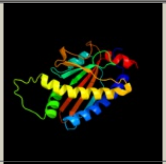
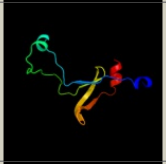
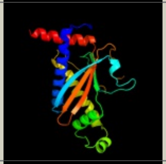
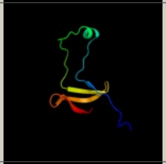
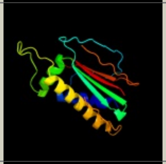
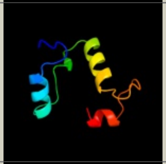
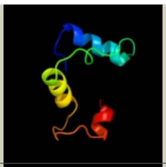
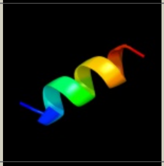
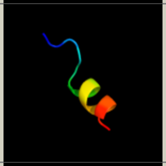
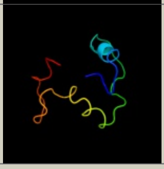
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P06974
Date	Thu Jan 5 10:59:40 GMT 2012
Unique Job ID	ce3da4c167b8e642

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hp7A_	Alignment		100.0	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein flim; **PDBTitle:** structure of flim provides insight into assembly of the2 switch complex in the bacterial flagella motor
2	d1o6aa_	Alignment		99.7	18	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
3	d1xkra_	Alignment		99.6	12	**Fold:**CheC-like **Superfamily:**CheC-like **Family:**CheC-like
4	c3qtaA_	Alignment		99.6	10	**PDB header:**attractant **Chain:** A: **PDB Molecule:**chemotaxis protein chec; **PDBTitle:** crystal structure of a hypothetical chec-like protein (rrnac0528) from2 haloarcula marismortui atcc 43049 at 2.00 a resolution
5	d1o9ya_	Alignment		99.6	19	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
6	d1xkoa_	Alignment		97.7	11	**Fold:**CheC-like **Superfamily:**CheC-like **Family:**CheC-like
7	c3hzhB_	Alignment		97.6	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**chemotaxis operon protein (chex); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
8	c3hm4A_	Alignment		97.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis protein chex; **PDBTitle:** crystal structure of a chemotaxis protein chex (dde_0281) from2 desulfovibrio desulfuricans subsp. at 1.30 a resolution
9	c3h2dA_	Alignment		96.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chec-like superfamily protein; **PDBTitle:** crystal structure of a chemotactic chec-like protein (so_3915) from2 shewanella oneidensis mr-1 at 1.86 a resolution
10	d1bu3a_	Alignment		58.0	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
11	c2w85A_	Alignment		46.1	32	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19

12	c3fs7D_	Alignment		39.3	21	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**parvalbumin, thymic; **PDBTitle:** crystal structure of gallus gallus beta-parvalbumin (avian2 thymic hormone)
13	d2evra2	Alignment		37.0	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
14	c2pl9D_	Alignment		28.3	33	**PDB header:**signaling protien **Chain:** D: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
15	c2pl9E_	Alignment		27.9	38	**PDB header:**signaling protien **Chain:** E: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
16	c2pl9F_	Alignment		27.9	38	**PDB header:**signaling protien **Chain:** F: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
17	c2fg0B_	Alignment		24.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
18	d2isba1	Alignment		23.7	48	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
19	c2jijA_	Alignment		18.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl-4 hydroxylase; **PDBTitle:** crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
20	c2kycA_	Alignment		17.2	25	**PDB header:**calcium binding protein **Chain:** A: **PDB Molecule:**parvalbumin, thymic cpv3; **PDBTitle:** solution structure of ca-free chicken parvalbumin 3 (cpv3)
21	c3jstA_	Alignment	not modelled	14.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of transcriptional coactivator/pterin dehydratase2 from brucella melitensis
22	d1rwya_	Alignment	not modelled	14.5	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
23	d1a0pa2	Alignment	not modelled	13.9	33	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
24	c3ff5B_	Alignment	not modelled	13.4	36	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
25	c2vywA_	Alignment	not modelled	13.2	38	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** hemoglobin (hb2) from trematode fasciola hepatica
26	c2e63A_	Alignment	not modelled	13.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1787 protein; **PDBTitle:** solution structure of the neuz domain in kiaa1787 protein
27	d1vyua1	Alignment	not modelled	12.6	21	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
28	d1pvaa_	Alignment	not modelled	11.9	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
						PDB header:rna binding protein

29	c2f9jP_	Alignment	not modelled	11.8	50	**Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
30	d1d1na_	Alignment	not modelled	11.8	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
31	c3nkhB_	Alignment	not modelled	11.0	18	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
32	c2glwA_	Alignment	not modelled	10.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
33	d2cqaa1	Alignment	not modelled	10.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
34	c3peiA_	Alignment	not modelled	9.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
35	d1wpga1	Alignment	not modelled	9.7	24	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
36	d5pala_	Alignment	not modelled	9.6	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
37	d1khda1	Alignment	not modelled	9.4	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
38	c2uzhB_	Alignment	not modelled	9.0	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
39	d1jz8a3	Alignment	not modelled	8.8	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
40	d1s04a_	Alignment	not modelled	8.7	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
41	c3fkhB_	Alignment	not modelled	8.5	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
42	c2pmzV_	Alignment	not modelled	8.5	10	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
43	d2elca1	Alignment	not modelled	8.2	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
44	c3q4nA_	Alignment	not modelled	8.1	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0754; **PDBTitle:** crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
45	c2kx2A_	Alignment	not modelled	8.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of mth1821
46	d1nr9a_	Alignment	not modelled	8.0	33	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
47	c1i7oC_	Alignment	not modelled	7.9	35	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
48	c3ouiA_	Alignment	not modelled	7.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** phd2-r717 with 40787422
49	c2krgA_	Alignment	not modelled	7.4	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1; **PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
50	c2dfuB_	Alignment	not modelled	7.2	32	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
51	d1eika_	Alignment	not modelled	7.0	10	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
52	c2ebbA_	Alignment	not modelled	7.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit

53	c3itqB_	Alignment	not modelled	7.0	36	domain protein; **PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
54	c2hc8A_	Alignment	not modelled	6.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
55	c3cp3A_	Alignment	not modelled	6.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
56	d1jjcb4	Alignment	not modelled	6.7	14	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
57	d1dzfa2	Alignment	not modelled	6.6	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
58	c2oxgE_	Alignment	not modelled	6.6	20	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
59	d1hmja_	Alignment	not modelled	6.5	19	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
60	c3rfuC_	Alignment	not modelled	6.4	13	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
61	d1u5la_	Alignment	not modelled	6.4	19	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
62	d1b10a_	Alignment	not modelled	6.1	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
63	d1yq2a3	Alignment	not modelled	6.0	16	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
64	d1v8ga1	Alignment	not modelled	5.9	14	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
65	d1v8ha1	Alignment	not modelled	5.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
66	d1tqba_	Alignment	not modelled	5.8	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
67	d1dcpa_	Alignment	not modelled	5.8	19	**Fold:**DCoH-like **Superfamily:**PCD-like **Family:**PCD-like
68	d1uw3a_	Alignment	not modelled	5.7	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
69	d1u69a_	Alignment	not modelled	5.7	40	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
70	d1xyua_	Alignment	not modelled	5.7	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
71	d1xyka_	Alignment	not modelled	5.5	25	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
72	d1sawa_	Alignment	not modelled	5.5	32	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
73	c2zjtB_	Alignment	not modelled	5.4	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation
74	d2vbua1	Alignment	not modelled	5.3	32	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
75	d1vgga_	Alignment	not modelled	5.3	17	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
76	d1ibxa_	Alignment	not modelled	5.2	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
77	c2gl0A_	Alignment	not modelled	5.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of pae2307 in complex with adenosine
78	d1b8la_	Alignment	not modelled	5.1	26	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
79	d1uoua1	Alignment	not modelled	5.1	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-

						terminal domain
80	d1ru0a_	Alignment	not modelled	5.0	15	**Fold:**DCoH-like **Superfamily:**PCD-like **Family:**PCD-like
81	d1xnea_	Alignment	not modelled	5.0	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
82	d2tpta1	Alignment	not modelled	5.0	25	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain