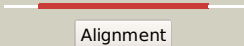

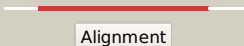

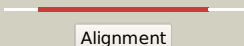







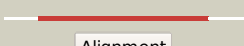




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1145_(mmpL13a)_1272428_1273339
Date	Wed Jul 31 22:05:23 BST 2019
Unique Job ID	4e6374aa1d7a3d2c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ajjA_</a>			100.0	24	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
2	<a href="#">c5khnB_</a>			100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
3	<a href="#">c3jd8A_</a>			100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> niemann-pick c1 protein; <b>PDBTitle:</b> cryo-em structure of the full-length human npc1 at 4.4 angstrom
4	<a href="#">c6dmoA_</a>			100.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein patched homolog 1; <b>PDBTitle:</b> cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
5	<a href="#">c6owsB_</a>			100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> efflux pump membrane transporter; <b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump
6	<a href="#">c6csxA_</a>			100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug efflux pump subunit acrb; <b>PDBTitle:</b> single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
7	<a href="#">c5lq3F_</a>			100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
8	<a href="#">c2v50A_</a>			100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein mexb; <b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
9	<a href="#">c4mt1A_</a>			100.0	16	<b>PDB header:</b> membrane protein, tranport protein <b>Chain:</b> A: <b>PDB Molecule:</b> drug efflux protein; <b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
10	<a href="#">c3k07A_</a>			100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
11	<a href="#">c1oy8A_</a>			99.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump

12	<a href="#">c4k0eC</a>	Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
13	<a href="#">c3aqpB</a>	Alignment		99.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus
14	<a href="#">c5xamA</a>	Alignment		99.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> crystal structure of secdf in i form at 4 a resolution
15	<a href="#">c4k0eA</a>	Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
16	<a href="#">c5mg3F</a>	Alignment		99.8	10	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> protein translocase subunit secf; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
17	<a href="#">d1iwga7</a>	Alignment		99.8	15	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
18	<a href="#">d1iwga8</a>	Alignment		99.7	14	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
19	<a href="#">c5mg3D</a>	Alignment		99.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
20	<a href="#">c4f0aB</a>	Alignment		46.3	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein wnt-8; <b>PDBTitle:</b> crystal structure of xwnt8 in complex with the cysteine-rich domain of2 frizzled 8
21	<a href="#">c1p58E</a>	Alignment	not modelled	36.0	21	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
22	<a href="#">c4av3A</a>	Alignment	not modelled	35.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> k(+)-stimulated pyrophosphate-energized sodium pump; <b>PDBTitle:</b> crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site
23	<a href="#">c1p58F</a>	Alignment	not modelled	32.0	29	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
24	<a href="#">c5awqA</a>	Alignment	not modelled	28.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isomaltodextranase; <b>PDBTitle:</b> arthrobacter globiformis t6 isomalto-dextranase complexed with panose
25	<a href="#">c5xknF</a>	Alignment	not modelled	26.2	67	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> epidermal patterning factor-like protein 4; <b>PDBTitle:</b> crystal structure of plant receptor eri2 in complex with epfl4
26	<a href="#">c5xknE</a>	Alignment	not modelled	26.2	67	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> epidermal patterning factor-like protein 4; <b>PDBTitle:</b> crystal structure of plant receptor eri2 in complex with epfl4
27	<a href="#">c2xzmE</a>	Alignment	not modelled	24.4	9	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> ribosomal protein s5 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
28	<a href="#">d2c4fl3</a>	Alignment	not modelled	21.9	50	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain

						<b>Family:</b> GLA-domain
29	<a href="#">c3j2pD</a>	Alignment	not modelled	21.8	29	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> cryoem structure of dengue virus envelope protein heterotetramer
30	<a href="#">c3na0C</a>	Alignment	not modelled	20.4	56	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> adrenodoxin, mitochondrial; <b>PDBTitle:</b> crystal structure of human cyp11a1 in complex with 20,22-2 dihydroxycholesterol
31	<a href="#">c3zeyP</a>	Alignment	not modelled	20.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s2, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
32	<a href="#">c3j20F</a>	Alignment	not modelled	19.5	22	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 30s ribosomal protein s5p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
33	<a href="#">c3a23A</a>	Alignment	not modelled	19.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted alpha-galactosidase; <b>PDBTitle:</b> crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
34	<a href="#">c5ireD</a>	Alignment	not modelled	18.2	19	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
35	<a href="#">c1n10G</a>	Alignment	not modelled	17.5	50	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> factor ix; <b>PDBTitle:</b> crystal structure of human factor ix gla domain in complex2 of an inhibitory antibody, 10c12
36	<a href="#">c5wsnD</a>	Alignment	not modelled	14.8	24	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
37	<a href="#">c5xyiC</a>	Alignment	not modelled	14.7	12	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
38	<a href="#">d1dan13</a>	Alignment	not modelled	14.3	50	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain <b>Family:</b> GLA-domain
39	<a href="#">c4cbfB</a>	Alignment	not modelled	13.3	14	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> near-atomic resolution cryo-em structure of dengue serotype 4 virus
40	<a href="#">c4a01B</a>	Alignment	not modelled	12.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proton pyrophosphatase; <b>PDBTitle:</b> crystal structure of the h-translocating pyrophosphatase
41	<a href="#">d3bzka3</a>	Alignment	not modelled	12.5	27	<b>Fold:</b> Tex N-terminal region-like <b>Superfamily:</b> Tex N-terminal region-like <b>Family:</b> Tex N-terminal region-like
42	<a href="#">c2ju5A</a>	Alignment	not modelled	12.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase
43	<a href="#">c6m97A</a>	Alignment	not modelled	11.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1
44	<a href="#">c4gj4A</a>	Alignment	not modelled	11.6	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble guanylyl cyclase alpha-1 subunit; <b>PDBTitle:</b> the crystal structure of the soluble guanylate cyclase pas alpha2 domain from manduca sexta
45	<a href="#">d2d32a1</a>	Alignment	not modelled	10.8	29	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Glutamate-cysteine ligase
46	<a href="#">c4y01A</a>	Alignment	not modelled	10.6	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmp111; <b>PDBTitle:</b> mycobacterial membrane protein mmp11d2
47	<a href="#">c5tw1J</a>	Alignment	not modelled	10.4	27	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> rna polymerase-binding protein rbpa; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
48	<a href="#">c4kzzC</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 40s ribosomal protein s2; <b>PDBTitle:</b> rabbit 40s ribosomal subunit in complex with mrna, initiator trna and2 eif1a
49	<a href="#">c2oceA</a>	Alignment	not modelled	10.1	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa5201; <b>PDBTitle:</b> crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
50	<a href="#">c2m4vA</a>	Alignment	not modelled	9.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase binding protein a (rbpa) and2 its interactions with sigma factors
51	<a href="#">c6c04J</a>	Alignment	not modelled	9.1	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> J: <b>PDB Molecule:</b> rna polymerase-binding protein rbpa; <b>PDBTitle:</b> mtb rnap holo/rbpa/double fork dna -closed clamp
52	<a href="#">c2cwoD</a>	Alignment	not modelled	8.7	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> rna silencing suppressor; <b>PDBTitle:</b> crystal structure of rna silencing suppressor p21 from beet yellows2 virus
53	<a href="#">c4owfG</a>	Alignment	not modelled	8.5	50	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf31; <b>PDBTitle:</b> crystal structure of the nemo cozi in complex with hoip nzf1 domain
54	<a href="#">c5fzxA</a>	Alignment	not modelled	8.2	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> u5-scytotoxin-sth1a; <b>PDBTitle:</b> high resolution solution nmr structure of the spider

						venom2 peptide u5-scytotoxin-sth1a
55	<a href="#">c4firB_</a>	Alignment	not modelled	8.2	42	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus
56	<a href="#">d1exta2</a>	Alignment	not modelled	7.7	50	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
57	<a href="#">c3c0uA_</a>	Alignment	not modelled	7.6	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaeq; <b>PDBTitle:</b> crystal structure of e.coli yaeq protein
58	<a href="#">c3lrmB_</a>	Alignment	not modelled	6.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase 1; <b>PDBTitle:</b> structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
59	<a href="#">c6hxgE_</a>	Alignment	not modelled	6.4	55	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate)
60	<a href="#">c3femB_</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine biosynthesis protein snz1; <b>PDBTitle:</b> structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
61	<a href="#">c3fhkF_</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> upf0403 protein yphp; <b>PDBTitle:</b> crystal structure of apc1446, b.subtilis yphp disulfide isomerase
62	<a href="#">c5b16C_</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
63	<a href="#">d2g3wa1</a>	Alignment	not modelled	6.1	5	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like
64	<a href="#">c3py7A_</a>	Alignment	not modelled	6.0	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,paxillin ld1,protein e6 <b>PDBTitle:</b> crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
65	<a href="#">d2gc6a1</a>	Alignment	not modelled	6.0	10	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
66	<a href="#">c2kr6A_</a>	Alignment	not modelled	5.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit
67	<a href="#">d1zpsa1</a>	Alignment	not modelled	5.9	37	<b>Fold:</b> Hisl-like <b>Superfamily:</b> Hisl-like <b>Family:</b> Hisl-like
68	<a href="#">c5b16B_</a>	Alignment	not modelled	5.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
69	<a href="#">c2nv2U_</a>	Alignment	not modelled	5.5	42	<b>PDB header:</b> lyase/transferase <b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
70	<a href="#">d2dk4a1</a>	Alignment	not modelled	5.5	22	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> PRP4-like <b>Family:</b> PRP4-like
71	<a href="#">c6ahyD_</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> proto-oncogene wnt-3; <b>PDBTitle:</b> wnt signaling complex
72	<a href="#">c2f51B_</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of trichomonas vaginalis thioredoxin
73	<a href="#">c2zkqe_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> rna expansion segment es6 part ii; <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
74	<a href="#">d2ot9a1</a>	Alignment	not modelled	5.1	9	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> YaeQ-like