
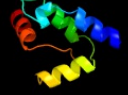



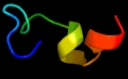

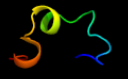
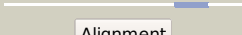

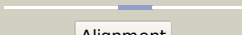





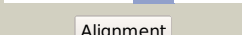
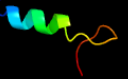


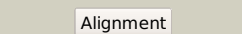

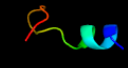

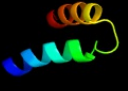

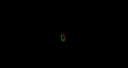

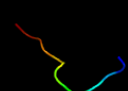

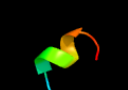


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3681c\_(whiB4)\_4121376\_4121732  
 Date Fri Aug 9 18:20:37 BST 2019  
 Unique Job ID 3df56510b1529ca8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5oayA_</a>	 Alignment		100.0	45	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator whib1; <b>PDBTitle:</b> 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	<a href="#">c4unfA_</a>	 Alignment		49.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> endonuclease iii-1; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-1
3	<a href="#">d1rrqa1</a>	 Alignment		27.7	38	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
4	<a href="#">c1rrqA_</a>	 Alignment		27.4	39	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
5	<a href="#">c4ywcD_</a>	 Alignment		22.4	54	<b>PDB header:</b> transcription regulator <b>Chain:</b> D; <b>PDB Molecule:</b> protein tify 7; <b>PDBTitle:</b> crystal structure of myc3(5-242) fragment in complex with jaz9(218-2 239) peptide
6	<a href="#">d1orna_</a>	 Alignment		21.1	31	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
7	<a href="#">c4ywcC_</a>	 Alignment		20.4	54	<b>PDB header:</b> transcription regulator <b>Chain:</b> C; <b>PDB Molecule:</b> protein tify 7; <b>PDBTitle:</b> crystal structure of myc3(5-242) fragment in complex with jaz9(218-2 239) peptide
8	<a href="#">d1kg2a_</a>	 Alignment		20.2	29	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
9	<a href="#">c3pybB_</a>	 Alignment		20.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> ent-copalyl diphosphate synthase, chloroplastic; <b>PDBTitle:</b> crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
10	<a href="#">c2wj8N_</a>	 Alignment		19.8	29	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> N; <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> respiratory syncytial virus ribonucleoprotein
11	<a href="#">c4uobA_</a>	 Alignment		19.8	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> endonuclease iii-3; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-3

12	<a href="#">c3saeA_</a>	Alignment		19.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-bisabolene synthase; <b>PDBTitle:</b> structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
13	<a href="#">d1keaa_</a>	Alignment		18.7	23	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
14	<a href="#">c5fvcF_</a>	Alignment		16.3	21	<b>PDB header:</b> viral protein <b>Chain:</b> F; <b>PDB Molecule:</b> hmpv nucleoprotein; <b>PDBTitle:</b> structure of rna-bound decameric hmpv nucleoprotein
15	<a href="#">c1vd3A_</a>	Alignment		16.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> rnase ngr3; <b>PDBTitle:</b> ribonuclease nt in complex with 2'-ump
16	<a href="#">c6f40P_</a>	Alignment		16.1	0	<b>PDB header:</b> transcription <b>Chain:</b> P; <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc6; <b>PDBTitle:</b> rna polymerase iii open complex
17	<a href="#">c2pqxA_</a>	Alignment		15.8	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ribonuclease i; <b>PDBTitle:</b> e. coli rnase 1 (in vivo folded)
18	<a href="#">c5fj9P_</a>	Alignment		15.3	8	<b>PDB header:</b> transcription <b>Chain:</b> P; <b>PDB Molecule:</b> dna-directed rna polymerase iii subunit rpc6; <b>PDBTitle:</b> cryo-em structure of yeast apo rna polymerase iii at 4.6 a
19	<a href="#">c3n5nX_</a>	Alignment		14.3	46	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> a/g-specific adenine dna glycosylase; <b>PDBTitle:</b> crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
20	<a href="#">c3m1uB_</a>	Alignment		13.8	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase; <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
21	<a href="#">c3p5rB_</a>	Alignment	not modelled	13.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> taxadiene synthase; <b>PDBTitle:</b> crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
22	<a href="#">c3zs9D_</a>	Alignment	not modelled	12.5	33	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> golgi to er traffic protein 2; <b>PDBTitle:</b> s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
23	<a href="#">c4rs9B_</a>	Alignment	not modelled	12.2	33	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> protein tify 7; <b>PDBTitle:</b> structure of myc3 n-terminal jaz-binding domain [44-238] in complex2 with jas motif of jaz9
24	<a href="#">c1i8yA_</a>	Alignment	not modelled	11.8	60	<b>PDB header:</b> cytokine <b>Chain:</b> A; <b>PDB Molecule:</b> granulin-1; <b>PDBTitle:</b> semi-automatic structure determination of the cg1 3-302 peptide based on aria
25	<a href="#">d1i8ya_</a>	Alignment	not modelled	11.8	60	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
26	<a href="#">c6dx2A_</a>	Alignment	not modelled	10.4	29	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from dera ghazi2 khan virus
27	<a href="#">d2abka_</a>	Alignment	not modelled	9.1	30	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
28	<a href="#">c3gycB_</a>	Alignment	not modelled	8.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative glycoside hydrolase; <b>PDBTitle:</b> crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at

						1.85 a resolution
29	<a href="#">d1k1xa1</a>	Alignment	not modelled	8.2	57	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> 4-alpha-glucanotransferase, domain 2
30	<a href="#">d1b4ua_</a>	Alignment	not modelled	6.9	23	<b>Fold:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Superfamily:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB <b>Family:</b> LigA subunit of an aromatic-ring-opening dioxygenase LigAB
31	<a href="#">d2f62a1</a>	Alignment	not modelled	6.8	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
32	<a href="#">c4l69A_</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase e; <b>PDBTitle:</b> rv2372c of mycobacterium tuberculosis is rsmc like methyltransferase
33	<a href="#">c1hjiB_</a>	Alignment	not modelled	6.3	42	<b>PDB header:</b> bacteriophage hk022 <b>Chain:</b> B: <b>PDB Molecule:</b> nun-protein; <b>PDBTitle:</b> bacteriophage hk022 nun-protein-nutboxb-rna complex
34	<a href="#">c2ru1A_</a>	Alignment	not modelled	6.2	44	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of esf3
35	<a href="#">c3zs9C_</a>	Alignment	not modelled	6.0	33	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> golgi to er traffic protein 2; <b>PDBTitle:</b> s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
36	<a href="#">c1y698_</a>	Alignment	not modelled	5.9	26	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> ribosome-recycling factor; <b>PDB Fragment:</b> unp residues 1-30 and 106-185; <b>PDBTitle:</b> rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
37	<a href="#">d1v54d_</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
38	<a href="#">c3s9vD_</a>	Alignment	not modelled	5.8	32	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> abietadiene synthase, chloroplastic; <b>PDBTitle:</b> abietadiene synthase from abies grandis
39	<a href="#">c2iu9C_</a>	Alignment	not modelled	5.7	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine <b>PDBTitle:</b> chlamydia trachomatis lpxd with 100mm udpglcna (complex ii)
40	<a href="#">c2y69Q_</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> electron transport <b>Chain:</b> Q: <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
41	<a href="#">c2ormA_</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase hp0924; <b>PDBTitle:</b> crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
42	<a href="#">d1wo9a_</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> PMP inhibitors <b>Superfamily:</b> PMP inhibitors <b>Family:</b> PMP inhibitors