
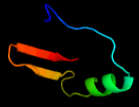
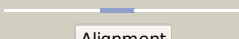
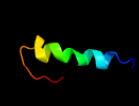
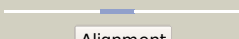
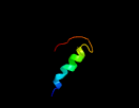

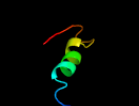

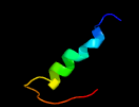

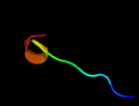

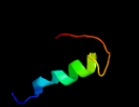

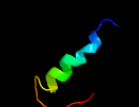
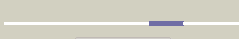







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3639c_(-)_4078063_4078629
Date	Fri Aug 9 18:20:32 BST 2019
Unique Job ID	5c89ff7959fffd58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4d0uD_	 Alignment		41.5	37	PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the atadenovirus snake2 adenovirus 1, selenomethionine-derivative
2	d1fy7a_	 Alignment		27.5	46	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
3	d2ozua1	 Alignment		27.2	46	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
4	c5gk9A_	 Alignment		20.8	38	PDB header: transferase/metal binding protein Chain: A: PDB Molecule: histone acetyltransferase kat7; PDBTitle: crystal structure of human hbo1 in complex with brpf2
5	c2ou2A_	 Alignment		20.7	50	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htip1; PDBTitle: acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
6	c3u2aA_	 Alignment		17.5	75	PDB header: hydrolase Chain: A: PDB Molecule: ggdef family protein; PDBTitle: adaptor dependent degradation of a cell-cycle regulator reveals2 diversity in substrate architectures
7	d2giva1	 Alignment		17.2	38	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
8	c2givA_	 Alignment		17.2	38	PDB header: transferase Chain: A: PDB Molecule: probable histone acetyltransferase myst1; PDBTitle: human myst histone acetyltransferase 1
9	c3r27A_	 Alignment		12.4	15	PDB header: protein binding Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein I; PDBTitle: crystal structure of the first rrm domain of heterogeneous nuclear2 ribonucleoprotein I (hnnp I)
10	d1wi8a_	 Alignment		11.5	23	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
11	c3eukL_	 Alignment		11.4	47	PDB header: cell cycle Chain: L: PDB Molecule: chromosome partition protein muke; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer

12	c3s8sA_	Alignment		11.0	29	PDB header: transcription Chain: A; PDB Molecule: histone-lysine n-methyltransferase setd1a; PDBTitle: crystal structure of the rrm domain of human setd1a
13	d1yuaa1	Alignment		10.8	63	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
14	d1sjqa_	Alignment		10.3	20	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
15	c2n3oA_	Alignment		10.1	19	PDB header: rna binding protein/rna Chain: A; PDB Molecule: polypyrimidine tract-binding protein 1; PDBTitle: structure of ptb rrm1(41-163) bound to an rna stemloop containing a2 structured loop derived from viral internal ribosomal entry site rna
16	c3c5mC_	Alignment		9.3	21	PDB header: lyase Chain: C; PDB Molecule: oligogalacturonate lyase; PDBTitle: crystal structure of oligogalacturonate lyase (vpa0088)2 from vibrio parahaemolyticus. northeast structural3 genomics consortium target vpr199
17	c1yuaA_	Alignment		9.1	63	PDB header: dna binding protein Chain: A; PDB Molecule: topoisomerase i; PDBTitle: c-terminal domain of escherichia coli topoisomerase i
18	c2kvxA_	Alignment		9.0	54	PDB header: plant protein Chain: A; PDB Molecule: kalata-b12; PDBTitle: solution structure of kalata b12
19	d1wdka2	Alignment		8.7	46	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
20	c3ctvA_	Alignment		7.0	38	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus
21	d2d1xa1	Alignment	not modelled	6.8	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: UAS domain
22	c2na7B_	Alignment	not modelled	6.7	44	PDB header: apoptosis Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of human fas/cd95 death receptor
23	c2na7C_	Alignment	not modelled	6.7	44	PDB header: apoptosis Chain: C; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of human fas/cd95 death receptor
24	c2na7A_	Alignment	not modelled	6.6	44	PDB header: apoptosis Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of human fas/cd95 death receptor
25	c3mjjD_	Alignment	not modelled	6.5	36	PDB header: hydrolase Chain: D; PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
26	c3couA_	Alignment	not modelled	6.5	62	PDB header: hydrolase Chain: A; PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
27	d1vqox1	Alignment	not modelled	6.3	24	Fold: Ribosomal protein L31e Superfamily: Ribosomal protein L31e Family: Ribosomal protein L31e
						PDB header: hydrolase

28	c2ii1A_	Alignment	not modelled	6.1	32	Chain: A: PDB Molecule: acetamidase; PDBTitle: crystal structure of acetamidase (10172637) from bacillus halodurans2 at 1.95 a resolution
29	c1z5wA_	Alignment	not modelled	6.0	25	PDB header: structural protein Chain: A: PDB Molecule: tubulin gamma-1 chain; PDBTitle: crystal structure of gamma-tubulin bound to gtp
30	c2j8aA_	Alignment	not modelled	6.0	33	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: x-ray structure of the n-terminus rrm domain of set1
31	d1su3a1	Alignment	not modelled	6.0	33	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
32	c5oayA_	Alignment	not modelled	5.8	32	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional regulator whib1; PDBTitle: m. tuberculosis [4fe-4s] protein whib1 is a four-helix bundle that2 forms a no-sensitive complex with sigmaa and regulates the major3 virulence factor esx-1
33	d2ad9a1	Alignment	not modelled	5.4	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD