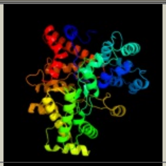
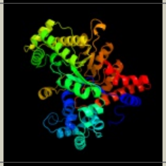
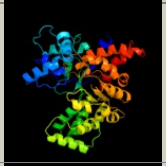
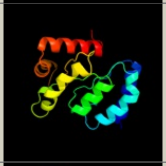
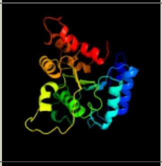
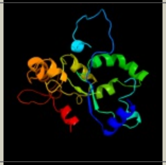
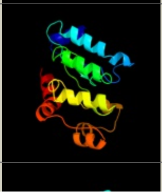
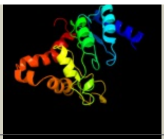
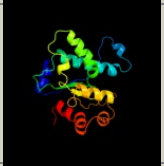
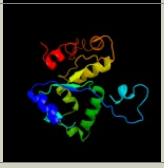
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8G3
Date	Thu Jan 5 11:07:46 GMT 2012
Unique Job ID	dd19131c69f38c89

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iacA_	Alignment		100.0	66	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucuronate isomerase; **PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
2	c2q01A_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uronate isomerase; **PDBTitle:** crystal structure of glucuronate isomerase from caulobacter crescentus
3	d1j5sa_	Alignment		100.0	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
4	d2qeec1	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
5	c2qpxA_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted metal-dependent hydrolase of the tim-barrel fold; **PDBTitle:** crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution
6	d1xwya1	Alignment		96.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
7	c3rcmA_	Alignment		95.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
8	d2dvta1	Alignment		94.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
9	d2f6ka1	Alignment		92.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
10	d1yixa1	Alignment		91.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
11	c3irsB_	Alignment		90.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bb4693; **PDBTitle:** crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica

12	c3k2gA_	Alignment		88.4	24	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
13	d2ffia1	Alignment		88.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
14	c3nurA_	Alignment		88.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus
15	d1j6oa_	Alignment		87.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
16	c2wm1A_	Alignment		85.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-amino-3-carboxymuconate-6-semialdehyde **PDBTitle:** the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis
17	c2ragB_	Alignment		78.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
18	c3pnzD_	Alignment		76.2	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphotriesterase family protein; **PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes
19	c3cjpA_	Alignment		70.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
20	d2hbva1	Alignment		69.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
21	c2xioA_	Alignment	not modelled	67.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
22	c2xi5D_	Alignment	not modelled	67.3	50	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
23	c2xi7B_	Alignment	not modelled	67.2	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rna polymerase l; **PDBTitle:** n-terminal endonuclease domain of la crosse virus l-protein
24	c3ipwA_	Alignment	not modelled	62.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
25	c1pscA_	Alignment	not modelled	61.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
26	d1vmea1	Alignment	not modelled	60.0	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	c2gzxB_	Alignment	not modelled	59.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative tatd related dnase; **PDBTitle:** crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
28	c3f4cA_	Alignment	not modelled	59.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
						PDB header:structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af 1765;

29	c3guwB_	Alignment	not modelled	58.9	14	**PDBTitle:** crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121
30	c3gg7A_	Alignment	not modelled	56.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
31	d1zzma1	Alignment	not modelled	56.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
32	d1bf6a_	Alignment	not modelled	55.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
33	d1e5da1	Alignment	not modelled	50.0	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
34	c2qahA_	Alignment	not modelled	49.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-pyrone-4,6-dicarboxylic acid hydrolase; **PDBTitle:** crystal structure of the 2-pyrone-4,6-dicarboxylic acid2 hydrolase from sphingomonas paucimobilis
35	c2fmoA_	Alignment	not modelled	47.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
36	d1xrta2	Alignment	not modelled	44.4	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
37	d2amxa1	Alignment	not modelled	44.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
38	c3ou8B_	Alignment	not modelled	38.6	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
39	d1yoba1	Alignment	not modelled	38.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
40	d1w5ra1	Alignment	not modelled	35.7	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
41	d1zbsa1	Alignment	not modelled	33.9	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
42	d1bpoa1	Alignment	not modelled	33.5	21	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin heavy-chain linker domain
43	c3ou8A_	Alignment	not modelled	33.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
44	c1deqF_	Alignment	not modelled	32.9	64	**PDB header:** **PDB COMPND:**
45	d2ffha2	Alignment	not modelled	31.9	32	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
46	c2w48D_	Alignment	not modelled	31.4	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
47	c3dzdA_	Alignment	not modelled	30.3	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
48	d2cbia2	Alignment	not modelled	29.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
49	c1zbsA_	Alignment	not modelled	28.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pg1100; **PDBTitle:** crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
50	c1ei3E_	Alignment	not modelled	28.2	45	**PDB header:** **PDB COMPND:**
51	d1k78a1	Alignment	not modelled	27.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
52	c3ghgK_	Alignment	not modelled	26.9	45	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
53	d2ajta2	Alignment	not modelled	26.7	15	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
54	c1deqO_	Alignment	not modelled	26.3	42	**PDB header:** **PDB COMPND:**
						PDB header:lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage

55	c2y7eA_	Alignment	not modelled	26.0	12	enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
56	c2yz5B_	Alignment	not modelled	25.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol phosphatase; **PDBTitle:** histidinol phosphate phosphatase complexed with phosphate
57	d1qb2a_	Alignment	not modelled	25.4	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
58	d1jjcb2	Alignment	not modelled	24.8	26	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
59	d1khda1	Alignment	not modelled	24.6	19	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
60	c1zxoB_	Alignment	not modelled	24.1	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein q8a1p1; **PDBTitle:** x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
61	c1ei3C_	Alignment	not modelled	23.5	64	**PDB header:** **PDB COMPND:**
62	d2tpta1	Alignment	not modelled	22.8	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
63	c2wc1A_	Alignment	not modelled	22.7	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
64	d2fvka2	Alignment	not modelled	22.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
65	c3h87D_	Alignment	not modelled	22.1	42	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
66	c1lwuH_	Alignment	not modelled	22.1	36	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from lamprey fibrinogen complexed with2 the peptide gly-his-arg-pro-amide
67	c2yguA_	Alignment	not modelled	21.1	35	**PDB header:**allergen **Chain:** A: **PDB Molecule:**venom allergen 2; **PDBTitle:** crystal structure of fire ant venom allergen, sol i 2
68	d1w4ta1	Alignment	not modelled	20.7	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
69	d1ra0a2	Alignment	not modelled	20.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
70	c3bvhC_	Alignment	not modelled	19.9	64	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
71	c1n73C_	Alignment	not modelled	19.4	64	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
72	c2hpcF_	Alignment	not modelled	19.2	64	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
73	c3bvhE_	Alignment	not modelled	19.2	50	**PDB header:**blood clotting **Chain:** E: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
74	d1qzxa2	Alignment	not modelled	19.0	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
75	c2infB_	Alignment	not modelled	18.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
76	d1lwuc1	Alignment	not modelled	18.9	64	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
77	c3kwkA_	Alignment	not modelled	18.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh dehydrogenase/nad(p)h nitroreductase; **PDBTitle:** crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
78	d1o17a1	Alignment	not modelled	18.4	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
79	c2hpcH_	Alignment	not modelled	18.3	42	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.

80	c2j61B_	Alignment	not modelled	18.1	27	**PDB header:**lectin **Chain:** B: **PDB Molecule:**ficolin-2; **PDBTitle:** l-ficolin complexed to n-acetylglucosamine (forme c)
81	d1m1jc1	Alignment	not modelled	18.1	64	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
82	d1lwub1	Alignment	not modelled	17.7	36	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
83	d6paxa1	Alignment	not modelled	17.7	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
84	c3m1eA_	Alignment	not modelled	17.6	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
85	c2vc7A_	Alignment	not modelled	16.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
86	d1fida_	Alignment	not modelled	16.3	64	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
87	d2paja2	Alignment	not modelled	16.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
88	c2i7hE_	Alignment	not modelled	15.9	8	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
89	d1re3b1	Alignment	not modelled	15.8	42	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
90	d1i0da_	Alignment	not modelled	15.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
91	c2vfbA_	Alignment	not modelled	15.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylamine n-acetyltransferase; **PDBTitle:** the structure of mycobacterium marinum arylamine n-2 acetyltransferase
92	d1jc9a_	Alignment	not modelled	15.4	27	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
93	c1jc9A_	Alignment	not modelled	15.4	27	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**techylectin-5a; **PDBTitle:** tachylectin 5a from tachypleus tridentatus (japanese horseshoe crab)
94	c3tgnA_	Alignment	not modelled	15.0	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
95	c3r6uA_	Alignment	not modelled	15.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**choline-binding protein; **PDBTitle:** crystal structure of choline binding protein opubc from bacillus2 subtilis
96	c2jubA_	Alignment	not modelled	14.7	38	**PDB header:**endonuclease inhibitor **Chain:** A: **PDB Molecule:**internal protein i; **PDBTitle:** solution structure of ipi*
97	c3pjwA_	Alignment	not modelled	14.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
98	c1af7A_	Alignment	not modelled	14.6	15	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**chemotaxis receptor methyltransferase cher; **PDBTitle:** cher from salmonella typhimurium
99	d1rrma_	Alignment	not modelled	14.5	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase