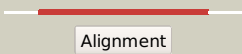

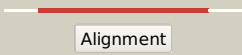

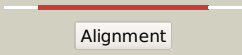



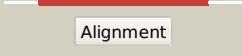

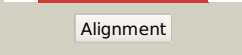

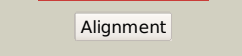

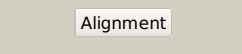

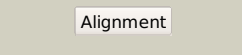
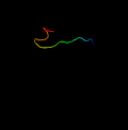
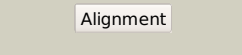
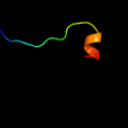
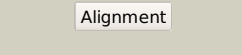

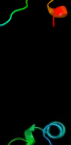


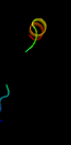
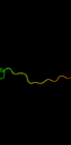
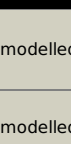
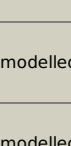
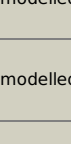
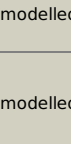


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3226c_(-)_3602561_3603319
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	1d3b117fd07e41dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ko9A_</a>	 Alignment		100.0	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> embryonic stem cell-specific 5-hydroxymethylcytosine- <b>PDBTitle:</b> crystal structure of the srp domain of human hmces protein
2	<a href="#">d2f20a1</a>	 Alignment		100.0	24	<b>Fold:</b> BB1717-like <b>Superfamily:</b> BB1717-like <b>Family:</b> BB1717-like
3	<a href="#">c2icuB_</a>	 Alignment		100.0	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein yedk; <b>PDBTitle:</b> crystal structure of hypothetical protein yedk from escherichia coli
4	<a href="#">d2bdva1</a>	 Alignment		100.0	24	<b>Fold:</b> BB1717-like <b>Superfamily:</b> BB1717-like <b>Family:</b> BB1717-like
5	<a href="#">d1zn6a1</a>	 Alignment		100.0	25	<b>Fold:</b> BB1717-like <b>Superfamily:</b> BB1717-like <b>Family:</b> BB1717-like
6	<a href="#">c2aegA_</a>	 Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein agr_pat_140; <b>PDBTitle:</b> x-ray crystal structure of protein atu5096 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr63.
7	<a href="#">d2aega1</a>	 Alignment		100.0	21	<b>Fold:</b> BB1717-like <b>Superfamily:</b> BB1717-like <b>Family:</b> BB1717-like
8	<a href="#">c3uksB_</a>	 Alignment		26.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sedoheptulose-1,7 bisphosphatase, putative; <b>PDBTitle:</b> 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
9	<a href="#">d1d9qa_</a>	 Alignment		22.4	35	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
10	<a href="#">c5oezA_</a>	 Alignment		22.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fbp protein; <b>PDBTitle:</b> crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
11	<a href="#">d1bk4a_</a>	 Alignment		21.8	39	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like

12	<a href="#">d1spia_</a>	Alignment		21.2	35	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
13	<a href="#">c2gq1A_</a>	Alignment		21.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase; <b>PDBTitle:</b> crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
14	<a href="#">d1nuwa_</a>	Alignment		21.1	44	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	<a href="#">d1ftaa_</a>	Alignment		19.6	39	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
16	<a href="#">c2fhyL_</a>	Alignment		18.1	39	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase 1; <b>PDBTitle:</b> structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor
17	<a href="#">c4eogA_</a>	Alignment		16.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of csx1 of pyrococcus furiosus
18	<a href="#">c5iz3B_</a>	Alignment		14.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> p. patens sedoheptulose-1,7-bisphosphatase
19	<a href="#">c4txvB_</a>	Alignment		14.4	24	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> crystal structure of the mixed disulfide intermediate between2 thioredoxin-like tlpas(c110s) and subunit ii of cytochrome c oxidase3 coxibd (c233s)
20	<a href="#">c3ulcA_</a>	Alignment		12.4	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> target of rapamycin complex 2 subunit avo1; <b>PDBTitle:</b> crystal structure of the pleckstrin homology domain of saccharomyces2 cerevisiae avo1, a torc2 subunit, in the p3121 crystal form
21	<a href="#">c1v55B_</a>	Alignment	not modelled	12.2	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> bovine heart cytochrome c oxidase at the fully reduced state
22	<a href="#">d2hewf1</a>	Alignment	not modelled	11.7	38	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
23	<a href="#">c2hewF_</a>	Alignment	not modelled	11.7	38	<b>PDB header:</b> cytokine <b>Chain:</b> F: <b>PDB Molecule:</b> tumor necrosis factor ligand superfamily member 4; <b>PDBTitle:</b> the x-ray crystal structure of murine ox40l
24	<a href="#">c6hu9n_</a>	Alignment	not modelled	11.4	29	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> N: <b>PDB Molecule:</b> cytochrome b; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
25	<a href="#">c6hwhL_</a>	Alignment	not modelled	11.1	18	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
26	<a href="#">d3dtub1</a>	Alignment	not modelled	10.9	41	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
27	<a href="#">c2yqpA_</a>	Alignment	not modelled	10.9	50	<b>PDB header:</b> gene regulation, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx59; <b>PDBTitle:</b> solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
28	<a href="#">c4uurB_</a>	Alignment	not modelled	10.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hemoglobin-like oxygen-binding protein; <b>PDBTitle:</b> cold-adapted truncated hemoglobin from the antarctic

					marine bacterium2 pseudoalteromonas haloplanktis tac125
29	<a href="#">d2hevf1</a>	Alignment	not modelled	9.7	38 <b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
30	<a href="#">c1t3bA</a>	Alignment	not modelled	9.4	22 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> x-ray structure of dsbc from haemophilus influenzae
31	<a href="#">d3ehbb1</a>	Alignment	not modelled	9.1	35 <b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
32	<a href="#">c2mxdA</a>	Alignment	not modelled	8.4	27 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> viral protein genome-linked; <b>PDBTitle:</b> solution structure of vpg of porcine sapovirus
33	<a href="#">c1m57H</a>	Alignment	not modelled	7.6	41 <b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
34	<a href="#">c2d0jD</a>	Alignment	not modelled	7.5	23 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> galactosylgalactosylxylosylprotein 3-beta- <b>PDBTitle:</b> crystal structure of human glcat-s apo form
35	<a href="#">c1qleB</a>	Alignment	not modelled	7.4	35 <b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
36	<a href="#">c1ar1B</a>	Alignment	not modelled	7.4	35 <b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
37	<a href="#">d1juha</a>	Alignment	not modelled	6.8	20 <b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Quercetin 2,3-dioxygenase-like
38	<a href="#">d1v54b1</a>	Alignment	not modelled	6.3	35 <b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
39	<a href="#">c2m4hA</a>	Alignment	not modelled	6.0	23 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> feline calicivirus vpg protein; <b>PDBTitle:</b> solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
40	<a href="#">d1eg3a3</a>	Alignment	not modelled	5.8	29 <b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
41	<a href="#">d2gysa1</a>	Alignment	not modelled	5.7	27 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
42	<a href="#">c3zf7v</a>	Alignment	not modelled	5.5	15 <b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 60s ribosomal protein l22, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
43	<a href="#">c3rbbA</a>	Alignment	not modelled	5.3	38 <b>PDB header:</b> viral protein, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein nef; <b>PDBTitle:</b> hiv-1 nef protein in complex with engineered hck sh3 domain