Phyre^2

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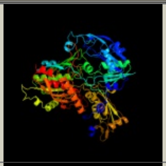
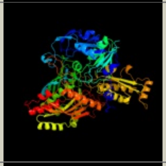
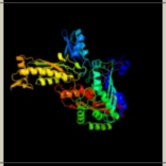
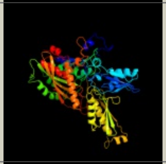
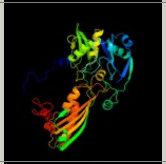
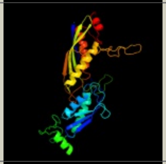
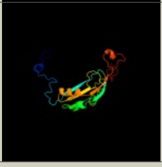
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ffvB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cutl, molybdoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
2	c1sb3D_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
3	c2w54F_	Alignment		100.0	25	**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
4	c1n62E_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase large chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
5	c1t3qB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
6	c1wygA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	c3eubL_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
8	c1vlbA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
9	c1dgjA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
10	d1jrob2	Alignment		100.0	24	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
11	d1rm6a2	Alignment		100.0	28	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain

12	d1n62b2	Alignment		100.0	21	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
13	d1ffvb2	Alignment		100.0	22	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
14	d1t3qb2	Alignment		100.0	24	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
15	d1v97a5	Alignment		100.0	23	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
16	d1vlba4	Alignment		100.0	26	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
17	d1dgja4	Alignment		100.0	25	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
18	c3hrdE_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nicotinate dehydrogenase large molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
19	c3hrdF_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
20	d1t3qb1	Alignment		100.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
21	d1n62b1	Alignment	not modelled	100.0	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
22	d1v97a3	Alignment	not modelled	100.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
23	d1ffvb1	Alignment	not modelled	100.0	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
24	d3b9jc1	Alignment	not modelled	100.0	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
25	d1rm6a1	Alignment	not modelled	100.0	29	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
26	d1jrob1	Alignment	not modelled	100.0	28	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
27	d1vlba3	Alignment	not modelled	100.0	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
28	d1dgja3	Alignment	not modelled	100.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
29	d1yh5a1	Alignment	not modelled	70.8	16	**Fold:**YggU-like **Superfamily:**YggU-like

						Family: YggU-like
30	c2rghA_	Alignment	not modelled	70.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
31	d1dpta_	Alignment	not modelled	67.5	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
32	d1gd0a_	Alignment	not modelled	63.8	22	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
33	d1knwa2	Alignment	not modelled	62.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
34	c3fwtA_	Alignment	not modelled	61.6	19	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
35	d2gdga1	Alignment	not modelled	61.5	19	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
36	c3n2oA_	Alignment	not modelled	60.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
37	d1otfa_	Alignment	not modelled	60.8	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
38	c2rgoA_	Alignment	not modelled	59.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
39	d1hfoa_	Alignment	not modelled	59.6	21	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
40	c2os5C_	Alignment	not modelled	58.0	16	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
41	c2xczA_	Alignment	not modelled	56.0	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
42	c3b64A_	Alignment	not modelled	53.6	17	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
43	d1fima_	Alignment	not modelled	53.4	20	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
44	d2fmra_	Alignment	not modelled	53.2	27	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
45	d1uiza_	Alignment	not modelled	53.1	17	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
46	c3gacD_	Alignment	not modelled	52.3	12	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
47	d2cpqa1	Alignment	not modelled	51.3	23	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
48	c2op8A_	Alignment	not modelled	50.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
49	c3t5sA_	Alignment	not modelled	49.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
50	c3abfB_	Alignment	not modelled	49.3	32	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
51	c3nzqB_	Alignment	not modelled	49.3	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
52	c3rr1B_	Alignment	not modelled	48.2	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative d-galactonate dehydratase; **PDBTitle:** crystal structure of enolase prk14017 (target efi-500653) from2 ralstonia pickettii 12j
53	c3nzpA_	Alignment	not modelled	47.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
54	d1bjpa_	Alignment	not modelled	46.8	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF

						Family:4-oxalocrotonate tautomerase-like
55	d1mwwa_	Alignment	not modelled	45.0	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
56	c2jwlB_	Alignment	not modelled	44.9	7	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
57	c3m20A_	Alignment	not modelled	44.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
58	c3ry0A_	Alignment	not modelled	44.1	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
59	c3mlcC_	Alignment	not modelled	43.5	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
60	c3mb2G_	Alignment	not modelled	41.8	23	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
61	d2aala1	Alignment	not modelled	40.7	26	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
62	c2kwpA_	Alignment	not modelled	38.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa
63	d1hh2p4	Alignment	not modelled	37.9	36	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
64	c2lfcA_	Alignment	not modelled	36.2	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
65	c2x4kB_	Alignment	not modelled	36.0	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
66	c1d7kB_	Alignment	not modelled	35.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**human ornithine decarboxylase; **PDBTitle:** crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
67	c2ormA_	Alignment	not modelled	31.1	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
68	d1nera_	Alignment	not modelled	29.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
69	d1d7ka2	Alignment	not modelled	29.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
70	d1d4ca3	Alignment	not modelled	27.4	29	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
71	d1y0pa3	Alignment	not modelled	26.8	24	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
72	d1gyxa_	Alignment	not modelled	26.6	5	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
73	c2hlhA_	Alignment	not modelled	26.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nodulation fucosyltransferase; **PDBTitle:** crystal structure of fucosyltransferase nodz from bradyrhizobium
74	c1vraA_	Alignment	not modelled	25.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
75	c1m8pB_	Alignment	not modelled	25.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
76	c3mt1B_	Alignment	not modelled	25.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
						PDB header:lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase;

77	c2on3A_	Alignment	not modelled	25.6	14	**PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
78	d1hnja2	Alignment	not modelled	24.1	19	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
79	d1f3ta2	Alignment	not modelled	23.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
80	c3da1A_	Alignment	not modelled	23.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
81	d1wufa2	Alignment	not modelled	22.6	9	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
82	c2ppgB_	Alignment	not modelled	22.3	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative isomerase; **PDBTitle:** crystal structure of putative isomerase from sinorhizobium meliloti
83	c3e0mB_	Alignment	not modelled	22.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
84	d7odca2	Alignment	not modelled	21.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
85	c1nwaA_	Alignment	not modelled	21.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
86	d1nwaa_	Alignment	not modelled	21.0	17	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
87	c2oo6A_	Alignment	not modelled	20.6	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative l-alanine-dl-glutamate epimerase; **PDBTitle:** crystal structure of putative l-alanine-dl-glutamate epimerase from2 burkholderia xenovorans strain lb400
88	c1jqkE_	Alignment	not modelled	20.2	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase; **PDBTitle:** crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
89	d1jqka_	Alignment	not modelled	20.2	26	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
90	d1w55a2	Alignment	not modelled	19.9	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
91	c3cb3B_	Alignment	not modelled	19.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of l-talarate dehydratase from polaromonas sp. js6662 complexed with mg and l-glucarate
92	d2dt5a1	Alignment	not modelled	19.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
93	d1u0ua2	Alignment	not modelled	19.2	8	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
94	c3tjiA_	Alignment	not modelled	19.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, n-terminal **PDBTitle:** crystal structure of an enolase from enterobacter sp. 638 (efi target2 efi-501662) with bound mg
95	c2jxuA_	Alignment	not modelled	19.1	44	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**terb; **PDBTitle:** nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
96	c3btnA_	Alignment	not modelled	18.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
97	c3bjsB_	Alignment	not modelled	18.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
98	d1up7a2	Alignment	not modelled	18.4	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
99	c2pmpA_	Alignment	not modelled	18.3	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana