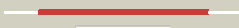
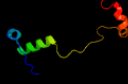

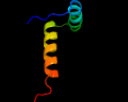

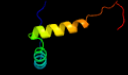

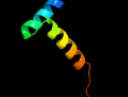

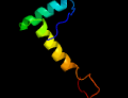










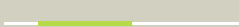









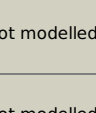


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0581 (-) _677713_677928
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	0d3f1b0c55378245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5x3tA_	 Alignment		100.0	97	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
2	c2k5jB_	 Alignment		95.4	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
3	c1q5vB_	 Alignment		92.7	21	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
4	c2h1oH_	 Alignment		91.5	30	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
5	c2bj3D_	 Alignment		91.1	17	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
6	d2bsqe1	 Alignment		91.1	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
7	d2bj7a1	 Alignment		89.1	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	d2hzaa1	 Alignment		87.4	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	d2hzab1	 Alignment		85.8	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	c2ca9B_	 Alignment		84.9	22	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
11	c2mvaA_	 Alignment		63.0	38	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein np_344732.1 from streptococcus pneumoniae2 tigr4

12	c2kelB	Alignment		48.8	26	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
13	c6iyaD	Alignment		44.5	33	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
14	d1mnta	Alignment		43.9	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
15	c2rbfB	Alignment		43.4	22	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
16	c3kxeD	Alignment		38.8	30	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
17	c3qoqC	Alignment		38.7	24	PDB header: transcription/dna Chain: C: PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
18	c5cegC	Alignment		35.7	22	PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
19	d1qh4a1	Alignment		35.7	21	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
20	d1g0wa1	Alignment		32.5	25	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
21	c6g1nB	Alignment	not modelled	31.2	11	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
22	d1a6qa1	Alignment	not modelled	29.7	29	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
23	d1i0ea1	Alignment	not modelled	28.1	23	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
24	d1u6ra1	Alignment	not modelled	26.9	19	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
25	d1qk1a1	Alignment	not modelled	25.6	19	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
26	d1crka1	Alignment	not modelled	24.4	21	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
27	c2oviA	Alignment	not modelled	22.8	29	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
28	d1vrpa1	Alignment	not modelled	20.9	16	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
29	d1cuka1	Alignment	not modelled	19.6	41	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain

						Family: DNA helicase RuvA subunit, C-terminal domain
30	c2ph0A	Alignment	not modelled	14.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
31	c1u9pA	Alignment	not modelled	14.8	18	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
32	d1m15a1	Alignment	not modelled	13.6	19	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
33	c3cwwB	Alignment	not modelled	12.5	25	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase, b subunit, truncated; PDBTitle: crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
34	c3s2xB	Alignment	not modelled	12.4	30	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
35	c4p7dA	Alignment	not modelled	11.9	18	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
36	c5exvD	Alignment	not modelled	11.6	29	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
37	c4me7E	Alignment	not modelled	11.4	27	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoa1; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
38	c6n2oB	Alignment	not modelled	10.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate ferredoxin/ferredoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
39	c1m1zB	Alignment	not modelled	10.7	41	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
40	c1no1C	Alignment	not modelled	10.6	30	PDB header: replication Chain: C: PDB Molecule: replisome organizer; PDBTitle: structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
41	d1no1a	Alignment	not modelled	10.6	30	Fold: Replisome organizer (g39p helicase loader/inhibitor protein) Superfamily: Replisome organizer (g39p helicase loader/inhibitor protein) Family: Replisome organizer (g39p helicase loader/inhibitor protein)
42	c5mrwG	Alignment	not modelled	10.3	25	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpcfabc complex
43	d1jcea1	Alignment	not modelled	9.6	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
44	c1algA	Alignment	not modelled	9.4	63	PDB header: oxidoreductase Chain: A: PDB Molecule: p11; PDBTitle: solution structure of an hgr inhibitor, nmr, 10 structures
45	c5ncrA	Alignment	not modelled	8.5	38	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine phosphatase; PDBTitle: oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
46	d2hqva1	Alignment	not modelled	8.3	21	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like
47	d2j0pa1	Alignment	not modelled	7.9	36	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
48	c4yczA	Alignment	not modelled	7.2	60	PDB header: structural protein Chain: A: PDB Molecule: fusion protein of sec13 and nup145c; PDBTitle: y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)
49	c2km1A	Alignment	not modelled	6.9	33	PDB header: protein binding Chain: A: PDB Molecule: protein dre2; PDBTitle: solution structure of the n-terminal domain of the yeast protein dre2
50	c2k29A	Alignment	not modelled	6.4	24	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
51	d1tfra1	Alignment	not modelled	6.2	38	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
52	c5b46B	Alignment	not modelled	6.1	27	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form
53	d2hq2a1	Alignment	not modelled	6.1	23	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
54	d1kska3	Alignment	not modelled	6.0	53	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
						PDB header: metal binding protein

55	c4lzxB_	Alignment	not modelled	5.9	47	Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
56	c1p9iA_	Alignment	not modelled	5.7	43	PDB header: unknown function Chain: A: PDB Molecule: cortexillin i/gcn4 hybrid peptide; PDBTitle: coiled-coil x-ray structure at 1.17 a resolution
57	c6gtsC_	Alignment	not modelled	5.5	26	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
58	c4wwrE_	Alignment	not modelled	5.5	50	PDB header: transport protein Chain: E: PDB Molecule: large proline-rich protein bag6; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
59	c2i0kA_	Alignment	not modelled	5.3	31	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
60	d1xria_	Alignment	not modelled	5.3	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like