

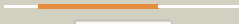

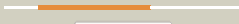

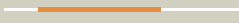
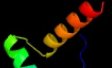



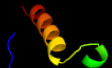







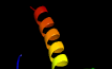






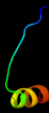
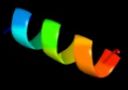





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1560_(-)_1764761_1764979
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	b9a26aa4e2d93c4a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vU	 Alignment		99.9	100	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vappb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	c2k5jB	 Alignment		81.5	13	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		81.1	30	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
4	d2bj7a1	 Alignment		80.3	17	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	c2ca9B	 Alignment		77.8	18	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
6	c2bj3D	 Alignment		74.0	17	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
7	c5cegC	 Alignment		64.2	13	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	c5vgtA	 Alignment		55.4	40	PDB header: viral protein Chain: A: PDB Molecule: gene 7 protein; PDBTitle: x-ray structure of bacteriophage sf6 tail adaptor protein gp7
9	c3kxeD	 Alignment		54.8	13	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	d2hzaa1	 Alignment		43.8	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	d2hzab1	 Alignment		39.9	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	c2l9iA_	Alignment		21.2	36	PDB header: peptide binding protein Chain: A: PDB Molecule: thymosin alpha-1; PDBTitle: nmr structure of thymosin alpha-1
13	d1dqua_	Alignment		19.3	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
14	c4zquB_	Alignment		19.3	42	PDB header: toxin Chain: B: PDB Molecule: cdii toxin; PDBTitle: cdiA-ct/cdii toxin and immunity complex from yersinia2 pseudotuberculosis
15	c1y66D_	Alignment		18.6	20	PDB header: de novo protein Chain: D: PDB Molecule: engrailed homeodomain; PDBTitle: dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
16	c2k29A_	Alignment		18.3	40	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
17	c2kelB_	Alignment		16.5	14	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
18	d1r0ma2	Alignment		15.5	21	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
19	d1kn0a_	Alignment		14.9	25	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: The homologous-pairing domain of Rad52 recombinase
20	d1irqa_	Alignment		14.6	20	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Omega transcriptional repressor
21	c2rnjA_	Alignment	not modelled	14.4	13	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
22	c1irqB_	Alignment	not modelled	14.4	20	PDB header: gene regulation Chain: B: PDB Molecule: omega transcriptional repressor; PDBTitle: crystal structure of omega transcriptional repressor at2 1.5a resolution
23	c2q2kA_	Alignment	not modelled	13.6	47	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
24	c2q2kB_	Alignment	not modelled	13.5	47	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
25	c4ehpB_	Alignment	not modelled	13.3	19	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: crystal structure of human vinculin head domain (residues 1-252) in2 complex with alpha-catenin (residues 277-382)
26	c2mnqA_	Alignment	not modelled	12.9	36	PDB header: protein binding Chain: A: PDB Molecule: thymosin alpha-1; PDBTitle: 1h, 13c, and 15n chemical shift assignments for thymosin alpha 1
27	d2gl5a2	Alignment	not modelled	12.3	31	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
28	c3sztB_	Alignment	not modelled	11.1	20	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
						Fold: Enolase N-terminal domain-like

29	d2gdqa2	Alignment	not modelled	10.3	19	Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
30	c3j47P	Alignment	not modelled	10.1	29	PDB header: protein binding Chain: P: PDB Molecule: 26s proteasome regulatory subunit rpn5; PDBTitle: formation of an intricate helical bundle dictates the assembly of the 26s proteasome lid
31	d2chra2	Alignment	not modelled	9.7	35	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
32	d1qf8a	Alignment	not modelled	9.4	17	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
33	d1muca2	Alignment	not modelled	9.1	23	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
34	c4zqvA	Alignment	not modelled	9.0	37	PDB header: immune system Chain: A: PDB Molecule: cdii immunity protein; PDBTitle: cdii immunity protein from yersinia kristensenii
35	c1xrxD	Alignment	not modelled	8.7	63	PDB header: replication inhibitor Chain: D: PDB Molecule: sega protein; PDBTitle: crystal structure of a dna-binding protein
36	d1xrx1	Alignment	not modelled	8.7	63	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
37	c6jqsA	Alignment	not modelled	8.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
38	d1jpm2	Alignment	not modelled	8.0	27	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
39	d1rvka2	Alignment	not modelled	7.8	35	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
40	c2jpcA	Alignment	not modelled	7.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
41	c5ep0A	Alignment	not modelled	7.4	19	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
42	c3b0dB	Alignment	not modelled	7.3	33	PDB header: dna binding protein Chain: B: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w complex,2 crystal form ii
43	c2jyaA	Alignment	not modelled	7.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
44	c2vixB	Alignment	not modelled	7.2	24	PDB header: transport protein Chain: B: PDB Molecule: protein mxic; PDBTitle: methylated shigella flexneri mxic
45	d1tzza2	Alignment	not modelled	7.2	15	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
46	d1nu5a2	Alignment	not modelled	7.1	31	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
47	c1zljE	Alignment	not modelled	7.0	14	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
48	d1l3la1	Alignment	not modelled	6.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
49	c1h2iG	Alignment	not modelled	6.9	25	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain
50	c4chgG	Alignment	not modelled	6.6	33	PDB header: toxin/antitoxin Chain: G: PDB Molecule: antitoxin vapb15; PDBTitle: crystal structure of vapbc15 complex from mycobacterium tuberculosis
51	c6exnD	Alignment	not modelled	6.4	26	PDB header: splicing Chain: D: PDB Molecule: pre-mrna-splicing factor cwc16; PDBTitle: post-catalytic p complex spliceosome with 3' splice site docked
52	d2mnra2	Alignment	not modelled	6.4	19	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
53	c3zc4G	Alignment	not modelled	6.4	33	PDB header: immune system Chain: G: PDB Molecule: ss01398; PDBTitle: the structure of csa5 from sulfolobus solfataricus.
54	c3lj4i	Alignment	not modelled	6.2	54	PDB header: viral protein Chain: I: PDB Molecule: portal protein; PDBTitle: bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
55	c4trbA	Alignment	not modelled	6.1	17	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase

56	c2zrrA_	Alignment	not modelled	6.0	31	PDB header: antimicrobial protein Chain: A: PDB Molecule: mundticin ks immunity protein; PDBTitle: crystal structure of an immunity protein that contributes to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
57	d1jjcb2	Alignment	not modelled	5.9	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
58	c4g6uB_	Alignment	not modelled	5.9	32	PDB header: toxin Chain: B: PDB Molecule: ec869 cdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from escherichia coli
59	c6iyaD_	Alignment	not modelled	5.8	20	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
60	c3oqvA_	Alignment	not modelled	5.6	21	PDB header: protein binding Chain: A: PDB Molecule: albc; PDBTitle: albc, a cyclodipeptide synthase from streptomyces noursei
61	c6gcsY_	Alignment	not modelled	5.5	29	PDB header: oxidoreductase Chain: Y: PDB Molecule: nuym subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
62	d1fsea_	Alignment	not modelled	5.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
63	d1wpda_	Alignment	not modelled	5.2	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins