Phyre2

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Description	P0A9U8
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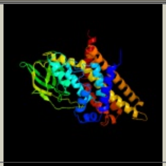
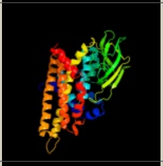
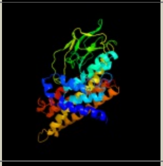
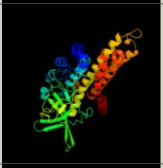
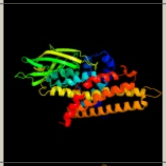
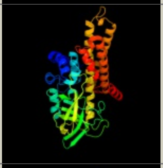
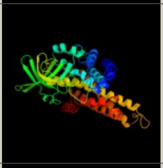
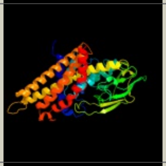
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a1tC_	Alignment		100.0	28	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase, medium-chain specific, **PDBTitle:** structure of the human mcad:etf e165betaa complex
2	c1egcB_	Alignment		100.0	28	**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
3	c1rx0B_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 8, **PDBTitle:** crystal structure of isobutyryl-coa dehydrogenase complexed2 with substrate/ligand.
4	c2z1qA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl coa dehydrogenase
5	c3owaC_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase complexed with fad from2 bacillus anthracis
6	c2ix5A_	Alignment		100.0	22	**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
7	c2cx9C_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase
8	c1ivhD_	Alignment		100.0	28	**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
9	c1ukwA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of medium-chain acyl-coa dehydrogenase2 from thermus thermophilus hb8
10	c2pg0B_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of acyl-coa dehydrogenase from geobacillus2 kaustophilus
11	c2jifA_	Alignment		100.0	25	**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)

12	c3swoA_	Alignment		100.0	21	**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
13	c2uxwA_	Alignment		100.0	28	**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)
14	c2vigC_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain specific acyl-coa dehydrogenase,; **PDBTitle:** crystal structure of human short-chain acyl coa2 dehydrogenase
15	c3sf6A_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of glutaryl-coa dehydrogenase from mycobacterium2 smegmatis
16	c3r7kB_	Alignment		100.0	28	**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
17	c1bucB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**butyryl-coa dehydrogenase; **PDBTitle:** three-dimensional structure of butyryl-coa dehydrogenase from2 megasphaera elsdenii
18	c1siqA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** the crystal structure and mechanism of human glutaryl-coa2 dehydrogenase
19	c3mpjG_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**glutaryl-coa dehydrogenase; **PDBTitle:** structure of the glutaryl-coenzyme a dehydrogenase
20	c3oibB_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak
21	c3eomD_	Alignment	not modelled	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
22	c3mkhC_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nitroalkane oxidase; **PDBTitle:** podospora anserina nitroalkane oxidase
23	c2dvlB_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of project tt0160 from thermus thermophilus hb8
24	c2ebaI_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**putative glutaryl-coa dehydrogenase; **PDBTitle:** crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus
25	c3nf4B_	Alignment	not modelled	100.0	29	**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
26	c3pfdB_	Alignment	not modelled	100.0	31	**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
27	c2rehD_	Alignment	not modelled	100.0	20	**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
						PDB header:oxidoreductase

28	c1r2jA_	Alignment	not modelled	100.0	19	**Chain:** A: **PDB Molecule:**protein fkbi; **PDBTitle:** fkbi for biosynthesis of methoxymalonyl extender unit of2 fk520 polyketide immunosuppresant
29	c2wbiB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 11; **PDBTitle:** crystal structure of human acyl-coa dehydrogenase 11
30	c3m9vA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent oxidoreductase; **PDBTitle:** x-ray structure of a kijd3 in complex with dtdp
31	c3djlA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein aidb; **PDBTitle:** crystal structure of alkylation response protein e. coli aidb
32	c2or0B_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxylase; **PDBTitle:** structural genomics, the crystal structure of a putative hydroxylase2 from rhodococcus sp. rha1
33	c2jbtA_	Alignment	not modelled	100.0	16	**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
34	c2rfqA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hsa hydroxylase, oxygenase; **PDBTitle:** crystal structure of 3-hsa hydroxylase from rhodococcus sp. rha1
35	c2ddhA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
36	c1w07A_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1
37	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)
38	c3mxlB_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrososynthase; **PDBTitle:** crystal structure of nitrososynthase from micromonospora carbonacea2 var. africana
39	d3mdea2	Alignment	not modelled	100.0	25	**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
40	d2d29a2	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
41	d1rx0a2	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
42	d1egda2	Alignment	not modelled	100.0	25	**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	d1ukwa2	Alignment	not modelled	100.0	25	**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	d1jqia2	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
45	d2c12a2	Alignment	not modelled	100.0	16	**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	d1buca2	Alignment	not modelled	100.0	26	**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	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
48	d1siqa2	Alignment	not modelled	100.0	19	**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	d1r2ja2	Alignment	not modelled	100.0	19	**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	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
51	d2ddha3	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
52	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
53	c2yyjA_	Alignment	not modelled	100.0	14	**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	14	**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	d3mdea1	Alignment	not modelled	100.0	33	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
56	d1egda1	Alignment	not modelled	100.0	34	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
57	d1jqia1	Alignment	not modelled	100.0	35	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
58	d1siqa1	Alignment	not modelled	100.0	27	**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	100.0	34	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
60	d1buca1	Alignment	not modelled	100.0	38	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
61	d1rx0a1	Alignment	not modelled	100.0	29	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
62	d2d29a1	Alignment	not modelled	100.0	38	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
63	d1ukwa1	Alignment	not modelled	100.0	40	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
64	d2c12a1	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
65	d2ddha1	Alignment	not modelled	99.9	19	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
66	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
67	d1r2ja1	Alignment	not modelled	99.9	21	**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	12	**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	d1u8va1	Alignment	not modelled	94.6	19	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
70	d1jhfa1	Alignment	not modelled	45.5	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
71	c3aqnA_	Alignment	not modelled	28.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
72	c3kxeD_	Alignment	not modelled	25.1	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
73	c2kngA_	Alignment	not modelled	16.0	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
74	c2pjpA_	Alignment	not modelled	15.8	20	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
75	d1vfga1	Alignment	not modelled	11.4	12	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
76	c1oizA_	Alignment	not modelled	11.2	20	**PDB header:**transport **Chain:** A: **PDB Molecule:**alpha-tocopherol transfer protein; **PDBTitle:** the molecular basis of vitamin e retention: structure of2 human alpha-tocopherol transfer protein
77	d1r5la2	Alignment	not modelled	9.3	19	**Fold:**SpoIIaa-like **Superfamily:**CRAL/TRIO domain **Family:**CRAL/TRIO domain
78	c2v79B_	Alignment	not modelled	9.1	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
						PDB header:structural genomics, unknown function

79	c1yx3A_	Alignment	not modelled	9.0	29	**Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
80	c3k2zA_	Alignment	not modelled	8.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
81	d1stza1	Alignment	not modelled	7.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
82	c2a5wC_	Alignment	not modelled	7.7	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
83	d1w96a2	Alignment	not modelled	7.7	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
84	d1rr7a_	Alignment	not modelled	7.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
85	c1rr7A_	Alignment	not modelled	7.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
86	d1ji8a_	Alignment	not modelled	7.2	21	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
87	d1kx9b_	Alignment	not modelled	6.9	26	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
88	d1jz8a5	Alignment	not modelled	6.8	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
89	d2v4jc1	Alignment	not modelled	6.2	9	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
90	c1k8gC_	Alignment	not modelled	5.9	13	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna
91	c2pheC_	Alignment	not modelled	5.8	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
92	c2phgB_	Alignment	not modelled	5.8	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
93	c2rkjM_	Alignment	not modelled	5.7	12	**PDB header:**ligase/rna **Chain:** M: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** cocrystal structure of a tyrosyl-trna synthetase splicing2 factor with a group i intron rna
94	c3c3jA_	Alignment	not modelled	5.6	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
95	c3hy5A_	Alignment	not modelled	5.3	42	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**retinaldehyde-binding protein 1; **PDBTitle:** crystal structure of cralbp