










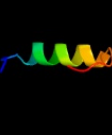





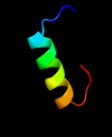

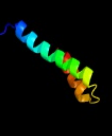

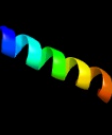



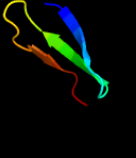


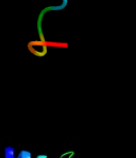




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0367C (-) _444845_445234
Date	Tue Jul 23 14:50:43 BST 2019
Unique Job ID	dcbbb513fe994e94

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u9pA	 Alignment		87.8	12	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
2	d1mnta	 Alignment		80.7	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
3	c3qoqC	 Alignment		80.0	14	PDB header: transcription/dna Chain: C: PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz1 in complex with the 2 18 base pair amrz1 binding site
4	c3bfmA	 Alignment		43.3	11	PDB header: unknown function Chain: A: PDB Molecule: biotin protein ligase-like protein of unknown function; PDBTitle: crystal structure of a biotin protein ligase-like protein of unknown2 function (tm1040_0394) from silicibacter sp. tm1040 at 1.70 a3 resolution
5	d2ay0a1	 Alignment		42.2	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
6	c6iyaD	 Alignment		38.9	17	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
7	c5j2vA	 Alignment		38.3	44	PDB header: gene regulation/dna Chain: A: PDB Molecule: regulatory protein; PDBTitle: molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
8	d1x4ta1	 Alignment		35.6	25	Fold: Long alpha-hairpin Superfamily: !SY1 domain-like Family: !SY1 N-terminal domain-like
9	c2rbfB	 Alignment		35.3	9	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)
10	d1tueb	 Alignment		33.5	12	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
11	c4u1eB	 Alignment		25.7	14	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of the eif3b-ctd/eif3i/eif3g-ntd translation2 initiation complex

12	c6f0hD_	Alignment		24.1	24	PDB header: chaperone Chain: D: PDB Molecule: ip4; PDBTitle: crystal structure asf1-ip4
13	c6f0hB_	Alignment		23.9	24	PDB header: chaperone Chain: B: PDB Molecule: ip4; PDBTitle: crystal structure asf1-ip4
14	d2proc1	Alignment		20.7	21	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
15	d1b2pa_	Alignment		16.9	15	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
16	c5whaF_	Alignment		16.4	33	PDB header: protein binding Chain: F: PDB Molecule: miniprotein 225-11; PDBTitle: kras g12v, bound to gdp and miniprotein 225-11
17	d1rk8c_	Alignment		14.8	83	Fold: WW domain-like Superfamily: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain Family: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
18	c1rk8C_	Alignment		14.8	83	PDB header: translation Chain: C: PDB Molecule: within the bgcn gene intron protein; PDBTitle: structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
19	d2g3ba2	Alignment		13.7	23	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
20	c4pdtA_	Alignment		13.3	16	PDB header: sugar binding protein Chain: A: PDB Molecule: mannose recognizing lectin; PDBTitle: japanese marasmius oreades lectin
21	d1bazb_	Alignment	not modelled	13.0	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
22	d1u9pa1	Alignment	not modelled	12.9	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
23	d1pn0a2	Alignment	not modelled	12.7	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
24	c6hbbA_	Alignment	not modelled	12.5	50	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein ccmm; PDBTitle: crystal structure of the small subunit-like domain 1 of ccmm from2 synechococcus elongatus (strain pcc 7942)
25	d1myka_	Alignment	not modelled	11.6	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
26	d1bdta_	Alignment	not modelled	10.9	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
27	d1p94a_	Alignment	not modelled	10.9	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
28	d3er7a1	Alignment	not modelled	10.8	38	Fold: Cystatin-like Superfamily: NTF2-like Family: Exig0174-like
						PDB header: transcription

29	c2jeuA_	Alignment	not modelled	10.6	10	Chain: A: PDB Molecule: regulatory protein e2; PDBTitle: transcription activator structure reveals redox control of a2 replication initiation reaction
30	d1baza_	Alignment	not modelled	10.5	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
31	c6c48E_	Alignment	not modelled	10.2	12	PDB header: cell cycle/dna binding Chain: E: PDB Molecule: protein lin-52 homolog; PDBTitle: crystal structure of b-myb-lin9-lin52 complex
32	c1fyfB_	Alignment	not modelled	10.2	5	PDB header: ligase Chain: B: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
33	d1kx5b_	Alignment	not modelled	9.7	12	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
34	d1dipa1	Alignment	not modelled	9.6	19	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
35	d1r6na_	Alignment	not modelled	9.3	13	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
36	c6b2zd_	Alignment	not modelled	9.1	30	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
37	d1biaa2	Alignment	not modelled	8.6	4	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)
38	c4xmnB_	Alignment	not modelled	8.5	25	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup145; PDBTitle: structure of the yeast coat nucleoporin complex, space group p212121
39	c1tueG_	Alignment	not modelled	8.1	16	PDB header: replication Chain: G: PDB Molecule: regulatory protein e2; PDBTitle: the x-ray structure of the papillomavirus helicase in2 complex with its molecular matchmaker e2
40	c4uy87_	Alignment	not modelled	7.9	55	PDB header: ribosome Chain: 7: PDB Molecule: tryptophanase; PDB Fragment: residues 7-85; PDBTitle: molecular basis for the ribosome functioning as a l-tryptophan sensor2 - cryo-em structure of a tnac stalled e.coli ribosome
41	c4i1oD_	Alignment	not modelled	7.7	25	PDB header: protein transport/hydrolase Chain: D: PDB Molecule: lepB; PDBTitle: crystal structure of the legionella pneumophila gap domain of lepB in2 complex with rab1b bound to gdp and bef3
42	d2nnaa1	Alignment	not modelled	7.4	10	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
43	c2w0cR_	Alignment	not modelled	7.4	30	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
44	c3j47O_	Alignment	not modelled	7.1	28	PDB header: protein binding Chain: O: PDB Molecule: 26s proteasome regulatory subunit rpn9; PDBTitle: formation of an intricate helical bundle dictates the assembly of the 26s proteasome lid
45	d1n1a2	Alignment	not modelled	6.8	27	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
46	d2cosa1	Alignment	not modelled	6.5	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
47	c6mcjA_	Alignment	not modelled	6.4	22	PDB header: protein binding Chain: A: PDB Molecule: orange carotenoid-binding protein; PDBTitle: structure of helical carotenoid protein 2 from fremyella diplosiphon
48	d1v2za_	Alignment	not modelled	6.4	24	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
49	d1mylb_	Alignment	not modelled	6.3	12	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
50	c2rmgA_	Alignment	not modelled	6.3	25	PDB header: hormone Chain: A: PDB Molecule: urocortin-2; PDBTitle: human urocortin 2
51	c2yh5A_	Alignment	not modelled	6.3	23	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
52	c2zzxD_	Alignment	not modelled	6.1	11	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
53	d2p4oa1	Alignment	not modelled	6.0	18	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
54	d1r8ja1	Alignment	not modelled	6.0	28	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
55	d1sv1a_	Alignment	not modelled	5.6	24	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain

56	d1s29a_	Alignment	not modelled	5.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: La domain
57	d1luxca_	Alignment	not modelled	5.6	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
58	d1g5ta_	Alignment	not modelled	5.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
59	d1toha_	Alignment	not modelled	5.5	17	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
60	d1luxda_	Alignment	not modelled	5.4	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
61	c3u65B_	Alignment	not modelled	5.2	9	PDB header: transport protein Chain: B: PDB Molecule: tp33 protein; PDBTitle: the crystal structure of tat-p(t) (tp0957)
62	d1q1va_	Alignment	not modelled	5.2	17	Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain
63	d1jm6a1	Alignment	not modelled	5.1	14	Fold: Bromodomain-like Superfamily: alpha-ketoacid dehydrogenase kinase, N-terminal domain Family: alpha-ketoacid dehydrogenase kinase, N-terminal domain