



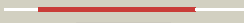



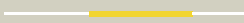


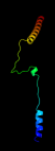



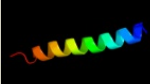

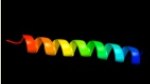



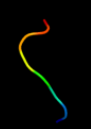
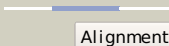

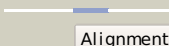



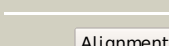

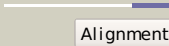

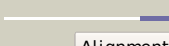

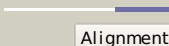


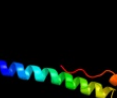
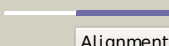

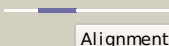

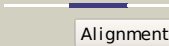




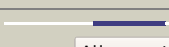


# Phyre2


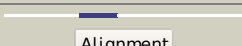
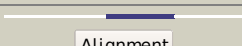



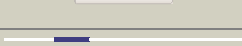
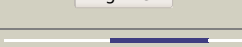
Email	I.a.kelley@imperial.ac.uk
Description	Q9NUG6
Date	Tue Apr 3 15:15:57 BST 2012
Unique Job ID	1314d70a36936970

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2zdiC_</a>	 Alignment		97.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> prefoldin subunit alpha; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
2	<a href="#">d1fxkc_</a>	 Alignment		96.8	15	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
3	<a href="#">c2zdiA_</a>	 Alignment		96.2	12	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> prefoldin subunit beta; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
4	<a href="#">d1fxka_</a>	 Alignment		89.9	17	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
5	<a href="#">c3aeiA_</a>	 Alignment		70.3	24	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> prefoldin beta subunit 2; <b>PDBTitle:</b> crystal structure of the prefoldin beta2 subunit from thermococcus2 strain ks-1
6	<a href="#">c1go4F_</a>	 Alignment		45.7	26	<b>PDB header:</b> cell cycle <b>Chain:</b> F; <b>PDB Molecule:</b> mad1 (mitotic arrest deficient)-like 1; <b>PDBTitle:</b> crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
7	<a href="#">d1k8ke_</a>	 Alignment		42.5	13	<b>Fold:</b> Arp2/3 complex 21 kDa subunit ARPC3 <b>Superfamily:</b> Arp2/3 complex 21 kDa subunit ARPC3 <b>Family:</b> Arp2/3 complex 21 kDa subunit ARPC3
8	<a href="#">c2gboB_</a>	 Alignment		27.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> upf0358 protein ef2458; <b>PDBTitle:</b> protein of unknown function ef2458 from enterococcus faecalis
9	<a href="#">d2gboa1</a>	 Alignment		27.2	14	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> EF2458-like <b>Family:</b> EF2458-like
10	<a href="#">c2ke4A_</a>	 Alignment		24.6	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
11	<a href="#">c3dwIE_</a>	 Alignment		23.2	25	<b>PDB header:</b> structural protein <b>Chain:</b> E; <b>PDB Molecule:</b> actin-related protein 2/3 complex subunit 3; <b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit

12	<a href="#">c2la3A_</a>		Alignment		21.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
13	<a href="#">c2kz6A_</a>		Alignment		21.0	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
14	<a href="#">c3lyvF_</a>		Alignment		18.8	31	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> ribosome-associated factor y; <b>PDBTitle:</b> crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
15	<a href="#">c3ka5A_</a>		Alignment		17.6	31	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome-associated protein y (psrp-1); <b>PDBTitle:</b> crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
16	<a href="#">c2ivfB_</a>		Alignment		16.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
17	<a href="#">c3he4A_</a>		Alignment		16.0	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> synzip6; <b>PDBTitle:</b> heterospecific coiled-coil pair synzip5:synzip6
18	<a href="#">c1t3jA_</a>		Alignment		14.2	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin 1; <b>PDBTitle:</b> mitofusin domain hr2 v686m/i708m mutant
19	<a href="#">c1yuzB_</a>		Alignment		12.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
20	<a href="#">c2ko2A_</a>		Alignment		11.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> reticulon-4; <b>PDBTitle:</b> nogo66
21	<a href="#">c2y0mB_</a>		Alignment	not modelled	10.4	30	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> male-specific lethal 1 homolog; <b>PDBTitle:</b> crystal structure of the complex between dosage2 compensation factors ms11 and mof
22	<a href="#">d1oqya1</a>		Alignment	not modelled	10.1	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
23	<a href="#">d1hh8a_</a>		Alignment	not modelled	9.9	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
24	<a href="#">c1y4mC_</a>		Alignment	not modelled	9.9	30	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> herv-frd_6p24.1 provirus ancestral env polyprotein; <b>PDBTitle:</b> crystal structure of human endogenous retrovirus herv-frd envelope2 protein (syncitin-2)
25	<a href="#">c2ykqC_</a>		Alignment	not modelled	9.8	19	<b>PDB header:</b> rna-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> line-1 orf1p; <b>PDBTitle:</b> structure of the human line-1 orf1p trimer
26	<a href="#">c1mofA_</a>		Alignment	not modelled	9.5	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> moloney murine leukemia virus p15; <b>PDBTitle:</b> coat protein
27	<a href="#">c1lb1C_</a>		Alignment	not modelled	9.2	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> guanine nucleotide exchange factor dbs; <b>PDBTitle:</b> crystal structure of the dbl and pleckstrin homology2 domains of dbs in complex with rhoa
28	<a href="#">c3hdeA_</a>		Alignment	not modelled	9.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> crystal structure of full-length endolysin r21 from phage 21

29	<a href="#">c2p3xA</a>	Alignment	not modelled	8.7	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyphenol oxidase, chloroplast; <b>PDBTitle:</b> crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
30	<a href="#">c2l5gB</a>	Alignment	not modelled	8.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ncor2; <b>PDBTitle:</b> co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
31	<a href="#">d1bt3a</a>	Alignment	not modelled	8.6	0	<b>Fold:</b> Di-copper centre-containing domain <b>Superfamily:</b> Di-copper centre-containing domain <b>Family:</b> Catechol oxidase
32	<a href="#">d1p37a</a>	Alignment	not modelled	8.4	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage lysozyme
33	<a href="#">d1lpya</a>	Alignment	not modelled	8.0	12	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage lysozyme
34	<a href="#">c2q7cC</a>	Alignment	not modelled	8.0	28	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> fusion protein between yeast variant gcn4 and <b>PDBTitle:</b> crystal structure of iqn17
35	<a href="#">c2ka6B</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> nmr structure of the cbp-taz2/stat1-tad complex
36	<a href="#">d1wpga2</a>	Alignment	not modelled	7.6	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
37	<a href="#">d2asra</a>	Alignment	not modelled	7.5	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Aspartate receptor, ligand-binding domain <b>Family:</b> Aspartate receptor, ligand-binding domain
38	<a href="#">d176la</a>	Alignment	not modelled	7.4	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage lysozyme
39	<a href="#">c2odmA</a>	Alignment	not modelled	7.4	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0358 protein mw0995; <b>PDBTitle:</b> crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
40	<a href="#">c2y9xC</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> polyphenol oxidase; <b>PDBTitle:</b> crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
41	<a href="#">c3kyzA</a>	Alignment	not modelled	7.1	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein pfes; <b>PDBTitle:</b> the crystal structure of the sensor domain of two-component2 sensor pfes from pseudomonas aeruginosa pa01
42	<a href="#">d1zl8a1</a>	Alignment	not modelled	6.9	19	<b>Fold:</b> L27 domain <b>Superfamily:</b> L27 domain <b>Family:</b> L27 domain
43	<a href="#">c3uuxD</a>	Alignment	not modelled	6.9	15	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial division protein 1; <b>PDBTitle:</b> crystal structure of yeast fis1 in complex with mdv1 fragment2 containing n-terminal extension and coiled coil domains
44	<a href="#">d1hqz1</a>	Alignment	not modelled	6.8	10	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Cofilin-like
45	<a href="#">d1udma</a>	Alignment	not modelled	6.8	21	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Cofilin-like
46	<a href="#">c2f9jP</a>	Alignment	not modelled	6.7	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> splicing factor 3b subunit 1; <b>PDBTitle:</b> 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
47	<a href="#">d1is1a</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
48	<a href="#">d1y74a1</a>	Alignment	not modelled	6.2	19	<b>Fold:</b> L27 domain <b>Superfamily:</b> L27 domain <b>Family:</b> L27 domain
49	<a href="#">c1u0iA</a>	Alignment	not modelled	6.0	47	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> iaal-e3; <b>PDBTitle:</b> iaal-e3/k3 heterodimer
50	<a href="#">d1xp8a2</a>	Alignment	not modelled	5.9	10	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
51	<a href="#">c2w9yA</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid/retinol binding protein protein 7, <b>PDBTitle:</b> the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
52	<a href="#">c1x67A</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> drebrin-like protein; <b>PDBTitle:</b> solution structure of the cofilin homology domain of hip-552 (drebrin-like protein)
53	<a href="#">c3obhA</a>	Alignment	not modelled	5.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
54	<a href="#">d1ubea2</a>	Alignment	not modelled	5.5	8	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain

55	<a href="#">c2wg6L_</a>	 Alignment	not modelled	5.5	21	<b>PDB header:</b> transcription,hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> general control protein gcn4, <b>PDBTitle:</b> proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
56	<a href="#">d2otaa1</a>	 Alignment	not modelled	5.5	26	<b>Fold:</b> YejL-like <b>Superfamily:</b> YejL-like <b>Family:</b> YejL-like
57	<a href="#">d1mo6a2</a>	 Alignment	not modelled	5.4	10	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
58	<a href="#">c1a3wB_</a>	 Alignment	not modelled	5.4	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
59	<a href="#">c2rdcA_</a>	 Alignment	not modelled	5.4	25	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
60	<a href="#">c3t07D_</a>	 Alignment	not modelled	5.3	22	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
61	<a href="#">d1wiva_</a>	 Alignment	not modelled	5.3	16	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
62	<a href="#">c1gk4A_</a>	 Alignment	not modelled	5.2	14	<b>PDB header:</b> vimentin <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> human vimentin coil 2b fragment (cys2)