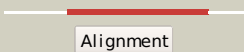

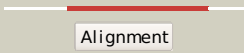

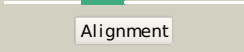

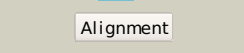
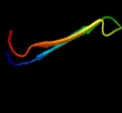


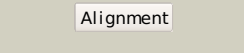

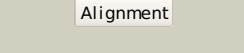

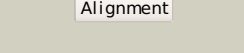
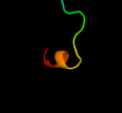

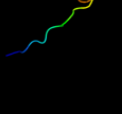
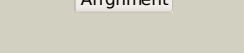

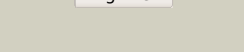

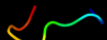

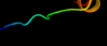
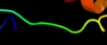



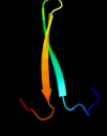



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PG75
Date	Fri May 25 09:45:32 BST 2012
Unique Job ID	16028dc78376965b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zxuA_	 Alignment		98.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g01750 protein; PDBTitle: x-ray structure of protein from arabidopsis thaliana2 at5g01750
2	d2q4ma1	 Alignment		98.8	16	Fold: Tubby C-terminal domain-like Superfamily: Tubby C-terminal domain-like Family: At5g01750-like
3	d1ppva_	 Alignment		40.4	11	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
4	c3dy0B_	 Alignment		38.1	36	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: c-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
5	c1lq8H_	 Alignment		37.1	38	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved protein c inhibitor
6	c2b26A_	 Alignment		27.3	22	PDB header: chaperone/protein transport Chain: A: PDB Molecule: sis1 protein; PDBTitle: the crystal structure of the protein complex of yeast hsp402 sis1 and hsp70 ssa1
7	c3i38F_	 Alignment		27.2	17	PDB header: chaperone Chain: F: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
8	c2qldA_	 Alignment		22.2	17	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 1; PDBTitle: human hsp40 hdj1
9	d1c3ga2	 Alignment		20.3	22	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
10	c3i38I_	 Alignment		18.5	18	PDB header: chaperone Chain: I: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
11	c3i38H_	 Alignment		18.1	17	PDB header: chaperone Chain: H: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578

12	d1x5wa2	Alignment		18.0	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	c3i38D_	Alignment		17.3	17	PDB header: chaperone Chain: D: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
14	c2q2gA_	Alignment		16.4	28	PDB header: chaperone Chain: A: PDB Molecule: heat shock 40 kda protein, putative (fragment); PDBTitle: crystal structure of dimerization domain of hsp40 from2 cryptosporidium parvum, cgd2_1800
15	d1msza_	Alignment		16.3	13	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
16	c1mszA_	Alignment		16.3	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: solution structure of the r3h domain from human smubp-2
17	c3i38K_	Alignment		15.8	17	PDB header: chaperone Chain: K: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
18	c3i38L_	Alignment		15.7	17	PDB header: chaperone Chain: L: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
19	c3s2xB_	Alignment		15.4	26	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
20	c3i38B_	Alignment		15.2	17	PDB header: chaperone Chain: B: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
21	c2k1A_	Alignment	not modelled	15.1	29	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
22	c2k1B_	Alignment	not modelled	15.1	29	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
23	c2k1kB_	Alignment	not modelled	15.1	29	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
24	c2k1kA_	Alignment	not modelled	15.1	29	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
25	c3kg6C_	Alignment	not modelled	14.5	4	PDB header: lyase Chain: C: PDB Molecule: curf; PDBTitle: dehydratase domain from curf module of curacin polyketide synthase
26	c3i38G_	Alignment	not modelled	14.1	17	PDB header: chaperone Chain: G: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
27	c3i38A_	Alignment	not modelled	14.1	17	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
28	d1eysh1	Alignment	not modelled	13.3	14	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain

29	c3lz8A	Alignment	not modelled	13.0	17	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
30	d2dmda3	Alignment	not modelled	12.5	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	c1eysH	Alignment	not modelled	12.5	14	PDB header: electron transport Chain: H: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
32	c3i38C	Alignment	not modelled	12.3	17	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
33	c3i38E	Alignment	not modelled	12.3	17	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
34	c3i38J	Alignment	not modelled	11.6	18	PDB header: chaperone Chain: J: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
35	d1gff1	Alignment	not modelled	11.6	22	Fold: Nucleoplamin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
36	c3mcrA	Alignment	not modelled	10.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
37	d2i5nh1	Alignment	not modelled	10.6	24	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
38	c1upsB	Alignment	not modelled	10.4	23	PDB header: glycosyl hydrolase Chain: B: PDB Molecule: glcnac-alpha-1,4-gal-releasing endo-beta- PDBTitle: glcnac[alpha]1-4gal releasing endo-[beta]-galactosidase2 from clostridium perfringens
39	d1rzhh1	Alignment	not modelled	10.2	16	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
40	c2i5nH	Alignment	not modelled	10.0	24	PDB header: photosynthesis Chain: H: PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
41	d2f1la1	Alignment	not modelled	9.9	10	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RimM C-terminal domain-like
42	c2pnyA	Alignment	not modelled	9.6	9	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
43	c3gita	Alignment	not modelled	9.4	30	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase/acetyl-coa synthase subunit PDBTitle: crystal structure of a truncated acetyl-coa synthase
44	d1c8ua2	Alignment	not modelled	9.0	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-CoA thioesterase
45	d1oaoc	Alignment	not modelled	8.7	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
46	d1svba1	Alignment	not modelled	8.6	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
47	c2khuA	Alignment	not modelled	8.6	45	PDB header: transferase/protein binding Chain: A: PDB Molecule: immunoglobulin g-binding protein g, dna PDBTitle: solution structure of the ubiquitin-binding motif of human2 polymerase iota
48	d1gg3a3	Alignment	not modelled	8.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
49	d4znfa	Alignment	not modelled	8.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	c3znfA	Alignment	not modelled	8.2	33	PDB header: zinc finger dna binding domain Chain: A: PDB Molecule: zinc finger; PDBTitle: high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
51	c4znfA	Alignment	not modelled	8.2	33	PDB header: zinc finger dna binding domain Chain: A: PDB Molecule: zinc finger; PDBTitle: high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
52	d1ru3a	Alignment	not modelled	8.1	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
53	c3f9uA	Alignment	not modelled	7.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported cytochrome c biogenesis-related protein; PDBTitle: crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis PDB header: photosynthesis

54	c1k6nH_	Alignment	not modelled	7.8	16	Chain: H: PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
55	c2l57A_	Alignment	not modelled	7.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoxin-like protein from2 clostridium perfringens
56	d2o5fa1	Alignment	not modelled	7.1	11	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
57	c1wyjA_	Alignment	not modelled	7.1	14	PDB header: cell adhesion Chain: A: PDB Molecule: protocadherin beta 14; PDBTitle: solution structure of mouse protocadherin beta 14 (26-137)
58	d1dmla2	Alignment	not modelled	7.0	18	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
59	d1z66a1	Alignment	not modelled	6.9	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
60	d2hq2a1	Alignment	not modelled	6.7	35	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
61	c3htrB_	Alignment	not modelled	6.7	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
62	d1e0na_	Alignment	not modelled	6.6	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
63	c3isyA_	Alignment	not modelled	6.6	25	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
64	c2k7iB_	Alignment	not modelled	6.5	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0339 protein atu0232; PDBTitle: solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 at3. ontario center for structural proteomics target atc0223.
65	d2k7ia1	Alignment	not modelled	6.5	27	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
66	c1b5fD_	Alignment	not modelled	6.5	11	PDB header: hydrolase Chain: D: PDB Molecule: protein (cardosin a); PDBTitle: native cardosin a from cynara cardunculus l.
67	d1nxxa_	Alignment	not modelled	6.3	18	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
68	d1a1ia3	Alignment	not modelled	6.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	c2v9kA_	Alignment	not modelled	6.1	7	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein flj32312; PDBTitle: crystal structure of human pus10, a novel pseudouridine2 synthase.
70	d2k8ea1	Alignment	not modelled	6.1	23	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
71	c1meyG_	Alignment	not modelled	6.1	33	PDB header: transferase/dna Chain: G: PDB Molecule: consensus zinc finger; PDBTitle: crystal structure of a designed zinc finger protein bound2 to dna
72	d1e2ya_	Alignment	not modelled	5.9	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
73	d2hqva1	Alignment	not modelled	5.9	9	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like
74	c1vf5R_	Alignment	not modelled	5.6	33	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
75	d2e74e1	Alignment	not modelled	5.6	33	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
76	c1vf5E_	Alignment	not modelled	5.6	33	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
77	c2e74E_	Alignment	not modelled	5.6	33	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
78	c2e75E_	Alignment	not modelled	5.6	33	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
79	c2e76E_	Alignment	not modelled	5.6	33	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
						Fold: beta-beta-alpha zinc fingers

80	d1llmc2	Alignment	not modelled	5.5	33	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
81	c2ph0A_	Alignment	not modelled	5.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
82	d1m06f_	Alignment	not modelled	5.5	22	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
83	d1st9a_	Alignment	not modelled	5.5	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
84	d2aqaa1	Alignment	not modelled	5.5	11	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
85	d1srka_	Alignment	not modelled	5.4	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
86	d2ibge1	Alignment	not modelled	5.3	13	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
87	d1a1ia2	Alignment	not modelled	5.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
88	c2i6kA_	Alignment	not modelled	5.1	12	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
89	d1fnna1	Alignment	not modelled	5.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
90	d2k49a2	Alignment	not modelled	5.1	15	Fold: YegP-like Superfamily: YegP-like Family: YegP-like