: BC3264-like
4	c3fysA_	 Alignment		26.2	12	PDB header: fatty acid-binding protein Chain: A: PDB Molecule: protein degv; PDBTitle: crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
5	c3ldaA_	 Alignment		23.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
6	c2of5K_	 Alignment		23.2	17	PDB header: apoptosis Chain: K: PDB Molecule: leucine-rich repeat and death domain-containing protein; PDBTitle: oligomeric death domain complex
7	c3kk4B_	 Alignment		22.9	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
8	c3lupA_	 Alignment		20.3	12	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: degv family protein; PDBTitle: crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
9	c4hdtA_	 Alignment		20.3	28	PDB header: isomerase Chain: A: PDB Molecule: 3-hydroxyisobutyryl-coa hydrolase; PDBTitle: crystal structure of a carnitiny-coa dehydratase from mycobacterium2 thermoresistibile
10	c4o9lA_	 Alignment		18.9	18	PDB header: antiviral protein Chain: A: PDB Molecule: mitochondrial antiviral signaling protein (mavs); PDBTitle: crystal structure of horse mavs card domain mutant e26r
11	c3bptA_	 Alignment		18.8	17	PDB header: hydrolase Chain: A: PDB Molecule: 3-hydroxyisobutyryl-coa hydrolase; PDBTitle: crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin

12	d1hiod_	Alignment		17.1	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
13	c6hqaK_	Alignment		16.1	12	PDB header: transcription Chain: K: PDB Molecule: subunit (61/68 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
14	c3eglC_	Alignment		15.7	9	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: degv family protein; PDBTitle: crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
15	c3rruA_	Alignment		14.9	15	PDB header: signaling protein Chain: A: PDB Molecule: tom111 protein; PDBTitle: x-ray crystal structure of the vhs domain of human tom1-like protein,2 northeast structural genomics consortium target hr3050e
16	c6dkeA_	Alignment		14.9	13	PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b1 protein; PDBTitle: the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution
17	c3jr7A_	Alignment		14.7	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized egv family protein cog1307; PDBTitle: the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
18	c2dfIA_	Alignment		14.7	10	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
19	d1p6ra_	Alignment		14.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
20	c4wzsB_	Alignment		14.2	5	PDB header: transcription Chain: B: PDB Molecule: tata-binding protein-associated phosphoprotein; PDBTitle: crystal structure of the mot1 n-terminal domain in complex with tbp2 and nc2 bound to a promoter dna fragment
21	d1h3ob_	Alignment	not modelled	13.1	12	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
22	c4wv4B_	Alignment	not modelled	12.4	15	PDB header: transcription Chain: B: PDB Molecule: transcription initiation factor tfiid subunit 8; PDBTitle: heterodimer of taf8/taf10
23	d1w2za3	Alignment	not modelled	11.9	15	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
24	c2npuA_	Alignment	not modelled	11.7	15	PDB header: transferase Chain: A: PDB Molecule: fkbp12-rapamycin complex-associated protein; PDBTitle: the solution structure of the rapamycin-binding domain of2 mtor (frb)
25	c4oa8A_	Alignment	not modelled	11.4	11	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase family protein; PDBTitle: x-ray crystal structure of o-methyltransferase from anaplasma2 phagocytophilum in apo form
26	c3r0rA_	Alignment	not modelled	11.1	22	PDB header: virus Chain: A: PDB Molecule: porcine circovirus 2 (pcv2) capsid protein; PDBTitle: the 2.3 a structure of porcine circovirus 2
27	d1pzxa_	Alignment	not modelled	10.4	23	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
28	c1t4gA_	Alignment	not modelled	10.2	14	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp

29	c1mgpA_	Alignment	not modelled	10.2	17	PDB header: lipid binding protein Chain: A: PDB Molecule: hypothetical protein tm841; PDBTitle: hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
30	d1mgpa_	Alignment	not modelled	10.2	17	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
31	c3pl5A_	Alignment	not modelled	10.2	17	PDB header: lipid binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: fatty acid binding protein
32	c3axjB_	Alignment	not modelled	10.2	19	PDB header: dna binding protein Chain: B: PDB Molecule: translin associated factor x, isoform b; PDBTitle: high resolution crystal structure of c3po
33	d2ev0a1	Alignment	not modelled	9.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
34	c5utoB_	Alignment	not modelled	9.5	17	PDB header: transport protein Chain: B: PDB Molecule: edd domain protein, degv family; PDBTitle: the crystal structure of the staphylococcus aureus fatty acid kinase2 (fak) b1 protein loaded with palmitic acid to 1.83 angstrom3 resolution
35	d2huec1	Alignment	not modelled	9.4	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
36	c4dg7D_	Alignment	not modelled	9.2	21	PDB header: dna binding protein Chain: D: PDB Molecule: gm27569p; PDBTitle: low resolution structure of drosophila translin
37	c2qrxA_	Alignment	not modelled	9.1	17	PDB header: dna binding protein Chain: A: PDB Molecule: gm27569p; PDBTitle: crystal structure of drosophila melanogaster translin protein
38	c3nyiA_	Alignment	not modelled	9.0	13	PDB header: lipid binding protein Chain: A: PDB Molecule: fat acid-binding protein; PDBTitle: the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
39	c1vw3D_	Alignment	not modelled	8.7	14	PDB header: ribosome Chain: D: PDB Molecule: 54s ribosomal protein yml6, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
40	d1l1ja_	Alignment	not modelled	8.4	19	Fold: alpha-alpha superhelix Superfamily: Translin Family: Translin
41	c6cngA_	Alignment	not modelled	8.4	12	PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b3 protein; PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b3 protein loaded with linoleic acid to 1.47 angstrom3 resolution
42	d1za0a1	Alignment	not modelled	8.2	18	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
43	c2dt8A_	Alignment	not modelled	8.2	17	PDB header: lipid binding protein Chain: A: PDB Molecule: degv family protein; PDBTitle: fatty acid binding of a degv family protein from thermus thermophilus
44	c2ev5B_	Alignment	not modelled	8.1	19	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
45	d1id3b_	Alignment	not modelled	7.8	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
46	d1e2ka_	Alignment	not modelled	7.7	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
47	c2i4cA_	Alignment	not modelled	7.5	24	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
48	c6dj6B_	Alignment	not modelled	7.4	22	PDB header: transferase Chain: B: PDB Molecule: fatty acid kinase (fak) b2 protein (spr1019); PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b2 protein loaded with cis-oleic acid to 1.9 angstrom3 resolution
49	c2g7zB_	Alignment	not modelled	7.3	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein spy1493; PDBTitle: conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
50	c3csvA_	Alignment	not modelled	7.3	11	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
51	c1g3wA_	Alignment	not modelled	7.2	12	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
52	d1xr4a1	Alignment	not modelled	7.2	35	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
53	c3pjaK_	Alignment	not modelled	6.9	30	PDB header: hydrolase Chain: K: PDB Molecule: translin-associated protein x; PDBTitle: crystal structure of human c3po complex

54	c4x9xA	Alignment	not modelled	6.6	22	PDB header: transferase Chain: A: PDB Molecule: degv domain-containing protein mw1315; PDBTitle: biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family
55	c4wv4A	Alignment	not modelled	6.5	17	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
56	d3ctaa1	Alignment	not modelled	6.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
57	c3t0yD	Alignment	not modelled	6.3	22	PDB header: transcription regulator/protein binding Chain: D: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
58	c3zmdD	Alignment	not modelled	6.2	13	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
59	d3fabp	Alignment	not modelled	6.1	15	Fold: Four-helical up-and-down bundle Superfamily: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) Family: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
60	d2isya1	Alignment	not modelled	6.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
61	d1juqa	Alignment	not modelled	6.0	15	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
62	c2pg1L	Alignment	not modelled	5.9	24	PDB header: structural protein Chain: L: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
63	c2pg1J	Alignment	not modelled	5.9	24	PDB header: structural protein Chain: J: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
64	c2rodB	Alignment	not modelled	5.9	50	PDB header: apoptosis Chain: B: PDB Molecule: noxaa; PDBTitle: solution structure of mcl-1 complexed with noxaa
65	d1w6ga3	Alignment	not modelled	5.9	4	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
66	c5cviB	Alignment	not modelled	5.9	16	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
67	d1g3wa1	Alignment	not modelled	5.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
68	c6mzdC	Alignment	not modelled	5.8	11	PDB header: transcription Chain: C: PDB Molecule: transcription initiation factor tfiid subunit 3; PDBTitle: human tfiid lobe a canonical
69	c2k4bA	Alignment	not modelled	5.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
70	c5y26A	Alignment	not modelled	5.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase epsilon subunit d; PDBTitle: crystal structure of native dpb4-dpb3
71	c3t0yB	Alignment	not modelled	5.6	22	PDB header: transcription regulator/protein binding Chain: B: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
72	d1okra	Alignment	not modelled	5.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
73	c4xlqB	Alignment	not modelled	5.4	21	PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: c. glabrata slx1 in complex with slx4ccd.
74	c3eo6B	Alignment	not modelled	5.4	36	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of unknown function (duf1255); PDBTitle: crystal structure of protein of unknown function (duf1255) (afe_2634)2 from acidithiobacillus ferrooxidans ncib8455 at 0.97 a resolution
75	c3zc1E	Alignment	not modelled	5.3	12	PDB header: hydrolase Chain: E: PDB Molecule: aftrax; PDBTitle: crystal structure of afc3po
76	c1zawZ	Alignment	not modelled	5.2	22	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
77	c1zavZ	Alignment	not modelled	5.2	22	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
78	d1zavz1	Alignment	not modelled	5.2	22	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain