

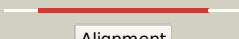

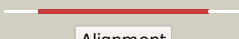











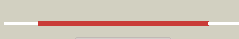




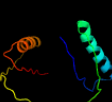


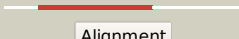
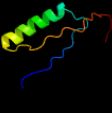
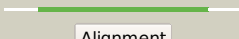
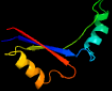

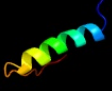
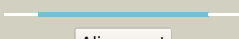
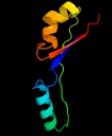



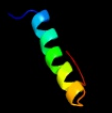
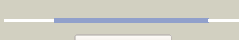

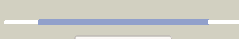
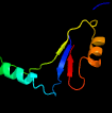
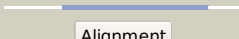
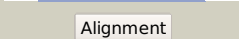

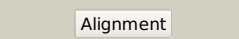


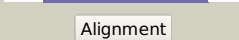



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0053\_(rpsF)\_58189\_58479  
 Date Tue Jul 23 14:50:08 BST 2019  
 Unique Job ID fb43ea73dbdb0e37

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o5jF_</a>	 Alignment		100.0	92	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">d2j5aa1</a>	 Alignment		100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
3	<a href="#">d1loua_</a>	 Alignment		100.0	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
4	<a href="#">d1qjha_</a>	 Alignment		100.0	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
5	<a href="#">c3bbnF_</a>	 Alignment		100.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> ribosomal protein s6; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
6	<a href="#">c3j0xl_</a>	 Alignment		100.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> I; <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
7	<a href="#">c1vmbA_</a>	 Alignment		100.0	29	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> crystal structure of 30s ribosomal protein s6 (tm0603) from thermotoga2 maritima at 1.70 a resolution
8	<a href="#">d1vmba_</a>	 Alignment		100.0	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
9	<a href="#">d2qalf1</a>	 Alignment		100.0	34	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
10	<a href="#">c2qbbF_</a>	 Alignment		100.0	34	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> crystal structure of the bacterial ribosome from escherichia coli in2 complex with gentamicin. this file contains the 30s subunit of the3 second 70s ribosome, with gentamicin bound. the entire crystal4 structure contains two 70s ribosomes and is described in remark 400.
11	<a href="#">c3r3tA_</a>	 Alignment		99.9	37	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> crystal structure of 30s ribosomal protein s from bacillus anthracis

12	<a href="#">c3j6vF_</a>	 Alignment		99.9	28	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 28s ribosomal protein s6, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
13	<a href="#">c2kjaA_</a>	 Alignment		99.7	41	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> solution structure and backbone dynamics of the permutant p54-55
14	<a href="#">c2zw2B_</a>	 Alignment		56.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein sts178; <b>PDBTitle:</b> crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfobolbus tokodaii (stpurs)
15	<a href="#">d1jcb4</a>	 Alignment		49.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Anticodon-binding domain of PheRS <b>Family:</b> Anticodon-binding domain of PheRS
16	<a href="#">d1gtda_</a>	 Alignment		37.1	14	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase
17	<a href="#">d1phza1</a>	 Alignment		32.2	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phenylalanine metabolism regulatory domain
18	<a href="#">c2akwB_</a>	 Alignment		29.8	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
19	<a href="#">d1sc6a3</a>	 Alignment		29.6	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
20	<a href="#">d1vq3a_</a>	 Alignment		27.8	18	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase
21	<a href="#">c2mdaB_</a>	 Alignment	not modelled	26.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine 3-monooxygenase; <b>PDBTitle:</b> the solution structure of the regulatory domain of tyrosine2 hydroxylase
22	<a href="#">c5a13j_</a>	 Alignment	not modelled	23.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> chlorite dismutase; <b>PDBTitle:</b> crystal structure of chlorite dismutase from2 magnetospirillum sp. in complex with thiocyanate
23	<a href="#">d3b5ha2</a>	 Alignment	not modelled	21.1	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
24	<a href="#">c3fmbA_</a>	 Alignment	not modelled	20.7	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dimeric protein of unknown function and ferredoxin-like <b>PDBTitle:</b> crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
25	<a href="#">c2ybvN_</a>	 Alignment	not modelled	18.9	26	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
26	<a href="#">d1uzhc1</a>	 Alignment	not modelled	15.4	14	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
27	<a href="#">d2nzca1</a>	 Alignment	not modelled	15.1	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> TM1266-like
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0106 protein ph0461;

28	<a href="#">c2yy8B_</a>	Alignment	not modelled	14.3	19	<b>PDBTitle:</b> crystal structure of archaeal trna-methylase for position256 (atrm56) from pyrococcus horikoshii, complexed with s-3adenosyl-l-methionine
29	<a href="#">d1svdm1</a>	Alignment	not modelled	13.9	10	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
30	<a href="#">d1t4aa_</a>	Alignment	not modelled	13.9	15	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase
31	<a href="#">d3bpdal</a>	Alignment	not modelled	12.9	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH889-like <b>Family:</b> MTH889-like
32	<a href="#">d2raqa1</a>	Alignment	not modelled	12.8	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH889-like <b>Family:</b> MTH889-like
33	<a href="#">c2yx5A_</a>	Alignment	not modelled	12.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0062 protein mj1593; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
34	<a href="#">c3nrbD_</a>	Alignment	not modelled	11.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
35	<a href="#">c2vxhF_</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> chlorite dismutase; <b>PDBTitle:</b> the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
36	<a href="#">c2x3dC_</a>	Alignment	not modelled	11.2	11	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ss06206; <b>PDBTitle:</b> crystal structure of sso6206 from sulfobolus solfataricus p2
37	<a href="#">c5ekaA_</a>	Alignment	not modelled	10.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein hu; <b>PDBTitle:</b> hu dna-binding protein from thermus thermophilus
38	<a href="#">c5fmsA_</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport protein 52 homolog; <b>PDBTitle:</b> mmift52 n-terminal domain
39	<a href="#">d1a6fa_</a>	Alignment	not modelled	9.9	12	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
40	<a href="#">c5by3A_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> btgh115a; <b>PDBTitle:</b> a novel family gh115 4-o-methyl-alpha-glucuronidase, btgh115a, with2 specificity for decorated arabinogalactans
41	<a href="#">c4qjuB_</a>	Alignment	not modelled	9.0	9	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein hu; <b>PDBTitle:</b> crystal structure of dna-bound nucleoid associated protein, sav1473
42	<a href="#">c4zmhA_</a>	Alignment	not modelled	9.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a five-domain gh115 alpha-glucuronidase from the2 marine bacterium saccharophagus degradans 2-40t
43	<a href="#">d3blhb1</a>	Alignment	not modelled	8.2	14	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
44	<a href="#">d1sqwa2</a>	Alignment	not modelled	8.2	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Nip7p homolog, N-terminal domain
45	<a href="#">d1f9ya_</a>	Alignment	not modelled	8.1	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK <b>Family:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
46	<a href="#">c4c90B_</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucuronidase gh115; <b>PDBTitle:</b> evidence that gh115 alpha-glucuronidase activity is2 dependent on conformational flexibility
47	<a href="#">c5nv3P_</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> lyase <b>Chain:</b> P: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small chain 1; <b>PDBTitle:</b> structure of rubisco from rhodobacter sphaeroides in complex with cabp
48	<a href="#">d1bwvs_</a>	Alignment	not modelled	7.3	13	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
49	<a href="#">c2ljpa_</a>	Alignment	not modelled	7.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease p protein component; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
50	<a href="#">c2rhsB_</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies
51	<a href="#">c1y9ja_</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> sec1 family domain containing protein 1; <b>PDBTitle:</b> solution structure of the rat sly1 n-terminal domain
52	<a href="#">c2jnvA_</a>	Alignment	not modelled	6.4	24	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 1, chloroplast; <b>PDBTitle:</b> solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
53	<a href="#">d1huua_</a>	Alignment	not modelled	6.4	11	<b>Fold:</b> IHF-like DNA-binding proteins <b>Superfamily:</b> IHF-like DNA-binding proteins

						<b>Family:</b> Prokaryotic DNA-bending protein
54	<a href="#">d1x4oa1</a>	Alignment	not modelled	6.3	13	<b>Fold:</b> Surp module (SWAP domain) <b>Superfamily:</b> Surp module (SWAP domain) <b>Family:</b> Surp module (SWAP domain)
55	<a href="#">d2gtln1</a>	Alignment	not modelled	6.3	19	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Extracellular hemoglobin linker subunit, receptor domain <b>Family:</b> Extracellular hemoglobin linker subunit, receptor domain
56	<a href="#">c2yy3B</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-beta; <b>PDBTitle:</b> crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
57	<a href="#">c3fpjA</a>	Alignment	not modelled	6.0	9	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
58	<a href="#">d1d6ta</a>	Alignment	not modelled	5.8	15	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
59	<a href="#">c2z51A</a>	Alignment	not modelled	5.7	29	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 2, chloroplast; <b>PDBTitle:</b> crystal structure of arabidopsis cnfu involved in iron-sulfur cluster2 biosynthesis
60	<a href="#">d2id1a1</a>	Alignment	not modelled	5.7	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> lojap/YbeB-like
61	<a href="#">c6eznG</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
62	<a href="#">c1kcfB</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical 30.2 kd protein c25g10.02 in <b>PDBTitle:</b> crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
63	<a href="#">c5d4pA</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrogen regulatory protein p-ii glnb; <b>PDBTitle:</b> structure of cpil bound to adp and bicarbonate, from thiomonas2 intermedia k12
64	<a href="#">d2o3aa1</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> AF0751-like
65	<a href="#">c2np2B</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hbb; <b>PDBTitle:</b> hbb-dna complex
66	<a href="#">d1th5a1</a>	Alignment	not modelled	5.4	24	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
67	<a href="#">d1ir1s</a>	Alignment	not modelled	5.3	17	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
68	<a href="#">c4wcbB</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal silencing factor rsfs; <b>PDBTitle:</b> ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis