








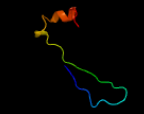

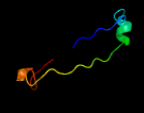

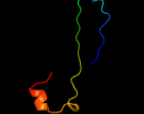

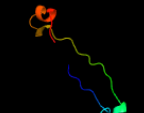









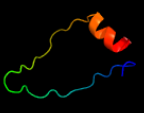




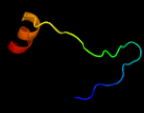


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1780 (-) _2014706_2015269
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	bc6d939a823ac754

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mwwA	 Alignment		39.3	17	PDB header: transferase Chain: A; PDB Molecule: rna polymerase sigma factor sigma; PDBTitle: sigma1.1 domain of sigmaa from bacillus subtilis
2	c2v3sB	 Alignment		36.8	21	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structural insights into the recognition of substrates and2 activators by the osr1 kinase
3	d1zmba1	 Alignment		32.7	33	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxytan esterase-like
4	c2k6xA	 Alignment		22.2	14	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
5	c2idcA	 Alignment		15.7	14	PDB header: replication/chaperone Chain: A; PDB Molecule: anti-silencing protein 1 and histone h3 chimera; PDBTitle: structure of the histone h3-asf1 chaperone interaction
6	c6a6yA	 Alignment		15.4	19	PDB header: chaperone Chain: A; PDB Molecule: histone chaperone asf1, putative; PDBTitle: crystal structure of asf1 from plasmodium falciparum
7	d2i32a1	 Alignment		15.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
8	c2i32A	 Alignment		15.1	14	PDB header: replication chaperone Chain: A; PDB Molecule: anti-silencing factor 1 paralog a; PDBTitle: structure of a human asf1a-hira complex and insights into specificity2 of histone chaperone complex assembly
9	d1roca	 Alignment		14.5	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
10	c3zpmA	 Alignment		13.6	18	PDB header: surfactant protein Chain: A; PDB Molecule: latherin; PDBTitle: solution structure of latherin
11	c3jb9E	 Alignment		13.4	45	PDB header: rna binding protein/rna Chain: E; PDB Molecule: small nuclear ribonucleoprotein-associated protein b; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution

12	c5fmnB_	Alignment		11.3	26	PDB header: dna binding protein Chain: B: PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
13	c3voqA_	Alignment		10.1	25	PDB header: membrane protein Chain: A: PDB Molecule: target of rapamycin complex 2 subunit mapkap1; PDBTitle: crystal structure of the pleckstrin homology domain of human sin1, a2 torc2 subunit
14	c5xtdK_	Alignment		9.9	67	PDB header: oxidoreductase/electron transport Chain: K: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 3, PDBTitle: cryo-em structure of human respiratory complex i
15	d1u3ua1	Alignment		9.6	18	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
16	c5lcyD_	Alignment		8.2	14	PDB header: transcription Chain: D: PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
17	c5lbnD_	Alignment		7.4	24	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor frmr; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
18	c2y69S_	Alignment		7.3	19	PDB header: electron transport Chain: S: PDB Molecule: cytochrome c oxidase subunit 5b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
19	d2dyja1	Alignment		6.9	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
20	d1u3wa1	Alignment		6.6	20	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
21	c2dcuB_	Alignment	not modelled	6.5	29	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
22	c2lkqA_	Alignment	not modelled	6.2	50	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
23	d2cu9a1	Alignment	not modelled	6.1	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
24	c2fsdB_	Alignment	not modelled	5.8	35	PDB header: viral protein Chain: B: PDB Molecule: putative baseplate protein; PDBTitle: a common fold for the receptor binding domains of2 lactococcal phages? the crystal structure of the head3 domain of phage bil170
25	d2b4va2	Alignment	not modelled	5.6	13	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RNA editing terminal uridyl transferase 2, RET2, catalytic domain
26	d2gu2a1	Alignment	not modelled	5.4	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
27	d2jhfa1	Alignment	not modelled	5.1	20	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain