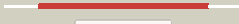

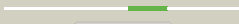
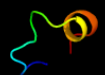

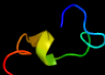






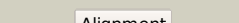








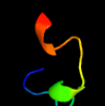


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3416_(whiB3)_3835072_3835380
 Date Fri Aug 9 18:20:08 BST 2019
 Unique Job ID 7438751fb2238bb6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oayA_	 Alignment		100.0	39	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
2	c4unfA_	 Alignment		53.7	33	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
3	d1rrqa1	 Alignment		26.4	38	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
4	c1rrqA_	 Alignment		23.6	39	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
5	c2wj8N_	 Alignment		22.6	21	PDB header: rna binding protein/rna Chain: N: PDB Molecule: nucleoprotein; PDBTitle: respiratory syncytial virus ribonucleoprotein
6	d1orna_	 Alignment		21.5	38	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
7	d1kq2a_	 Alignment		21.0	29	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
8	d1keaa_	 Alignment		18.7	23	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
9	c1vd3A_	 Alignment		17.6	24	PDB header: hydrolase Chain: A: PDB Molecule: rnase ngr3; PDBTitle: ribonuclease nt in complex with 2'-ump
10	c3saeA_	 Alignment		16.5	22	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
11	c4uobA_	 Alignment		16.1	38	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3

12	c2pqxA_			15.6	28	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease i; PDBTitle: e. coli rnae 1 (in vivo folded)
13	c3pybB_			15.6	23	PDB header: isomerase Chain: B: PDB Molecule: ent-copalyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
14	c5c2mA_			15.3	29	PDB header: structural protein Chain: A: PDB Molecule: predicted protein; PDBTitle: the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
15	c6f40P_			14.0	0	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase iii subunit rpc6; PDBTitle: rna polymerase iii open complex
16	c3n5nX_			13.2	46	PDB header: hydrolase Chain: X: PDB Molecule: a/g-specific adenine dna glycosylase; PDBTitle: crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
17	c5fvcF_			12.9	18	PDB header: viral protein Chain: F: PDB Molecule: hmpv nucleoprotein; PDBTitle: structure of rna-bound decameric hmpv nucleoprotein
18	c5fj9P_			11.9	0	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase iii subunit rpc6; PDBTitle: cryo-em structure of yeast apo rna polymerase iii at 4.6 a
19	c3p5rB_			11.2	17	PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
20	c1hjiB_			10.5	25	PDB header: bacteriophage hk022 Chain: B: PDB Molecule: nun-protein; PDBTitle: bacteriophage hk022 nun-protein-nutboxb-rna complex
21	c6dx2A_		not modelled	10.2	33	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of the viral otu domain protease from dera ghazi2 khan virus
22	c3s9vD_		not modelled	10.2	22	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
23	d2abka_		not modelled	10.0	30	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
24	d1i8ya_		not modelled	9.9	83	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat
25	c1i8yA_		not modelled	9.9	83	PDB header: cytokine Chain: A: PDB Molecule: granulin-1; PDBTitle: semi-automatic structure determination of the cg1 3-302 peptide based on aria
26	c2ru1A_		not modelled	9.9	67	PDB header: hormone Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of esf3
27	c3zs9D_		not modelled	9.0	31	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
28	d1k1xa1		not modelled	8.8	57	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: 4-alpha-glucanotransferase, domain 2
						Fold: Flavodoxin-like

29	d2f62a1	Alignment	not modelled	8.8	14	Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
30	d1wo9a_	Alignment	not modelled	6.8	67	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
31	d1gl0i_	Alignment	not modelled	6.6	83	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
32	c3gycB_	Alignment	not modelled	6.3	14	PDB header: hydrolase Chain: B: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
33	c2f91B_	Alignment	not modelled	6.1	67	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: serine protease inhibitor i/ii; PDBTitle: 1.2a resolution structure of a crayfish trypsin complexed2 with a peptide inhibitor, sgti
34	d1dixa_	Alignment	not modelled	6.1	24	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
35	d1b4ua_	Alignment	not modelled	5.8	15	Fold: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Superfamily: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Family: LigA subunit of an aromatic-ring-opening dioxygenase LigAB
36	d1u61a_	Alignment	not modelled	5.3	21	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: RNase III catalytic domain-like