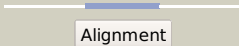
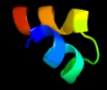
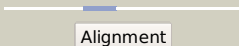

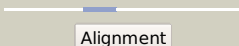

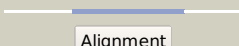
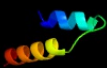
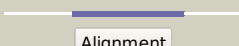

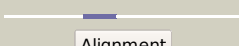
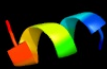
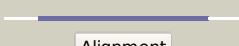
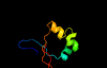
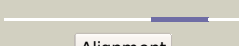
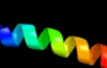







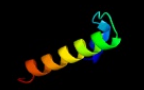


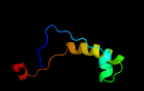






# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3190A\_(RVBD3190A)\_3556852\_3557061  
 Date Thu Aug 8 16:20:38 BST 2019  
 Unique Job ID 19fc9499f6358a2e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5fimA_</a>	 Alignment		24.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ygau; <b>PDBTitle:</b> the structure of kbp.k from e. coli
2	<a href="#">d1y7ma2</a>	 Alignment		24.5	20	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
3	<a href="#">c2mkxA_</a>	 Alignment		21.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> solution structure of lysm the peptidoglycan binding domain of 2 autolysin atla from enterococcus faecalis
4	<a href="#">c1ks9A_</a>	 Alignment		20.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> ketopantoate reductase from escherichia coli
5	<a href="#">d1ks9a1</a>	 Alignment		18.7	19	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Ketopantoate reductase PanE
6	<a href="#">d1e0ga_</a>	 Alignment		16.3	40	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
7	<a href="#">c4pqlB_</a>	 Alignment		14.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> truncated replication protein repa; <b>PDBTitle:</b> n-terminal domain of dna binding protein
8	<a href="#">c2yonA_</a>	 Alignment		14.3	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> sensory box protein; <b>PDBTitle:</b> solution nmr structure of the c-terminal extension of two bacterial 2 light, oxygen, voltage (lov) photoreceptor proteins from 3 pseudomonas putida
9	<a href="#">c3no7A_</a>	 Alignment		13.8	53	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative plasmid related protein; <b>PDBTitle:</b> crystal structure of the centromere-binding protein parb from plasmid 2 pccx100
10	<a href="#">c5zhcA_</a>	 Alignment		12.4	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv
11	<a href="#">d2ev0a1</a>	 Alignment		12.4	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein

12	<a href="#">c3k96B_</a>	Alignment		12.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
13	<a href="#">c5ocdD_</a>	Alignment		12.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cyclodipeptide synthase; <b>PDBTitle:</b> structure of a cdps from fluoribacter dumoffii
14	<a href="#">c5nbcD_</a>	Alignment		10.6	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> structure of prokaryotic transcription factors
15	<a href="#">c2djpA_</a>	Alignment		10.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sb145; <b>PDBTitle:</b> the solution structure of the lysm domain of human2 hypothetical protein sb145
16	<a href="#">d2nrac1</a>	Alignment		10.2	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Replication initiation protein
17	<a href="#">d1fipa_</a>	Alignment		10.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
18	<a href="#">c4b3nA_</a>	Alignment		10.1	29	<b>PDB header:</b> sugar binding protein/ligase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, tripartite motif- <b>PDBTitle:</b> crystal structure of rhesus trim5alpha pry/spry domain
19	<a href="#">c4pxvC_</a>	Alignment		10.1	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> chitinase a; <b>PDBTitle:</b> crystal structure of lysm domain from pteris ryukyensis chitinase a
20	<a href="#">c6hu9e_</a>	Alignment		9.8	23	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
21	<a href="#">d1g3wa1</a>	Alignment	not modelled	9.7	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
22	<a href="#">d1dj0a_</a>	Alignment	not modelled	9.6	21	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase I TruA
23	<a href="#">c5k2IA_</a>	Alignment	not modelled	9.3	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase, lysozyme; <b>PDBTitle:</b> crystal structure of lysm domain from volvox carteri chitinase
24	<a href="#">c5I9wb_</a>	Alignment	not modelled	9.2	58	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
25	<a href="#">d2itba1</a>	Alignment	not modelled	9.2	19	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> MiaE-like
26	<a href="#">c5bumA_</a>	Alignment	not modelled	8.5	40	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase a; <b>PDBTitle:</b> crystal structure of lysm domain from equisetum arvense chitinase a
27	<a href="#">c3bjqA_</a>	Alignment	not modelled	8.4	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phage-related protein; <b>PDBTitle:</b> crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
28	<a href="#">c5I9wB_</a>	Alignment	not modelled	8.4	67	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
29	<a href="#">d2isya1</a>	Alignment	not modelled	7.8	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

						<b>Family:</b> Iron-dependent repressor protein
30	<a href="#">d1q6za2</a>	Alignment	not modelled	7.8	31	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
31	<a href="#">d1v9pa3</a>	Alignment	not modelled	7.7	25	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD <sup>+</sup> -dependent DNA ligase
32	<a href="#">d1mzba_</a>	Alignment	not modelled	7.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FUR-like
33	<a href="#">c1jpxA_</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp41 envelope protein; <b>PDBTitle:</b> mutation that destabilize the gp41 core: determinants for stabilizing2 the siv/cpma envelope glycoprotein complex. wild type.
34	<a href="#">c4p96B_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae
35	<a href="#">c2l9yA_</a>	Alignment	not modelled	6.4	30	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cvnh-lysm lectin; <b>PDBTitle:</b> solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
36	<a href="#">c1hsjA_</a>	Alignment	not modelled	6.2	26	<b>PDB header:</b> transcription/sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein consisting of staphylococcus accessory <b>PDBTitle:</b> sarr mbp fusion structure
37	<a href="#">d3lada3</a>	Alignment	not modelled	6.1	27	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
38	<a href="#">c5fgmA_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
39	<a href="#">d1w7pd1</a>	Alignment	not modelled	5.8	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
40	<a href="#">c3g17H_</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> similar to 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
41	<a href="#">c6dlcB_</a>	Alignment	not modelled	5.7	43	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein dhd1:234_b; <b>PDBTitle:</b> designed protein dhd1:234_a, designed protein dhd1:234_b
42	<a href="#">c4bryB_</a>	Alignment	not modelled	5.7	35	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> multicilin; <b>PDBTitle:</b> the idas:geminin heterodimeric parallel coiled-coil
43	<a href="#">c2kelB_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein 56b; <b>PDBTitle:</b> structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
44	<a href="#">c4uz2D_</a>	Alignment	not modelled	5.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the n-terminal lysm domains from the putative2 nlpc/p60 d,l endopeptidase from t. thermophilus
45	<a href="#">c3f10A_</a>	Alignment	not modelled	5.4	8	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-oxoguanine-dna-glycosylase; <b>PDBTitle:</b> crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
46	<a href="#">c3mwmA_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal uptake regulation protein; <b>PDBTitle:</b> graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur