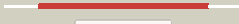

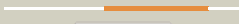
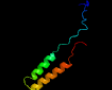











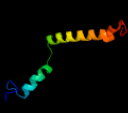

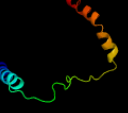

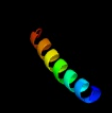

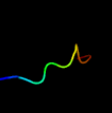

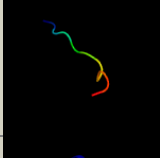
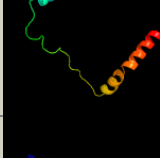
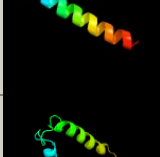
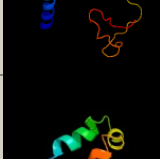
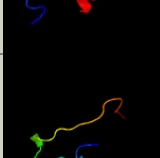
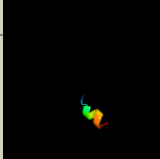

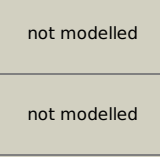


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2199c_(-)_2463241_2463660
Date	Mon Aug 5 13:25:32 BST 2019
Unique Job ID	f7a41ee49e53b97b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hwhX_</a>	 Alignment		100.0	78	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	<a href="#">c2yevA_</a>	 Alignment		89.7	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide i+iii; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
3	<a href="#">d1qlc_</a>	 Alignment		88.7	33	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
4	<a href="#">d1m56c_</a>	 Alignment		87.1	27	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
5	<a href="#">d1v54c_</a>	 Alignment		86.0	20	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
6	<a href="#">c6hu9o_</a>	 Alignment		80.6	22	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> O: <b>PDB Molecule:</b> cytochrome c1, heme protein, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
7	<a href="#">d1g2913</a>	 Alignment		41.6	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
8	<a href="#">c6btmC_</a>	 Alignment		39.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
9	<a href="#">c3eh4A_</a>	 Alignment		38.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
10	<a href="#">c2l9uB_</a>	 Alignment		36.8	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
11	<a href="#">c6mupK_</a>	 Alignment		36.3	45	<b>PDB header:</b> nuclear protein <b>Chain:</b> K: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and two copies2 cenp-n(nt)

12	<a href="#">c6mupL_</a>	Alignment		35.4	45	<b>PDB header:</b> nuclear protein <b>Chain:</b> L: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and two copies2 cenp-n(nt)
13	<a href="#">c6muoK_</a>	Alignment		35.4	45	<b>PDB header:</b> nuclear protein <b>Chain:</b> K: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> cenp-a nucleosome bound by two copies of cenp-c(cd) and one copy cenp-2 n(nt)
14	<a href="#">d1xmea1</a>	Alignment		30.7	9	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
15	<a href="#">c2l9uA_</a>	Alignment		30.1	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-3; <b>PDBTitle:</b> spatial structure of dimeric erbB3 transmembrane domain
16	<a href="#">c4djiA_</a>	Alignment		26.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
17	<a href="#">c3eweD_</a>	Alignment		22.8	16	<b>PDB header:</b> protein transport,structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> nucleoporin nup85; <b>PDBTitle:</b> crystal structure of the nup85/seh1 complex
18	<a href="#">d2bm8a1</a>	Alignment		22.2	36	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Cmcl-like
19	<a href="#">c5xavB_</a>	Alignment		22.1	50	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> intracellular polyhydroxyalkanoate synthase; <b>PDBTitle:</b> structure of phac from chromobacterium sp. usm2
20	<a href="#">c2lx0A_</a>	Alignment		20.1	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane fusion protein p14; <b>PDBTitle:</b> arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
21	<a href="#">c6cfwI_</a>	Alignment	not modelled	19.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
22	<a href="#">c5t6oA_</a>	Alignment	not modelled	19.0	50	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> poly-beta-hydroxybuterate polymerase; <b>PDBTitle:</b> structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
23	<a href="#">c2jlnA_</a>	Alignment	not modelled	17.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
24	<a href="#">c2nuuF_</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> ammonia channel; <b>PDBTitle:</b> regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex
25	<a href="#">c2mtpB_</a>	Alignment	not modelled	17.6	29	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> the structure of filamin repeat 21 bound to integrin
26	<a href="#">c3a0hj_</a>	Alignment	not modelled	16.8	26	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
27	<a href="#">d2axtj1</a>	Alignment	not modelled	16.8	26	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, PsbJ <b>Family:</b> PsbJ-like
28	<a href="#">c5mpoA_</a>	Alignment	not modelled	16.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin synthase sulfur carrier subunit; <b>PDBTitle:</b> crystal structure of human molybdopterin synthase complex

29	<a href="#">c6f0kC_</a>	Alignment	not modelled	15.1	12	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> polysulphide reductase nrfd; <b>PDBTitle:</b> alternative complex iii
30	<a href="#">c5aexB_</a>	Alignment	not modelled	15.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
31	<a href="#">c2m4eA_</a>	Alignment	not modelled	14.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of vv2_0175 from vibrio vulnificus, nesg target2 vnr1 and csqid target idp91333
32	<a href="#">d1ci3m1</a>	Alignment	not modelled	14.0	30	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
33	<a href="#">c2k74A_</a>	Alignment	not modelled	13.7	13	<b>PDB header:</b> membrane protein, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond formation protein b; <b>PDBTitle:</b> solution nmr structure of dsbb-ubiquinone complex
34	<a href="#">c1jjoB_</a>	Alignment	not modelled	13.1	50	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> neuroserpin; <b>PDBTitle:</b> crystal structure of mouse neuroserpin (cleaved form)
35	<a href="#">c3jcuJ_</a>	Alignment	not modelled	11.3	21	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
36	<a href="#">c5xnmj_</a>	Alignment	not modelled	10.6	26	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
37	<a href="#">c1s4wA_</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> nmr structure of the cytoplasmic domain of integrin aiib in2 dpc micelles
38	<a href="#">c1dPKA_</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB subunit; <b>PDBTitle:</b> solution structure of the cytoplasmic domain of the2 integrin alpha-iiB subunit
39	<a href="#">c1m8oA_</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> platelet integrin alfaIiB subunit: cytoplasmic <b>PDBTitle:</b> platelet integrin alfaIiB-beta3 cytoplasmic domain
40	<a href="#">c2kncA_</a>	Alignment	not modelled	9.6	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIiB-beta3 transmembrane-cytoplasmic2 heterocomplex
41	<a href="#">c2b2hA_</a>	Alignment	not modelled	9.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter; <b>PDBTitle:</b> ammonium transporter amt-1 from a. fulgidus (as)
42	<a href="#">c5abvF_</a>	Alignment	not modelled	9.0	100	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> gh11071p; <b>PDBTitle:</b> complex of d. melanogaster eif4e with the 4e-binding2 protein mexTli
43	<a href="#">d1u7ga_</a>	Alignment	not modelled	9.0	19	<b>Fold:</b> Ammonium transporter <b>Superfamily:</b> Ammonium transporter <b>Family:</b> Ammonium transporter
44	<a href="#">c1cirA_</a>	Alignment	not modelled	9.0	38	<b>PDB header:</b> serine protease inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> chymotrypsin inhibitor 2; <b>PDBTitle:</b> complex of two fragments of ci2 [(1-40)(dot)(41-64)]
45	<a href="#">c4ewcA_</a>	Alignment	not modelled	7.8	38	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleoprotein; <b>PDBTitle:</b> crystal structure of the infectious salmon anemia virus nucleoprotein
46	<a href="#">c5lC5m_</a>	Alignment	not modelled	7.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
47	<a href="#">c6itcB_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> translocating peptide; <b>PDBTitle:</b> structure of a substrate engaged seca-secy protein translocation2 machine
48	<a href="#">c6g2jJ_</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 6; <b>PDBTitle:</b> mouse mitochondrial complex i in the active state
49	<a href="#">c4n6eB_</a>	Alignment	not modelled	7.0	28	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> this/moad family protein; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
50	<a href="#">d1d0da_</a>	Alignment	not modelled	7.0	31	<b>Fold:</b> BPTI-like <b>Superfamily:</b> BPTI-like <b>Family:</b> Soft tick anticoagulant proteins
51	<a href="#">c5t13A_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanuric acid amidohydrolase; <b>PDBTitle:</b> structure of the cyanuric acid hydrolase trzd reveals product exit2 channel
52	<a href="#">c5ir6A_</a>	Alignment	not modelled	6.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bd-type quinol oxidase subunit i; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
53	<a href="#">c1tapA_</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> proteinase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> factor xa inhibitor; <b>PDBTitle:</b> nmr solution structure of recombinant tick anticoagulant2 protein (rtap), a factor xa inhibitor from the tick3 ornithodoros moubata
54	<a href="#">d1ldna2</a>	Alignment	not modelled	6.8	16	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
						<b>Fold:</b> Common fold of diphtheria toxin/transcription

55	<a href="#">d1tu2b1</a>	Alignment	not modelled	6.7	32	Factors/cytochrome f <b>Superfamily:</b> Cytochrome f, large domain <b>Family:</b> Cytochrome f, large domain
56	<a href="#">d1ckma1</a>	Alignment	not modelled	6.6	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
57	<a href="#">c3i31A</a>	Alignment	not modelled	6.4	40	<b>PDB header:</b> rna binding protein,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> hera helicase rna binding domain is an rrm fold
58	<a href="#">c2l52A</a>	Alignment	not modelled	6.4	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> methanosarcina acetivorans samp1 homolog; <b>PDBTitle:</b> solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
59	<a href="#">c2g1eA</a>	Alignment	not modelled	6.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
60	<a href="#">d2r8ca1</a>	Alignment	not modelled	5.8	23	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
61	<a href="#">c4kppA</a>	Alignment	not modelled	5.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
62	<a href="#">d1m9la</a>	Alignment	not modelled	5.5	18	<b>Fold:</b> Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) <b>Superfamily:</b> Outer arm dynein light chain 1 <b>Family:</b> Outer arm dynein light chain 1
63	<a href="#">c1dpgA</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB subunit; <b>PDBTitle:</b> solution structure of the constitutively active mutant of2 the integrin alpha iiB cytoplasmic domain.
64	<a href="#">c3dcC</a>	Alignment	not modelled	5.4	37	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> tm1086; <b>PDBTitle:</b> crystal structure of tm1086
65	<a href="#">c6jzbD</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> moad/this family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
66	<a href="#">d2hi7b1</a>	Alignment	not modelled	5.3	13	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> DsbB-like <b>Family:</b> DsbB-like
67	<a href="#">c1tu2B</a>	Alignment	not modelled	5.3	32	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
68	<a href="#">c5xtdo</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> O: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] flavoprotein 2, <b>PDBTitle:</b> cryo-em structure of human respiratory complex i
69	<a href="#">c3e9jC</a>	Alignment	not modelled	5.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol/disulfide oxidoreductase dsbb; <b>PDBTitle:</b> structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
70	<a href="#">d1tsfa</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> Rof/RNase P subunit-like <b>Superfamily:</b> Rof/RNase P subunit-like <b>Family:</b> RNase P subunit p29-like
71	<a href="#">c6jc0A</a>	Alignment	not modelled	5.2	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein d2 <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
72	<a href="#">d1gywb</a>	Alignment	not modelled	5.2	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> gamma-adaptin C-terminal appendage domain-like
73	<a href="#">c3zguA</a>	Alignment	not modelled	5.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanuric acid amidohydrolase; <b>PDBTitle:</b> the 'tricorn' fold: a novel fold for a unique family of ring-opening2 amidases.
74	<a href="#">c4inmV</a>	Alignment	not modelled	5.1	38	<b>PDB header:</b> structural protein/dna <b>Chain:</b> V: <b>PDB Molecule:</b> cenp-c; <b>PDBTitle:</b> crystal structure of cenp-c in complex with the nucleosome core2 particle