Phyre2

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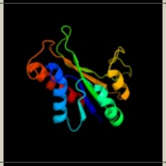
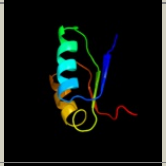
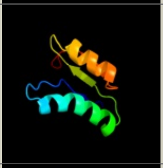
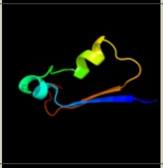
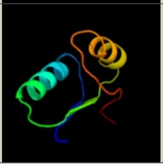
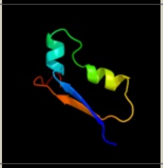
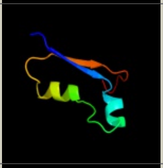
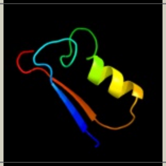
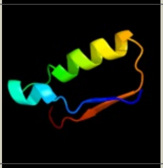
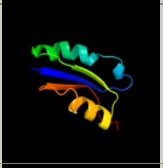
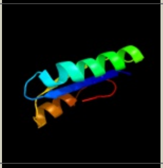
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2e85B_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
2	d1cfza_	Alignment		100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Hydrogenase maturating endopeptidase HybD
3	c3pu6A_	Alignment		100.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
4	d1c8ba_	Alignment		96.5	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
5	c3neaA_	Alignment		94.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
6	d2ptha_	Alignment		91.6	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
7	d1lssa_	Alignment		82.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
8	c3l4bG_	Alignment		81.9	11	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
9	c2z2jA_	Alignment		81.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
10	d2vapa1	Alignment		78.4	13	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
11	c3eywA_	Alignment		76.7	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff

12	c1w5fA_	Alignment		76.5	15	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
13	d1w5fa1	Alignment		76.1	15	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
14	c1w59B_	Alignment		73.0	13	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
15	c3rh0A_	Alignment		71.5	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
16	c3vh3A_	Alignment		71.1	24	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
17	d2g2ca1	Alignment		66.3	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
18	c2pjkA_	Alignment		66.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
19	c3ic5A_	Alignment		62.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
20	c3gucB_	Alignment		60.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
21	c2zklA_	Alignment	not modelled	60.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
22	c3jviA_	Alignment	not modelled	56.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
23	d1ryba_	Alignment	not modelled	56.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
24	c2yxbA_	Alignment	not modelled	55.2	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
25	d2f1ka2	Alignment	not modelled	51.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
26	c3ckyA_	Alignment	not modelled	50.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase; **PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
27	c3rfqC_	Alignment	not modelled	49.8	17	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
						PDB header:structural genomics, unknown function **Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-

28	c3g17H_	Alignment	not modelled	49.6	13	reductase; **PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
29	c1u2pA_	Alignment	not modelled	49.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
30	d1mv8a2	Alignment	not modelled	49.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
31	c3gznB_	Alignment	not modelled	49.0	26	**PDB header:**protein binding/ligase **Chain:** B: **PDB Molecule:**nedd8-activating enzyme e1 catalytic subunit; **PDBTitle:** structure of nedd8-activating enzyme in complex with nedd82 and mln4924
32	d1y1la_	Alignment	not modelled	48.7	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
33	c3rofA_	Alignment	not modelled	48.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
34	c2z2vA_	Alignment	not modelled	47.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
35	d1mkza_	Alignment	not modelled	46.7	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
36	d1txga2	Alignment	not modelled	45.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
37	c2vxyA_	Alignment	not modelled	44.8	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
38	c2ofpB_	Alignment	not modelled	44.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
39	c2f1kD_	Alignment	not modelled	44.1	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
40	d2nqra3	Alignment	not modelled	44.0	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
41	d1q0qa2	Alignment	not modelled	43.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	d1ks9a2	Alignment	not modelled	43.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
43	c3qhaB_	Alignment	not modelled	43.4	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
44	c2fekA_	Alignment	not modelled	43.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
45	c3c85A_	Alignment	not modelled	42.9	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
46	c2is8A_	Alignment	not modelled	42.4	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
47	c2r6r1_	Alignment	not modelled	42.2	13	**PDB header:**cell cycle **Chain:** 1: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** aquifex aeolicus ftsz
48	d1pgja2	Alignment	not modelled	40.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
49	c2cwdA_	Alignment	not modelled	40.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
50	d1t2da1	Alignment	not modelled	40.3	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
51	c1ks9A_	Alignment	not modelled	40.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
52	d1j5pa4	Alignment	not modelled	39.3	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						Fold:NAD(P)-binding Rossmann-fold domains

53	d1n1ea2	Alignment	not modelled	38.9	20	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
54	c2vawA_	Alignment	not modelled	38.3	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
55	d1jlja_	Alignment	not modelled	38.0	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
56	d1vl0a_	Alignment	not modelled	37.9	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
57	c3vh1A_	Alignment	not modelled	37.2	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
58	c3lcmB_	Alignment	not modelled	36.9	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
59	d1yovb1	Alignment	not modelled	36.9	26	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
60	c3dojA_	Alignment	not modelled	36.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
61	c1nhqA_	Alignment	not modelled	35.9	16	**PDB header:**oxidoreductase (h2o2(a)) **Chain:** A: **PDB Molecule:**nadh peroxidase; **PDBTitle:** crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
62	c2gf2B_	Alignment	not modelled	35.6	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
63	c2rhoB_	Alignment	not modelled	34.4	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
64	c1a5zA_	Alignment	not modelled	33.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
65	c1vkzA_	Alignment	not modelled	33.4	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
66	c1ojuA_	Alignment	not modelled	33.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
67	d5pnta_	Alignment	not modelled	33.1	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
68	c2cduB_	Alignment	not modelled	33.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
69	d1a5za1	Alignment	not modelled	32.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
70	c2uyyD_	Alignment	not modelled	31.8	13	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
71	c2h1fB_	Alignment	not modelled	31.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
72	c2gi4A_	Alignment	not modelled	31.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
73	d1nhpa1	Alignment	not modelled	30.9	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
74	d1ofua1	Alignment	not modelled	30.4	18	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
75	c1zfnA_	Alignment	not modelled	29.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
76	c3fvwA_	Alignment	not modelled	29.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
77	c1zggA_	Alignment	not modelled	29.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis

78	d1jw9b_	Alignment	not modelled	28.5	11	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
79	d1c1da1	Alignment	not modelled	28.4	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
80	c3ghyA_	Alignment	not modelled	28.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
81	d1yzfa1	Alignment	not modelled	28.0	22	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
82	d1guza1	Alignment	not modelled	27.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
83	d1rq2a1	Alignment	not modelled	27.5	16	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
84	c3oc4A_	Alignment	not modelled	27.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, pyridine nucleotide-disulfide family; **PDBTitle:** crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
85	c3qjaA_	Alignment	not modelled	26.6	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
86	d1jf8a_	Alignment	not modelled	26.5	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
87	c1ofuB_	Alignment	not modelled	26.5	18	**PDB header:**bacterial cell division inhibitor **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
88	d1d1qa_	Alignment	not modelled	25.9	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
89	d2blla1	Alignment	not modelled	25.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	c2nvuB_	Alignment	not modelled	25.3	27	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
91	d1uz5a3	Alignment	not modelled	25.1	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
92	c3hp7A_	Alignment	not modelled	24.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
93	d2bfdb2	Alignment	not modelled	24.7	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
94	d1ojua1	Alignment	not modelled	24.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
95	c3lp8A_	Alignment	not modelled	24.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
96	c3l6dB_	Alignment	not modelled	23.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
97	c3grzA_	Alignment	not modelled	23.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
98	d1dg9a_	Alignment	not modelled	23.8	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
99	c2dc1A_	Alignment	not modelled	22.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
100	d1o0sa2	Alignment	not modelled	22.7	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
101	d1y0ya2	Alignment	not modelled	22.6	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
102	c2wmyH_	Alignment	not modelled	22.5	14	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
103	c2g1uA_	Alignment	not modelled	22.3	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
						PDB header:oxidoreductase

104	c3prjB_	Alignment	not modelled	21.6	16	**Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
105	d1a53a_	Alignment	not modelled	21.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
106	d1i36a2	Alignment	not modelled	21.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
107	d1v8da_	Alignment	not modelled	21.2	14	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679
108	d1leha1	Alignment	not modelled	21.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
109	d1a4ia1	Alignment	not modelled	21.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
110	c2y0dB_	Alignment	not modelled	21.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
111	c2qytA_	Alignment	not modelled	21.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
112	d1jaya_	Alignment	not modelled	20.4	37	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
113	c1d4fD_	Alignment	not modelled	20.2	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase