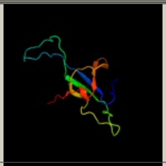
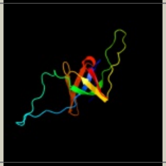
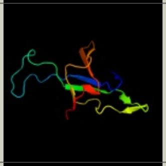
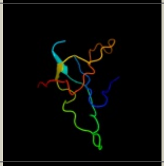
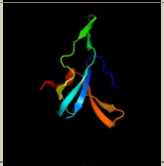
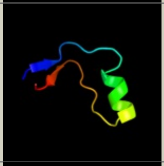
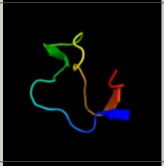
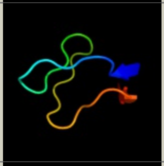
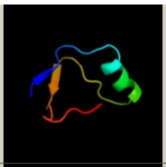
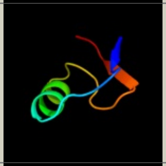
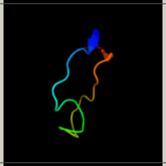
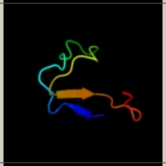
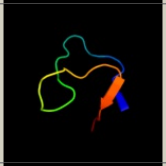
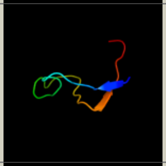
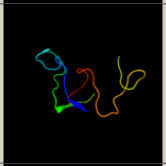
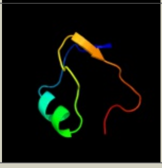
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6F9
Date	Thu Jan 5 11:03:04 GMT 2012
Unique Job ID	d570d63c00d7beaa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1aono_	Alignment		100.0	100	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
2	d1p3ha_	Alignment		100.0	45	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
3	d1we3o_	Alignment		100.0	53	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
4	d1lepa_	Alignment		99.9	48	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
5	c3nx6A_	Alignment		99.9	49	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**10kda chaperonin; **PDBTitle:** crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
6	d1g31a_	Alignment		95.7	19	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
7	c1p82A_	Alignment		76.7	43	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**10 kda chaperonin; **PDBTitle:** nmr structure of 1-25 fragment of mycobacterium2 tuberculosis cpn10
8	c1yqxB_	Alignment		76.0	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sinapyl alcohol dehydrogenase; **PDBTitle:** sinapyl alcohol dehydrogenase at 2.5 angstrom resolution
9	c1lluD_	Alignment		72.3	50	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate
10	c4a10A_	Alignment		71.3	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**octenoyl-coa reductase/carboxylase; **PDBTitle:** apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
11	c2ejvA_	Alignment		70.3	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-threonine 3-dehydrogenase; **PDBTitle:** crystal structure of threonine 3-dehydrogenase complexed with nad+

12	c1kevB_	Alignment		70.2	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** structure of nadp-dependent alcohol dehydrogenase
13	c1rjwA_	Alignment		69.9	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r
14	c3m6iA_	Alignment		69.6	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arabinitol 4-dehydrogenase; **PDBTitle:** l-arabinitol 4-dehydrogenase
15	c1kolA_	Alignment		69.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formaldehyde dehydrogenase; **PDBTitle:** crystal structure of formaldehyde dehydrogenase
16	c2ouiB_	Alignment		68.9	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
17	c1piwA_	Alignment		68.4	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical zinc-type alcohol dehydrogenase- **PDBTitle:** apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae
18	d1uufa1	Alignment		67.7	35	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
19	c1pl6A_	Alignment		67.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sorbitol dehydrogenase; **PDBTitle:** human sdh/nadh/inhibitor complex
20	c2hcyD_	Alignment		67.2	30	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 1; **PDBTitle:** yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme
21	c1r37B_	Alignment	not modelled	66.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent alcohol dehydrogenase; **PDBTitle:** alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol
22	c1h2bA_	Alignment	not modelled	66.1	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a3 resolution
23	c2cf5A_	Alignment	not modelled	65.9	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cinnamyl alcohol dehydrogenase; **PDBTitle:** crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5
24	c2xaaC_	Alignment	not modelled	65.0	36	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**secondary alcohol dehydrogenase; **PDBTitle:** alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol
25	c3krtC_	Alignment	not modelled	63.8	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**crotonyl coa reductase; **PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
26	c1f8fA_	Alignment	not modelled	63.7	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzyl alcohol dehydrogenase; **PDBTitle:** crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus
27	c2eihA_	Alignment	not modelled	63.1	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** crystal structure of nad-dependent alcohol dehydrogenase
28	c1e3jA_	Alignment	not modelled	62.2	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp(h)-dependent ketose reductase; **PDBTitle:** ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly

29	c1vj0B_	Alignment	not modelled	61.4	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase, zinc-containing; **PDBTitle:** crystal structure of alcohol dehydrogenase (tm0436) from thermotoga2 maritima at 2.00 a resolution
30	c1cdoB_	Alignment	not modelled	60.0	36	**PDB header:**oxidoreductase (ch-oh(d)-nad(a)) **Chain:** B: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc
31	c2dphA_	Alignment	not modelled	59.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formaldehyde dismutase; **PDBTitle:** crystal structure of formaldehyde dismutase
32	c1ma0B_	Alignment	not modelled	58.7	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione-dependent formaldehyde dehydrogenase; **PDBTitle:** ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid
33	c3uogB_	Alignment	not modelled	58.5	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021
34	d1pl8a1	Alignment	not modelled	56.9	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
35	c2dfvB_	Alignment	not modelled	55.3	45	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable l-threonine 3-dehydrogenase; **PDBTitle:** hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii
36	d2eyqa1	Alignment	not modelled	54.9	15	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
37	c1uufA_	Alignment	not modelled	54.7	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**zinc-type alcohol dehydrogenase-like protein **PDBTitle:** crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk
38	c3cosD_	Alignment	not modelled	53.8	39	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 4; **PDBTitle:** crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn
39	c1p0fA_	Alignment	not modelled	51.7	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp
40	d1piwa1	Alignment	not modelled	51.7	33	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
41	c1hf3A_	Alignment	not modelled	51.3	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase e chain; **PDBTitle:** atomic x-ray structure of liver alcohol dehydrogenase2 containing cadmium and a hydroxide adduct to nadh
42	c3b70A_	Alignment	not modelled	46.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl reductase; **PDBTitle:** crystal structure of aspergillus terreus trans-acting lovastatin2 polyketide enoyl reductase (lovc) with bound nadp
43	d2vnud3	Alignment	not modelled	44.2	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
44	c2cdaA_	Alignment	not modelled	41.6	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose dehydrogenase; **PDBTitle:** sulfolobus solfataricus glucose dehydrogenase 1 in complex2 with nadp
45	c2h6eA_	Alignment	not modelled	40.8	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arabinose 1-dehydrogenase; **PDBTitle:** crystal structure of the d-arabinose dehydrogenase from sulfolobus2 solfataricus
46	d2z1ca1	Alignment	not modelled	40.6	37	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
47	d1kola1	Alignment	not modelled	39.6	38	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
48	d1p0fa1	Alignment	not modelled	37.4	21	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
49	d1x82a_	Alignment	not modelled	36.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
50	c3ip1C_	Alignment	not modelled	30.4	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**alcohol dehydrogenase, zinc-containing; **PDBTitle:** structure of putative alcohol dehydrogenase (tm_042) from thermotoga2 maritima
51	c2fg0B_	Alignment	not modelled	29.7	26	**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
52	d1iuza_	Alignment	not modelled	29.0	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
53	d1j3pa_	Alignment	not modelled	28.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
						PDB header:oxidoreductase

54	c2j8zA_	Alignment	not modelled	26.3	30	**Chain:** A: **PDB Molecule:**quinone oxidoreductase; **PDBTitle:** crystal structure of human p53 inducible oxidoreductase (2 tp53i3,pig3)
55	c2vnuD_	Alignment	not modelled	26.1	27	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
56	c1n9gF_	Alignment	not modelled	25.4	30	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** mitochondrial 2-enoyl thioester reductase etr1p/etr2p2 heterodimer from candida tropicalis
57	c3n2bD_	Alignment	not modelled	23.4	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
58	d1uika1	Alignment	not modelled	23.2	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
59	d1dgwa_	Alignment	not modelled	22.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
60	d2ot2a1	Alignment	not modelled	21.6	24	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
61	c2c0cB_	Alignment	not modelled	21.1	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**zinc binding alcohol dehydrogenase, domain **PDBTitle:** structure of the mgc45594 gene product
62	c3npfB_	Alignment	not modelled	20.2	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
63	d1jt8a_	Alignment	not modelled	17.7	40	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
64	c3h41A_	Alignment	not modelled	16.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
65	d2d6fa1	Alignment	not modelled	16.7	30	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
66	c2l55A_	Alignment	not modelled	16.3	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
67	d1knwa1	Alignment	not modelled	15.1	23	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
68	c2kijA_	Alignment	not modelled	15.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
69	c3gt2A_	Alignment	not modelled	14.4	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
70	c3d3rA_	Alignment	not modelled	14.2	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
71	c3gazA_	Alignment	not modelled	13.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase superfamily protein; **PDBTitle:** crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans
72	d2oyza1	Alignment	not modelled	13.8	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
73	d1gppa_	Alignment	not modelled	13.5	23	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
74	d1g7sa1	Alignment	not modelled	13.5	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
75	d1xa0a1	Alignment	not modelled	13.3	17	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
76	c3gjbA_	Alignment	not modelled	13.3	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
77	d1oe1a2	Alignment	not modelled	12.8	42	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
78	d1mzya2	Alignment	not modelled	12.8	58	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
79	c2xivA_	Alignment	not modelled	12.6	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
						Fold:PUA domain-like

80	d1zcea1	Alignment	not modelled	12.6	40	**Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
81	c1dgsB_	Alignment	not modelled	12.6	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
82	d2evra2	Alignment	not modelled	12.6	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
83	d2jfga2	Alignment	not modelled	12.5	27	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
84	c3pjyB_	Alignment	not modelled	12.3	29	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
85	d3d3ra1	Alignment	not modelled	12.2	20	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
86	d1u0la1	Alignment	not modelled	12.1	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
87	c2k1gA_	Alignment	not modelled	12.1	28	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
88	d1smxa_	Alignment	not modelled	12.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
89	c2fqpD_	Alignment	not modelled	12.0	9	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hypothetical protein bp2299; **PDBTitle:** crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
90	d2gbsa1	Alignment	not modelled	11.8	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
91	c3anuA_	Alignment	not modelled	11.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of d-serine dehydratase from chicken kidney
92	d1uija1	Alignment	not modelled	11.6	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
93	c2e4fA_	Alignment	not modelled	11.2	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**g protein-activated inward rectifier potassium channel 2; **PDBTitle:** crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2
94	d1xnea_	Alignment	not modelled	11.1	64	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
95	c1qorA_	Alignment	not modelled	11.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinone oxidoreductase; **PDBTitle:** crystal structure of escherichia coli quinone2 oxidoreductase complexed with nadph
96	c3pbiA_	Alignment	not modelled	10.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
97	c3kgzA_	Alignment	not modelled	10.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
98	d1rc6a_	Alignment	not modelled	10.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
99	d1e2wa2	Alignment	not modelled	10.4	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain