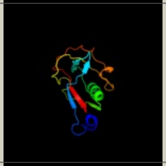
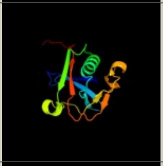
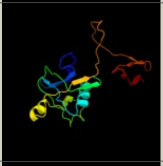
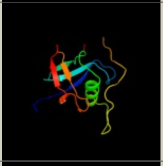
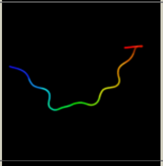
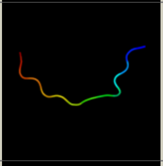
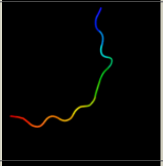
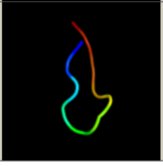
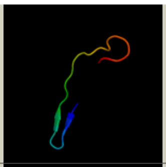
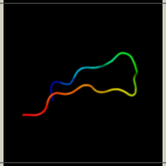
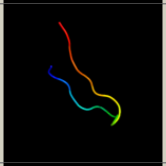
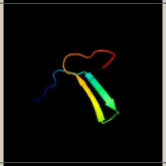
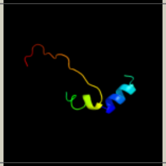
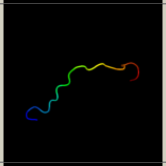
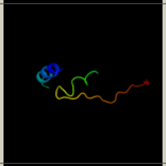
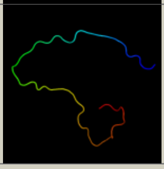
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A1L0T3
Date	Tue Jul 30 13:14:16 BST 2013
Unique Job ID	91d36cd811f2fc8c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1by2a_	Alignment		100.0	49	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Scavenger receptor cysteine-rich (SRCR) domain
2	c2oyaA_	Alignment		100.0	46	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**macrophage receptor marco; **PDBTitle:** crystal structure analysis of the dimeric form of the srcr domain of2 mouse marco
3	c2jopA_	Alignment		100.0	28	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** solution structure of the n-terminal extracellular domain2 of the lymphocyte receptor cd5 (cd5 domain 1)
4	c2ottY_	Alignment		100.0	33	**PDB header:**immune system **Chain:** Y: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** crystal structure of cd5_diii
5	d1z8ga2	Alignment		99.9	18	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Hepsin, N-terminal domain
6	c1z8gA_	Alignment		99.8	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease hepsin; **PDBTitle:** crystal structure of the extracellular region of the transmembrane2 serine protease hepsin with covalently bound preferred substrate.
7	c2xrcD_	Alignment		96.8	24	**PDB header:**immune system **Chain:** D: **PDB Molecule:**human complement factor i; **PDBTitle:** human complement factor i
8	c2dvkA_	Alignment		19.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0130 protein ape0816; **PDBTitle:** crystal structure of hypothetical protein from aeropyrum pernix
9	d1tlja_	Alignment		17.0	29	**Fold:**SSo0622-like **Superfamily:**SSo0622-like **Family:**SSo0622-like
10	c1tljA_	Alignment		17.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0130 protein sso0622; **PDBTitle:** crystal structure of conserved protein of unknown function2 sso0622 from sulfolobus solfataricus
11	c2lw6A_	Alignment		15.9	27	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**avrpiz-t protein; **PDBTitle:** solution structure of an avirulence protein avrpiz-t from pathogen2 magnaportheoryzae

12	d1pbya5	Alignment		15.3	22	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
13	c2aklA_	Alignment		13.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
14	d2akka1	Alignment		13.1	24	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
15	d2akla1	Alignment		12.7	24	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
16	c2qg3B_	Alignment		9.1	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0130 protein af_2059; **PDBTitle:** crystal structure of a tyw3 methyltransferase-like protein (af_2059)2 from archaeoglobus fulgidus dsm 4304 at 1.95 a resolution
17	c1iicA_	Alignment		8.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**peptide n-myristoyltransferase; **PDBTitle:** crystal structure of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoylcoa
18	d2vxfa1	Alignment		8.8	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**LSM14 N-terminal domain-like
19	c2p6fA_	Alignment		8.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structures of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoyl-coa and inhibitors
20	c1dzlA_	Alignment		8.6	16	**PDB header:**virus **Chain:** A: **PDB Molecule:**late major capsid protein l1; **PDBTitle:** l1 protein of human papillomavirus 16
21	d1dzla_	Alignment	not modelled	8.6	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
22	d2ns0a1	Alignment	not modelled	8.4	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
23	c1jpeA_	Alignment	not modelled	8.4	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dsbd-alpha; **PDBTitle:** crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd
24	c2vxeA_	Alignment	not modelled	8.1	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cg10686-pa; **PDBTitle:** solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch)
25	c2it3B_	Alignment	not modelled	8.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0130 protein ph1069; **PDBTitle:** structure of ph1069 protein from pyrococcus horikoshii
26	d1tn3a_	Alignment	not modelled	8.0	25	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
27	d1iica2	Alignment	not modelled	7.8	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
28	c1iylC_	Alignment	not modelled	7.8	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**myristoyl-coa:protein n-myristoyltransferase; **PDBTitle:** crystal structure of candida albicans n-myristoyltransferase with non-2 peptidic inhibitor
						PDB header:hydrolase

29	c1fwoA_	Alignment	not modelled	7.7	19	**Chain:** A: **PDB Molecule:**oryzain beta chain; **PDBTitle:** the solution structure of a 35-residue fragment from the2 granulin/epithelin-like subdomain of rice oryzain beta3 (rob 382-416 (c398s,c399s,c407s,c413s))
30	d1oz7a_	Alignment	not modelled	7.7	25	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
31	c4dx94_	Alignment	not modelled	7.6	23	**PDB header:**protein binding **Chain:** 4: **PDB Molecule:**integrin beta-1-binding protein 1; **PDBTitle:** icap1 in complex with integrin beta 1 cytoplasmic tail
32	c2r5kE_	Alignment	not modelled	7.6	13	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
33	c2k0rA_	Alignment	not modelled	7.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbd; **PDBTitle:** solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
34	d1rxta2	Alignment	not modelled	7.2	37	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
35	d1l6pa_	Alignment	not modelled	7.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha) **Family:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)
36	d1iyka2	Alignment	not modelled	7.1	30	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
37	c3iu2B_	Alignment	not modelled	6.9	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase 1; **PDBTitle:** crystal structure of human type-i n-myristoyltransferase with bound2 myristoyl-coa and inhibitor ddd90096
38	c1nj3A_	Alignment	not modelled	6.6	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**npl4; **PDBTitle:** structure and ubiquitin interactions of the conserved nzf2 domain of npl4
39	c2a45J_	Alignment	not modelled	6.4	32	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
40	c3a57A_	Alignment	not modelled	6.3	32	**PDB header:**toxin **Chain:** A: **PDB Molecule:**thermostable direct hemolysin 2; **PDBTitle:** crystal structure of thermostable direct hemolysin
41	d1wk1a_	Alignment	not modelled	6.3	32	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
42	c2vpnB_	Alignment	not modelled	6.3	8	**PDB header:**transport **Chain:** B: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata
43	c3ke2A_	Alignment	not modelled	6.2	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
44	c2jtkA_	Alignment	not modelled	6.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dickkopf-related protein 2; **PDBTitle:** a functional domain of a wnt signal protein
45	d1jmxa5	Alignment	not modelled	5.9	13	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
46	c4g5eD_	Alignment	not modelled	5.9	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2,4,6-trichlorophenol 4-monooxygenase; **PDBTitle:** 2,4,6-trichlorophenol 4-monooxygenase
47	c3fxbB_	Alignment	not modelled	5.7	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
48	d2pf5a1	Alignment	not modelled	5.6	27	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Link domain
49	d1k42a_	Alignment	not modelled	5.5	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**CBM4/9
50	c3djmA_	Alignment	not modelled	5.4	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf427; **PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
51	c3iyjE_	Alignment	not modelled	5.4	9	**PDB header:**virus **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** bovine papillomavirus type 1 outer capsid
52	c4ag4A_	Alignment	not modelled	5.4	13	**PDB header:**immune system/transferase **Chain:** A: **PDB Molecule:**epithelial discoidin domain-containing receptor 1; **PDBTitle:** crystal structure of a ddr1-fab complex