Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75867
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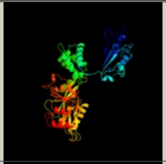
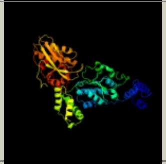
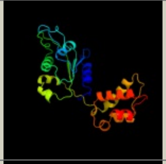
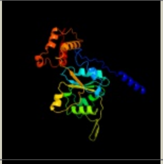
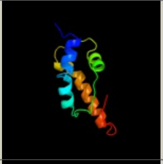
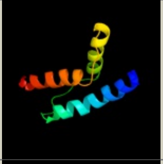
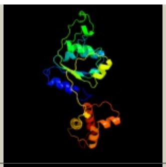
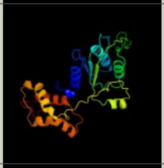
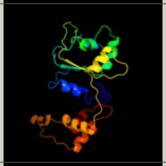
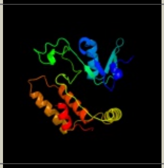
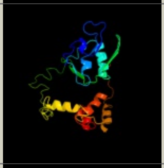
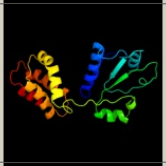
Unique Job ID	0af580f1a2cd6074

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k1jA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
2	c3m6aC_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon c-terminal domain
3	c1z0eF_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative protease la homolog type; **PDBTitle:** crystal structure of a. fulgidus lon proteolytic domain
4	d1xhka_	Alignment		100.0	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**ATP-dependent protease Lon (La), catalytic domain
5	c2x36F_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**lon protease homolog, mitochondrial; **PDBTitle:** structure of the proteolytic domain of the human2 mitochondrial lon protease
6	d1rrea_	Alignment		100.0	27	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**ATP-dependent protease Lon (La), catalytic domain
7	c1ny5A_	Alignment		99.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
8	c3dzdA_	Alignment		99.2	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
9	d1qzma_	Alignment		99.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	c1x37A_	Alignment		99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** structure of bacillus subtilis lon protease ssd domain
11	d1ny5a2	Alignment		97.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

12	c2c99A_	Alignment		97.6	12	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
13	c3pxgA_	Alignment		97.0	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
14	c1ojlF_	Alignment		96.8	15	**PDB header:**response regulator **Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
15	c1qvrB_	Alignment		96.8	14	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
16	c3f8tA_	Alignment		96.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
17	c3f9vA_	Alignment		95.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
18	c2gefA_	Alignment		94.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
19	d1r6bx2	Alignment		92.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
20	c3nbxX_	Alignment		92.1	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
21	c1r6bX_	Alignment	not modelled	91.9	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
22	d1um8a_	Alignment	not modelled	91.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
23	c3pxiB_	Alignment	not modelled	90.7	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
24	d1g8pa_	Alignment	not modelled	90.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	c3co5B_	Alignment	not modelled	88.0	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
26	c3u5zM_	Alignment	not modelled	85.8	14	**PDB header:**dna binding protein/dna **Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44; **PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
27	c3pfiB_	Alignment	not modelled	84.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate

28	c3b9pA_	Alignment	not modelled	82.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
29	c1sxjA_	Alignment	not modelled	82.5	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**activator 1 95 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
30	d1iqpa2	Alignment	not modelled	81.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
31	c1in8A_	Alignment	not modelled	81.1	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
32	d1sxjb2	Alignment	not modelled	80.7	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
33	c2r44A_	Alignment	not modelled	79.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
34	d1qvra3	Alignment	not modelled	79.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
35	c1iy2A_	Alignment	not modelled	78.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
36	c3d8bB_	Alignment	not modelled	77.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
37	d2ce7a2	Alignment	not modelled	76.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	d1ixza_	Alignment	not modelled	73.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
39	c3pvsA_	Alignment	not modelled	72.6	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
40	c2r65A_	Alignment	not modelled	68.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
41	c2z4rB_	Alignment	not modelled	68.0	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
42	d1sxjc2	Alignment	not modelled	68.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
43	d1dvoa_	Alignment	not modelled	67.0	13	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
44	d1r6bx3	Alignment	not modelled	63.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
45	c2x8aA_	Alignment	not modelled	61.5	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear valosin-containing protein-like; **PDBTitle:** human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
46	c3bosA_	Alignment	not modelled	61.1	13	**PDB header:**hydrolase regulator,dna binding protein **Chain:** A: **PDB Molecule:**putative dna replication factor; **PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
47	d2hxja1	Alignment	not modelled	56.1	9	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
48	d1qvra2	Alignment	not modelled	54.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	c2dhrC_	Alignment	not modelled	53.1	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
50	d1yvua1	Alignment	not modelled	47.3	44	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
51	c3hteC_	Alignment	not modelled	46.1	8	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
52	c3hu2C_	Alignment	not modelled	45.4	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs

53	d1njfa_	Alignment	not modelled	43.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
54	c3cf1C_	Alignment	not modelled	41.4	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
55	c1sxjE_	Alignment	not modelled	38.0	12	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
56	d1in4a2	Alignment	not modelled	34.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
57	c3pi7A_	Alignment	not modelled	33.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidoreductase; **PDBTitle:** crystal structure of a putative nadph:quinone reductase (mll3093) from2 mesorhizobium loti at 1.71 a resolution
58	d1rm6a2	Alignment	not modelled	32.8	8	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
59	c1wygA_	Alignment	not modelled	32.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
60	c2w54F_	Alignment	not modelled	30.9	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
61	d1ofha_	Alignment	not modelled	30.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
62	c2c0cB_	Alignment	not modelled	28.9	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**zinc binding alcohol dehydrogenase, domain **PDBTitle:** structure of the mgc45594 gene product
63	d1qf8a_	Alignment	not modelled	26.9	24	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
64	c2hcyD_	Alignment	not modelled	25.9	9	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 1; **PDBTitle:** yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme
65	c1wlyA_	Alignment	not modelled	25.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-haloacrylate reductase; **PDBTitle:** crystal structure of 2-haloacrylate reductase
66	c2c9kA_	Alignment	not modelled	24.3	23	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
67	d1d2na_	Alignment	not modelled	24.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	c2z5wA_	Alignment	not modelled	23.5	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bcla protein; **PDBTitle:** tbcla, a recombinant spore surface protein from bacillus anthracis
69	d1v97a5	Alignment	not modelled	23.3	14	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
70	c1wckA_	Alignment	not modelled	23.2	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**bcla protein; **PDBTitle:** crystal structure of the c-terminal domain of bcla, the2 major antigen of the exosporium of the bacillus anthracis3 spore.
71	c3eihB_	Alignment	not modelled	23.1	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
72	c2pnmA_	Alignment	not modelled	22.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of vp4 protease from infectious pancreatic necrosis2 virus (ipnv) in space group p6122
73	c2qz4A_	Alignment	not modelled	21.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
74	c1nsfA_	Alignment	not modelled	21.3	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
75	d1hiod_	Alignment	not modelled	21.3	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	c3gazA_	Alignment	not modelled	20.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase superfamily protein; **PDBTitle:** crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans
77	c1hk8A_	Alignment	not modelled	20.2	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2

						regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
78	d1hk8a_	Alignment	not modelled	20.2	28	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
79	d1sxja2	Alignment	not modelled	20.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
80	c1uufA_	Alignment	not modelled	19.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**zinc-type alcohol dehydrogenase-like protein **PDBTitle:** crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk
81	d1o75a2	Alignment	not modelled	19.3	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains
82	c2p65A_	Alignment	not modelled	19.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063; **PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
83	d1jrob2	Alignment	not modelled	19.0	10	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
84	c1x59A_	Alignment	not modelled	19.0	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** solution structures of the whep-trs domain of human2 histidyl-trna synthetase
85	d2hfqa1	Alignment	not modelled	18.8	16	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
86	c2hfqA_	Alignment	not modelled	18.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
87	c1zsvB_	Alignment	not modelled	18.7	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent leukotriene b4 12- **PDBTitle:** crystal structure of human nadp-dependent leukotriene b4 12-2 hydroxydehydrogenase
88	c3jynA_	Alignment	not modelled	18.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinone oxidoreductase; **PDBTitle:** crystal structures of pseudomonas syringae pv. tomato dc30002 quinone oxidoreductase complexed with nadph
89	c1k47F_	Alignment	not modelled	16.3	12	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
90	c3eubL_	Alignment	not modelled	16.1	14	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
91	c1sb3D_	Alignment	not modelled	16.1	8	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
92	c2vcyA_	Alignment	not modelled	16.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trans-2-enoyl-coa reductase; **PDBTitle:** crystal structure of 2-enoyl thioester reductase of human2 fas ii
93	c1iqpF_	Alignment	not modelled	15.8	16	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
94	c2om6A_	Alignment	not modelled	15.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable phosphoserine phosphatase; **PDBTitle:** hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
95	d1sxjd2	Alignment	not modelled	15.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
96	d1x6va3	Alignment	not modelled	15.3	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
97	c3gohA_	Alignment	not modelled	15.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase, zinc-containing; **PDBTitle:** crystal structure of alcohol dehydrogenase superfamily protein2 (np_718042.1) from shewanella oneidensis at 1.55 a resolution
98	c3hrdE_	Alignment	not modelled	15.0	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nicotinate dehydrogenase large molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
99	c1yadD_	Alignment	not modelled	14.8	23	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis