


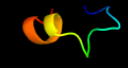





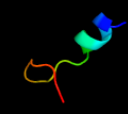

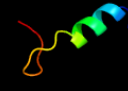







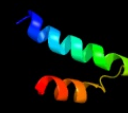

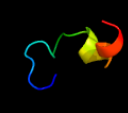


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3219_(whiB1)_3595710_3595964
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	5ba29ebbd17d27a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5oayA_</a>	 Alignment		100.0	100	<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		47.9	28	<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		24.3	29	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
4	<a href="#">c1vd3A_</a>	 Alignment		23.7	18	<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
5	<a href="#">c3saeA_</a>	 Alignment		23.5	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
6	<a href="#">c3pybB_</a>	 Alignment		22.3	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
7	<a href="#">c1rrqa_</a>	 Alignment		22.1	30	<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
8	<a href="#">d1orna_</a>	 Alignment		21.3	31	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
9	<a href="#">c2pqxA_</a>	 Alignment		20.7	24	<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)
10	<a href="#">c2wj8N_</a>	 Alignment		20.4	24	<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="#">d1kg2a_</a>	 Alignment		20.2	29	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase

12	<a href="#">c3p5rB_</a>	Alignment		18.9	33	<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
13	<a href="#">c4uobA_</a>	Alignment		18.3	31	<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
14	<a href="#">d1keaa_</a>	Alignment		17.7	23	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
15	<a href="#">c3s9vD_</a>	Alignment		17.3	33	<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
16	<a href="#">c5fvcF_</a>	Alignment		16.8	24	<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
17	<a href="#">c5fj9P_</a>	Alignment		14.9	0	<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
18	<a href="#">c6f40P_</a>	Alignment		14.5	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
19	<a href="#">c3n5nX_</a>	Alignment		12.9	38	<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="#">d2f62a1</a>	Alignment		12.6	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
21	<a href="#">c1i8yA_</a>	Alignment	not modelled	11.1	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
22	<a href="#">d1i8ya_</a>	Alignment	not modelled	11.1	60	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
23	<a href="#">c1hjiB_</a>	Alignment	not modelled	10.7	33	<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
24	<a href="#">c3zs9D_</a>	Alignment	not modelled	9.8	35	<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
25	<a href="#">d2abka_</a>	Alignment	not modelled	9.0	30	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
26	<a href="#">d1dixa_</a>	Alignment	not modelled	8.8	18	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
27	<a href="#">c4fdxB_</a>	Alignment	not modelled	8.8	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonase tautomerase isozyme; <b>PDBTitle:</b> kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
28	<a href="#">d1b4ua_</a>	Alignment	not modelled	8.6	15	<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
						<b>Fold:</b> immunoglobulin/albumin-binding domain-like

29	<a href="#">d1k1xa1</a>	Alignment	not modelled	7.9	57	<b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> 4-alpha-glucanotransferase, domain 2
30	<a href="#">c6dx2A_</a>	Alignment	not modelled	7.5	33	<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
31	<a href="#">d1wo9a_</a>	Alignment	not modelled	7.2	50	<b>Fold:</b> PMP inhibitors <b>Superfamily:</b> PMP inhibitors <b>Family:</b> PMP inhibitors
32	<a href="#">c3gycB_</a>	Alignment	not modelled	7.1	18	<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
33	<a href="#">d1iqqa_</a>	Alignment	not modelled	7.0	18	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
34	<a href="#">d1jy5a_</a>	Alignment	not modelled	7.0	18	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
35	<a href="#">c2ru1A_</a>	Alignment	not modelled	6.6	56	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of esf3
36	<a href="#">d1gl0i_</a>	Alignment	not modelled	6.6	67	<b>Fold:</b> PMP inhibitors <b>Superfamily:</b> PMP inhibitors <b>Family:</b> PMP inhibitors
37	<a href="#">c2f91B_</a>	Alignment	not modelled	6.4	50	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease inhibitor i/ji; <b>PDBTitle:</b> 1.2a resolution structure of a crayfish trypsin complexed2 with a peptide inhibitor, sgti
38	<a href="#">d1sgla_</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
39	<a href="#">d1sl8a_</a>	Alignment	not modelled	5.9	25	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
40	<a href="#">d1iooa_</a>	Alignment	not modelled	5.7	12	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
41	<a href="#">d1iyba_</a>	Alignment	not modelled	5.2	24	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
42	<a href="#">d1g26a_</a>	Alignment	not modelled	5.1	67	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat