


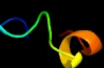


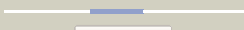
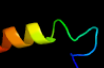




















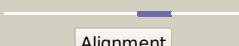
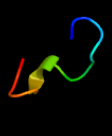
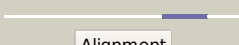
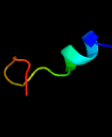
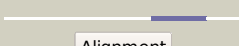
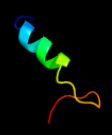
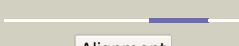
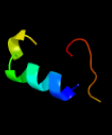



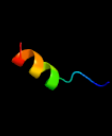



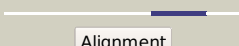






# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3260c\_(whiB2)\_3639869\_3640138  
 Date Thu Aug 8 16:20:46 BST 2019  
 Unique Job ID 72c948fa272b0eca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5oayA_</a>	 Alignment		100.0	47	<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		43.0	44	<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="#">c4bjsC_</a>	 Alignment		26.1	38	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> telomere length regulator protein rif1; <b>PDBTitle:</b> crystal structure of the rif1 c-terminal domain (rif1-ctd)2 from saccharomyces cerevisiae
4	<a href="#">d2f62a1</a>	 Alignment		23.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
5	<a href="#">c2wj8N_</a>	 Alignment		22.9	21	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> respiratory syncytial virus ribonucleoprotein
6	<a href="#">c1hjiB_</a>	 Alignment		20.6	58	<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
7	<a href="#">d1rrqa1</a>	 Alignment		20.5	29	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
8	<a href="#">c1rrqA_</a>	 Alignment		18.5	26	<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
9	<a href="#">c1vd3A_</a>	 Alignment		18.0	24	<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
10	<a href="#">c5fvcF_</a>	 Alignment		17.9	18	<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
11	<a href="#">d1orna_</a>	 Alignment		17.7	38	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III

12	<a href="#">d1kg2a_</a>	 Alignment		16.9	29	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
13	<a href="#">c4uobA_</a>	 Alignment		16.5	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
14	<a href="#">c2pqxA_</a>	 Alignment		15.4	29	<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)
15	<a href="#">d1keaa_</a>	 Alignment		15.1	31	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
16	<a href="#">c3saeA_</a>	 Alignment		13.6	22	<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
17	<a href="#">c3pybB_</a>	 Alignment		12.9	14	<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
18	<a href="#">c6dx2A_</a>	 Alignment		12.8	25	<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
19	<a href="#">c3n5nX_</a>	 Alignment		11.7	31	<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="#">c2ormA_</a>	 Alignment		10.4	25	<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.
21	<a href="#">c6f40P_</a>	 Alignment	not modelled	9.2	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
22	<a href="#">c3p5rB_</a>	 Alignment	not modelled	9.1	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
23	<a href="#">c5fj9P_</a>	 Alignment	not modelled	9.0	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
24	<a href="#">c3gycB_</a>	 Alignment	not modelled	8.0	23	<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
25	<a href="#">d2abka_</a>	 Alignment	not modelled	7.9	30	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
26	<a href="#">c3s9vD_</a>	 Alignment	not modelled	7.9	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
27	<a href="#">c3abfB_</a>	 Alignment	not modelled	7.5	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase; <b>PDBTitle:</b> crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
28	<a href="#">d1otfa_</a>	 Alignment	not modelled	7.4	24	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like

29	<a href="#">c2x4kB_</a>	Alignment	not modelled	7.3	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase; <b>PDBTitle:</b> crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
30	<a href="#">d1k1xa1</a>	Alignment	not modelled	7.3	35	<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
31	<a href="#">c1i8yA_</a>	Alignment	not modelled	7.2	40	<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
32	<a href="#">d1i8ya_</a>	Alignment	not modelled	7.2	40	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
33	<a href="#">c2ru1A_</a>	Alignment	not modelled	7.0	44	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of esf3
34	<a href="#">d1b4ua_</a>	Alignment	not modelled	7.0	8	<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
35	<a href="#">c2mvmA_</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-delta; <b>PDBTitle:</b> solution structure of eef1bdelta car domain in tctp-bound state
36	<a href="#">c5m6qA_</a>	Alignment	not modelled	6.8	54	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of kutzneria albida transglutaminase
37	<a href="#">c3mb2G_</a>	Alignment	not modelled	6.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase family enzyme - alpha subunit; <b>PDBTitle:</b> kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
38	<a href="#">c3j20T_</a>	Alignment	not modelled	6.7	54	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 30s ribosomal protein s19p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
39	<a href="#">c4fazB_</a>	Alignment	not modelled	6.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate isomerase protein; <b>PDBTitle:</b> kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphillum
40	<a href="#">c2mvmA_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-delta; <b>PDBTitle:</b> solution structure of eef1bdelta car domain
41	<a href="#">c4fdxB_</a>	Alignment	not modelled	6.4	18	<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 petroleiphillum
42	<a href="#">c2xzmS_</a>	Alignment	not modelled	6.1	54	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rps15e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
43	<a href="#">c2op8A_</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase ywhb; <b>PDBTitle:</b> crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
44	<a href="#">d1dixa_</a>	Alignment	not modelled	5.9	35	<b>Fold:</b> Ribonuclease Rh-like <b>Superfamily:</b> Ribonuclease Rh-like <b>Family:</b> Ribonuclease Rh-like
45	<a href="#">c3ry0A_</a>	Alignment	not modelled	5.7	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tautomerase; <b>PDBTitle:</b> crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
46	<a href="#">d1bjpa_</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
47	<a href="#">c5xxuP_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> ribosomal protein us19; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
48	<a href="#">c4bozA_</a>	Alignment	not modelled	5.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin thioesterase otu1; <b>PDBTitle:</b> structure of otud2 otu domain in complex with k11-linked di ubiquitin
49	<a href="#">c3j38P_</a>	Alignment	not modelled	5.4	46	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s15, isoform a; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins