Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P00936
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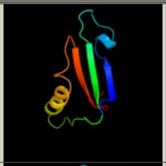
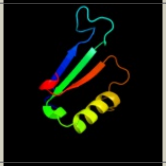
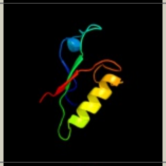
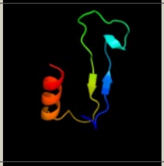
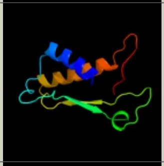
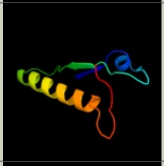
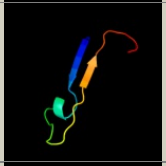
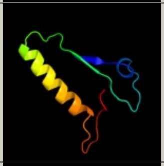
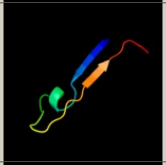
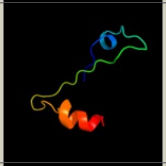
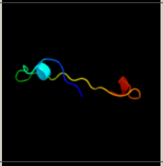
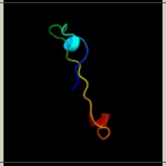
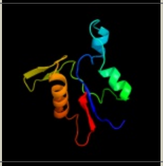
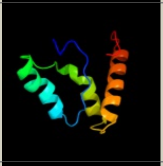
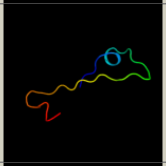
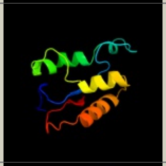
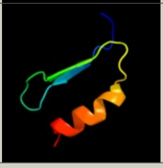
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rffA_	Alignment		94.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
2	d1ylqa1	Alignment		93.6	16	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
3	d1wota_	Alignment		93.6	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
4	d1no5a_	Alignment		93.1	28	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
5	c3k7dA_	Alignment		91.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenylyltransferase
6	c1v4aA_	Alignment		91.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenylyltransferase
7	d1knya2	Alignment		89.8	13	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
8	d1v4aa2	Alignment		85.7	15	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GlnE-like domain
9	c1knyA_	Alignment		76.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kanamycin nucleotidyltransferase; **PDBTitle:** kanamycin nucleotidyltransferase
10	d2q66a2	Alignment		75.2	20	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
11	d1mzja2	Alignment		73.1	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like

12	d1ub7a2	Alignment		72.6	17	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
13	d1u6ea2	Alignment		70.6	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
14	c1q78A_	Alignment		70.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase alpha; **PDBTitle:** crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride
15	d1q79a2	Alignment		68.7	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
16	d1hnja2	Alignment		66.3	25	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
17	c1cmlA_	Alignment		64.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (chalcone synthase); **PDBTitle:** chalcone synthase from alfalfa complexed with malonyl-coa
18	d1u0ma2	Alignment		63.6	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
19	c3c66B_	Alignment		59.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
20	c1u0mA_	Alignment		52.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative polyketide synthase; **PDBTitle:** crystal structure of 1,3,6,8-tetrahydroxynaphthalene synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
21	d1gp1a_	Alignment		51.4	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
22	c3u80A_	Alignment	not modelled	51.1	32	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii; **PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
23	d1t1ra2	Alignment	not modelled	50.8	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
24	c3a5qA_	Alignment	not modelled	50.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**benzalacetone synthase; **PDBTitle:** benzalacetone synthase from rheum palmatum
25	c3n8kG_	Alignment	not modelled	49.4	25	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
26	d2f8aa1	Alignment	not modelled	48.5	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
27	c2uygF_	Alignment	not modelled	48.1	29	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus

28	d1h05a_	Alignment	not modelled	44.7	23	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
29	d1gtza_	Alignment	not modelled	42.4	21	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
30	c3nybA_	Alignment	not modelled	41.2	27	**PDB header:**transferase/rna binding protein **Chain:** A: **PDB Molecule:**poly(a) rna polymerase protein 2; **PDBTitle:** structure and function of the polymerase core of tramp, a rna2 surveillance complex
31	d1bi5a2	Alignment	not modelled	39.0	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
32	c2r37A_	Alignment	not modelled	38.5	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
33	c3o6xC_	Alignment	not modelled	37.8	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
34	c1k5hB_	Alignment	not modelled	37.4	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
35	c3au9A_	Alignment	not modelled	36.8	46	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
36	d1xhna1	Alignment	not modelled	36.6	31	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
37	d1fsfa_	Alignment	not modelled	34.8	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
38	d1ee0a2	Alignment	not modelled	33.0	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
39	d1q0qa2	Alignment	not modelled	32.4	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	c2h84A_	Alignment	not modelled	31.5	21	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**steely1; **PDBTitle:** crystal structure of the c-terminal type iii polyketide synthase (pks2 iii) domain of 'steely1' (a type i/iii pks hybrid from dictyostelium)
41	c3oitB_	Alignment	not modelled	31.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** crystal structure of curcuminoid synthase cus from oryza sativa
42	c2i6hA_	Alignment	not modelled	31.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0120; **PDBTitle:** structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
43	d2i6ha1	Alignment	not modelled	31.2	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Atu0120-like
44	c2he3A_	Alignment	not modelled	30.1	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
45	c2p0uB_	Alignment	not modelled	29.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stilbenecarboxylate synthase 2; **PDBTitle:** crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
46	c3jz0B_	Alignment	not modelled	28.8	18	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**lincosamide nucleotidyltransferase; **PDBTitle:** linb complexed with clindamycin and ampcpp
47	d1uqra_	Alignment	not modelled	28.6	27	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
48	c2obiA_	Alignment	not modelled	28.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phospholipid hydroperoxide glutathione **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpx4)
49	c2eghA_	Alignment	not modelled	27.8	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
50	c2p5qA_	Alignment	not modelled	26.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
51	d1u0ua2	Alignment	not modelled	26.6	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
52	c1sz1A_	Alignment	not modelled	26.3	15	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
						PDB header:oxidoreductase

53	c2p31B_	Alignment	not modelled	26.2	16	**Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
54	c2x3eA_	Alignment	not modelled	25.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase iii, fabh from pseudomonas aeruginosa pao1
55	c1ee0A_	Alignment	not modelled	25.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-pyrone synthase; **PDBTitle:** 2-pyrone synthase complexed with acetoacetyl-coa
56	c2jcyA_	Alignment	not modelled	25.0	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
57	d1r0ka2	Alignment	not modelled	24.9	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
58	d1rh2a_	Alignment	not modelled	24.9	31	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
59	d1thga_	Alignment	not modelled	24.6	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
60	d1teda_	Alignment	not modelled	24.6	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
61	c3cynC_	Alignment	not modelled	24.2	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
62	c3hn6D_	Alignment	not modelled	24.2	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
63	c3hczA_	Alignment	not modelled	23.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
64	c3l76B_	Alignment	not modelled	22.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
65	c2kw7A_	Alignment	not modelled	22.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
66	c3ng0A_	Alignment	not modelled	21.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
67	c1w17A_	Alignment	not modelled	21.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
68	d1xdpa1	Alignment	not modelled	21.2	73	**Fold:**Spectrin repeat-like **Superfamily:**PPK N-terminal domain-like **Family:**PPK N-terminal domain-like
69	d1z21a1	Alignment	not modelled	21.0	47	**Fold:**Type III secretion system domain **Superfamily:**Type III secretion system domain **Family:**YopR Core
70	c3fkyD_	Alignment	not modelled	20.8	12	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
71	d1qo7a_	Alignment	not modelled	20.6	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
72	c1zowB_	Alignment	not modelled	20.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase iii; **PDBTitle:** crystal structure of s. aureus fabh, beta-ketoacyl carrier protein2 synthase iii
73	d2h7ca1	Alignment	not modelled	20.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
74	c1r0lD_	Alignment	not modelled	19.9	46	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
75	d1ne7a_	Alignment	not modelled	19.6	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
76	c3dwvB_	Alignment	not modelled	19.6	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
77	c1icfB_	Alignment	not modelled	19.5	63	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cathepsin l: light chain); **PDBTitle:** crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin l
						PDB header:oxidoreductase

78	c3a14B_	Alignment	not modelled	19.2	31	**Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
79	c2djgC_	Alignment	not modelled	19.0	38	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dipeptidyl-peptidase 1; **PDBTitle:** re-determination of the native structure of human dipeptidyl peptidase2 i (cathepsin c)
80	c3il3A_	Alignment	not modelled	19.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of haemophilus influenzae fabh
81	c2v1mA_	Alignment	not modelled	18.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
82	c2qm2B_	Alignment	not modelled	18.7	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hopj type iii effector protein; **PDBTitle:** putative hopj type iii effector protein from vibrio parahaemolyticus
83	c3eytA_	Alignment	not modelled	18.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
84	c1xetD_	Alignment	not modelled	18.1	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dihydropinosylvin synthase; **PDBTitle:** crystal structure of stilbene synthase from pinus2 sylvestris, complexed with methylmalonyl coa
85	d1qhma_	Alignment	not modelled	18.0	7	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
86	d1z5ye1	Alignment	not modelled	17.9	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
87	c3pw3E_	Alignment	not modelled	17.9	38	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**aminopeptidase c; **PDBTitle:** crystal structure of a cysteine protease (bdi_2249) from2 parabacteroides distasonis atcc 8503 at 2.23 a resolution
88	d1gqoa_	Alignment	not modelled	17.8	27	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
89	c3lwzC_	Alignment	not modelled	17.7	32	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
90	c3se4B_	Alignment	not modelled	17.3	17	**PDB header:**immune system receptor **Chain:** B: **PDB Molecule:**interferon omega-1; **PDBTitle:** human ifnw-ifnar ternary complex
91	c3ndjA_	Alignment	not modelled	17.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
92	c3aleB_	Alignment	not modelled	16.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**os07g0271500 protein; **PDBTitle:** a type iii polyketide synthase that produces diarylheptanoid
93	d1b5la_	Alignment	not modelled	16.4	16	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
94	c2rliA_	Alignment	not modelled	16.2	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
95	c2d3aJ_	Alignment	not modelled	16.1	18	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
96	d1thea_	Alignment	not modelled	16.1	63	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
97	c2rcnA_	Alignment	not modelled	15.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
98	d1wu3i_	Alignment	not modelled	15.9	31	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
99	d1u0la2	Alignment	not modelled	15.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins