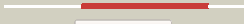
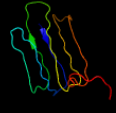
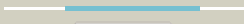
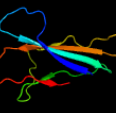

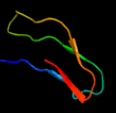

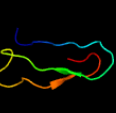



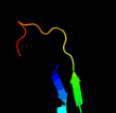
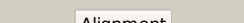


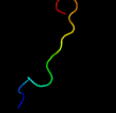

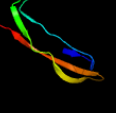


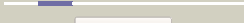



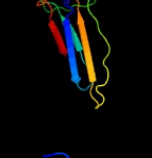
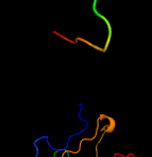

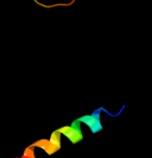


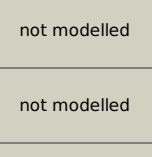


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0451c_(mmpS4)_541491_541913
 Date Tue Jul 23 14:50:52 BST 2019
 Unique Job ID 3b627673b93eced9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lw3A_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmps4; PDBTitle: solution structure of the soluble domain of mmps4 from mycobacterium2 tuberculosis
2	d1fv1b1	 Alignment		30.5	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
3	d1ok0a_	 Alignment		26.2	14	Fold: alpha-Amylase inhibitor tendamistat Superfamily: alpha-Amylase inhibitor tendamistat Family: alpha-Amylase inhibitor tendamistat
4	c2kerA_	 Alignment		23.6	17	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase inhibitor z-2685; PDBTitle: alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
5	d1muja1	 Alignment		21.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
6	d2cs4a1	 Alignment		21.3	40	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
7	c3osvC_	 Alignment		21.1	7	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
8	c2kvzA_	 Alignment		20.1	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ispe; PDBTitle: structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
9	d3d85d2	 Alignment		18.7	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
10	c4ux5B_	 Alignment		18.5	22	PDB header: transcription Chain: B: PDB Molecule: transcription factor mbp1; PDBTitle: structure of dna complex of pcg2
11	c2amnA_	 Alignment		17.0	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: cathelicidin; PDBTitle: solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken

12	d1d5mb1	Alignment		16.1	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
13	c5lnkm_	Alignment		13.4	24	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
14	d1zs8a1	Alignment		12.8	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
15	d1kska3	Alignment		12.3	45	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
16	d1nkg2	Alignment		12.0	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Rhamnogalacturonase B, RhgB, C-terminal domain
17	d2rb6a1	Alignment		11.9	17	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Ygdl/YgdR-like
18	c2na6B_	Alignment		10.0	12	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
19	c2na6C_	Alignment		10.0	12	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
20	c2na6A_	Alignment		10.0	12	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
21	d1l3ga_	Alignment	not modelled	9.9	16	Fold: DNA-binding domain of Mlu1-box binding protein MBP1 Superfamily: DNA-binding domain of Mlu1-box binding protein MBP1 Family: DNA-binding domain of Mlu1-box binding protein MBP1
22	d1dmla1	Alignment	not modelled	9.7	17	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
23	c2nykA_	Alignment	not modelled	9.5	16	PDB header: viral protein Chain: A: PDB Molecule: m157; PDBTitle: crystal structure of m157 from mouse cytomegalovirus
24	d1c16a1	Alignment	not modelled	9.4	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
25	d1ywka1	Alignment	not modelled	9.2	38	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Kdul-like
26	c1q40C_	Alignment	not modelled	9.2	33	PDB header: translation Chain: C: PDB Molecule: mrna transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
27	c2xkuA_	Alignment	not modelled	8.9	10	PDB header: immune system Chain: A: PDB Molecule: beta-2-microglobulin; PDBTitle: prion-like conversion during amyloid formation at atomic resolution
28	c5ee2A_	Alignment	not modelled	8.6	38	PDB header: metal transport Chain: A: PDB Molecule: hemoglobin-haptoglobin-utilization protein; PDBTitle: the crystal structure of the c-terminal beta-barrel of hpua from2 neisseria gonorrhoeae
29	c6ee7A_	Alignment	not modelled	8.6	13	PDB header: sugar binding protein Chain: A: PDB Molecule: anti-sigma factor domain-containing

29	c4qe7A	Alignment	not modelled	8.6	13	protein; PDBTitle: anti-sigma factor domain-containing protein
30	d1klub1	Alignment	not modelled	8.5	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
31	c6ansD	Alignment	not modelled	8.4	41	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from 2 burkholderia cenocepacia
32	c2kt7A	Alignment	not modelled	8.2	13	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: putative peptidoglycan bound protein (lpxtg) PDBTitle: solution nmr structure of mucin-binding domain of protein 2 lmo0835 from listeria monocytogenes, northeast structural genomics consortium target lmr64a
33	c2obkE	Alignment	not modelled	8.1	37	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: sel/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas 2 fluorescens. northeast structural genomics consortium target plr6.
34	d2fa8a1	Alignment	not modelled	8.1	37	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
35	d2ra2a1	Alignment	not modelled	8.0	33	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
36	c4kw3A	Alignment	not modelled	8.0	24	PDB header: viral protein Chain: A: PDB Molecule: ns1; PDBTitle: crystal structure of the non-structural protein 1 n-terminal origin-2 recognition/nickase domain from the emerging human bocavirus
37	d1jk8a1	Alignment	not modelled	7.9	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
38	c2k9yA	Alignment	not modelled	7.9	42	PDB header: transferase Chain: A: PDB Molecule: ephryn type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
39	c3owrA	Alignment	not modelled	7.8	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized hypothetical protein; PDBTitle: crystal structure of a putative secreted protein (bf4250) from 2 bacteroides fragilis nctc 9343 at 1.81 a resolution
40	c1ywke	Alignment	not modelled	7.8	38	PDB header: isomerase Chain: E: PDB Molecule: 4-deoxy-l-threo-5-hexosulose-uronate ketol- PDBTitle: crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate 2 ketol-isomerase from enterococcus faecalis
41	c2kppA	Alignment	not modelled	7.6	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0431 protein; PDBTitle: solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
42	c2yxyA	Alignment	not modelled	7.5	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein, gk0453; PDBTitle: crystal structure of hypothetical conserved protein, gk0453
43	c5aeoA	Alignment	not modelled	7.3	18	PDB header: immune system Chain: A: PDB Molecule: r. equi vapg protein; PDBTitle: virulence-associated protein vapg from the intracellular 2 pathogen rhodococcus equi
44	d2rd1a1	Alignment	not modelled	7.0	17	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
45	c2k9yB	Alignment	not modelled	7.0	42	PDB header: transferase Chain: B: PDB Molecule: ephryn type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
46	c2jmbA	Alignment	not modelled	7.0	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu4866; PDBTitle: solution structure of the protein atu4866 from agrobacterium 2 tumefaciens
47	d1mhca1	Alignment	not modelled	7.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
48	d1xrua1	Alignment	not modelled	7.0	63	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Kdul-like
49	d1f32a	Alignment	not modelled	6.8	45	Fold: Pepsin inhibitor-3 Superfamily: Pepsin inhibitor-3 Family: Pepsin inhibitor-3
50	d1kona	Alignment	not modelled	6.7	35	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
51	d1of5b	Alignment	not modelled	6.7	27	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
52	c2l7yA	Alignment	not modelled	6.6	16	PDB header: structural protein Chain: A: PDB Molecule: putative endo-beta-n-acetylglucosaminidase; PDBTitle: solution structure of a putative surface protein
53	c4csbA	Alignment	not modelled	6.5	15	PDB header: unknown function Chain: A: PDB Molecule: virulence associated protein vapd; PDBTitle: structure of the virulence-associated protein vapd from the 2 intracellular pathogen rhodococcus equi.
54	d1eg3a3	Alignment	not modelled	6.5	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain

55	d1pkla1	Alignment	not modelled	6.4	14	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
56	d1toqr2	Alignment	not modelled	6.4	40	Fold: BPTI-like Superfamily: BPTI-like Family: Soft tick anticoagulant proteins
57	d1o0va1	Alignment	not modelled	6.4	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
58	c4cv7A_	Alignment	not modelled	6.3	15	PDB header: toxin Chain: A; PDB Molecule: virulence associated protein vapb; PDBTitle: crystal structure of rhodococcus equi vapb
59	d1vlba2	Alignment	not modelled	6.1	50	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
60	d2jn0a1	Alignment	not modelled	6.0	17	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
61	d1dgia2	Alignment	not modelled	5.9	50	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
62	c5o31b_	Alignment	not modelled	5.9	24	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
63	c5lc5b_	Alignment	not modelled	5.9	24	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
64	d1n6za_	Alignment	not modelled	5.8	33	Fold: Hypothetical protein Yml108w Superfamily: Hypothetical protein Yml108w Family: Hypothetical protein Yml108w
65	d2gpia1	Alignment	not modelled	5.7	24	Fold: Shew3726-like Superfamily: Shew3726-like Family: Shew3726-like
66	d1a3xa1	Alignment	not modelled	5.6	11	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
67	d1lk2a1	Alignment	not modelled	5.6	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
68	d1sawa_	Alignment	not modelled	5.6	19	Fold: FAH Superfamily: FAH Family: FAH
69	c4gdzA_	Alignment	not modelled	5.6	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4251 family protein (bacegg_02002) from <i>Bacteroides eggerthii</i> DSM 20697 at 1.95 Å resolution
70	d1xtda2	Alignment	not modelled	5.3	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
71	d1lfpa_	Alignment	not modelled	5.3	22	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
72	c2p0gB_	Alignment	not modelled	5.3	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from <i>Vibrio cholerae</i> . northeast structural genomics target vcr75
73	c3mk7F_	Alignment	not modelled	5.2	9	PDB header: oxidoreductase Chain: F; PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
74	c3rolA_	Alignment	not modelled	5.1	16	PDB header: immune system Chain: A; PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain; PDBTitle: murine class i major histocompatibility complex h-2kb in complex with 2 post-translationally modified Icmv-derived gp34-41 peptide, 3 comprising a nitrotyrosine at position 3