Phyre²

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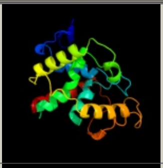
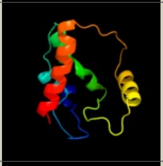
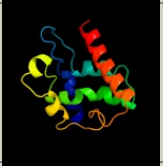
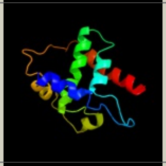
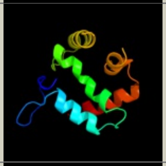
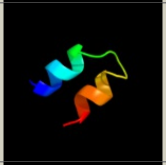
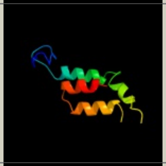
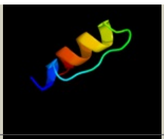
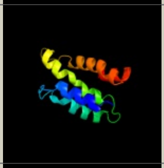
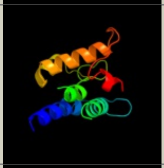
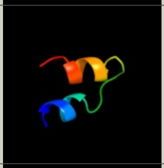
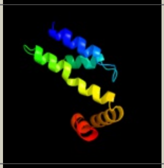
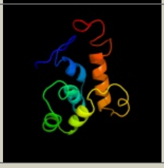
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gz4a1	Alignment		100.0	29	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
2	c3mzoA_	Alignment		99.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lin2634 protein; **PDBTitle:** crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution
3	d2paqa1	Alignment		99.2	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
4	c2cqzA_	Alignment		98.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
5	d1xx7a_	Alignment		98.8	25	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
6	d1ynba1	Alignment		98.2	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
7	c3kh1B_	Alignment		98.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
8	d3b57a1	Alignment		80.3	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
9	c2ogiA_	Alignment		76.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein sag1661; **PDBTitle:** crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
10	c2pgsA_	Alignment		73.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
11	c2o08B_	Alignment		71.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh1327 protein; **PDBTitle:** crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution

12	c3ccgA_	Alignment		70.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd superfamily hydrolase; **PDBTitle:** crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
13	d2pq7a1	Alignment		70.2	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
14	c3nr1A_	Alignment		65.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain-containing protein 3; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
15	c1vj7B_	Alignment		58.9	13	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
16	c2dqbB_	Alignment		49.5	36	**PDB header:**hydrolase, dna binding protein **Chain:** B: **PDB Molecule:**deoxyguanosinetriphosphate triphosphohydrolase, putative; **PDBTitle:** crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
17	c3m1tA_	Alignment		48.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
18	d2heka1	Alignment		47.5	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
19	d2pjqa1	Alignment		45.6	25	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
20	c3nqwB_	Alignment		42.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
21	c3hc1A_	Alignment	not modelled	41.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized hdod domain protein; **PDBTitle:** crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
22	c3u1nC_	Alignment	not modelled	40.2	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
23	d3dtoa1	Alignment	not modelled	38.3	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
24	d1vqra_	Alignment	not modelled	36.0	11	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
25	d2qgsa1	Alignment	not modelled	29.3	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
26	d1rm6c1	Alignment	not modelled	29.0	29	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
27	c2o6iA_	Alignment	not modelled	28.5	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
28	d2o6ia1	Alignment	not modelled	28.5	41	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
29	c3aqnA_	Alignment	not modelled	27.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase;

						PDBTitle: complex structure of bacterial protein (apo form ii)
30	d1n62a1	Alignment	not modelled	27.3	24	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
31	c2q14A_	Alignment	not modelled	27.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
32	d1zxia1	Alignment	not modelled	26.3	24	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
33	c3hrdH_	Alignment	not modelled	22.3	38	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
34	d3djba1	Alignment	not modelled	21.1	30	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
35	d1ffva1	Alignment	not modelled	20.6	29	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
36	c1ffuA_	Alignment	not modelled	20.4	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
37	c3memA_	Alignment	not modelled	20.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
38	d1t3qa1	Alignment	not modelled	19.5	24	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
39	c3l09B_	Alignment	not modelled	19.5	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
40	c3gw7A_	Alignment	not modelled	17.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj; **PDBTitle:** crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
41	c3skdA_	Alignment	not modelled	17.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb187; **PDBTitle:** crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
42	c1t3qD_	Alignment	not modelled	17.2	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
43	d1v97a1	Alignment	not modelled	17.0	29	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
44	d1b93a_	Alignment	not modelled	17.0	11	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
45	c3bg2A_	Alignment	not modelled	16.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
46	d1vj7a1	Alignment	not modelled	16.4	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
47	d1vmda_	Alignment	not modelled	15.8	16	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
48	c1n60D_	Alignment	not modelled	13.6	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
49	c2jo7A_	Alignment	not modelled	12.9	23	**PDB header:**surface active protein **Chain:** A: **PDB Molecule:**glycosylphosphatidylinositol-anchored merozoite **PDBTitle:** solution structure of the adhesion protein bd37 from2 babesia divergens
50	c1rm6F_	Alignment	not modelled	11.7	29	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
51	d1dgja1	Alignment	not modelled	11.5	25	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
52	c3ljvA_	Alignment	not modelled	11.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mmoq response regulator; **PDBTitle:** crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
						Fold:alpha-alpha superhelix

53	d1z2cb1	Alignment	not modelled	10.7	17	**Superfamily:**ARM repeat **Family:**Diap1 N-terninal region-like
54	d1vlba1	Alignment	not modelled	10.3	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
55	d1ei1a1	Alignment	not modelled	10.3	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
56	d1tuza_	Alignment	not modelled	9.2	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
57	c2zklA_	Alignment	not modelled	9.1	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
58	c3eu8D_	Alignment	not modelled	8.9	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucoamylase; **PDBTitle:** crystal structure of putative glucoamylase (yp_210071.1) from2 bacteroides fragilis nctc 9343 at 2.12 a resolution
59	c2lbbA_	Alignment	not modelled	8.5	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acyl coa binding protein; **PDBTitle:** solution structure of acyl coa binding protein from babesia bovis t2bo
60	c2bnxA_	Alignment	not modelled	8.4	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**diaphanous protein homolog 1; **PDBTitle:** crystal structure of the dimeric regulatory domain of mouse2 diaphaneous-related formin (drf), mdia1
61	d2bnxa1	Alignment	not modelled	8.4	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Diap1 N-terninal region-like
62	d2enda_	Alignment	not modelled	8.0	50	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
63	c1vlbA_	Alignment	not modelled	7.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
64	d1kija1	Alignment	not modelled	7.7	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
65	d1mx3a2	Alignment	not modelled	7.7	33	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
66	d1b4ua_	Alignment	not modelled	7.6	11	**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
67	c2it8A_	Alignment	not modelled	7.5	67	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**trypsin inhibitor 2; **PDBTitle:** solution structure of a linear analog of the cyclic squash2 trypsin inhibitor mcoti-ii
68	d2it8a1	Alignment	not modelled	7.5	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
69	c2copA_	Alignment	not modelled	7.4	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coenzyme a binding domain containing 6; **PDBTitle:** solution structure of rsgi ruh-040, an acbp domain from2 human cdna
70	d2ibna1	Alignment	not modelled	7.4	27	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
71	c2huoA_	Alignment	not modelled	7.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
72	d3bxda1	Alignment	not modelled	7.3	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
73	d1ivza_	Alignment	not modelled	7.0	5	**Fold:**Ferredoxin-like **Superfamily:**SEA domain **Family:**SEA domain
74	d1y8xb1	Alignment	not modelled	6.8	31	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
75	c3i7aA_	Alignment	not modelled	6.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
76	c3fnvB_	Alignment	not modelled	6.8	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**cdgsh iron sulfur domain-containing protein 2; **PDBTitle:** crystal structure of miner1: the redox-active 2fe-2s protein causative2 in wolfram syndrome 2
77	c3ojlA_	Alignment	not modelled	6.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cap5o; **PDBTitle:** native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
						PDB header:ribosome/hydrolase

78	c4a2iV_	Alignment	not modelled	6.7	11	**Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga; **PDBTitle:** cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
79	d1ha9a_	Alignment	not modelled	6.5	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
80	d1hbka_	Alignment	not modelled	6.3	11	**Fold:**Acyl-CoA binding protein-like **Superfamily:**Acyl-CoA binding protein **Family:**Acyl-CoA binding protein
81	d1dw0a_	Alignment	not modelled	6.3	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
82	c2cquA_	Alignment	not modelled	6.2	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peroxisomal d3,d2-enoyl-coa isomerase; **PDBTitle:** solution structure of rsgi ruh-045, a human acyl-coa2 binding protein
83	c3gwnA_	Alignment	not modelled	6.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-linked sulfhydryl oxidase r596; **PDBTitle:** crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
84	d2raqa1	Alignment	not modelled	6.1	23	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
85	c2po8A_	Alignment	not modelled	6.1	67	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**mcoti-ii; **PDBTitle:** the structure of a two-disulfide intermediate of mcoti-ii
86	d1hjra_	Alignment	not modelled	6.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
87	c1tg6G_	Alignment	not modelled	5.9	8	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**putative atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
88	c1m3wA_	Alignment	not modelled	5.8	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**h10h24; **PDBTitle:** crystal structure of a molecular maquette scaffold
89	c1m3wB_	Alignment	not modelled	5.8	30	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**h10h24; **PDBTitle:** crystal structure of a molecular maquette scaffold
90	c1m3wC_	Alignment	not modelled	5.8	30	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**h10h24; **PDBTitle:** crystal structure of a molecular maquette scaffold
91	c1m3wD_	Alignment	not modelled	5.8	30	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**h10h24; **PDBTitle:** crystal structure of a molecular maquette scaffold
92	d1hyoa1	Alignment	not modelled	5.7	29	**Fold:**SH3-like barrel **Superfamily:**Fumarylacetoacetate hydrolase, FAH, N-terminal domain **Family:**Fumarylacetoacetate hydrolase, FAH, N-terminal domain
93	c3kfwX_	Alignment	not modelled	5.7	12	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**uncharacterized protein; **PDBTitle:** uncharacterized protein rv0674 from mycobacterium tuberculosis
94	c1dgjA_	Alignment	not modelled	5.5	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
95	d1jroa1	Alignment	not modelled	5.4	40	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
96	c3q7hM_	Alignment	not modelled	5.4	13	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii
97	d1tg6a1	Alignment	not modelled	5.3	8	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
98	d1hb6a_	Alignment	not modelled	5.2	11	**Fold:**Acyl-CoA binding protein-like **Superfamily:**Acyl-CoA binding protein **Family:**Acyl-CoA binding protein