Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFI2
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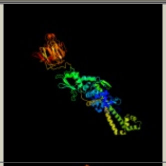
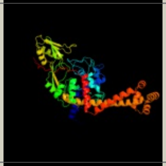
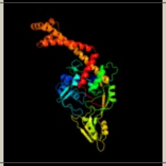
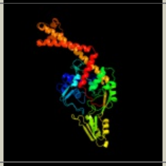
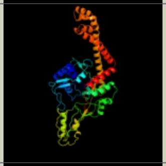
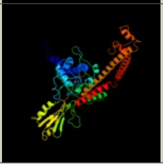
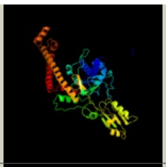
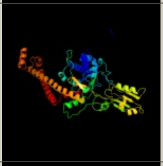
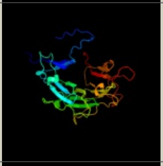
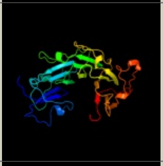
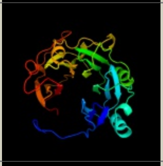
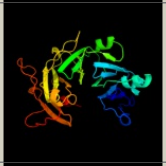
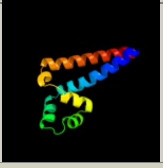
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zvuA_	Alignment		100.0	99	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
2	c2xcsD_	Alignment		100.0	45	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
3	c2xkjE_	Alignment		100.0	67	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**topoisomerase iv; **PDBTitle:** crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate)
4	c2wl2B_	Alignment		100.0	46	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
5	c3ifzA_	Alignment		100.0	41	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
6	d1ab4a_	Alignment		100.0	47	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
7	c2xcqA_	Alignment		100.0	47	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
8	c3ilwA_	Alignment		100.0	41	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
9	c2inrA_	Alignment		100.0	42	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
10	c2novD_	Alignment		100.0	42	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
11	c3qx3B_	Alignment		100.0	22	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide

12	c1bjtA_	Alignment		100.0	23	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
13	d1bjta_	Alignment		100.0	23	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
14	c3l6vA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the xanthomonas campestris gyrase a c-2 terminal domain
15	d1wp5a_	Alignment		100.0	15	**Fold:**6-bladed beta-propeller **Superfamily:**GyrA/ParC C-terminal domain-like **Family:**GyrA/ParC C-terminal domain-like
16	c1zvtA_	Alignment		100.0	100	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the e. coli parc c-terminal domain
17	c1zi0A_	Alignment		100.0	18	**PDB header:**isomerase, dna bindng protein **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** a superhelical spiral in escherichia coli dna gyrase a c-2 terminal domain imparts unidirectional supercoiling bias
18	d1suua_	Alignment		100.0	16	**Fold:**6-bladed beta-propeller **Superfamily:**GyrA/ParC C-terminal domain-like **Family:**GyrA/ParC C-terminal domain-like
19	c3no0B_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** aquifex aeolicus type iia topoisomerase c-terminal domain
20	d1x75a1	Alignment		99.9	48	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
21	c3ku8A_	Alignment	not modelled	99.9	48	**PDB header:**toxin/isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** ccdbvfi:gyra14ec
22	c1t3jA_	Alignment	not modelled	91.6	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
23	c3fokH_	Alignment	not modelled	63.4	23	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
24	c2qjhH_	Alignment	not modelled	47.9	11	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
25	c1c9lA_	Alignment	not modelled	44.7	10	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
26	c3a7pB_	Alignment	not modelled	44.7	17	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
27	d2v8qb1	Alignment	not modelled	43.3	28	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
28	c1xi4D_	Alignment	not modelled	41.4	10	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**clathrin heavy chain; **PDBTitle:** clathrin d6 coat

29	c2oajA_	Alignment	not modelled	40.4	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
30	d1q1ha_	Alignment	not modelled	38.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
31	c1q1hA_	Alignment	not modelled	38.6	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
32	d1iwpa_	Alignment	not modelled	37.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
33	d1ivsa1	Alignment	not modelled	34.4	23	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
34	c1bpoA_	Alignment	not modelled	33.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (clathrin); **PDBTitle:** clathrin heavy-chain terminal domain and linker
35	c3gndC_	Alignment	not modelled	33.0	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
36	c1u0iA_	Alignment	not modelled	33.0	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
37	c2q6tB_	Alignment	not modelled	32.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
38	d2qrdb1	Alignment	not modelled	32.4	27	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
39	c2vyeA_	Alignment	not modelled	31.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
40	d2c6ya1	Alignment	not modelled	28.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
41	c1ik9B_	Alignment	not modelled	28.6	12	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
42	c2pqaB_	Alignment	not modelled	28.4	33	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
43	c3ushB_	Alignment	not modelled	25.9	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
44	d1ji6a1	Alignment	not modelled	25.7	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
45	d1b4ua_	Alignment	not modelled	25.6	18	**Fold:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Superfamily:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Family:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB
46	d2ajfa1	Alignment	not modelled	25.6	18	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
47	d1a6qa1	Alignment	not modelled	25.2	21	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
48	c2zezC_	Alignment	not modelled	25.1	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**s-layer associated multidomain endoglucanase; **PDBTitle:** family 16 carbohydrate binding module-2
49	d2pi2e1	Alignment	not modelled	25.0	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
50	c1deqF_	Alignment	not modelled	24.1	16	**PDB header:** **PDB COMPND:**
51	d1utca2	Alignment	not modelled	23.5	10	**Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain
52	d1wi9a_	Alignment	not modelled	23.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
53	c1n73C_	Alignment	not modelled	22.9	10	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
54	c3dm0A_	Alignment	not modelled	22.1	13	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
						PDB header:signaling protein

55	c3afcB_	Alignment	not modelled	21.9	13	**Chain:** B: **PDB Molecule:**semaphorin-6a; **PDBTitle:** mouse semaphorin 6a extracellular domain
56	c3lssA_	Alignment	not modelled	21.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
57	c3icgD_	Alignment	not modelled	21.3	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
58	d1a06a_	Alignment	not modelled	21.2	25	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
59	c3a7mA_	Alignment	not modelled	20.6	20	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
60	c2hpcF_	Alignment	not modelled	20.2	19	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
61	c2r60A_	Alignment	not modelled	20.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
62	c2xzrA_	Alignment	not modelled	20.1	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
63	c2jjmH_	Alignment	not modelled	19.9	26	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
64	d1k32a3	Alignment	not modelled	19.8	9	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
65	c2dfdD_	Alignment	not modelled	19.6	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
66	d1n0ua3	Alignment	not modelled	19.4	26	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
67	c3al8B_	Alignment	not modelled	19.3	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**plexin-a2; **PDBTitle:** plexin a2 / semaphorin 6a complex
68	d2a84a1	Alignment	not modelled	19.3	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
69	c1xp4C_	Alignment	not modelled	19.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**d-alanyl-d-alanine carboxypeptidase; **PDBTitle:** crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae
70	c2jesG_	Alignment	not modelled	18.9	10	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**portal protein; **PDBTitle:** portal protein from bacteriophage spp1
71	c2pwzG_	Alignment	not modelled	18.6	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase
72	c1tvfA_	Alignment	not modelled	18.2	14	**PDB header:**penicillin binding **Chain:** A: **PDB Molecule:**penicillin binding protein 4; **PDBTitle:** crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus
73	d1mlda2	Alignment	not modelled	17.9	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
74	c3dzcA_	Alignment	not modelled	17.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
75	d2dloa1	Alignment	not modelled	17.7	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
76	d1xata_	Alignment	not modelled	16.7	9	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
77	d1egwa_	Alignment	not modelled	16.4	8	**Fold:**SRF-like **Superfamily:**SRF-like **Family:**SRF-like
78	d1qpoa1	Alignment	not modelled	16.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
79	c2paxA_	Alignment	not modelled	16.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(adp-ribose) polymerase; **PDBTitle:** the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide
80	d1flca2	Alignment	not modelled	16.1	28	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1
						PDB header:hydrolase **Chain:** B: **PDB Molecule:**probable manganase-dependent

81	c3l31B_	Alignment	not modelled	16.1	17	inorganic **PDBTitle:** crystal structure of the cbs and drtgg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
82	c1mldA_	Alignment	not modelled	16.0	18	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
83	d2g0da1	Alignment	not modelled	15.9	14	**Fold:**alpha/alpha toroid **Superfamily:**LanC-like **Family:**LanC-like
84	d1j36a_	Alignment	not modelled	15.9	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
85	c3al9B_	Alignment	not modelled	15.7	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**plexin-a2; **PDBTitle:** mouse plexin a2 extracellular domain
86	c3idwA_	Alignment	not modelled	15.6	13	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
87	c1dpuA_	Alignment	not modelled	15.1	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
88	d1dpua_	Alignment	not modelled	15.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
89	c3oktA_	Alignment	not modelled	15.0	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-a2; **PDBTitle:** mouse plexin a2, extracellular domains 1-4
90	d1rp3a2	Alignment	not modelled	14.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
91	d1y0ua_	Alignment	not modelled	14.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
92	c3okyA_	Alignment	not modelled	14.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-a2; **PDBTitle:** plexin a2 in complex with semaphorin 6a
93	c1flcA_	Alignment	not modelled	14.3	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haemagglutinin-esterase-fusion glycoprotein; **PDBTitle:** x-ray structure of the haemagglutinin-esterase-fusion glycoprotein of2 influenza c virus
94	c2gejA_	Alignment	not modelled	14.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
95	d1ku7a_	Alignment	not modelled	14.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
96	c3c4vB_	Alignment	not modelled	14.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
97	c2p9mD_	Alignment	not modelled	14.0	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
98	d1mi8a_	Alignment	not modelled	13.8	18	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
99	d1dlca1	Alignment	not modelled	13.7	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain