Phyre^2

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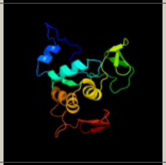
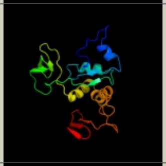
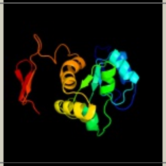
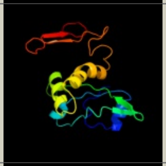
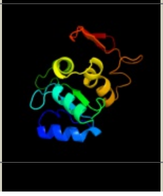
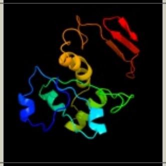
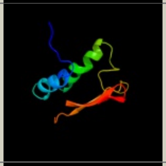
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yrra2	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
2	d1un7a2	Alignment		100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
3	c3egjA_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
4	c2vhlB_	Alignment		100.0	36	**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
5	c1o12B_	Alignment		100.0	39	**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
6	c2p50C_	Alignment		99.9	37	**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
7	c2gokA_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
8	c2bb0A_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis
9	c3e0lB_	Alignment		99.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine deaminase; **PDBTitle:** computationally designed ammelide deaminase
10	c3hm7A_	Alignment		99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
11	c2aqoB_	Alignment		99.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase; **PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q

12	c2q09A_	Alignment		99.7	17	**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
13	c2vr2A_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
14	c3lnpA_	Alignment		99.7	19	**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
15	c3ooqC_	Alignment		99.7	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of amidohydrolase from thermotoga maritima msb8
16	c1gkrA_	Alignment		99.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
17	c2ftwA_	Alignment		99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase; **PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum
18	c2p9bA_	Alignment		99.7	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible prolidase; **PDBTitle:** crystal structure of putative prolidase from2 bifidobacterium longum
19	c1gkpD_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**hydantoinase; **PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
20	c2gseC_	Alignment		99.7	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2; **PDBTitle:** crystal structure of human dihydropyrimidinease-like 2
21	c3gnhA_	Alignment	not modelled	99.7	23	**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.
22	c3hpaB_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
23	c2i9uA_	Alignment	not modelled	99.7	19	**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
24	c3feqB_	Alignment	not modelled	99.7	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eah89906
25	c3nqbB_	Alignment	not modelled	99.7	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
26	c1k1dF_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**d-hydantoinase; **PDBTitle:** crystal structure of d-hydantoinase
27	c2oodA_	Alignment	not modelled	99.7	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr3880 protein; **PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum
28	c3dc8B_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from

						sinorhizobium meliloti
29	c3griB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** the crystal structure of a dihydroorotase from staphylococcus aureus
30	c1nfgA_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-hydantoinase; **PDBTitle:** structure of d-hydantoinase
31	d1o12a2	Alignment	not modelled	99.7	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
32	c1p1mA_	Alignment	not modelled	99.7	13	**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
33	c2z00A_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus
34	c2r8cB_	Alignment	not modelled	99.7	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eaj56179
35	c3be7B_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase; **PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase
36	c2gwnA_	Alignment	not modelled	99.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis.
37	c2fvmA_	Alignment	not modelled	99.6	19	**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
38	c2qs8A_	Alignment	not modelled	99.6	23	**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
39	c1xrfA_	Alignment	not modelled	99.6	15	**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
40	c3e74D_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of e. coli allantoinase with iron ions at2 the metal center
41	c2ogjB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of a dihydroorotase
42	c2pajA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/guanine deaminase; **PDBTitle:** crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
43	c3mpgB_	Alignment	not modelled	99.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** dihydroorotase from bacillus anthracis
44	c3gipB_	Alignment	not modelled	99.6	23	**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.
45	c1rjqA_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminoacylase; **PDBTitle:** the crystal structure of the d-aminoacylase mutant d366a
46	c3mduA_	Alignment	not modelled	99.6	23	**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
47	c3d6nA_	Alignment	not modelled	99.6	30	**PDB header:**hydrolase/transferase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
48	c1fwcC_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**urease; **PDBTitle:** klebsiella aerogenes urease, c319a variant at ph 8.5
49	c3lsbA_	Alignment	not modelled	99.6	15	**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
50	c2vunC_	Alignment	not modelled	99.6	21	**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
51	c2ubpC_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (urease alpha subunit); **PDBTitle:** structure of native urease from bacillus pasteurii
52	c1e9yB_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease subunit beta; **PDBTitle:** crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
53	c1r9yA_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine deaminase; **PDBTitle:** bacterial cytosine deaminase d314a mutant.

54	c2icsA_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenine deaminase; **PDBTitle:** crystal structure of an adenine deaminase
55	c2qt3A_	Alignment	not modelled	99.5	19	**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
56	c3la4A_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease; **PDBTitle:** crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
57	c3etkA_	Alignment	not modelled	99.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
58	c3ighX_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
59	d4ubpc2	Alignment	not modelled	99.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
60	d1gkpa2	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
61	c2imrA_	Alignment	not modelled	99.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dr_0824; **PDBTitle:** crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
62	d3be7a1	Alignment	not modelled	99.1	22	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
63	d2bb0a1	Alignment	not modelled	98.9	26	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
64	d1nfga1	Alignment	not modelled	98.8	13	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
65	c3msrA_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
66	d1ra0a2	Alignment	not modelled	98.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
67	d2bb0a2	Alignment	not modelled	98.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
68	d2paja1	Alignment	not modelled	98.7	19	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
69	d2q09a2	Alignment	not modelled	98.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
70	d2puza2	Alignment	not modelled	98.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
71	d2uz9a2	Alignment	not modelled	98.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
72	d1kcxa2	Alignment	not modelled	98.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
73	d2ftwa2	Alignment	not modelled	98.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
74	d2p9ba2	Alignment	not modelled	98.4	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
75	d2paja2	Alignment	not modelled	98.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
76	d2icsa2	Alignment	not modelled	98.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
77	d2qs8a1	Alignment	not modelled	98.3	27	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
78	d1p1ma1	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
79	d2ooda1	Alignment	not modelled	98.3	28	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
						Fold: Composite domain of metallo-dependent hydrolases

80	d1gkra1	Alignment	not modelled	98.2	13	**Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
81	d1xrta1	Alignment	not modelled	98.2	31	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
82	d2ooda2	Alignment	not modelled	98.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
83	d1ynya2	Alignment	not modelled	98.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
84	d3be7a2	Alignment	not modelled	98.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
85	d2r8ca2	Alignment	not modelled	98.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
86	d2qs8a2	Alignment	not modelled	97.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
87	d2i9ua2	Alignment	not modelled	97.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
88	d1nfga2	Alignment	not modelled	97.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
89	d1k1da2	Alignment	not modelled	97.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
90	d1onwa2	Alignment	not modelled	97.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
91	d1m7ja2	Alignment	not modelled	97.5	21	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
92	d2imra2	Alignment	not modelled	97.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
93	d1gkra2	Alignment	not modelled	97.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
94	d1p1ma2	Alignment	not modelled	97.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
95	d1kcxa1	Alignment	not modelled	97.3	21	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
96	d1o12a1	Alignment	not modelled	97.3	31	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
97	d2fvka2	Alignment	not modelled	97.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
98	d1i0da_	Alignment	not modelled	97.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
99	d1xrta2	Alignment	not modelled	97.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
100	c3pnuA_	Alignment	not modelled	96.4	2	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
101	d2puza1	Alignment	not modelled	95.9	26	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
102	d1ynya1	Alignment	not modelled	95.8	24	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
103	d1e9yb2	Alignment	not modelled	95.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
104	d1k1da1	Alignment	not modelled	95.5	21	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
105	d2i9ua1	Alignment	not modelled	95.5	12	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
106	d1gkpa1	Alignment	not modelled	95.4	32	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
107	d2d2ja1	Alignment	not modelled	94.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like

108	d1m7ja3	Alignment	not modelled	94.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**D-aminoacylase, catalytic domain
109	c1pscA_	Alignment	not modelled	94.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
110	d1yixa1	Alignment	not modelled	94.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
111	c3ou8A_	Alignment	not modelled	94.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
112	c3ou8B_	Alignment	not modelled	94.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
113	d1un7a1	Alignment	not modelled	93.9	31	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
114	d2eg6a1	Alignment	not modelled	92.5	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase
115	c3jzeC_	Alignment	not modelled	92.4	15	**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
116	d1bf6a_	Alignment	not modelled	92.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
117	d2uz9a1	Alignment	not modelled	91.4	21	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
118	c2zc1A_	Alignment	not modelled	89.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
119	d1a4ma_	Alignment	not modelled	89.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
120	c2vc7A_	Alignment	not modelled	89.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities