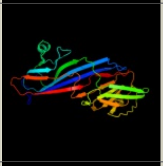
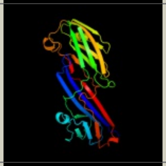
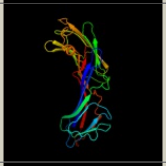
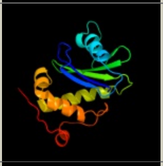
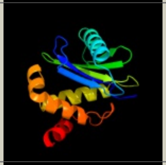
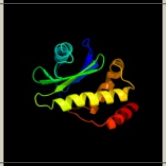
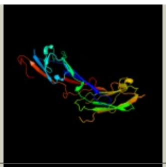
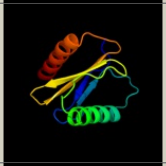
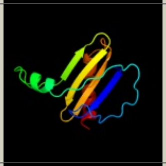
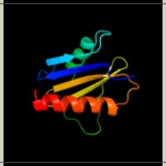
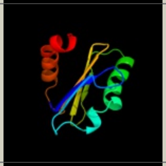
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O94669
Date	Sun Jul 8 11:54:00 BST 2012
Unique Job ID	9ab4a24c790e374c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w63P_	Alignment		100.0	23	**PDB header:**endocytosis **Chain:** P: **PDB Molecule:**adaptor-related protein complex 1, mu 1 subunit; **PDBTitle:** ap1 clathrin adaptor core
2	c2jkrM_	Alignment		100.0	21	**PDB header:**endocytosis **Chain:** M: **PDB Molecule:**ap-2 complex subunit mu-1; **PDBTitle:** ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
3	c1bw8A_	Alignment		100.0	23	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein (mu2 adaptin subunit); **PDBTitle:** mu2 adaptin subunit (ap50) of ap2 adaptor (second domain),2 complexed with egfr internalization peptide fyralm
4	c4en2M_	Alignment		100.0	26	**PDB header:**viral protein/immune system **Chain:** M: **PDB Molecule:**ap-1 complex subunit mu-1; **PDBTitle:** hiv-1 nef in complex with mhc-i cytoplasmic domain and mu1 adaptin2 subunit of ap1 adaptor (second domain)
5	d2pr9a1	Alignment		100.0	24	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor **Family:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor
6	c3ml6D_	Alignment		100.0	23	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2 **PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2
7	c3l81A_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ap-4 complex subunit mu-1; **PDBTitle:** crystal structure of adaptor protein complex 4 (ap-4) mu4 subunit c-2 terminal domain, in complex with a sorting peptide from the amyloid3 precursor protein (app)
8	d1gw5m2	Alignment		100.0	17	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Clathrin coat assembly domain
9	c2hf6A_	Alignment		100.0	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit zeta-1; **PDBTitle:** solution structure of human zeta-cop
10	d1gw5s_	Alignment		100.0	16	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Clathrin coat assembly domain
11	c1w63T_	Alignment		100.0	13	**PDB header:**endocytosis **Chain:** T: **PDB Molecule:**adapter-related protein complex 1 sigma 1a **PDBTitle:** ap1 clathrin adaptor core

12	c3g9hA_	Alignment		99.1	17	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**suppressor of yeast profilin deletion; **PDBTitle:** crystal structure of the c-terminal mu homology domain of2 syp1
13	c3cueM_	Alignment		96.0	13	**PDB header:**protein transport **Chain:** M: **PDB Molecule:**transport protein particle 23 kda subunit; **PDBTitle:** crystal structure of a trapp subassembly activating the rab ypt1p
14	c1skoA_	Alignment		95.9	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase 1 **PDBTitle:** mp1-p14 complex
15	c2dmwA_	Alignment		95.3	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**synaptobrevin-like 1 variant; **PDBTitle:** solution structure of the longin domain of synaptobrevin-2 like protein 1
16	c4afiB_	Alignment		95.2	12	**PDB header:**endocytosis **Chain:** B: **PDB Molecule:**ap-3 complex subunit delta-1, vesicle-associated membrane **PDBTitle:** complex between vamp7 longin domain and fragment of delta-2 adaptin from ap3
17	c3cueO_	Alignment		94.9	11	**PDB header:**protein transport **Chain:** O: **PDB Molecule:**transport protein particle 18 kda subunit; **PDBTitle:** crystal structure of a trapp subassembly activating the rab ypt1p
18	d3cpta1	Alignment		94.9	8	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
19	c2j3tC_	Alignment		94.8	17	**PDB header:**transport **Chain:** C: **PDB Molecule:**trafficking protein particle complex subunit 1; **PDBTitle:** the crystal structure of the bet3-trs33-bet5-trs23 complex.
20	c3kyqA_	Alignment		94.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**synaptobrevin homolog ykt6; **PDBTitle:** lipid-induced conformational switch controls fusion activity of longin2 domain snare ykt6
21	d1ioua_	Alignment	not modelled	93.3	15	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Synatpobrevin N-terminal domain
22	c3egdC_	Alignment	not modelled	90.8	11	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vesicle-trafficking protein sec22b; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22 and bound3 to the transport signal sequence of vesicular stomatitis4 virus glycoprotein
23	c2nupC_	Alignment	not modelled	90.8	11	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vesicle-trafficking protein sec22b; **PDBTitle:** crystal structure of the human sec23a/24a heterodimer,2 complexed with the snare protein sec22b
24	c2vx8D_	Alignment	not modelled	90.3	13	**PDB header:**endocytosis,exocytosis **Chain:** D: **PDB Molecule:**nucleoporin-like protein rip, vesicle-associated **PDBTitle:** vamp7 longin domain hrb peptide complex
25	d1ifqa_	Alignment	not modelled	88.8	12	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Synatpobrevin N-terminal domain
26	c2zmvB_	Alignment	not modelled	83.1	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trafficking protein particle complex subunit 4; **PDBTitle:** crystal structure of synbindin
27	d2j3wa1	Alignment	not modelled	80.3	10	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Sedlin (SEDL)
28	d2fh5a1	Alignment	not modelled	56.9	6	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like

29	c2go51_	Alignment	not modelled	55.6	7	**PDB header:**translation/rna **Chain:** 1: **PDB Molecule:**signal recognition particle receptor alpha **PDBTitle:** structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex
30	c2pnyA_	Alignment	not modelled	37.3	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
31	d3buxb3	Alignment	not modelled	30.3	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
32	c2wl8D_	Alignment	not modelled	30.3	14	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
33	c3npkB_	Alignment	not modelled	25.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**geranyltranstransferase; **PDBTitle:** the crystal structure of geranyltranstransferase from campylobacter2 jejuni
34	c1r77A_	Alignment	not modelled	25.6	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell wall targeting domain of glycylglycine **PDBTitle:** crystal structure of the cell wall targeting domain of2 peptidylglycan hydrolase ale-1
35	c2i6kA_	Alignment	not modelled	22.9	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
36	d2zcta1	Alignment	not modelled	18.1	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
37	c3op0B_	Alignment	not modelled	17.4	15	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
38	d1k4na_	Alignment	not modelled	15.1	22	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YecM (EC4020)
39	c2v2gC_	Alignment	not modelled	15.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
40	d1prxa_	Alignment	not modelled	13.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
41	d1hzta_	Alignment	not modelled	13.0	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
42	c2wxoA_	Alignment	not modelled	12.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
43	d1xcca_	Alignment	not modelled	12.0	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d1vetb_	Alignment	not modelled	11.9	13	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
45	d2cv4a1	Alignment	not modelled	11.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
46	c2l0rA_	Alignment	not modelled	11.7	17	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
47	d1e7ua4	Alignment	not modelled	11.2	12	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Phoshoinositide 3-kinase (PI3K), catalytic domain
48	d2fi0a1	Alignment	not modelled	11.2	13	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
49	c1e8zA_	Alignment	not modelled	10.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit; **PDBTitle:** structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
50	d1qmva_	Alignment	not modelled	10.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
51	d1n8va_	Alignment	not modelled	9.9	15	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
52	c3e6qL_	Alignment	not modelled	9.7	19	**PDB header:**isomerase **Chain:** L: **PDB Molecule:**putative 5-carboxymethyl-2-hydroxymuconate isomerase; **PDBTitle:** putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
						PDB header:transferase/oncoprotein

53	c2rd0A_	Alignment	not modelled	9.4	12	**Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a human p110alpha/p85alpha complex
54	d1mqea_	Alignment	not modelled	9.4	29	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
55	d1uula_	Alignment	not modelled	9.0	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
56	c1n4kA_	Alignment	not modelled	9.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inositol 1,4,5-trisphosphate receptor type 1; **PDBTitle:** crystal structure of the inositol 1,4,5-trisphosphate2 receptor binding core in complex with ip3
57	d1so9a_	Alignment	not modelled	8.5	6	**Fold:**Ctag/Cox11 **Superfamily:**Ctag/Cox11 **Family:**Ctag/Cox11
58	c1so9A_	Alignment	not modelled	8.5	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cytochrome c oxidase assembly protein ctag; **PDBTitle:** solution structure of apocox11, 30 structures
59	d1w5ra1	Alignment	not modelled	8.2	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
60	d2aeea1	Alignment	not modelled	7.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
61	d1iyjb2	Alignment	not modelled	7.8	22	**Fold:**BRCA2 tower domain **Superfamily:**BRCA2 tower domain **Family:**BRCA2 tower domain
62	c2y3aA_	Alignment	not modelled	7.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
63	d1n8ja_	Alignment	not modelled	7.5	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
64	c2cblA_	Alignment	not modelled	7.3	23	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
65	c3bunB_	Alignment	not modelled	6.9	23	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
66	d1ppva_	Alignment	not modelled	6.8	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
67	c2ifoA_	Alignment	not modelled	6.6	57	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** model-building studies of inovirus: genetic variations on a2 geometric theme
68	c2e6xD_	Alignment	not modelled	6.5	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ttha1281; **PDBTitle:** x-ray structure of tt1592 from thermus thermophilus hb8
69	d1sxjd1	Alignment	not modelled	6.3	9	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
70	c3qf7D_	Alignment	not modelled	6.2	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
71	c1bp1A_	Alignment	not modelled	6.2	12	**PDB header:**bactericidal **Chain:** A: **PDB Molecule:**bactericidal/permeability-increasing protein; **PDBTitle:** crystal structure of bpi, the human bactericidal2 permeability-increasing protein
72	d1fskb1	Alignment	not modelled	6.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
73	c1w3gA_	Alignment	not modelled	5.8	54	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.
74	c3klqB_	Alignment	not modelled	5.8	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative pilus anchoring protein; **PDBTitle:** crystal structure of the minor pilin fctb from streptococcus pyogenes2 90/306s
75	c2zjbB_	Alignment	not modelled	5.6	10	**PDB header:**recombination **Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog; **PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant
76	d1vola2	Alignment	not modelled	5.6	9	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
77	d1n0wa_	Alignment	not modelled	5.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
78	d1qhda1	Alignment	not modelled	5.5	20	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain

						Family:vp6, the major capsid protein of group A rotavirus
79	c2ihfA_	Alignment	not modelled	5.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
80	d1szpa2	Alignment	not modelled	5.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
81	c3q91D_	Alignment	not modelled	5.5	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
82	c1v7wA_	Alignment	not modelled	5.4	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
83	c2kdvA_	Alignment	not modelled	5.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
84	c2w4eA_	Alignment	not modelled	5.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
85	d1h54a2	Alignment	not modelled	5.3	9	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
86	c1j3wB_	Alignment	not modelled	5.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**giding protein-mglb; **PDBTitle:** structure of gliding protein-mglb from thermus thermophilus hb8
87	c3lsoA_	Alignment	not modelled	5.2	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane anchored protein; **PDBTitle:** crystal structure of putative membrane anchored protein from2 corynebacterium diphtheriae
88	c3l9bA_	Alignment	not modelled	5.2	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**otoferlin; **PDBTitle:** crystal structure of rat otoferlin c2a
89	d2bjra1	Alignment	not modelled	5.1	17	**Fold:**MFPT repeat-like **Superfamily:**MFPT repeat-like **Family:**MFPT repeat