
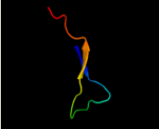
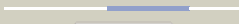







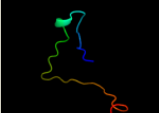

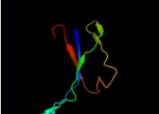



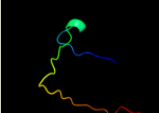

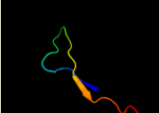




# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PJW6
Date	Fri May 25 09:28:59 BST 2012
Unique Job ID	2896c7f53cbc3de2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1gtra1</a>	 Alignment		31.4	32	<b>Fold:</b> Ribosomal protein L25-like <b>Superfamily:</b> Ribosomal protein L25-like <b>Family:</b> Gln-tRNA synthetase (GlnRS), C-terminal (anti codon-binding) domain
2	<a href="#">d1sr8a_</a>	 Alignment		23.1	21	<b>Fold:</b> CbiD-like <b>Superfamily:</b> CbiD-like <b>Family:</b> CbiD-like
3	<a href="#">d2zcta1</a>	 Alignment		21.3	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
4	<a href="#">d1z5ye1</a>	 Alignment		19.6	38	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
5	<a href="#">d2v3ia1</a>	 Alignment		19.5	24	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
6	<a href="#">d1gpia_</a>	 Alignment		19.5	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
7	<a href="#">d1k3ia1</a>	 Alignment		19.4	20	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
8	<a href="#">c2rfyB_</a>	 Alignment		18.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
9	<a href="#">d1q9ha_</a>	 Alignment		18.9	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
10	<a href="#">c1exdA_</a>	 Alignment		17.6	32	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
11	<a href="#">c3k44D_</a>	 Alignment		17.1	17	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> purine-rich binding protein-alpha, isoform b; <b>PDBTitle:</b> crystal structure of drosophila melanogaster pur-alpha

12	<a href="#">c3ia1A_</a>	Alignment		16.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thio-disulfide isomerase/thioredoxin; <b>PDBTitle:</b> crystal structure of thio-disulfide isomerase from thermus2 thermophilus
13	<a href="#">d2b5xa1</a>	Alignment		16.7	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
14	<a href="#">c3fkfC_</a>	Alignment		16.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
15	<a href="#">c3razA_</a>	Alignment		14.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
16	<a href="#">c1yycA_</a>	Alignment		14.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative late embryogenesis abundant protein; <b>PDBTitle:</b> solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
17	<a href="#">c3ewlA_</a>	Alignment		14.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein bf1870; <b>PDBTitle:</b> crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
18	<a href="#">d2e9xb2</a>	Alignment		13.4	40	<b>Fold:</b> GINS/PriA/YqbF domain <b>Superfamily:</b> PriA/YqbF domain <b>Family:</b> PSF2 N-terminal domain-like
19	<a href="#">c215oA_</a>	Alignment		12.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution structure of a putative thioredoxin from neisseria2 meningitidis
20	<a href="#">c3eytA_</a>	Alignment		12.6	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein spoa0173; <b>PDBTitle:</b> crystal structure of thioredoxin-like superfamily protein spoa0173
21	<a href="#">d1hdfa_</a>	Alignment	not modelled	12.6	23	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
22	<a href="#">c2hz7A_</a>	Alignment	not modelled	12.2	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
23	<a href="#">d1gefa_</a>	Alignment	not modelled	12.1	14	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Hjc-like
24	<a href="#">c3eurA_</a>	Alignment	not modelled	12.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
25	<a href="#">d1knga_</a>	Alignment	not modelled	12.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
26	<a href="#">d2fy6a1</a>	Alignment	not modelled	11.9	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
27	<a href="#">c2lrta_</a>	Alignment	not modelled	11.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the uncharacterized thioredoxin-like protein2 bvu_1432 from bacteroides vulgatus
28	<a href="#">c3hdca_</a>	Alignment	not modelled	11.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from geobacter2 metallireducens
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3kh7A_</a>	Alignment	not modelled	11.4	38	<b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
30	<a href="#">d1rubx4</a>	Alignment	not modelled	11.3	44	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
31	<a href="#">d1hvcA_</a>	Alignment	not modelled	11.0	29	<b>Fold:</b> Acid proteases <b>Superfamily:</b> Acid proteases <b>Family:</b> Retroviral protease (retropepsin)
32	<a href="#">c2lrnA_</a>	Alignment	not modelled	10.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> solution structure of a thiol:disulfide interchange protein from2 bacteroides sp.
33	<a href="#">d1eg1a_</a>	Alignment	not modelled	10.7	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
34	<a href="#">d1u2ma_</a>	Alignment	not modelled	10.7	17	<b>Fold:</b> OmpH-like <b>Superfamily:</b> OmpH-like <b>Family:</b> OmpH-like
35	<a href="#">d1qmva_</a>	Alignment	not modelled	10.7	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
36	<a href="#">c1uv7A_</a>	Alignment	not modelled	10.6	36	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein m; <b>PDBTitle:</b> periplasmic domain of epsm from vibrio cholerae
37	<a href="#">d1uv7a_</a>	Alignment	not modelled	10.6	36	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> General secretion pathway protein M, EpsM <b>Family:</b> General secretion pathway protein M, EpsM
38	<a href="#">c3ztB_</a>	Alignment	not modelled	10.6	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin peroxidase; <b>PDBTitle:</b> crystal structure of decameric form of peroxiredoxin i from2 schistosoma mansoni
39	<a href="#">d1n8ja_</a>	Alignment	not modelled	10.1	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
40	<a href="#">c3kv1A_</a>	Alignment	not modelled	9.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor; <b>PDBTitle:</b> crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
41	<a href="#">c3kcmC_</a>	Alignment	not modelled	9.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from geobacter2 metallireducens
42	<a href="#">c4evmA_</a>	Alignment	not modelled	9.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of soluble domain of membrane-anchored2 thioredoxin family protein from streptococcus pneumoniae strain3 canada mdr_19a
43	<a href="#">c3or5A_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein, thioredoxin family <b>PDBTitle:</b> crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum t5
44	<a href="#">d2owna2</a>	Alignment	not modelled	9.1	36	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
45	<a href="#">d1ib8a1</a>	Alignment	not modelled	9.1	11	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> YhbC-like, C-terminal domain <b>Family:</b> YhbC-like, C-terminal domain
46	<a href="#">d1zzoa1</a>	Alignment	not modelled	8.9	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
47	<a href="#">c2ls5A_</a>	Alignment	not modelled	8.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of a putative protein disulfide isomerase from2 bacteroides thetaiotaomicron
48	<a href="#">c3hn5B_</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative exported protein bf0290; <b>PDBTitle:</b> crystal structure of bf0290 (yp_210027.1) from bacteroides fragilis2 nctc 9343 at 1.70 a resolution
49	<a href="#">c2xdhA_</a>	Alignment	not modelled	8.7	36	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cohesin; <b>PDBTitle:</b> non-cellulosomal cohesin from the hyperthermophilic2 archaeon archaeoglobus fulgidus
50	<a href="#">d1sgua_</a>	Alignment	not modelled	8.5	29	<b>Fold:</b> Acid proteases <b>Superfamily:</b> Acid proteases <b>Family:</b> Retroviral protease (retropepsin)
51	<a href="#">c3erwG_</a>	Alignment	not modelled	8.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation thiol-disulfide oxidoreductase a; <b>PDBTitle:</b> crystal structure of stoa from bacillus subtilis
52	<a href="#">d1ojja_</a>	Alignment	not modelled	8.4	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
53	<a href="#">d1xo8a_</a>	Alignment	not modelled	8.4	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> LEA14-like <b>Family:</b> LEA14-like
54	<a href="#">d2essa2</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-ACP thioesterase-like
55	<a href="#">c3ha9A_</a>	Alignment	not modelled	7.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized thioredoxin-like protein; <b>PDBTitle:</b> the 1.7a crystal structure of a thioredoxin-like protein

						from2 aeropyrum pernix
56	<a href="#">c3ohnA</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane usher protein fimd; <b>PDBTitle:</b> crystal structure of the fimd translocation domain
57	<a href="#">dlprxa</a>	Alignment	not modelled	7.6	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
58	<a href="#">dl1u4a</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
59	<a href="#">dlxcca</a>	Alignment	not modelled	7.5	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
60	<a href="#">c2v2gC</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> peroxiredoxin 6; <b>PDBTitle:</b> crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
61	<a href="#">c3cmiA</a>	Alignment	not modelled	7.3	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin hyr1; <b>PDBTitle:</b> crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
62	<a href="#">c3lorB</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol-disulfide isomerase and thioredoxins; <b>PDBTitle:</b> the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
63	<a href="#">c3fw2A</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
64	<a href="#">c2lcmA</a>	Alignment	not modelled	7.2	57	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> voltage-dependent n-type calcium channel subunit alpha-1b; <b>PDBTitle:</b> nmr structure of s3-4 peptide
65	<a href="#">c2ownA</a>	Alignment	not modelled	7.1	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oleoyl-[acyl-carrier protein] thioesterase; <b>PDBTitle:</b> crystal structure of oleoyl thioesterase (putative) (np_784467.1) from2 lactobacillus plantarum at 2.00 a resolution
66	<a href="#">dluula</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
67	<a href="#">dljfua</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
68	<a href="#">dlst9a</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
69	<a href="#">c2zt9E</a>	Alignment	not modelled	6.9	53	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
70	<a href="#">c3gf6B</a>	Alignment	not modelled	6.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized bacterial lipoprotein; <b>PDBTitle:</b> crystal structure of a bacterial lipoprotein (bt_1233) from2 bacteroides thetaiotaomicron vpi-5482 at 1.69 a resolution
71	<a href="#">c3lwaA</a>	Alignment	not modelled	6.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
72	<a href="#">d3efba1</a>	Alignment	not modelled	6.4	18	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> SorC sugar-binding domain-like
73	<a href="#">c2e9xF</a>	Alignment	not modelled	6.3	40	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> dna replication complex gins protein psf2; <b>PDBTitle:</b> the crystal structure of human gins core complex
74	<a href="#">c3nzeB</a>	Alignment	not modelled	6.2	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator, sugar-binding family; <b>PDBTitle:</b> the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
75	<a href="#">d2f8aa1</a>	Alignment	not modelled	6.2	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
76	<a href="#">c2he3A</a>	Alignment	not modelled	6.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 2; <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gp2)
77	<a href="#">d3ovwa</a>	Alignment	not modelled	6.1	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
78	<a href="#">c3dvvB</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
79	<a href="#">c3hczA</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
80	<a href="#">d3ecga1</a>	Alignment	not modelled	5.9	24	<b>Fold:</b> Acid proteases <b>Superfamily:</b> Acid proteases <b>Family:</b> Retroviral protease (retropepsin)
81	<a href="#">dlwe0a1</a>	Alignment	not modelled	5.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like

						<b>Family:</b> Glutathione peroxidase-like
82	<a href="#">d2rcrh2</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
83	<a href="#">d2fzpa1</a>	Alignment	not modelled	5.6	71	<b>Fold:</b> NRDP1 C-terminal domain-like <b>Superfamily:</b> NRDP1 C-terminal domain-like <b>Family:</b> USP8 interacting domain
84	<a href="#">d1d7ka1</a>	Alignment	not modelled	5.6	32	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
85	<a href="#">c2p5qA_</a>	Alignment	not modelled	5.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 5; <b>PDBTitle:</b> crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
86	<a href="#">c2r1fB_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> predicted aminodeoxychorismate lyase; <b>PDBTitle:</b> crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli
87	<a href="#">d1jv2a3</a>	Alignment	not modelled	5.5	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Integrin domains <b>Family:</b> Integrin domains
88	<a href="#">c2ywiA_</a>	Alignment	not modelled	5.5	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
89	<a href="#">c2b1kA_</a>	Alignment	not modelled	5.4	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein
90	<a href="#">d1f3ta1</a>	Alignment	not modelled	5.4	31	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
91	<a href="#">c2c0dA_</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin peroxidase 2; <b>PDBTitle:</b> structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
92	<a href="#">d1njbb1</a>	Alignment	not modelled	5.3	32	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
93	<a href="#">d1y5oa1</a>	Alignment	not modelled	5.3	13	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> TFIIH domain
94	<a href="#">d1li4a2</a>	Alignment	not modelled	5.1	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
95	<a href="#">c3f9uA_</a>	Alignment	not modelled	5.0	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported cytochrome c biogenesis-related protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
96	<a href="#">d1bdqa_</a>	Alignment	not modelled	5.0	29	<b>Fold:</b> Acid proteases <b>Superfamily:</b> Acid proteases <b>Family:</b> Retroviral protease (retropepsin)