Phyre^2

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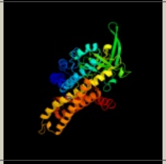
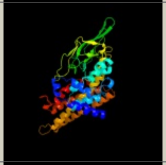
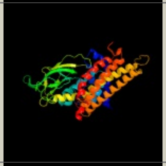
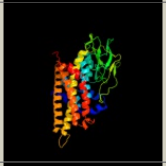
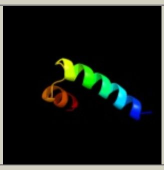
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2uxwA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**very-long-chain specific acyl-coa dehydrogenase; **PDBTitle:** crystal structure of human very long chain acyl-coa2 dehydrogenase (acadvl)
2	c3owaC_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase complexed with fad from2 bacillus anthracis
3	c2z1qA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl coa dehydrogenase
4	c2ix5A_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coenzyme a oxidase 4, peroxisomal; **PDBTitle:** short chain specific acyl-coa oxidase from arabidopsis2 thaliana, acx4 in complex with acetoacetyl-coa
5	c1rx0B_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 8, **PDBTitle:** crystal structure of isobutyryl-coa dehydrogenase complexed2 with substrate/ligand.
6	c3sf6A_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of glutaryl-coa dehydrogenase from mycobacterium2 smegmatis
7	c2a1tC_	Alignment		100.0	19	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase, medium-chain specific, **PDBTitle:** structure of the human mcad:etf e165betaa complex
8	c2vigC_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain specific acyl-coa dehydrogenase,; **PDBTitle:** crystal structure of human short-chain acyl coa2 dehydrogenase
9	c1siqA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** the crystal structure and mechanism of human glutaryl-coa2 dehydrogenase
10	c3oibB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak
11	c2pg0B_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase from geobacillus2 kaustophilus

12	c1ivhD_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isovaleryl-coa dehydrogenase; **PDBTitle:** structure of human isovaleryl-coa dehydrogenase at 2.62 angstroms resolution: structural basis for substrate3 specificity
13	c2jifA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short/branched chain specific acyl-coa dehydrogenase; **PDBTitle:** structure of human short-branched chain acyl-coa2 dehydrogenase (acadsb)
14	c3r7kB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable acyl coa dehydrogenase; **PDBTitle:** crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196
15	c1egcB_	Alignment		100.0	19	**PDB header:**electron transfer **Chain:** B: **PDB Molecule:**medium chain acyl-coa dehydrogenase; **PDBTitle:** structure of t255e, e376g mutant of human medium chain acyl-2 coa dehydrogenase complexed with octanoyl-coa
16	c2ddhA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
17	c3swoA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of a glutaryl-coa dehydrogenase from mycobacterium2 smegmatis in complex with fadh2
18	c1w07A_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1
19	c2cx9C_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase
20	c3eomD_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** 2.4 a crystal structure of native glutaryl-coa dehydrogenase from2 burkholderia pseudomallei
21	c1ukwA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of medium-chain acyl-coa dehydrogenase2 from thermus thermophilus hb8
22	c2dvlB_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of project tt0160 from thermus thermophilus hb8
23	c2fonA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal acyl-coa oxidase 1a; **PDBTitle:** x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
24	c3nf4B_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to flavin adenine dinucleotide
25	c1bucB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**butyryl-coa dehydrogenase; **PDBTitle:** three-dimensional structure of butyryl-coa dehydrogenase from2 megasphaera elsdenii
26	c3mkhC_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nitroalkane oxidase; **PDBTitle:** podospora anserina nitroalkane oxidase
27	c1r2jA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein fkbi; **PDBTitle:** fkbi for biosynthesis of methoxymalonyl extender unit of2 fk520 polyketide immunosuppresant
28	c3djlA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein aidb; **PDBTitle:** crystal structure of alkylation response protein e. coli aidb
						PDB header:oxidoreductase

29	c2ebaI_	Alignment	not modelled	100.0	25	**Chain:** I: **PDB Molecule:**putative glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus
30	c3mpjG_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** structure of the glutaryl-coenzyme a dehydrogenase
31	c3pfdB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of an acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to reduced flavin adenine dinucleotide solved3 by combined iodide ion sad mr
32	c2wbiB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 11; **PDBTitle:** crystal structure of human acyl-coa dehydrogenase 11
33	c2rehD_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitroalkane oxidase; **PDBTitle:** mechanistic and structural analyses of the roles of arg4092 and asp402 in the reaction of the flavoprotein nitroalkane3 oxidase
34	c3m9vA_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent oxidoreductase; **PDBTitle:** x-ray structure of a kijd3 in complex with dtdp
35	c2jbtA_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**p-hydroxyphenylacetate hydroxylase c2\:oxygenase **PDBTitle:** structure of the monooxygenase component of p-2 hydroxyphenylacetate hydroxylase from acinetobacter3 baumannii
36	c2or0B_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxylase; **PDBTitle:** structural genomics, the crystal structure of a putative hydroxylase2 from rhodococcus sp. rha1
37	c2rfqA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hsa hydroxylase, oxygenase; **PDBTitle:** crystal structure of 3-hsa hydroxylase from rhodococcus sp. rha1
38	c3mxlB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrososynthase; **PDBTitle:** crystal structure of nitrososynthase from micromonospora carbonacea2 var. africana
39	d2ddha3	Alignment	not modelled	100.0	14	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**acyl-CoA oxidase N-terminal domains
40	c3hwcD_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**chlorophenol-4-monooxygenase component 2; **PDBTitle:** crystal structure of chlorophenol 4-monooxygenase (tftd) of2 burkholderia cepacia ac1100
41	d1w07a3	Alignment	not modelled	100.0	17	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**acyl-CoA oxidase N-terminal domains
42	d1jqia2	Alignment	not modelled	100.0	23	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
43	d1rx0a2	Alignment	not modelled	100.0	21	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
44	d3mdea2	Alignment	not modelled	100.0	20	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
45	d2c12a2	Alignment	not modelled	100.0	14	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
46	d1r2ja2	Alignment	not modelled	100.0	22	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
47	d2d29a2	Alignment	not modelled	100.0	28	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
48	d1ukwa2	Alignment	not modelled	100.0	22	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
49	d1egda2	Alignment	not modelled	100.0	20	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
50	d1buca2	Alignment	not modelled	100.0	24	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
51	d1ivha2	Alignment	not modelled	100.0	23	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
52	d1siqa2	Alignment	not modelled	100.0	22	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
53	c2yyjA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylacetate-3-hydroxylase; **PDBTitle:** crystal structure of the oxygenase component (hpab) of 4-2 hydroxyphenylacetate 3-monooxygenase complexed with fad and 4-3 hydroxyphenylacetate

54	c1u8vA_	Alignment	not modelled	100.0	17	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**gamma-aminobutyrate metabolism **PDBTitle:** crystal structure of 4-hydroxybutyryl-coa dehydratase from2 clostridium aminobutyricum: radical catalysis involving a3 [4fe-4s] cluster and flavin
55	d1siqa1	Alignment	not modelled	99.9	17	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
56	d1rx0a1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
57	d1egda1	Alignment	not modelled	99.9	18	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
58	d3mdea1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
59	d1ivha1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
60	d1jqia1	Alignment	not modelled	99.9	22	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
61	d1buca1	Alignment	not modelled	99.9	23	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
62	d1ukwa1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
63	d2ddha1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
64	d1w07a1	Alignment	not modelled	99.9	16	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
65	d2d29a1	Alignment	not modelled	99.9	20	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
66	d2c12a1	Alignment	not modelled	99.9	15	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
67	d1r2ja1	Alignment	not modelled	99.9	19	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
68	d1u8va2	Alignment	not modelled	99.8	15	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
69	d1k8ke_	Alignment	not modelled	87.9	20	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
70	d1u8va1	Alignment	not modelled	76.0	17	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
71	c2jobA_	Alignment		53.7	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
72	c2r7bA_	Alignment	not modelled	43.3	12	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**phosphoinositide-dependent protein kinase 1; **PDBTitle:** crystal structure of the phosphoinositide-dependent kinase-2 1 (pdk-1)catalytic domain bound to a dibenzonaphthyridine3 inhibitor
73	c2vywA_	Alignment	not modelled	41.8	10	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** hemoglobin (hb2) from trematode fasciola hepatica
74	d1pbya2	Alignment	not modelled	34.7	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
75	d2lhba_	Alignment	not modelled	32.4	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
76	d1dgna_	Alignment	not modelled	31.2	12	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
77	c3exmA_	Alignment	not modelled	30.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
						Fold:PEP carboxykinase-like

78	d1khba1	Alignment	not modelled	30.1	18	**Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
79	d2p12a1	Alignment	not modelled	29.2	16	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
80	d2cb5a_	Alignment	not modelled	29.1	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
81	d1h16a_	Alignment	not modelled	29.0	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
82	d2hgsa4	Alignment	not modelled	28.7	31	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Eukaryotic glutathione synthetase ATP-binding domain
83	d2duca1	Alignment	not modelled	26.8	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
84	c2hgsA_	Alignment	not modelled	26.1	31	**PDB header:**amine/carboxylate ligase **Chain:** A: **PDB Molecule:**protein (glutathione synthetase); **PDBTitle:** human glutathione synthetase
85	c3ebnD_	Alignment	not modelled	25.2	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
86	c3h0dB_	Alignment	not modelled	24.5	10	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
87	c3hf3A_	Alignment	not modelled	22.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
88	d1cqxa1	Alignment	not modelled	21.3	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
89	d2io8a3	Alignment	not modelled	21.0	21	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Glutathionylspermidine synthase ATP-binding domain-like
90	c1pbyA_	Alignment	not modelled	20.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
91	d1hbga_	Alignment	not modelled	20.8	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
92	c1ylmA_	Alignment	not modelled	20.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu32300; **PDBTitle:** structure of cytosolic protein of unknown function yute2 from bacillus subtilis
93	d1oyaa_	Alignment	not modelled	20.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	d1uu3a_	Alignment	not modelled	19.7	12	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
95	c2q6fB_	Alignment	not modelled	19.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**infectious bronchitis virus (ibv) main protease; **PDBTitle:** crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
96	c2zs0A_	Alignment	not modelled	19.0	14	**PDB header:**oxygen storage, oxygen transport **Chain:** A: **PDB Molecule:**extracellular giant hemoglobin major globin subunit a1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
97	d1djqa1	Alignment	not modelled	18.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	c2hbpA_	Alignment	not modelled	18.1	14	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
99	c3dxrA_	Alignment	not modelled	18.1	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the yeast inter-membrane space2 chaperone assembly tim9.10