




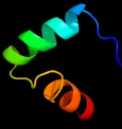
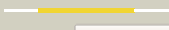





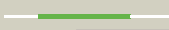

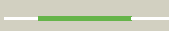










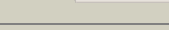
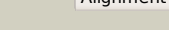
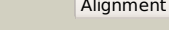

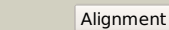
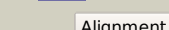


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2801A_(RVBD2801A)_3110517_3110747
 Date Wed Aug 7 12:50:46 BST 2019
 Unique Job ID 979795da78f0a15e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bj7a1	 Alignment		97.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
2	c2bj3D_	 Alignment		97.6	21	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nkr-apo
3	d2hzaa1	 Alignment		97.5	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c1q5vB_	 Alignment		97.5	26	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nkr
5	d2hzaa1	 Alignment		97.4	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c2ca9B_	 Alignment		97.4	32	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nkr from helicobacter pylori in closed trans-2 conformation
7	c5cegC_	 Alignment		94.5	19	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
8	c5yrzC_	 Alignment		93.8	26	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
9	c3kxeD_	 Alignment		93.3	22	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
10	c6g1nB_	 Alignment		92.4	29	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
11	c2k5jB_	 Alignment		88.4	23	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

12	c4me7E_	 Alignment		82.1	31	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
13	c4p7dA_	 Alignment		78.0	25	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
14	c6a6xC_	 Alignment		55.0	30	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
15	d2cpga_	 Alignment		51.9	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
16	c1ea4K_	 Alignment		51.9	30	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
17	c6qeqD_	 Alignment		51.6	14	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcff from enterococcus faecalis pcf10
18	c2mdvB_	 Alignment		27.1	33	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
19	d2vy4a1	 Alignment		21.2	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: CHHC finger
20	c5cwwC_	 Alignment		16.0	33	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup159; PDBTitle: crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex
21	d1jdfa2	 Alignment	not modelled	15.0	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
22	c1mszA_	 Alignment	not modelled	14.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: solution structure of the r3h domain from human smubp-2
23	d1msza_	 Alignment	not modelled	14.9	21	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
24	d1rvka2	 Alignment	not modelled	13.3	33	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
25	c4l6tA_	 Alignment	not modelled	13.0	46	PDB header: hydrolase Chain: A: PDB Molecule: ecxa; PDBTitle: gm1 bound form of the ecx ab5 holotoxin
26	d2chra2	 Alignment	not modelled	12.9	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
27	d2hh6a1	 Alignment	not modelled	12.6	32	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
28	d1t98a1	 Alignment	not modelled	12.5	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MukF N-terminal domain-like
29	d1bqga2	 Alignment	not modelled	12.0	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like

						Family: Enolase N-terminal domain-like
30	d1jpma2	Alignment	not modelled	10.6	33	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
31	d1wuea2	Alignment	not modelled	10.3	40	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
32	c1t98B	Alignment	not modelled	10.2	33	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of mukf(1-287)
33	c2rrfA	Alignment	not modelled	10.2	14	PDB header: unknown function Chain: A: PDB Molecule: zinc finger fyve domain-containing protein 21; PDBTitle: the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
34	d2gl5a2	Alignment	not modelled	9.9	40	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
35	d2mnra2	Alignment	not modelled	9.9	40	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
36	d1nu5a2	Alignment	not modelled	9.8	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
37	d1wufa2	Alignment	not modelled	9.7	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
38	d2b0la1	Alignment	not modelled	9.6	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CodY HTH domain
39	d1lqaa	Alignment	not modelled	8.8	29	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
40	d1yeya2	Alignment	not modelled	8.8	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
41	c4n2sA	Alignment	not modelled	8.6	18	PDB header: splicing/rna Chain: A: PDB Molecule: tha8 rna binding protein; PDBTitle: crystal structure of tha8 in complex with zm1a-6 rna
42	d1sjda2	Alignment	not modelled	8.3	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
43	c5b0nA	Alignment	not modelled	8.1	26	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase ipah9.8; PDBTitle: structure of shigella effector lrr domain
44	d2c5ra1	Alignment	not modelled	7.9	50	Fold: Phage replication organizer domain Superfamily: Phage replication organizer domain Family: Phage replication organizer domain
45	c3jviA	Alignment	not modelled	7.8	19	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
46	c4h3uB	Alignment	not modelled	7.5	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein with ketosteroid isomerase-2 like protein fold from catenulispora acidiphila dsm 44928
47	d2gdqa2	Alignment	not modelled	6.9	20	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
48	d1jpdx2	Alignment	not modelled	6.7	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
49	d2ezwa1	Alignment	not modelled	6.5	28	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
50	c4f9kA	Alignment	not modelled	6.4	22	PDB header: transferase regulator Chain: A: PDB Molecule: camp-dependent protein kinase type i-beta regulatory PDBTitle: crystal structure of human camp-dependent protein kinase type i-beta2 regulatory subunit (fragment 11-73), northeast structural genomics3 consortium (nesg) target hr8613a
51	c5ey0A	Alignment	not modelled	6.4	35	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from staphylococcus aureus with gtp and ile
52	d1muca2	Alignment	not modelled	6.3	60	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
53	c3tadB	Alignment	not modelled	6.1	20	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
54	d1tzza2	Alignment	not modelled	6.1	53	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like

55	d1r0ma2	Alignment	not modelled	6.0	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
56	c4zriC_	Alignment	not modelled	5.8	50	PDB header: signaling protein/transferase Chain: C: PDB Molecule: serine/threonine-protein kinase lats2; PDBTitle: crystal structure of merlin-ferm and lats2
57	c4zriD_	Alignment	not modelled	5.7	50	PDB header: signaling protein/transferase Chain: D: PDB Molecule: serine/threonine-protein kinase lats2; PDBTitle: crystal structure of merlin-ferm and lats2
58	c5o5jR_	Alignment	not modelled	5.7	30	PDB header: ribosome Chain: R: PDB Molecule: 30s ribosomal protein s18 2; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
59	d1h99a1	Alignment	not modelled	5.6	30	Fold: PTS-regulatory domain, PRD Superfamily: PTS-regulatory domain, PRD Family: PTS-regulatory domain, PRD
60	d2fq4a2	Alignment	not modelled	5.6	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
61	c2pijB_	Alignment	not modelled	5.3	24	PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
62	c3h87D_	Alignment	not modelled	5.3	39	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
63	c6g1oA_	Alignment	not modelled	5.3	21	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: structure of pseudomonas aeruginosa isocitrate lyase, icl
64	d2ftra1	Alignment	not modelled	5.2	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
65	d1q2za_	Alignment	not modelled	5.1	20	Fold: alpha-alpha superhelix Superfamily: C-terminal domain of Ku80 Family: C-terminal domain of Ku80