




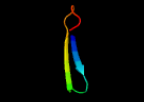

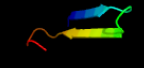

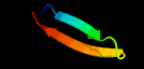



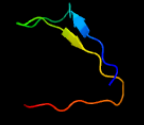

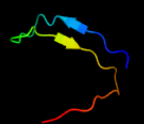

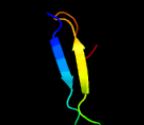

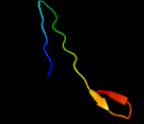


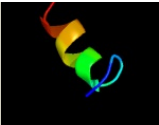
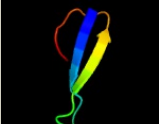

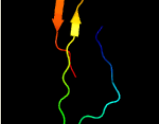

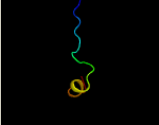

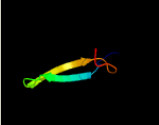
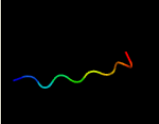


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0603 (-) _699859_700170
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	e56bf8ff5a1d9547

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kgyA_	 Alignment		100.0	84	PDB header: immune system Chain: A: PDB Molecule: possible exported protein; PDBTitle: solution structure of rv0603 protein from mycobacterium2 tuberculosis h37rv
2	c4exrA_	 Alignment		74.9	18	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (cd1622) from clostridium2 difficile 630 at 1.85 a resolution
3	c2vldA_	 Alignment		58.6	20	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssi
4	c5gkeB_	 Alignment		57.0	25	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
5	c3riqA_	 Alignment		21.5	37	PDB header: viral protein Chain: A: PDB Molecule: tailspike protein; PDBTitle: siphovirus 9na tailspike receptor binding domain
6	c3hd4A_	 Alignment		19.9	29	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: mhv nucleocapsid protein ntd
7	d1s21a_	 Alignment		18.3	31	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector
8	c1s21A_	 Alignment		18.3	31	PDB header: chaperone Chain: A: PDB Molecule: orf2; PDBTitle: crystal structure of avrpphf orf2, a type iii effector from p.2 syringae
9	d2cjoa_	 Alignment		13.6	37	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
10	c6hosB_	 Alignment		13.6	28	PDB header: cell adhesion Chain: B: PDB Molecule: ba75_04148t0; PDBTitle: structure of the kpfl02 adhesin domain in complex with glycerol
11	d3duea1	 Alignment		13.2	17	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like

12	d2gyc31	Alignment		11.8	64	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
13	c4v194_	Alignment		11.6	29	PDB header: ribosome Chain: 4: PDB Molecule: mitoribosomal protein b131m, mrp155; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
14	c5n76C_	Alignment		10.6	54	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
15	d2d7na1	Alignment		10.5	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
16	c5e4rA_	Alignment		9.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of domain-duplicated synthetic class ii ketol-acid2 reductoisomerase 2ia_kari-dd
17	c5xcxB_	Alignment		9.3	22	PDB header: immune system Chain: B: PDB Molecule: vl-sarah(s37c) chimera; PDBTitle: crystal structure of ts2/16 fv-clasp fragment
18	d1dlja2	Alignment		8.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
19	d1v2ya_	Alignment		8.5	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
20	c3d8tB_	Alignment		7.2	0	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
21	c3witA_	Alignment	not modelled	7.0	50	PDB header: structural protein Chain: A: PDB Molecule: putative vgr protein; PDBTitle: crystal structure of the c-terminal region of vgrg1 from e. coli o1572 edl933
22	c2e12B_	Alignment	not modelled	7.0	31	PDB header: translation Chain: B: PDB Molecule: hypothetical protein xcc3642; PDBTitle: the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
23	c5kdvA_	Alignment	not modelled	6.7	22	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: impa metallopeptidase from pseudomonas aeruginosa
24	d1np3a2	Alignment	not modelled	6.7	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
25	c2qtzA_	Alignment	not modelled	6.6	46	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine synthase reductase; PDBTitle: crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
26	d1dd3a1	Alignment	not modelled	6.3	39	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
27	c5cb9A_	Alignment	not modelled	5.9	30	PDB header: lyase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of c-as lyase with mercaptoethonal
28	c4oleD_	Alignment	not modelled	5.7	38	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: next to brca1 gene 1 protein; PDBTitle: crystal structure of a neighbor of brca1 gene 1 (nbr1) from homo2 sapiens at 2.52 a resolution
						PDB header: oxidoreductase

29	c1f20A_	Alignment	not modelled	5.7	46	Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
30	d3elga1	Alignment	not modelled	5.7	17	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like
31	c2m7yA_	Alignment	not modelled	5.7	67	PDB header: viral protein Chain: A: PDB Molecule: leader peptide; PDBTitle: the mengovirus leader protein
32	c3qftA_	Alignment	not modelled	5.7	38	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh--cytochrome p450 reductase; PDBTitle: crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
33	c6j7aB_	Alignment	not modelled	5.5	46	PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1,nadh--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
34	c5omtA_	Alignment	not modelled	5.5	44	PDB header: hydrolase Chain: A: PDB Molecule: nucb; PDBTitle: endonuclease nucb
35	d1jb9a2	Alignment	not modelled	5.4	38	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
36	c1yrlD_	Alignment	not modelled	5.3	30	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
37	c5igrA_	Alignment	not modelled	5.2	26	PDB header: transferase/antibiotic Chain: A: PDB Molecule: macrolide 2'-phosphotransferase; PDBTitle: macrolide 2'-phosphotransferase type i - complex with gdp and2 oleandomycin
38	c5wecB_	Alignment	not modelled	5.2	36	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein; PDBTitle: structure of an alternative pilotin from the type ii secretion system2 of vibrio cholerae
39	c4dqkA_	Alignment	not modelled	5.1	38	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional p-450/nadph-p450 reductase; PDBTitle: crystal structure of the fad binding domain of cytochrome p450 bm3