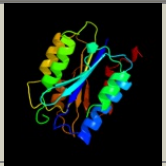
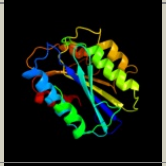
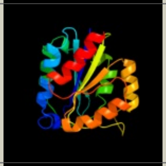
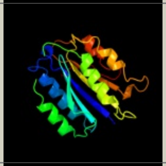
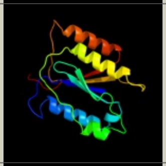
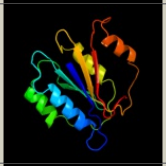
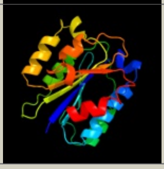
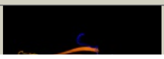
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76481
Date	Thu Jan 5 12:23:23 GMT 2012
Unique Job ID	4c7b07eb16f18151

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rs0A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
2	c2ok5A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** human complement factor b
3	c3ibsA_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein batb; **PDBTitle:** crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
4	d2ok5a1	Alignment		100.0	19	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
5	c2i6sA_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement c2a fragment; **PDBTitle:** complement component c2a
6	c2x5nA_	Alignment		99.9	18	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn10; **PDBTitle:** crystal structure of the sprpn10 vwa domain
7	c2x31F_	Alignment		99.9	21	**PDB header:**ligase **Chain:** F: **PDB Molecule:**magnesium-chelatase 60 kda subunit; **PDBTitle:** modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
8	d1shux_	Alignment		99.9	22	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
9	d1pd0a3	Alignment		99.9	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
10	d1ijba_	Alignment		99.9	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
11	d1u0oc1	Alignment		99.9	17	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain

12	c3n2nC_	Alignment		99.9	20	**PDB header:**toxin receptor **Chain:** C: **PDB Molecule:**anthrax toxin receptor 1; **PDBTitle:** the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
13	c3gxbB_	Alignment		99.9	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**von willebrand factor; **PDBTitle:** crystal structure of vwf a2 domain
14	c2iueA_	Alignment		99.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pactolus i-domain; **PDBTitle:** pactolus i-domain: functional switching of the rossmann2 fold
15	c2b2xB_	Alignment		99.9	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**integrin alpha-1; **PDBTitle:** vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
16	d1q0pa_	Alignment		99.9	21	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
17	d1jeya2	Alignment		99.8	19	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku70 subunit N-terminal domain
18	d1atza_	Alignment		99.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
19	d1jeyb2	Alignment		99.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku80 subunit N-terminal domain
20	d1ck4a_	Alignment		99.8	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
21	d1v7pc_	Alignment	not modelled	99.8	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
22	d1n3ya_	Alignment	not modelled	99.8	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
23	c2xggB_	Alignment	not modelled	99.8	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**microneme protein 2; **PDBTitle:** structure of toxoplasma gondii micronemal protein 2 a_i2 domain
24	d1pt6a_	Alignment	not modelled	99.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
25	d1yvra2	Alignment	not modelled	99.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**RoRNP C-terminal domain-like
26	d1mf7a_	Alignment	not modelled	99.7	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
27	d1mjna_	Alignment	not modelled	99.7	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
28	c2nvoA_	Alignment	not modelled	99.7	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ro sixty-related protein, rsr; **PDBTitle:** crystal structure of deinococcus radiodurans ro (rsr) protein
						**PDB header:**transport protein

29	c1pd0A_	Alignment		99.7	14	**Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
30	c1m2vB_	Alignment	not modelled	99.6	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
31	c3eh2B_	Alignment	not modelled	99.6	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
32	c3egxB_	Alignment	not modelled	99.6	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
33	c3eg9B_	Alignment	not modelled	99.6	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
34	c3eg9A_	Alignment	not modelled	99.6	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
35	c1jeyB_	Alignment	not modelled	99.6	13	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**ku80; **PDBTitle:** crystal structure of the ku heterodimer bound to dna
36	c1m2oA_	Alignment	not modelled	99.6	18	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
37	d1tyeb2	Alignment	not modelled	99.6	20	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
38	c3v4pB_	Alignment	not modelled	99.5	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-7; **PDBTitle:** crystal structure of a4b7 headpiece complexed with fab act-1
39	d2qtva3	Alignment	not modelled	99.5	18	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
40	c3fcuB_	Alignment	not modelled	99.5	17	**PDB header:**cell adhesion/blood clotting **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation
41	c3ragA_	Alignment	not modelled	99.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
42	c1jeqA_	Alignment	not modelled	99.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ku70; **PDBTitle:** crystal structure of the ku heterodimer
43	c1u8cB_	Alignment	not modelled	99.1	18	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
44	c1yvrA_	Alignment	not modelled	99.0	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**60-kda ss-a/ro ribonucleoprotein; **PDBTitle:** ro autoantigen
45	c3k6sB_	Alignment	not modelled	98.6	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
46	d1vlpa2	Alignment	not modelled	53.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
47	d1o98a1	Alignment	not modelled	49.3	20	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
48	d1jsca3	Alignment	not modelled	48.7	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
49	d2fcja1	Alignment	not modelled	48.5	17	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
50	c2e5cA_	Alignment	not modelled	48.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinamide phosphoribosyltransferase; **PDBTitle:** crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
51	c1vlpA_	Alignment	not modelled	41.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
52	d2hk6a1	Alignment	not modelled	35.8	9	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
53	d1xpma1	Alignment	not modelled	32.1	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like

54	c3d3kD_	Alignment	not modelled	30.4	15	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
55	c3igzB_	Alignment	not modelled	26.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
56	c2bdqA_	Alignment	not modelled	25.3	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
57	c3lq1A_	Alignment	not modelled	24.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
58	c1m6yA_	Alignment	not modelled	23.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
59	c1iszA_	Alignment	not modelled	21.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-d-xylanase; **PDBTitle:** crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
60	c1txtB_	Alignment	not modelled	20.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coa synthase; **PDBTitle:** staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
61	c2dunA_	Alignment	not modelled	19.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** solution structure of brct domain of dna polymerase mu
62	c1t10A_	Alignment	not modelled	19.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
63	c2coeA_	Alignment	not modelled	19.3	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**deoxynucleotidyltransferase, terminal variant; **PDBTitle:** solution structure of brct domain of terminal2 deoxynucleotidyltransferase
64	d2ihta3	Alignment	not modelled	18.9	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
65	d1hm5a_	Alignment	not modelled	18.6	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
66	c1wg8B_	Alignment	not modelled	18.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
67	c3euoB_	Alignment	not modelled	17.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii pentaketide synthase; **PDBTitle:** crystal structure of a fungal type iii polyketide synthase,2 oras
68	c1o98A_	Alignment	not modelled	17.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
69	d1r85a_	Alignment	not modelled	17.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
70	c3os4A_	Alignment	not modelled	15.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
71	c2gfqC_	Alignment	not modelled	15.6	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
72	d2csua1	Alignment	not modelled	15.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
73	c1jscA_	Alignment	not modelled	15.3	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
74	d1u0fa_	Alignment	not modelled	15.3	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
75	c1tllA_	Alignment	not modelled	14.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
76	c1x9eB_	Alignment	not modelled	14.0	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hmg-coa synthase; **PDBTitle:** crystal structure of hmg-coa synthase from enterococcus2 faecalis
77	c3hjbA_	Alignment	not modelled	13.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
78	c3nbuC_	Alignment	not modelled	13.4	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase;

						PDBTitle: crystal structure of pgi glucosephosphate isomerase
79	c2jvfA_	Alignment	not modelled	13.0	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
80	d1iata_	Alignment	not modelled	12.7	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
81	c2p8uB_	Alignment	not modelled	12.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, cytoplasmic; **PDBTitle:** crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
82	c1nuiA_	Alignment	not modelled	12.2	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
83	c2i2xD_	Alignment	not modelled	12.1	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
84	c3ugsB_	Alignment	not modelled	12.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
85	c2og2A_	Alignment	not modelled	11.9	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
86	d1twda_	Alignment	not modelled	11.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
87	c3hl0B_	Alignment	not modelled	11.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
88	d1isia_	Alignment	not modelled	11.6	21	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
89	c2vjjA_	Alignment	not modelled	11.6	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike protein; **PDBTitle:** tailspike protein of e.coli bacteriophage hk620 in complex2 with hexasaccharide
90	d2ji7a3	Alignment	not modelled	11.3	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
91	d1gzda_	Alignment	not modelled	11.2	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
92	c2wu8A_	Alignment	not modelled	11.1	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
93	c3ca8B_	Alignment	not modelled	11.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
94	c3lklB_	Alignment	not modelled	11.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
95	c3lehA_	Alignment	not modelled	10.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative hydroxymethylglutaryl-coa synthase; **PDBTitle:** the crystal structure of smu.943c from streptococcus mutans ua159
96	d1ozha3	Alignment	not modelled	10.9	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
97	c3e1hA_	Alignment	not modelled	10.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a type iii polyketide synthase2 pksiiinc from neurospora crassa
98	d1csca_	Alignment	not modelled	10.5	11	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
99	d2d1pa1	Alignment	not modelled	10.5	16	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like