Phyre2

Email	l.a.kelley@imperial.ac.uk
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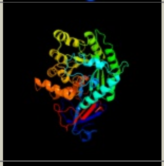
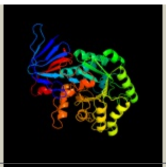
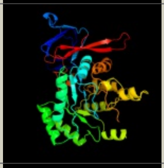
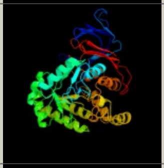
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qt3A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-isopropylammelide isopropyl amidohydrolase; **PDBTitle:** crystal structure of n-isopropylammelide isopropylaminohydrolase atzc2 from pseudomonas sp. strain adp complexed with zn
2	c1r9yA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine deaminase; **PDBTitle:** bacterial cytosine deaminase d314a mutant.
3	c3hpaB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
4	c3lnpA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase family protein olei01672_1_465; **PDBTitle:** crystal structure of amidohydrolase family protein2 olei01672_1_465 from oleispira antarctica
5	c2i9uA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine/guanine deaminase related protein; **PDBTitle:** crystal structure of guanine deaminase from c. acetobutylicum with2 bound guanine in the active site
6	c3lsbA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**triazine hydrolase; **PDBTitle:** crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aurescens tc1 complexed with zinc and ametrin
7	c1p1mA_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tm0936; **PDBTitle:** structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
8	c2q09A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxo-imidazolidin-4-yl)-propionic acid
9	c2gokA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
10	c3e0lB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine deaminase; **PDBTitle:** computationally designed ammelide deaminase
11	c2bb0A_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis

12	c2pajA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/guanine deaminase; **PDBTitle:** crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
13	c3gnhA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-lysine, l-arginine carboxypeptidase cc2672; **PDBTitle:** crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.
14	c1gkpD_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**hydantoinase; **PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
15	c2ftwA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase; **PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum
16	c2gseC_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2; **PDBTitle:** crystal structure of human dihydropyrimidinease-like 2
17	c3hm7A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
18	c3mduA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-formimino-l-glutamate iminohydrolase; **PDBTitle:** the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
19	c3be7B_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase; **PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase
20	c2oodA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr3880 protein; **PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum
21	c1gkrA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
22	c3v7pA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase family protein; **PDBTitle:** crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
23	c3d6nA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase/transferase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
24	c2r8cB_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eaj56179
25	c2vr2A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
26	c3dc8B_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from sinorhizobium meliloti
27	c2vunC_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**enamidase; **PDBTitle:** the crystal structure of enamidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
28	c1k1dF_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**d-hydantoinase; **PDBTitle:** crystal structure of d-hydantoinase

29	c2qs8A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of a xaa-pro dipeptidase with bound2 methionine in the active site
30	c1nfgA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-hydantoinase; **PDBTitle:** structure of d-hydantoinase
31	c2p9bA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible prolidase; **PDBTitle:** crystal structure of putative prolidase from2 bifidobacterium longum
32	c1xrfA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution
33	c3gipB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-acyl-d-glutamate deacylase; **PDBTitle:** crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
34	c2fvmA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
35	c3mpgB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** dihydroorotase from bacillus anthracis
36	c3feqB_	Alignment	not modelled	100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eah89906
37	c1rjqA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminoacylase; **PDBTitle:** the crystal structure of the d-aminoacylase mutant d366a
38	c2ubpC_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (urease alpha subunit); **PDBTitle:** structure of native urease from bacillus pasteurii
39	c2vhlB_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis
40	c3griB_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** the crystal structure of a dihydroorotase from staphylococcus aureus
41	c3nqbB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
42	c2aqoB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase; **PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
43	c3e74D_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of e. coli allantoinase with iron ions at2 the metal center
44	c2gwnA_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis.
45	c1e9yB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease subunit beta; **PDBTitle:** crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
46	c2p50C_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
47	c1fwcC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**urease; **PDBTitle:** klebsiella aerogenes urease, c319a variant at ph 8.5
48	c2z00A_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus
49	c3ooqC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of amidohydrolase from thermotoga maritima msb8
50	c3etkA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
51	c3egjA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
52	c2imrA_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dr_0824; **PDBTitle:** crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
						PDB header:hydrolase **Chain:** X: **PDB Molecule:**uncharacterized metal-dependent

53	c3ighX_	Alignment	not modelled	100.0	15	hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
54	c3la4A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease; **PDBTitle:** crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
55	c2icsA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenine deaminase; **PDBTitle:** crystal structure of an adenine deaminase
56	c2ogjB_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of a dihydroorotase
57	c1o12B_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** crystal structure of n-acetylglucosamine-6-phosphate2 deacetylase (tm0814) from thermotoga maritima at 2.5 a3 resolution
58	d1ra0a2	Alignment	not modelled	99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
59	d2uz9a2	Alignment	not modelled	99.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
60	d2i9ua2	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
61	d1p1ma2	Alignment	not modelled	99.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
62	d2imra2	Alignment	not modelled	99.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
63	d2ooda2	Alignment	not modelled	99.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
64	d2bb0a2	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
65	c3msrA_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
66	d2puza2	Alignment	not modelled	99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
67	d2q09a2	Alignment	not modelled	99.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
68	d2paja2	Alignment	not modelled	99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
69	d4ubpc2	Alignment	not modelled	99.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
70	d1gkpa2	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
71	d2p9ba1	Alignment	not modelled	99.5	18	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
72	d2qs8a2	Alignment	not modelled	99.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
73	d1yrra1	Alignment	not modelled	99.5	18	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
74	d2p9ba2	Alignment	not modelled	99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
75	d1kcxa2	Alignment	not modelled	99.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
76	d3be7a2	Alignment	not modelled	99.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
77	c3ggmB_	Alignment	not modelled	99.4	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bt9727_2919; **PDBTitle:** crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
78	c3ou8B_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
79	d2r8ca2	Alignment	not modelled	99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
						Fold: Composite domain of metallo-dependent hydrolases

80	d1ejxc1	Alignment	not modelled	99.4	19	**Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
81	d1onwa1	Alignment	not modelled	99.4	15	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase
82	c3ou8A_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
83	d1e9yb1	Alignment	not modelled	99.3	20	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
84	d1xrta2	Alignment	not modelled	99.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
85	d2r8ca1	Alignment	not modelled	99.3	17	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
86	c3pnuA_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
87	d2ftwa2	Alignment	not modelled	99.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
88	d2fvka1	Alignment	not modelled	99.3	19	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
89	d1i0da_	Alignment	not modelled	99.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
90	d1ynya2	Alignment	not modelled	99.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
91	d1k1da2	Alignment	not modelled	99.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
92	d2d2ja1	Alignment	not modelled	99.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
93	c1pscA_	Alignment	not modelled	99.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
94	d1nfga2	Alignment	not modelled	99.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
95	d1gkra2	Alignment	not modelled	99.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
96	d2eg6a1	Alignment	not modelled	99.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase
97	d2fvka2	Alignment	not modelled	99.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
98	c3jzeC_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydroorotase; **PDBTitle:** 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
99	d2ftwa1	Alignment	not modelled	99.0	23	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
100	c3rysA_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
101	c2zc1A_	Alignment	not modelled	98.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
102	c3pnzD_	Alignment	not modelled	98.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphotriesterase family protein; **PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes
103	d1k1da1	Alignment	not modelled	98.9	29	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
104	d2icsa2	Alignment	not modelled	98.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
105	d1vfla1	Alignment	not modelled	98.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
106	d1onwa2	Alignment	not modelled	98.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
						Fold:TIM beta/alpha-barrel

107	d1a4ma_	Alignment	not modelled	98.8	12	**Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
108	d1gkpa1	Alignment	not modelled	98.8	19	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
109	d1ynya1	Alignment	not modelled	98.8	22	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
110	c3f4cA_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
111	d2amxa1	Alignment	not modelled	98.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
112	d1bf6a_	Alignment	not modelled	98.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
113	d1m7ja1	Alignment	not modelled	98.7	20	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
114	c2vc7A_	Alignment	not modelled	98.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
115	d3be7a1	Alignment	not modelled	98.7	10	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
116	d2bb0a1	Alignment	not modelled	98.6	18	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
117	d1kcxa1	Alignment	not modelled	98.4	17	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
118	d2paja1	Alignment	not modelled	98.3	17	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
119	d1m7ja3	Alignment	not modelled	98.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**D-aminoacylase, catalytic domain
120	d1zzma1	Alignment	not modelled	98.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like