























# Phyre2

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Description	RVBD3456c_rplQ_3877069_3877611
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o600_</a>	 Alignment		100.0	92	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 50s ribosomal protein l17; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">c1vw4L_</a>	 Alignment		100.0	30	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 54s ribosomal protein l8, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
3	<a href="#">d2qamn1</a>	 Alignment		100.0	49	<b>Fold:</b> Prokaryotic ribosomal protein L17 <b>Superfamily:</b> Prokaryotic ribosomal protein L17 <b>Family:</b> Prokaryotic ribosomal protein L17
4	<a href="#">c4v19R_</a>	 Alignment		100.0	37	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> mitoribosomal protein bl17m, mrpl17; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
5	<a href="#">c3bboP_</a>	 Alignment		100.0	50	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> ribosomal protein l17; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
6	<a href="#">d2zjrk1</a>	 Alignment		100.0	47	<b>Fold:</b> Prokaryotic ribosomal protein L17 <b>Superfamily:</b> Prokaryotic ribosomal protein L17 <b>Family:</b> Prokaryotic ribosomal protein L17
7	<a href="#">c3j3vN_</a>	 Alignment		100.0	46	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 50s ribosomal protein l17; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
8	<a href="#">d1gd8a_</a>	 Alignment		100.0	54	<b>Fold:</b> Prokaryotic ribosomal protein L17 <b>Superfamily:</b> Prokaryotic ribosomal protein L17 <b>Family:</b> Prokaryotic ribosomal protein L17
9	<a href="#">d2cqma1</a>	 Alignment		100.0	40	<b>Fold:</b> Prokaryotic ribosomal protein L17 <b>Superfamily:</b> Prokaryotic ribosomal protein L17 <b>Family:</b> Prokaryotic ribosomal protein L17
10	<a href="#">c5vn4A_</a>	 Alignment		36.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenine phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate
11	<a href="#">c3w6kC_</a>	 Alignment		35.8	11	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> scpb; <b>PDBTitle:</b> crystal structure of dimer of scpb n-terminal domain complexed with2 scpa peptide

12	<a href="#">c3w6jC_</a>	Alignment		33.8	11	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> scpb; <b>PDBTitle:</b> crystal structure of scpb core complex
13	<a href="#">c5yhhA_</a>	Alignment		33.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein yim; <b>PDBTitle:</b> crystal structure of yim from geobacillus stearothermophilus
14	<a href="#">c3h0dB_</a>	Alignment		24.6	50	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> ctsr; <b>PDBTitle:</b> crystal structure of ctsr in complex with a 26bp dna duplex
15	<a href="#">c2z99A_</a>	Alignment		21.1	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of scpb from mycobacterium tuberculosis
16	<a href="#">d1o65a_</a>	Alignment		20.3	16	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> MOSC (MOCO sulphurase C-terminal) domain
17	<a href="#">d1xd7a_</a>	Alignment		16.5	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
18	<a href="#">c3kowH_</a>	Alignment		14.8	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> d-ornithine aminomutase s component; <b>PDBTitle:</b> crystal structure of ornithine 4,5 aminomutase backsoaked complex
19	<a href="#">c5he9E_</a>	Alignment		14.1	33	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> phage inhibitor protein; <b>PDBTitle:</b> bacterial initiation protein in complex with phage inhibitor protein
20	<a href="#">c2ic6B_</a>	Alignment		13.4	21	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> the coiled-coil domain (residues 1-75) structure of the sin nombre2 virus nucleocapsid protein
21	<a href="#">c5wlbF_</a>	Alignment	not modelled	11.5	71	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> 225-15 b; <b>PDBTitle:</b> kras g12v, bound to gppnhp and miniprotein 225-15a/b
22	<a href="#">d1v66a_</a>	Alignment	not modelled	11.3	23	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
23	<a href="#">c2op8A_</a>	Alignment	not modelled	11.2	10	<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
24	<a href="#">c5tv6A_</a>	Alignment	not modelled	10.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-carboxyhexanoate--coa ligase; <b>PDBTitle:</b> a. aeolicus biow with pelimate
25	<a href="#">c1x4qA_</a>	Alignment	not modelled	10.4	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
26	<a href="#">d1t6sa1</a>	Alignment	not modelled	10.1	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ScpB/YpuH-like
27	<a href="#">c5wlbC_</a>	Alignment	not modelled	9.5	71	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> 225-15 b; <b>PDBTitle:</b> kras g12v, bound to gppnhp and miniprotein 225-15a/b
28	<a href="#">c4fipG_</a>	Alignment	not modelled	9.0	55	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> structure of the saga ubp8(s144n)/sgf11(1-72, delta-znf)/sus1/sgf732 dub module <b>PDB header:</b> toxin

29	<a href="#">c4dtfA_</a>	Alignment	not modelled	8.5	24	<b>Chain:</b> A: <b>PDB Molecule:</b> vrgg protein; <b>PDBTitle:</b> structure of a vrgg vibrio cholerae toxin acd domain in complex with 2 amp-pnp and mg++
30	<a href="#">c2wb1_</a>	Alignment	not modelled	8.3	25	<b>PDB header:</b> transcription <b>Chain:</b> J: <b>PDB Molecule:</b> dna-directed rna polymerase rpo13 subunit; <b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
31	<a href="#">c1pqrA_</a>	Alignment	not modelled	7.7	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-a-conotoxin eiva; <b>PDBTitle:</b> solution conformation of alphaa-conotoxin eiva
32	<a href="#">d1otfa_</a>	Alignment	not modelled	7.3	5	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
33	<a href="#">c2llrA_</a>	Alignment	not modelled	7.0	45	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> alvinellacin; <b>PDBTitle:</b> nmr structure of alvinellacin
34	<a href="#">c4i0wA_</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease cspb; <b>PDBTitle:</b> structure of the clostridium perfringens cspb protease
35	<a href="#">c3ry0A_</a>	Alignment	not modelled	6.9	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 in 2 tomaymycin biosynthetic pathway
36	<a href="#">c2bnIE_</a>	Alignment	not modelled	6.8	7	<b>PDB header:</b> stress-response <b>Chain:</b> E: <b>PDB Molecule:</b> modulator protein rsbr; <b>PDBTitle:</b> the structure of the n-terminal domain of rsbr
37	<a href="#">c4acrA_</a>	Alignment	not modelled	6.3	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glypican-1; <b>PDBTitle:</b> crystal structure of n-glycosylated, c-terminally truncated human 2 glypican-1
38	<a href="#">d1qb7a_</a>	Alignment	not modelled	6.3	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
39	<a href="#">c2cqiA_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein <b>PDBTitle:</b> solution structure of the s4 domain of u3 small nucleolar 2 ribonucleoprotein protein imp3 homolog
40	<a href="#">c4fdxB_</a>	Alignment	not modelled	6.2	10	<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-oxalocrotonate 2 tautomerase isozymes from methylbium petroleiphilum
41	<a href="#">d1bjpa_</a>	Alignment	not modelled	6.1	10	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
42	<a href="#">c4if2A_</a>	Alignment	not modelled	6.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase homology protein; <b>PDBTitle:</b> structure of the phosphotriesterase from mycobacterium tuberculosis
43	<a href="#">c2x4kB_</a>	Alignment	not modelled	5.8	14	<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-oxalocrotonate 2 tautomerase from the methicillin-resistant staphylococcus 3 aureus (mrsa)
44	<a href="#">c5x5wC_</a>	Alignment	not modelled	5.6	27	<b>PDB header:</b> viral protein/cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> gd; <b>PDBTitle:</b> crystal structure of pseudorabies virus glycoprotein d
45	<a href="#">c3mkoA_</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycoprotein c; <b>PDBTitle:</b> crystal structure of the lymphocytic choriomeningitis virus membrane 2 fusion glycoprotein gp2 in its postfusion conformation
46	<a href="#">c5wd9A_</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lem22; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector lpg2328
47	<a href="#">d2incb1</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
48	<a href="#">c6nd4K_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> utp9; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic 2 small ribosomal subunit
49	<a href="#">d1ht6a1</a>	Alignment	not modelled	5.3	17	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
50	<a href="#">c2d3o1_</a>	Alignment	not modelled	5.2	54	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> structure of ribosome binding domain of the trigger factor on the 50s 2 ribosomal subunit from d. radiodurans
51	<a href="#">c3kmiB_</a>	Alignment	not modelled	5.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative membrane protein cog4129; <b>PDBTitle:</b> crystal structure of putative membrane protein from clostridium 2 difficile 630
52	<a href="#">c3dhgB_</a>	Alignment	not modelled	5.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> toluene 4-monoxygenase hydroxylase beta subunit; <b>PDBTitle:</b> crystal structure of toluene 4-monoxygenase hydroxylase