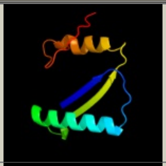
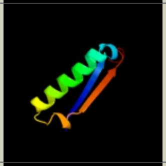
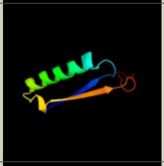
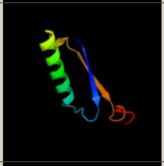
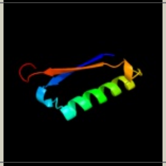
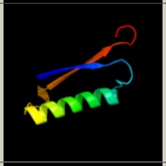
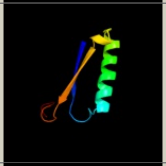
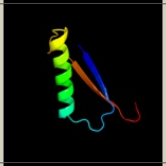
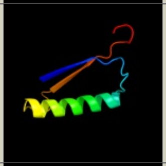
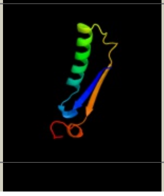
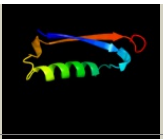
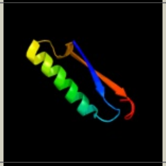
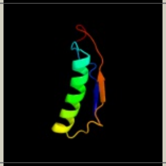
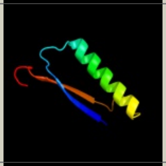
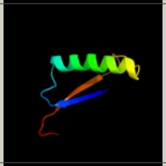
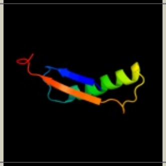
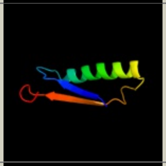
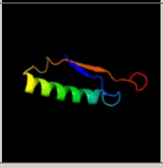
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P31992
Date	Thu Jan 5 11:48:57 GMT 2012
Unique Job ID	764e78dae7f62102

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gyxa_	Alignment		100.0	100	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
2	c2x4kB_	Alignment		99.5	16	**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)
3	c3mb2G_	Alignment		99.5	20	**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
4	c3abfB_	Alignment		99.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
5	d1otfa_	Alignment		99.5	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
6	d1bjpa_	Alignment		99.4	18	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
7	c3ry0A_	Alignment		99.4	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
8	c2op8A_	Alignment		99.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
9	c2ormA_	Alignment		99.4	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
10	c3m20A_	Alignment		99.2	22	**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
11	d1mwwa_	Alignment		99.1	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1

12	c3mlcC_	Alignment		99.1	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
13	c2flzC_	Alignment		98.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cis-3-chloroacrylic acid dehalogenase; **PDBTitle:** the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
14	d2aala1	Alignment		98.9	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
15	c3n4dF_	Alignment		98.8	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
16	c3c6vB_	Alignment		97.9	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable tautomerase/dehalogenase au4130; **PDBTitle:** crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
17	d1uiza_	Alignment		97.9	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
18	c3gacD_	Alignment		97.8	16	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
19	c2xczA_	Alignment		97.8	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
20	c2os5C_	Alignment		97.6	16	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
21	d1dpta_	Alignment	not modelled	97.6	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
22	d1hfoa_	Alignment	not modelled	97.6	8	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
23	d2gdga1	Alignment	not modelled	97.5	6	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
24	d1gd0a_	Alignment	not modelled	97.4	6	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
25	c3e6qL_	Alignment	not modelled	97.4	14	**PDB header:**isomerase **Chain:** L: **PDB Molecule:**putative 5-carboxymethyl-2-hydroxymuconate isomerase; **PDBTitle:** putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
26	d1s0ya_	Alignment	not modelled	97.4	23	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
27	c3fwtA_	Alignment	not modelled	97.2	22	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
28	c3b64A_	Alignment	not modelled	97.0	18	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
						PDB header:immune system

29	c3t5sA_	Alignment	not modelled	97.0	16	**Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
30	d1otga_	Alignment	not modelled	96.9	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
31	d1fima_	Alignment	not modelled	96.3	7	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
32	d1s0yb_	Alignment	not modelled	96.0	22	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
33	c3ej9D_	Alignment	not modelled	96.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-subunit of trans-3-chloroacrylic acid dehalogenase; **PDBTitle:** structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
34	c3mb2J_	Alignment	not modelled	94.7	23	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - beta 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
35	d1u9da_	Alignment	not modelled	92.0	21	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**VC0714-like
36	d2ivya1	Alignment	not modelled	45.1	14	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
37	d1wh9a_	Alignment	not modelled	40.0	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
38	d2daya1	Alignment	not modelled	32.0	20	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**RWD domain
39	c2eg5C_	Alignment	not modelled	28.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
40	d1zj8a1	Alignment	not modelled	24.8	6	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
41	c3hrdF_	Alignment	not modelled	21.1	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
42	c3fxeA_	Alignment	not modelled	21.0	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein icmq; **PDBTitle:** crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
43	d1wjwa_	Alignment	not modelled	20.2	6	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
44	c2ebmA_	Alignment	not modelled	19.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rwd domain-containing protein 1; **PDBTitle:** solution structure of the rwd domain of human rwd domain2 containing protein 1
45	d1v97a5	Alignment	not modelled	17.8	23	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
46	d2akja1	Alignment	not modelled	17.4	14	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
47	c2y9jt_	Alignment	not modelled	17.2	15	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
48	d2i0xa1	Alignment	not modelled	16.9	11	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
49	d1lq9a_	Alignment	not modelled	16.2	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Actinorhodin biosynthesis monooxygenase ActVa-Orf6
50	c2kl0A_	Alignment	not modelled	16.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
51	d1wh5a_	Alignment	not modelled	14.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
52	d1ukxa_	Alignment	not modelled	13.4	17	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**RWD domain
53	c2v4iA_	Alignment	not modelled	12.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate n-acetyltransferase 2 alpha chain; **PDBTitle:** structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
54	d1vkua_	Alignment	not modelled	12.3	8	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)

55	d1lcda_	Alignment	not modelled	12.2	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
56	d1t3qb2	Alignment	not modelled	11.8	14	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
57	d1yh5a1	Alignment	not modelled	11.6	10	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
58	d3e11a1	Alignment	not modelled	11.2	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
59	d1a3qa1	Alignment	not modelled	10.8	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
60	d1ffvb2	Alignment	not modelled	10.8	14	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
61	d1p5dx4	Alignment	not modelled	10.8	13	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
62	d1zud21	Alignment	not modelled	10.7	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
63	c1sb3D_	Alignment	not modelled	10.7	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
64	d2ejqa1	Alignment	not modelled	10.5	3	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
65	d1n62b2	Alignment	not modelled	10.5	18	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
66	c3eubL_	Alignment	not modelled	10.2	23	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
67	d1aopa1	Alignment	not modelled	10.1	10	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
68	d1hlva1	Alignment	not modelled	9.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
69	c2ebkA_	Alignment	not modelled	9.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rwd domain-containing protein 3; **PDBTitle:** solution structure of the rwd domain of human rwd domain2 containing protein 3
70	c3epvB_	Alignment	not modelled	9.6	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
71	c2w54F_	Alignment	not modelled	9.6	14	**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
72	d2bjca1	Alignment	not modelled	9.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
73	d1tygb_	Alignment	not modelled	9.1	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
74	d1qpza1	Alignment	not modelled	9.0	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
75	c1t3qB_	Alignment	not modelled	8.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
76	c1a3qA_	Alignment	not modelled	8.9	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b p52); **PDBTitle:** human nf-kappa-b p52 bound to dna
77	c3oq2A_	Alignment	not modelled	8.7	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**crispr-associated protein cas2; **PDBTitle:** structure of a crispr associated protein cas2 from desulfovibrio2 vulgaris
78	c2wwaJ_	Alignment	not modelled	8.7	15	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
79	c2a67C_	Alignment	not modelled	8.6	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
80	d1jrob2	Alignment	not modelled	8.4	14	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain

81	d1w55a2	Alignment	not modelled	8.4	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
82	d1ooha_	Alignment	not modelled	8.3	11	**Fold:**EF Hand-like **Superfamily:**Insect pheromone/odorant-binding proteins **Family:**Insect pheromone/odorant-binding proteins
83	c2qnwA_	Alignment	not modelled	8.3	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
84	d2cu3a1	Alignment	not modelled	8.1	3	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
85	c1tygG_	Alignment	not modelled	8.1	6	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
86	d1zpwx1	Alignment	not modelled	7.9	19	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
87	d1iv3a_	Alignment	not modelled	7.8	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
88	c2d4gA_	Alignment	not modelled	7.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu11850; **PDBTitle:** structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
89	d1wpia1	Alignment	not modelled	7.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YKR049C-like
90	c2jnsA_	Alignment	not modelled	7.5	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bromodomain-containing protein 4; **PDBTitle:** solution structure of the bromodomain-containing protein 42 et domain
91	d1m6ex_	Alignment	not modelled	7.4	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Salicylic acid carboxyl methyltransferase (SAMT)
92	d1my7a_	Alignment	not modelled	7.4	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
93	c3f0gA_	Alignment	not modelled	7.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
94	d2v4jb2	Alignment	not modelled	7.4	5	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
95	c2fvfA_	Alignment	not modelled	7.2	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
96	c1vraA_	Alignment	not modelled	7.2	7	**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
97	d2jpqa1	Alignment	not modelled	7.2	12	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
98	d1oy3c_	Alignment	not modelled	7.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
99	d1hska2	Alignment	not modelled	7.2	3	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain