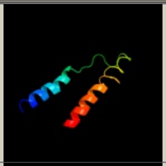
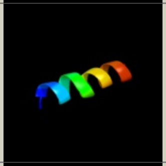
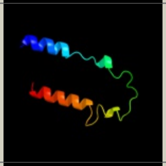
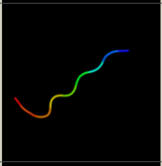
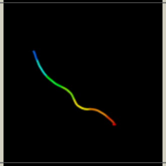
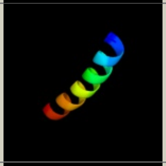
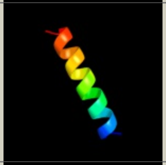
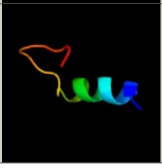
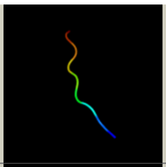
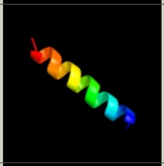
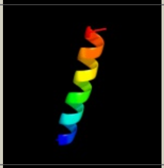
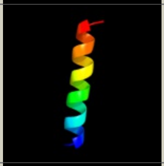
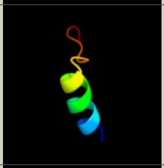
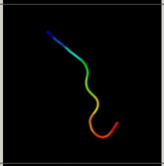
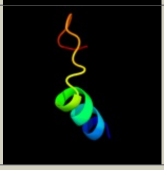
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADL6
Date	Thu Jan 5 11:21:18 GMT 2012
Unique Job ID	2e35e9fc47d711be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3chxG_	Alignment		59.5	30	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
2	d1prtf_	Alignment		51.7	59	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
3	c1yewC_	Alignment		44.7	30	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
4	d1pjwa_	Alignment		25.8	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
5	d1s6na_	Alignment		24.6	56	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
6	c3egpA_	Alignment		24.6	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure analysis of dengue-1 envelope protein2 domain iii
7	c3lbwB_	Alignment		24.3	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** high resolution crystal structure of transmembrane domain of m2
8	c3lbwD_	Alignment		24.3	38	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** high resolution crystal structure of transmembrane domain of m2
9	c3lbwC_	Alignment		24.3	38	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** high resolution crystal structure of transmembrane domain of m2
10	c3lbwA_	Alignment		24.3	38	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** high resolution crystal structure of transmembrane domain of m2
11	d1v32a_	Alignment		19.4	23	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain

12	c2jqmA_	Alignment		18.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**envelope protein e; **PDBTitle:** yellow fever envelope protein domain iii nmr structure2 (s288-k398)
13	c3c9jC_	Alignment		18.2	38	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
14	c3c9jB_	Alignment		18.2	38	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
15	c3c9jA_	Alignment		18.2	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
16	c3c9jD_	Alignment		18.2	38	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
17	d1v31a_	Alignment		17.6	26	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
18	d1ixra1	Alignment		14.6	43	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
19	c2h0pA_	Alignment		14.0	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
20	d1uhra_	Alignment		12.6	27	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
21	c2kncA_	Alignment	not modelled	12.1	31	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
22	d2iuba2	Alignment	not modelled	11.9	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
23	c2wwbC_	Alignment	not modelled	11.9	36	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**protein transport protein sec61 subunit beta; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
24	c1nyjB_	Alignment	not modelled	9.6	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
25	c2kqtC_	Alignment	not modelled	9.6	33	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
26	c2kqtA_	Alignment	not modelled	9.6	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
27	c1nyjA_	Alignment	not modelled	9.6	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
						PDB header:viral protein

28	c1nyjD_	Alignment	not modelled	9.6	33	**Chain:** D: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
29	c2kqtB_	Alignment	not modelled	9.6	33	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
30	c1nyjC_	Alignment	not modelled	9.6	33	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
31	c1mp6A_	Alignment	not modelled	9.6	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
32	c2kqtD_	Alignment	not modelled	9.6	33	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
33	c2bbjB_	Alignment	not modelled	9.0	14	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
34	d2fp7b1	Alignment	not modelled	8.3	55	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
35	c3bkdE_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** E: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
36	c3bkdG_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** G: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
37	c3bkdH_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** H: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
38	c3bkdD_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** D: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
39	c3bkdC_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** C: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
40	c3bkdA_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** A: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
41	c3bkdF_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** F: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
42	c3bkdB_	Alignment	not modelled	8.1	33	**PDB header:**viral protein, membrane protein **Chain:** B: **PDB Molecule:**transmembrane domain of matrix protein m2; **PDBTitle:** high resolution crystal structure of transmembrane domain of m22 protein
43	c3c6dB_	Alignment	not modelled	7.1	33	**PDB header:**virus **Chain:** B: **PDB Molecule:**polyprotein; **PDBTitle:** the pseudo-atomic structure of dengue immature virus
44	c2ehoL_	Alignment	not modelled	6.8	16	**PDB header:**replication **Chain:** L: **PDB Molecule:**gins complex subunit 3; **PDBTitle:** crystal structure of human gins complex
45	c3i9yA_	Alignment	not modelled	6.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. parahaemolyticus histidine2 kinase sensor tors sensor domain
46	d1ok8a1	Alignment	not modelled	6.5	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
47	d2fomb1	Alignment	not modelled	6.2	55	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
48	c3e90B_	Alignment	not modelled	6.2	55	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ns3 protease; **PDBTitle:** west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
49	c2rlfA_	Alignment	not modelled	6.2	33	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**matrix protein 2; **PDBTitle:** proton channel m2 from influenza a in complex with2 inhibitor rimantadine
50	d2ijob1	Alignment	not modelled	6.2	55	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
51	c3uajA_	Alignment	not modelled	5.8	22	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab

						fragment of the chimpanzee3 monoclonal antibody 5h2
52	c2w8xB_	Alignment	not modelled	5.7	40	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**ion-channel modulator raklp; **PDBTitle:** structure of the tick ion-channel modulator ra-klp
53	c1urzC_	Alignment	not modelled	5.6	44	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
54	d2f2ab1	Alignment	not modelled	5.5	39	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
55	d1befa_	Alignment	not modelled	5.4	55	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
56	c3lkwA_	Alignment	not modelled	5.4	55	**PDB header:**viral protein,hydrolase **Chain:** A: **PDB Molecule:**fusion protein of nonstructural protein 2b and **PDBTitle:** crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
57	d1ztxe1	Alignment	not modelled	5.3	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
58	c2kadD_	Alignment	not modelled	5.3	29	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
59	c2kadA_	Alignment	not modelled	5.3	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
60	c2kadC_	Alignment	not modelled	5.3	29	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
61	c2kadB_	Alignment	not modelled	5.3	29	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane peptide of matrix protein 2; **PDBTitle:** magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain