




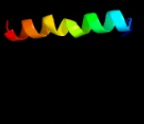







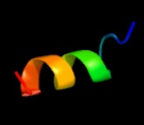







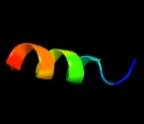
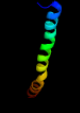



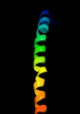






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1109c_(-)_1235462_1236100
Date	Wed Jul 31 22:05:19 BST 2019
Unique Job ID	0e5b51e7894d2650

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ov9a_	 Alignment		57.4	35	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
2	c3cqbB_	 Alignment		56.8	42	PDB header: hydrolase Chain: B: PDB Molecule: probable protease htpx homolog; PDBTitle: crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
3	c3sl9F_	 Alignment		33.6	25	PDB header: signaling protein, protein binding Chain: F: PDB Molecule: b-cell cl/lymphoma 9 protein; PDBTitle: x-ray structure of beta catenin in complex with bcl9
4	c3sl9C_	 Alignment		33.5	25	PDB header: signaling protein, protein binding Chain: C: PDB Molecule: b-cell cl/lymphoma 9 protein; PDBTitle: x-ray structure of beta catenin in complex with bcl9
5	d1zara1	 Alignment		32.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rio2 serine protein kinase N-terminal domain
6	d1k1va_	 Alignment		30.9	22	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
7	c5cwsF_	 Alignment		29.4	57	PDB header: protein transport Chain: F: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
8	c5cwsL_	 Alignment		27.1	57	PDB header: protein transport Chain: L: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
9	d1dl6a_	 Alignment		24.6	46	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
10	c2n90B_	 Alignment		24.5	50	PDB header: transferase Chain: B: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
11	c2n90A_	 Alignment		24.5	50	PDB header: transferase Chain: A: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles

12	c2jo8B_	Alignment		24.5	21	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
13	d1q08a_	Alignment		23.8	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
14	c4il3B_	Alignment		23.6	17	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
15	d2ga1a1	Alignment		22.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
16	c4l0nG_	Alignment		20.8	26	PDB header: transferase Chain: G: PDB Molecule: serine/threonine-protein kinase 3; PDBTitle: crystal structure of stk3 (mst2) sarah domain
17	d1h1js_	Alignment		17.8	44	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
18	d1pfta_	Alignment		14.8	60	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
19	c1dpuA_	Alignment		14.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
20	d1dpua_	Alignment		14.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
21	c2kvuA_	Alignment	not modelled	14.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: mkl/myocardin-like protein 1; PDBTitle: solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
22	c3lmoA_	Alignment	not modelled	12.8	19	PDB header: transferase Chain: A: PDB Molecule: specialized acyl carrier protein; PDBTitle: crystal structure of specialized acyl carrier protein (rpa2022) from2 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr324
23	c2kz5A_	Alignment	not modelled	12.0	16	PDB header: transcription Chain: A: PDB Molecule: transcription factor nf-e2 45 kda subunit; PDBTitle: solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
24	c2lz1A_	Alignment	not modelled	11.9	10	PDB header: transcription Chain: A: PDB Molecule: nuclear factor erythroid 2-related factor 2; PDBTitle: solution nmr structure of the dna-binding domain of human nf-e2-2 related factor 2, northeast structural genomics consortium (nesg)3 target hr3520o
25	c4aw6B_	Alignment	not modelled	10.5	14	PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
26	c6bn1A_	Alignment	not modelled	10.3	20	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo; PDBTitle: salvador hippo sarah domain complex
27	d1q9ca_	Alignment	not modelled	10.2	13	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
						Fold: Chemotaxis receptor methyltransferase CheR, N-terminal

28	d1af7a1	Alignment	not modelled	9.6	23	domain Superfamily: Chemotaxis receptor methyltransferase CheR, N-terminal domain Family: Chemotaxis receptor methyltransferase CheR, N-terminal domain
29	d1sknp_	Alignment	not modelled	9.4	18	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
30	d1dd4c_	Alignment	not modelled	9.2	27	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
31	c3m0dC_	Alignment	not modelled	8.3	15	PDB header: signaling protein Chain: C; PDB Molecule: tnf receptor-associated factor 1; PDBTitle: crystal structure of the traf1:traf2:ciap2 complex
32	d1dd3a1	Alignment	not modelled	8.0	27	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
33	c3m06F_	Alignment	not modelled	7.9	7	PDB header: protein binding Chain: F; PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
34	d1zrja1	Alignment	not modelled	7.6	31	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
35	d1kx5c_	Alignment	not modelled	7.4	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
36	d1ttha_	Alignment	not modelled	7.1	12	Fold: Anti-sigma factor AsiA Superfamily: Anti-sigma factor AsiA Family: Anti-sigma factor AsiA
37	c2jssA_	Alignment	not modelled	6.5	22	PDB header: chaperone/nuclear protein Chain: A; PDB Molecule: chimera of histone h2b.1 and histone h2a.z; PDBTitle: nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
38	d1jdla_	Alignment	not modelled	6.5	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
39	d1eqza_	Alignment	not modelled	6.5	21	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
40	c3c37B_	Alignment	not modelled	6.3	17	PDB header: hydrolase Chain: B; PDB Molecule: peptidase, m48 family; PDBTitle: x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
41	d1jeia_	Alignment	not modelled	6.0	22	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
42	d1i8oa_	Alignment	not modelled	6.0	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
43	c1motA_	Alignment	not modelled	5.7	33	PDB header: membrane protein Chain: A; PDB Molecule: glycine receptor alpha-1 chain; PDBTitle: nmr structure of extended second transmembrane domain of2 glycine receptor alpha1 subunit in sds micelles
44	d3c2ca_	Alignment	not modelled	5.6	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
45	d1hroa_	Alignment	not modelled	5.4	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
46	d1fcdc2	Alignment	not modelled	5.3	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
47	c3oa8B_	Alignment	not modelled	5.2	25	PDB header: heme-binding protein/heme-binding protei Chain: B; PDB Molecule: soxx; PDBTitle: diheme soxax
48	c3ouvA_	Alignment	not modelled	5.1	16	PDB header: transferase Chain: A; PDB Molecule: serine/threonine protein kinase; PDBTitle: semet derivative of I512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb