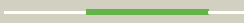
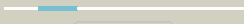
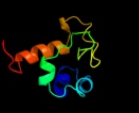
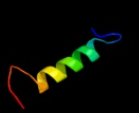
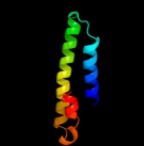
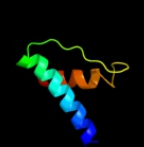
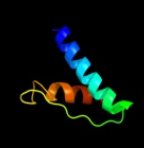


Phyre2

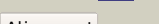
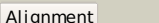
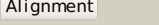
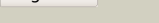
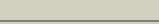
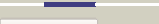
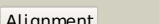
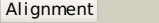
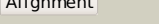
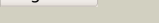
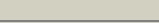
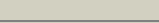
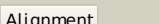
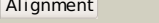
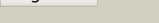
Email	I.a.kelley@imperial.ac.uk
Description	O13539
Date	Mon Jul 2 19:10:10 BST 2012
Unique Job ID	204bab2d0bd130c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nfoA_	 Alignment		59.1	14	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoe2, d154a mutation)
2	d1eo0a_	 Alignment		39.7	15	Fold: N-cbl like Superfamily: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70 Family: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70
3	c2is9A_	 Alignment		35.1	14	PDB header: transcription Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
4	c2eaoA_	 Alignment		30.7	23	PDB header: signaling protein, transferase Chain: A: PDB Molecule: ephrin type-b receptor 1; PDBTitle: solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
5	d2ebfx2	 Alignment		27.4	7	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
6	d2dk4a1	 Alignment		24.7	26	Fold: LEM/SAP HeH motif Superfamily: PRP4-like Family: PRP4-like
7	d1hjra_	 Alignment		22.8	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
8	c1n0fF_	 Alignment		22.5	20	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
9	c1lw3A_	 Alignment		22.1	24	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of myotubularin-related protein 22 complexed with phosphate
10	c3teqB_	 Alignment		21.0	32	PDB header: signaling protein Chain: B: PDB Molecule: stromal interaction molecule 1; PDBTitle: crystal structure of soar domain
11	c3qf7D_	 Alignment		20.7	41	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

12	c3gbgA_	Alignment		19.9	8	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
13	c2ltaA_	Alignment		19.6	40	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein; PDBTitle: solution nmr structure of de novo designed protein, rossmann 3x1 fold,2 northeast structural genomics consortium target or157
14	c2c5iT_	Alignment		18.7	21	PDB header: protein transport Chain: T: PDB Molecule: t-snare affecting a late golgi compartment PDBTitle: n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
15	dlzsqa2	Alignment		17.7	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myotubularin-like phosphatases
16	c1wq6A_	Alignment		17.4	22	PDB header: oncoprotein Chain: A: PDB Molecule: aml1-eto; PDBTitle: the tetramer structure of the nervy homolgy two (nhr2) domain of aml1-2 eto is critical for aml1-eto's activity
17	c1zsqA_	Alignment		16.5	24	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of mtmr2 in complex with2 phosphatidylinositol 3-phosphate
18	dlnoea_	Alignment		16.4	20	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
19	c3t4aG_	Alignment		16.1	50	PDB header: immune system Chain: G: PDB Molecule: fibrinogen-binding protein; PDBTitle: structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
20	c3terA_	Alignment		15.5	25	PDB header: metal binding protein Chain: A: PDB Molecule: mammalian stromal interaction molecule-1; PDBTitle: crystal structure of soar domain with inhibition helix from c. elegans
21	c2yf0A_	Alignment	not modelled	15.3	24	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 6; PDBTitle: human myotubularin related protein 6 (mtmr6)
22	dl4oa_	Alignment	not modelled	14.7	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
23	c2qffA_	Alignment	not modelled	14.7	38	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
24	c3ha4C_	Alignment	not modelled	14.2	19	PDB header: unknown function Chain: C: PDB Molecule: mix1; PDBTitle: crystal structure of the type one membrane protein mix1 from2 leishmania
25	c1pt9B_	Alignment	not modelled	14.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
26	dlpnoa_	Alignment	not modelled	13.9	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
27	c2bruC_	Alignment	not modelled	13.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
28	c3fmyA_	Alignment	not modelled	12.1	9	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
						PDB header: hydrolase inhibitor

29	c3f02A_	Alignment	not modelled	11.9	12	Chain: A: PDB Molecule: neuroserpin; PDBTitle: cleaved human neuroserpin
30	d1ft8e_	Alignment	not modelled	11.7	8	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
31	c3kkaD_	Alignment	not modelled	11.5	21	PDB header: transferase Chain: D: PDB Molecule: ephrin type-a receptor 2; PDBTitle: co-crystal structure of the sam domains of epha1 and epha2
32	cli25A_	Alignment	not modelled	11.4	40	PDB header: toxin Chain: A: PDB Molecule: huwentoxin-ii; PDBTitle: three dimensional solution structure of huwentoxin-ii by 2d2 1h-nmr
33	dli25a_	Alignment	not modelled	11.4	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
34	c2yxhB_	Alignment	not modelled	11.0	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
35	d2icta1	Alignment	not modelled	10.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
36	dlgs9a_	Alignment	not modelled	10.9	13	Fold: Four-helical up-and-down bundle Superfamily: Apolipoprotein Family: Apolipoprotein
37	dlidra_	Alignment	not modelled	10.7	5	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
38	c2jqqa_	Alignment	not modelled	10.5	26	PDB header: protein transport Chain: A: PDB Molecule: conserved oligomeric golgi complex subunit 2; PDBTitle: solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit2 protein (cog2p)
39	c2e8nA_	Alignment	not modelled	10.3	22	PDB header: transferase, signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
40	d1wmhb_	Alignment	not modelled	10.1	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
41	c2v4hA_	Alignment	not modelled	10.0	29	PDB header: transcription Chain: A: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cc2-lz domain - 1d5 darpin complex
42	d1z9ha1	Alignment	not modelled	9.4	15	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
43	c2q0oC_	Alignment	not modelled	9.2	25	PDB header: transcription Chain: C: PDB Molecule: probable transcriptional repressor tram; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
44	c2fjrB_	Alignment	not modelled	9.0	10	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
45	c3cecA_	Alignment	not modelled	9.0	12	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
46	c1b0xA_	Alignment	not modelled	9.0	17	PDB header: transferase Chain: A: PDB Molecule: protein (epha4 receptor tyrosine kinase); PDBTitle: the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
47	d1b0xa_	Alignment	not modelled	9.0	17	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
48	c2ktrA_	Alignment	not modelled	8.9	11	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
49	d1knxa1	Alignment	not modelled	8.8	14	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phosphatase HprK N-terminal domain
50	c2qyaA_	Alignment	not modelled	8.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of an uncharacterized conserved protein2 from methanopyrus kandleri
51	c2riwA_	Alignment	not modelled	8.7	13	PDB header: signaling protein Chain: A: PDB Molecule: thyroxine-binding globulin; PDBTitle: the reactive loop cleaved human thyroxine binding globulin complexed2 with thyroxine
52	c2zvnF_	Alignment	not modelled	8.6	29	PDB header: signaling protein/transcription Chain: F: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cozi domain incomplex with diubiquitin in p2121212 space group
53	d1pzra_	Alignment	not modelled	8.5	22	Fold: HLH-like Superfamily: Docking domain B of the erythromycin polyketide synthase (DEBS) Family: Docking domain B of the erythromycin polyketide synthase (DEBS)
54	c2ebyA_	Alignment	not modelled	8.2	18	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli

55	c2hx1D	 Alignment	not modelled	8.0	28	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had PDBTitle: crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
56	c3vejB	 Alignment	not modelled	7.9	33	PDB header: protein binding Chain: B: PDB Molecule: ubiquitin-like protein mdy2; PDBTitle: crystal structure of the get5 carboxyl domain from s. cerevisiae
57	d1ioka2	 Alignment	not modelled	7.7	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
58	c1ow5A	 Alignment	not modelled	7.7	19	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase ste11; PDBTitle: nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
59	d1ow5a	 Alignment	not modelled	7.7	19	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
60	c2lnzA	 Alignment	not modelled	7.6	33	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-like protein mdy2; PDBTitle: solution structure of the get5 carboxyl domain from s. cerevisiae
61	c2q2kA	 Alignment	not modelled	7.6	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
62	d2nr5a1	 Alignment	not modelled	7.6	17	Fold: Ferritin-like Superfamily: SO2669-like Family: SO2669-like
63	c3m1fC	 Alignment	not modelled	7.5	16	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
64	d1ydxal	 Alignment	not modelled	7.4	12	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
65	c2h4bC	 Alignment	not modelled	7.4	20	PDB header: de novo protein Chain: C: PDB Molecule: pancreatic hormone; PDBTitle: cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
66	c2h3sB	 Alignment	not modelled	7.4	20	PDB header: de novo protein Chain: B: PDB Molecule: pancreatic hormone; PDBTitle: cis-azobenzene-avian pancreatic polypeptide bound to dpc2 micelles
67	c2h4bD	 Alignment	not modelled	7.4	20	PDB header: de novo protein Chain: D: PDB Molecule: pancreatic hormone; PDBTitle: cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
68	c3vp8B	 Alignment	not modelled	7.4	14	PDB header: transcription Chain: B: PDB Molecule: general transcriptional corepressor tup1; PDBTitle: crystal structure of the n-terminal domain of the yeast general2 corepressor tup1p
69	d1b4fa	 Alignment	not modelled	7.4	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
70	c3mtuE	 Alignment	not modelled	7.3	30	PDB header: contractile protein Chain: E: PDB Molecule: head morphogenesis protein, tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
71	d1whua	 Alignment	not modelled	7.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
72	c3n8uB	 Alignment	not modelled	7.0	16	PDB header: hydrolase Chain: B: PDB Molecule: imelysin peptidase; PDBTitle: crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
73	c2ns6A	 Alignment	not modelled	7.0	24	PDB header: hydrolase Chain: A: PDB Molecule: mobilization protein a; PDBTitle: crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
74	d1ft8a2	 Alignment	not modelled	6.9	7	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
75	c2h3tB	 Alignment	not modelled	6.8	20	PDB header: de novo protein Chain: B: PDB Molecule: pancreatic hormone; PDBTitle: trans-(4-aminomethyl)phenylazobenzoic acid-app bound to dpc2 micelles
76	c3odsA	 Alignment	not modelled	6.8	28	PDB header: protein binding Chain: A: PDB Molecule: sympleskin; PDBTitle: crystal structure of the k185a mutant of the n-terminal domain of2 human symplekin
77	d1ykhb1	 Alignment	not modelled	6.8	17	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
78	d1rkua	 Alignment	not modelled	6.7	17	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
79	c2bf9A	 Alignment	not modelled	6.7	20	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
80	c2ppxA	Alignment	not modelled	6.7	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from

					agrobacterium2 tumefaciens
81	d2ppxa1	Alignment	not modelled	6.7	9 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
82	d2hbka1	Alignment	not modelled	6.5	29 Fold: SAM domain-like Superfamily: HRDC-like Family: EXOSC10 HRDC domain-like
83	c2kg5A_	Alignment	not modelled	6.5	12 PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
84	c3o2qD_	Alignment	not modelled	6.4	28 PDB header: hydrolase Chain: D: PDB Molecule: sympleskin; PDBTitle: crystal structure of the human sympleskin-ssu72-ctd phosphopeptide2 complex
85	d1rkqa_	Alignment	not modelled	6.4	24 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
86	c1vdiA_	Alignment	not modelled	6.4	19 PDB header: contractile protein Chain: A: PDB Molecule: troponin i, fast skeletal muscle; PDBTitle: solution structure of actin-binding domain of troponin in2 ca2+-free state
87	c2ef8A_	Alignment	not modelled	6.3	19 PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
88	d1r9da_	Alignment	not modelled	6.1	25 Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
89	c1tz5A_	Alignment	not modelled	6.1	30 PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
90	c3l9aX_	Alignment	not modelled	6.1	30 PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: structure of the c-terminal domain from a streptococcus2 mutans hypothetical
91	c3aq8A_	Alignment	not modelled	6.0	8 PDB header: oxygen binding Chain: A: PDB Molecule: group 1 truncated hemoglobin; PDBTitle: crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
92	c3odrA_	Alignment	not modelled	6.0	28 PDB header: protein binding Chain: A: PDB Molecule: sympleskin; PDBTitle: crystal structure of the n-terminal domain of human sympleskin
93	c2d7cD_	Alignment	not modelled	5.9	24 PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of human rab11 in complex with fip3 rab-2 binding domain
94	d1h9aa1	Alignment	not modelled	5.9	40 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	c3h8mB_	Alignment	not modelled	5.8	18 PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 7; PDBTitle: sam domain of human ephrin type-a receptor 7 (epha7)
96	d2grrb1	Alignment	not modelled	5.8	9 Fold: alpha-alpha superhelix Superfamily: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain Family: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain
97	c3u88B_	Alignment	not modelled	5.7	16 PDB header: transcription Chain: B: PDB Molecule: menin; PDBTitle: crystal structure of human menin in complex with mll1 and ledgf
98	c3nkuA_	Alignment	not modelled	5.7	40 PDB header: protein transport Chain: A: PDB Molecule: drda; PDBTitle: crystal structure of the n-terminal domain of drda/sidm from2 legionella pneumophila
99	d2hwna1	Alignment	not modelled	5.7	17 Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit