



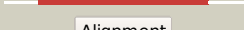

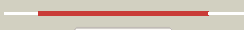




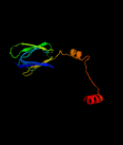


















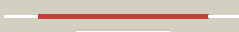
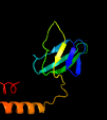



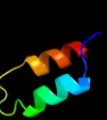








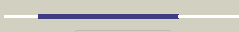





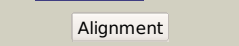
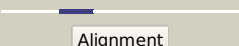
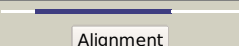
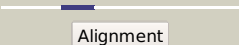
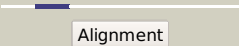

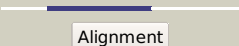
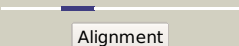
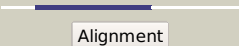
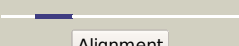

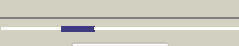
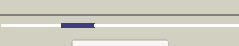

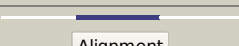
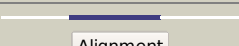
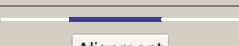

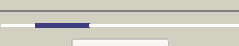
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1311_(atpC)_1467321_1467686
Date	Wed Jul 31 22:05:40 BST 2019
Unique Job ID	3a63d75ce2e84af2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5yioA_</a>	 Alignment		100.0	100	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> nmr solution structure of subunit epsilon of the mycobacterium2 tuberculosis f-atp synthase
2	<a href="#">c6q45P_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> P; <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> f1-atpase from fusobacterium nucleatum
3	<a href="#">c2e5yA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
4	<a href="#">c2rq7A_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
5	<a href="#">c6fkhe_</a>	 Alignment		100.0	32	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> atp synthase subunit alpha, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 2
6	<a href="#">c1fs0E_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> atp synthase epsilon subunit; <b>PDBTitle:</b> complex of gamma/epsilon atp synthase from e.coli
7	<a href="#">c6f5dH_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> atp synthase subunit delta, mitochondrial; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
8	<a href="#">c2qe7H_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> atp synthase subunit epsilon; <b>PDBTitle:</b> crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
9	<a href="#">c6refR_</a>	 Alignment		100.0	21	<b>PDB header:</b> proton transport <b>Chain:</b> R; <b>PDB Molecule:</b> mitochondrial atp synthase subunit delta; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 3b,2 monomer-masked refinement
10	<a href="#">c2wssQ_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> Q; <b>PDB Molecule:</b> atp synthase subunit delta, mitochondrial; <b>PDBTitle:</b> the structure of the membrane extrinsic region of bovine atp synthase
11	<a href="#">c5lqzH_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> atp synthase delta subunit; <b>PDBTitle:</b> structure of f-atpase from pichia angusta, state1

12	<a href="#">c2hldH_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> atp synthase delta chain, mitochondrial; <b>PDBTitle:</b> crystal structure of yeast mitochondrial f1-atpase
13	<a href="#">d1aqt2</a>	 Alignment		99.9	25	<b>Fold:</b> Epsilon subunit of F1F0-ATP synthase N-terminal domain <b>Superfamily:</b> Epsilon subunit of F1F0-ATP synthase N-terminal domain <b>Family:</b> Epsilon subunit of F1F0-ATP synthase N-terminal domain
14	<a href="#">c1h8eH_</a>	 Alignment		99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> bovine mitochondrial f1-atpase; <b>PDBTitle:</b> (adp.alf4)2(adp.so4) bovine f1-atpase2 (all three catalytic sites occupied)
15	<a href="#">c5dn6L_</a>	 Alignment		99.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> atp synthase from paracoccus denitrificans
16	<a href="#">c2w6jH_</a>	 Alignment		97.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> f1-atpase delta subunit; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
17	<a href="#">c2e5tA_</a>	 Alignment		91.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase epsilon chain; <b>PDBTitle:</b> c-terminal domain of epsilon subunit of f1f0-atp synthase2 from the thermophilic bacillus ps3 in the presence of atp3 condition
18	<a href="#">d1aqt1</a>	 Alignment		78.5	39	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Epsilon subunit of F1F0-ATP synthase C-terminal domain <b>Family:</b> Epsilon subunit of F1F0-ATP synthase C-terminal domain
19	<a href="#">c3hqxA_</a>	 Alignment		59.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0345 protein aciad0356; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
20	<a href="#">c4cv7A_</a>	 Alignment		23.3	16	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> virulence associated protein vapb; <b>PDBTitle:</b> crystal structure of rhodococcus equi vapb
21	<a href="#">c3vtoR_</a>	 Alignment	not modelled	18.6	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> R: <b>PDB Molecule:</b> protein gp45; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of mu phage central2 spike
22	<a href="#">d2ezla_</a>	 Alignment	not modelled	18.2	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
23	<a href="#">c4er8A_</a>	 Alignment	not modelled	12.7	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> tnparep for protein; <b>PDBTitle:</b> structure of the rep associates tyrosine transposase bound to a rep2 hairpin
24	<a href="#">d1y60a_</a>	 Alignment	not modelled	12.1	13	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Formaldehyde-activating enzyme, FAE
25	<a href="#">c3eo6B_</a>	 Alignment	not modelled	8.8	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of unknown function (duf1255); <b>PDBTitle:</b> crystal structure of protein of unknown function (duf1255) (afe_2634)2 from acidithiobacillus ferrooxidans ncib8455 at 0.97 a resolution
26	<a href="#">c4c5eH_</a>	 Alignment	not modelled	8.5	25	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> polycomb protein pho; <b>PDBTitle:</b> crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
27	<a href="#">c4c5eG_</a>	 Alignment	not modelled	8.5	25	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> polycomb protein pho; <b>PDBTitle:</b> crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
28	<a href="#">c2vhgB_</a>	 Alignment	not modelled	8.4	24	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transposase orfa; <b>PDBTitle:</b> crystal structure of the ishp608 transposase in complex2 with right end 31-mer dna

29	<a href="#">c4gdxB</a>	 Alignment	not modelled	8.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase 1 light chain; <b>PDBTitle:</b> crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
30	<a href="#">c3j6vR</a>	 Alignment	not modelled	8.1	56	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 28s ribosomal protein s18a, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
31	<a href="#">d2oyza1</a>	 Alignment	not modelled	7.7	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> VPA0057-like
32	<a href="#">d2f5ga1</a>	 Alignment	not modelled	7.3	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Transposase IS200-like <b>Family:</b> Transposase IS200-like
33	<a href="#">c4l6uB</a>	 Alignment	not modelled	6.8	27	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
34	<a href="#">c3frnA</a>	 Alignment	not modelled	6.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flga; <b>PDBTitle:</b> crystal structure of flagellar protein flga from thermotoga maritima2 msb8
35	<a href="#">d1od5a1</a>	 Alignment	not modelled	6.4	20	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
36	<a href="#">c2vicA</a>	 Alignment	not modelled	6.2	24	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transposase orfa; <b>PDBTitle:</b> crystal structure of the ishp608 transposase in complex2 with left end 26-mer dna and manganese
37	<a href="#">c5dudA</a>	 Alignment	not modelled	6.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ybgk; <b>PDBTitle:</b> crystal structure of e. coli ybgk
38	<a href="#">c3j20G</a>	 Alignment	not modelled	6.0	14	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 30s ribosomal protein s6e; <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="#">c5aeeA</a>	 Alignment	not modelled	6.0	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> r. equi vapg protein; <b>PDBTitle:</b> virulence-associated protein vapg from the intracellular2 pathogen rhodococcus equi
40	<a href="#">d2fyxa1</a>	 Alignment	not modelled	5.9	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Transposase IS200-like <b>Family:</b> Transposase IS200-like
41	<a href="#">d2viva1</a>	 Alignment	not modelled	5.9	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Transposase IS200-like <b>Family:</b> Transposase IS200-like
42	<a href="#">d1e3ha5</a>	 Alignment	not modelled	5.7	22	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
43	<a href="#">c5wlyA</a>	 Alignment	not modelled	5.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-2,3-diacetylglucosamine hydrolase; <b>PDBTitle:</b> e. coli lpxh- 8 mutations
44	<a href="#">c3stjC</a>	 Alignment	not modelled	5.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degq; <b>PDBTitle:</b> crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
45	<a href="#">c4bkwA</a>	 Alignment	not modelled	5.4	21	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 9; <b>PDBTitle:</b> crystal structure of the c-terminal region of human zfyve9
46	<a href="#">c1tr8A</a>	 Alignment	not modelled	5.3	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein (mth177); <b>PDBTitle:</b> crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
47	<a href="#">c3pm9A</a>	 Alignment	not modelled	5.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution