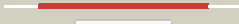



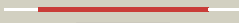


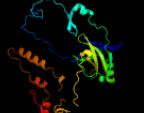





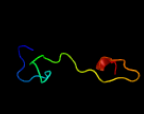

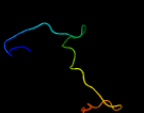

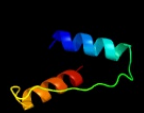

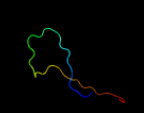



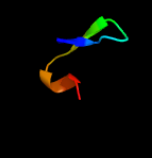

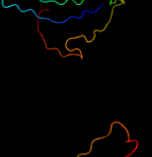
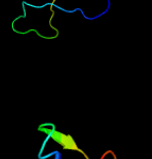
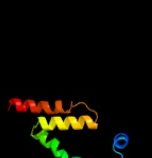
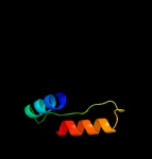

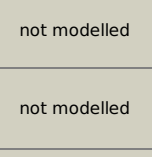


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0937c_(-)_1045203_1046024
Date	Fri Jul 26 01:50:53 BST 2019
Unique Job ID	f6932964688455ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dljeya1	 Alignment		100.0	14	Fold: SPOC domain-like Superfamily: SPOC domain-like Family: Ku70 subunit middle domain
2	dljeyb1	 Alignment		100.0	15	Fold: SPOC domain-like Superfamily: SPOC domain-like Family: Ku80 subunit middle domain
3	cljeqA_	 Alignment		100.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
4	cljeyB_	 Alignment		100.0	14	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
5	c5y58E_	 Alignment		100.0	17	PDB header: rna binding protein Chain: E: PDB Molecule: atp-dependent dna helicase ii subunit 1; PDBTitle: crystal structure of ku70/80 and tlc1
6	c5y58D_	 Alignment		100.0	17	PDB header: rna binding protein Chain: D: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku70/80 and tlc1
7	c4gcvD_	 Alignment		55.4	14	PDB header: transcription Chain: D: PDB Molecule: putative transcription protein; PDBTitle: structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
8	d2f2ea1	 Alignment		55.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
9	c2jwB_	 Alignment		34.8	14	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
10	c4xjcD_	 Alignment		33.5	21	PDB header: hydrolase Chain: D: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: dctp deaminase-dutpase from bacillus halodurans
11	c2r9qD_	 Alignment		33.3	25	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens

12	c5kxfA	Alignment		22.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: flowering time control protein fpa; PDBTitle: crystal structure of the spoc domain of the arabidopsis flowering2 regulator fpa
13	c3mhsE	Alignment		22.8	38	PDB header: hydrolase/transcription regulator/protei Chain: E: PDB Molecule: saga-associated factor 73; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
14	c4dn7B	Alignment		20.8	17	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of putative abc transporter, atp-binding protein2 from methanosarcina mazei go1
15	c1f8vA	Alignment		18.7	13	PDB header: virus/rna Chain: A: PDB Molecule: mature capsid protein beta; PDBTitle: the structure of pariacoto virus reveals a dodecahedral cage of duplex2 rna
16	c2qxxA	Alignment		16.3	16	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
17	c2lo3A	Alignment		15.7	38	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 73; PDBTitle: solution structure of sgf73(59-102) zinc finger domain
18	d2cw9a1	Alignment		15.5	12	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
19	c5by4A	Alignment		13.8	10	PDB header: protein transport Chain: A: PDB Molecule: protein tol; PDBTitle: structure and function of the escherichia coli tol-pal stator protein2 tol
20	c1ow1A	Alignment		12.2	14	PDB header: transcription Chain: A: PDB Molecule: smart/hdac1 associated repressor protein; PDBTitle: crystal structure of the spoc domain of the human2 transcriptional corepressor, sharp.
21	d1ow1a	Alignment	not modelled	12.2	14	Fold: SPOC domain-like Superfamily: SPOC domain-like Family: SPOC domain
22	c2yueA	Alignment	not modelled	12.0	29	PDB header: rna binding protein Chain: A: PDB Molecule: protein neuralized; PDBTitle: solution structure of the neuz (nhr) domain in neuralized2 from drosophila melanogaster
23	c1vbjB	Alignment	not modelled	11.1	6	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from trypanosoma2 brucei
24	c5awfA	Alignment	not modelled	10.2	14	PDB header: transport protein/protein binding Chain: A: PDB Molecule: fes cluster assembly protein sufB; PDBTitle: crystal structure of sufB-sufC-sufD complex from escherichia coli
25	c5y0tD	Alignment	not modelled	9.4	11	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
26	d2bbvc	Alignment	not modelled	8.9	17	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Nodaviridae-like VP
27	d2p8ia1	Alignment	not modelled	8.5	15	Fold: Ferredoxin-like Superfamily: DOPA-like Family: DOPA dioxygenase-like
28	d2c35b2	Alignment	not modelled	8.2	17	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
						Fold: beta-clip

29	d1xs1a_	Alignment	not modelled	7.8	16	Superfamily: dUTPase-like Family: dUTPase-like
30	c5d5nA_	Alignment	not modelled	7.7	11	PDB header: viral protein Chain: A: PDB Molecule: virion egress protein ul34 homolog; PDBTitle: crystal structure of the human cytomegalovirus pul50-pul53 complex
31	d1go3e2	Alignment	not modelled	7.6	21	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
32	c3gmiA_	Alignment	not modelled	7.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: supf0348 protein mj0951; PDBTitle: crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
33	c2k5cA_	Alignment	not modelled	7.5	29	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
34	d1wpga3	Alignment	not modelled	7.5	17	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
35	d1tuaa1	Alignment	not modelled	7.4	30	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
36	c3monE_	Alignment	not modelled	7.3	24	PDB header: sweet-tasting protein Chain: E: PDB Molecule: monellin; PDBTitle: crystal structures of two intensely sweet proteins
37	c4nohA_	Alignment	not modelled	7.1	16	PDB header: lipid binding protein Chain: A: PDB Molecule: lipoprotein, putative; PDBTitle: 1.5 angstrom crystal structure of putative lipoprotein from bacillus2 anthracis.
38	c4m01D_	Alignment	not modelled	6.9	12	PDB header: cell adhesion Chain: D: PDB Molecule: serine-rich adhesin for platelets; PDBTitle: n terminal fragment(residues 245-575) of binding region of srap
39	c3f5hB_	Alignment	not modelled	6.9	42	PDB header: protein binding Chain: B: PDB Molecule: type i polyketide synthase pikaiii, type i polyketide PDBTitle: crystal structure of fused docking domains from pikaiii and pikaiv of2 the pikromycin polyketide synthase
40	c2x7aB_	Alignment	not modelled	6.7	33	PDB header: immune system Chain: B: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
41	c2e63A_	Alignment	not modelled	6.6	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa1787 protein; PDBTitle: solution structure of the neuz domain in kiaa1787 protein
42	c6qj4E_	Alignment	not modelled	6.6	30	PDB header: cell cycle Chain: E: PDB Molecule: condensin complex subunit 2; PDBTitle: crystal structure of the c. thermophilum condensin ycs4-brn12 subcomplex bound to the smc4 atpase head in complex with the c-3 terminal domain of brn1
43	c5a3gA_	Alignment	not modelled	6.5	13	PDB header: viral protein Chain: A: PDB Molecule: m50; PDBTitle: structure of herpesvirus nuclear egress complex subunit m50
44	d1mo7a_	Alignment	not modelled	6.5	12	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
45	d2cdqa3	Alignment	not modelled	6.3	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
46	c5fwhA_	Alignment	not modelled	6.3	18	PDB header: structural protein Chain: A: PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
47	c4ddvA_	Alignment	not modelled	6.1	22	PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
48	c2x0dA_	Alignment	not modelled	6.0	9	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
49	c3bk5A_	Alignment	not modelled	5.9	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative outer membrane lipoprotein-sorting protein; PDBTitle: crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
50	c6iicC_	Alignment	not modelled	5.9	27	PDB header: virus Chain: C: PDB Molecule: vp3 of mud crab dicistrovirus; PDBTitle: cryoem structure of mud crab dicistrovirus
51	d1k1fa_	Alignment	not modelled	5.9	21	Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
52	c2d7cD_	Alignment	not modelled	5.7	13	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of human rab11 in complex with fip3 rab-2 binding domain
53	c2xuvB_	Alignment	not modelled	5.7	28	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
54	c4v1ai_	Alignment	not modelled	5.7	6	PDB header: ribosome Chain: I: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
						Fold: beta-beta-alpha zinc fingers

55	d1bboa1	Alignment	not modelled	5.6	63	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
56	c2pfuA_	Alignment	not modelled	5.5	15	PDB header: transport protein Chain: A: PDB Molecule: biopolymer transport exbd protein; PDBTitle: nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
57	c2kpoA_	Alignment	not modelled	5.4	19	PDB header: de novo protein Chain: A: PDB Molecule: rossmann 2x2 fold protein; PDBTitle: solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
58	d1zhva2	Alignment	not modelled	5.4	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
59	c3ec7C_	Alignment	not modelled	5.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
60	c4odrB_	Alignment	not modelled	5.4	17	PDB header: isomerase, chaperone Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase slyd, peptidyl-prolyl PDBTitle: structure of slyd delta-if from thermus thermophilus in complex with2 fk506
61	c4ce4i_	Alignment	not modelled	5.2	6	PDB header: ribosome Chain: I: PDB Molecule: mrpl9; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
62	c3buuB_	Alignment	not modelled	5.2	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized lola superfamily protein ne2245; PDBTitle: crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
63	d2gtlo1	Alignment	not modelled	5.2	14	Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
64	c2qluA_	Alignment	not modelled	5.1	11	PDB header: transferase Chain: A: PDB Molecule: activin receptor type iib; PDBTitle: crystal structure of activin receptor type ii kinase domain2 from human