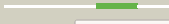

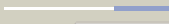









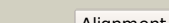

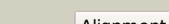
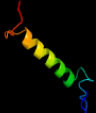








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2653c (-) _2976596_2976919
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	5518525e8cbc2c58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mhjA_	 Alignment		55.5	50	PDB header: transcription Chain: A; PDB Molecule: major viral transcription factor icp4; PDBTitle: icp4 dna-binding domain, lacking intrinsically disordered region, in2 complex with 12mer dna duplex from its own promoter
2	d1s0pa_	 Alignment		23.5	13	Fold: N-terminal domain of adenylcyclase associated protein, CAP Superfamily: N-terminal domain of adenylcyclase associated protein, CAP Family: N-terminal domain of adenylcyclase associated protein, CAP
3	d2dara2	 Alignment		20.3	67	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
4	c6f1uf_	 Alignment		18.3	21	PDB header: motor protein Chain: F; PDB Molecule: arp1 actin related protein 1 homolog a; PDBTitle: n terminal region of dynein tail domains in complex with dynactin2 filament and bicdr-1
5	c6adqP_	 Alignment		16.5	75	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
6	c6f1yf_	 Alignment		13.6	18	PDB header: motor protein Chain: F; PDB Molecule: PDBTitle: dynein light intermediate chain region of the dynein2 tail/dynactin/bicdr1 complex
7	d2i9ca1	 Alignment		12.2	23	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: RPA1889-like
8	d1hn0a1	 Alignment		10.3	13	Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Hyaluronate lyase-like catalytic, N-terminal domain
9	c2kitA_	 Alignment		8.6	30	PDB header: transferase Chain: A; PDB Molecule: serine/threonine-protein kinase tor1; PDBTitle: the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k
10	d1fafa_	 Alignment		8.3	24	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
11	c1w1nA_	 Alignment		8.3	30	PDB header: transferase Chain: A; PDB Molecule: phosphatidylinositol 3-kinase tor1; PDBTitle: the solution structure of the fatc domain of the protein kinase tor12 from yeast

12	c2ogfD_	Alignment		7.8	43	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
13	d1xw3a1	Alignment		7.6	18	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Sulfiredoxin-like
14	d2i52a1	Alignment		7.4	50	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
15	c5loiA_	Alignment		6.5	41	PDB header: signaling protein Chain: A: PDB Molecule: rad26; PDBTitle: crystal structure of myceliophthora thermophila rad26 (residues 373-2 841)
16	c1u9fA_	Alignment		6.4	36	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15))(16)
17	c3iynR_	Alignment		6.4	32	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
18	c4jj9A_	Alignment		6.3	25	PDB header: isomerase Chain: A: PDB Molecule: 5-carboxymethyl-2-hydroxymuconate delta-isomerase; PDBTitle: crystal structure of 5-carboxymethyl-2-hydroxymuconate delta-isomerase
19	c3j2wS_	Alignment		6.3	40	PDB header: virus Chain: S: PDB Molecule: glycoprotein e2; PDBTitle: electron cryo-microscopy of chikungunya virus
20	c6gbrA_	Alignment		6.2	46	PDB header: viral protein Chain: A: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
21	c4cgbE_	Alignment	not modelled	6.2	56	PDB header: cell cycle Chain: E: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
22	c4qsgA_	Alignment	not modelled	6.2	38	PDB header: structural protein Chain: A: PDB Molecule: gas vesicle protein; PDBTitle: crystal structure of gas vesicle protein gvpf from microcystis2 aeruginosa
23	c1u9fB_	Alignment	not modelled	6.1	36	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15))(16)
24	c1u9fC_	Alignment	not modelled	6.1	36	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15))(16)
25	c1u9fD_	Alignment	not modelled	5.9	36	PDB header: transcription Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pII based coiled2 coils: replacement of k(15))(16)
26	d1x3ha1	Alignment	not modelled	5.7	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
27	c4dfdB_	Alignment	not modelled	5.7	19	PDB header: hydrolase Chain: B: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family enzyme bt-2542 (target efi-501088)2 from bacteroides thetaiotaomicron, magnesium complex
28	c6bn1A_	Alianment	not modelled	5.5	50	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo;

						PDBTitle: salvador hippo sarah domain complex
29	c4cgbA_	Alignment	not modelled	5.3	56	PDB header: cell cycle Chain: A: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
30	c6gboG_	Alignment	not modelled	5.2	46	PDB header: viral protein Chain: G: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from ebola2 virus
31	c1ij3A_	Alignment	not modelled	5.1	41	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
32	d2ciwa2	Alignment	not modelled	5.1	83	Fold: EF Hand-like Superfamily: Cloroperoxidase Family: Cloroperoxidase
33	d2pgca1	Alignment	not modelled	5.1	44	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Marine metagenome family DABB3