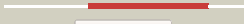
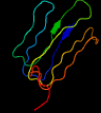
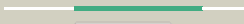
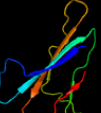



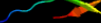







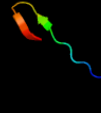





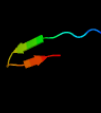
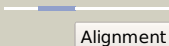
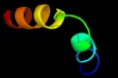
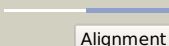
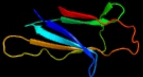
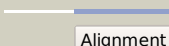
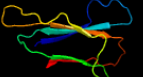
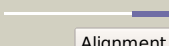
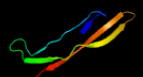
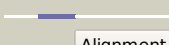

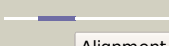

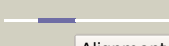


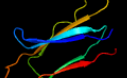

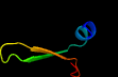
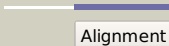
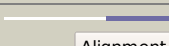

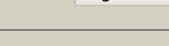
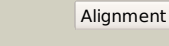


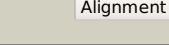


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0506\_(mmpS2)\_596762\_597205  
 Date Fri Jul 26 01:50:05 BST 2019  
 Unique Job ID 57f9effbfe0a23e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lw3A_</a>	 Alignment		100.0	44	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmps4; <b>PDBTitle:</b> solution structure of the soluble domain of mmps4 from mycobacterium2 tuberculosis
2	<a href="#">d1fv1b1</a>	 Alignment		45.6	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
3	<a href="#">c5lnkm_</a>	 Alignment		40.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> mitochondrial complex i, nd4 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
4	<a href="#">d1kona_</a>	 Alignment		34.9	38	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
5	<a href="#">d1d5mb1</a>	 Alignment		32.5	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
6	<a href="#">c3osvC_</a>	 Alignment		32.5	5	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
7	<a href="#">c2kvzA_</a>	 Alignment		31.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ispe; <b>PDBTitle:</b> structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
8	<a href="#">d1lfpA_</a>	 Alignment		28.4	31	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
9	<a href="#">c4f3qA_</a>	 Alignment		26.4	39	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cbu_1566; <b>PDBTitle:</b> structure of a yebc family protein (cbu_1566) from coxiella burnetii
10	<a href="#">d1muja1</a>	 Alignment		25.8	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
11	<a href="#">d1mw7a_</a>	 Alignment		24.2	25	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like

12	<a href="#">c5o31b_</a>	 Alignment		24.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, <b>PDBTitle:</b> mitochondrial complex i in the deactive state
13	<a href="#">d1uvqb1</a>	 Alignment		23.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
14	<a href="#">d1klub1</a>	 Alignment		21.7	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
15	<a href="#">d3d85d2</a>	 Alignment		19.6	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
16	<a href="#">c5lc5b_</a>	 Alignment		19.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
17	<a href="#">c5ldxb_</a>	 Alignment		19.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.
18	<a href="#">c5ldwb_</a>	 Alignment		19.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
19	<a href="#">d1es0b1</a>	 Alignment		16.3	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
20	<a href="#">c5aaoA_</a>	 Alignment		16.2	15	<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
21	<a href="#">d1fngb1</a>	 Alignment	not modelled	15.1	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
22	<a href="#">c5e09A_</a>	 Alignment	not modelled	15.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
23	<a href="#">c2amnA_</a>	 Alignment	not modelled	14.1	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin; <b>PDBTitle:</b> solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken
24	<a href="#">c2na6A_</a>	 Alignment	not modelled	13.5	26	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
25	<a href="#">c2na6C_</a>	 Alignment	not modelled	13.5	26	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
26	<a href="#">c4csbA_</a>	 Alignment	not modelled	13.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> virulence associated protein vapd; <b>PDBTitle:</b> structure of the virulence-associated protein vapd from the2 intracellular pathogen rhodococcus equi.
27	<a href="#">c2na6B_</a>	 Alignment	not modelled	13.0	26	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
						<b>Fold:</b> Alpha-L RNA-binding motif

28	<a href="#">d1kska3</a>	Alignment	not modelled	12.7	27	<b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
29	<a href="#">d1jk8a1</a>	Alignment	not modelled	12.5	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
30	<a href="#">d1c16a1</a>	Alignment	not modelled	12.5	7	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
31	<a href="#">c4cv7A</a>	Alignment	not modelled	12.4	12	<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
32	<a href="#">d1ok0a</a>	Alignment	not modelled	11.9	14	<b>Fold:</b> alpha-Amylase inhibitor tendamistat <b>Superfamily:</b> alpha-Amylase inhibitor tendamistat <b>Family:</b> alpha-Amylase inhibitor tendamistat
33	<a href="#">d1zs8a1</a>	Alignment	not modelled	11.3	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
34	<a href="#">c2xkuA</a>	Alignment	not modelled	10.7	10	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> prion-like conversion during amyloid formation at atomic resolution
35	<a href="#">d1qqda1</a>	Alignment	not modelled	10.4	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
36	<a href="#">d2iada1</a>	Alignment	not modelled	9.7	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
37	<a href="#">d1mhca1</a>	Alignment	not modelled	9.7	8	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
38	<a href="#">d1uvqa1</a>	Alignment	not modelled	9.5	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
39	<a href="#">c2kerA</a>	Alignment	not modelled	9.5	23	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase inhibitor z-2685; <b>PDBTitle:</b> alpha-amylase inhibitor parvulstat (z-2685) from2 streptomyces parvulus
40	<a href="#">d1xtda2</a>	Alignment	not modelled	9.1	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
41	<a href="#">d1ywka1</a>	Alignment	not modelled	9.0	38	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmC-like cupins <b>Family:</b> Kdul-like
42	<a href="#">d1lk2a1</a>	Alignment	not modelled	8.9	6	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
43	<a href="#">c1q40C</a>	Alignment	not modelled	8.5	67	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> mRNA transport regulator mtr2; <b>PDBTitle:</b> crystal structure of the c. albicans mtr2-mex67 m domain complex
44	<a href="#">c2kt7A</a>	Alignment	not modelled	8.5	23	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidoglycan bound protein (lpxtg) <b>PDBTitle:</b> solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
45	<a href="#">c6b6B</a>	Alignment	not modelled	8.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 2, sugar binding domain protein; <b>PDBTitle:</b> the crystal structure of glycosyl hydrolase family 2 (gh2) member from2 bacteroides cellulosilyticus dsm 14838
46	<a href="#">c2kpaA</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0431 protein; <b>PDBTitle:</b> solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
47	<a href="#">d1fnga1</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
48	<a href="#">d1dmla1</a>	Alignment	not modelled	7.7	22	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
49	<a href="#">c1ywkE</a>	Alignment	not modelled	7.7	38	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-l-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
50	<a href="#">d2rb6a1</a>	Alignment	not modelled	7.5	28	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
51	<a href="#">d1k8ib1</a>	Alignment	not modelled	7.2	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
52	<a href="#">c2nykA</a>	Alignment	not modelled	7.2	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> m157; <b>PDBTitle:</b> crystal structure of m157 from mouse cytomegalovirus
53	<a href="#">c3owrA</a>	Alignment	not modelled	7.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative secreted protein (bf4250) from2 bacteroides fragilis nctc 9343 at 1.81 a resolution
						<b>Fold:</b> Sm-like fold

54	<a href="#">d3bdua1</a>	Alignment	not modelled	7.1	20	<b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
55	<a href="#">d1x6oa2</a>	Alignment	not modelled	7.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
56	<a href="#">d1xrua1</a>	Alignment	not modelled	6.8	38	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Kdul-like
57	<a href="#">d1pkla1</a>	Alignment	not modelled	6.8	8	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
58	<a href="#">d2fa8a1</a>	Alignment	not modelled	6.7	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Selenoprotein W-related
59	<a href="#">c3a5pD</a>	Alignment	not modelled	6.4	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> haemagglutinin i; <b>PDBTitle:</b> crystal structure of hemagglutinin
60	<a href="#">c2obkE</a>	Alignment	not modelled	6.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E; <b>PDB Molecule:</b> sel/selw/selh selenoprotein domain; <b>PDBTitle:</b> x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
61	<a href="#">c4gdzA</a>	Alignment	not modelled	6.3	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4251 family protein (bacegg_02002) from2 bacteroides eggerthii dsm 20697 at 1.95 a resolution
62	<a href="#">d1eg3a3</a>	Alignment	not modelled	6.3	27	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
63	<a href="#">c6mhqE</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> gap junction alpha-3 protein, connexin-46; <b>PDBTitle:</b> structure of connexin-46 intercellular gap junction channel at 3.42 angstrom resolution by cryoem
64	<a href="#">d2cs4a1</a>	Alignment	not modelled	6.0	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
65	<a href="#">c5ee2A</a>	Alignment	not modelled	6.0	50	<b>PDB header:</b> metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> hemoglobin-haptoglobin-utilization protein; <b>PDBTitle:</b> the crystal structure of the c-terminal beta-barrel of hpua from2 neisseria gonorrhoeae
66	<a href="#">d2ra2a1</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
67	<a href="#">c3py9A</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein kinase; <b>PDBTitle:</b> x-ray structural studies of the entire extra-cellular region of the2 ser/thr kinase prkc from staphylococcus aureus
68	<a href="#">c2mgyA</a>	Alignment	not modelled	5.5	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> translocator protein; <b>PDBTitle:</b> solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
69	<a href="#">d1ydwa2</a>	Alignment	not modelled	5.5	33	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
70	<a href="#">c2k9yA</a>	Alignment	not modelled	5.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
71	<a href="#">c2k9yB</a>	Alignment	not modelled	5.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
72	<a href="#">d1iaka1</a>	Alignment	not modelled	5.4	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
73	<a href="#">d1of5b</a>	Alignment	not modelled	5.3	33	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> NTF2-like
74	<a href="#">d2jn0a1</a>	Alignment	not modelled	5.2	15	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> YgdI/YgdR-like
75	<a href="#">d1s9va1</a>	Alignment	not modelled	5.2	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
76	<a href="#">d1a3xa1</a>	Alignment	not modelled	5.0	5	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
77	<a href="#">d1dgia2</a>	Alignment	not modelled	5.0	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins