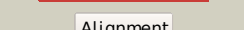
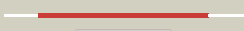


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1r9yA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
2	c2qt3A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: n-isopropylammelide isopropyl amidohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase atzc2 from pseudomonas sp. strain adp complexed with zn
3	c3hpaB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
4	c3lnpA_	 Alignment		100.0	18	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	c2bb0A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
6	c3lsbA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureusens tc1 complexed with zinc and ametrin
7	c2gokA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
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	c1plmA_	 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
10	c2i9uA_	 Alignment		100.0	16	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
11	c2gseC_	 Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinase-like 2

12	c2ftwA_	Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
13	c2vr2A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
14	c2pajA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of 2 sargasso sea
15	c3dc8B_	Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
16	c3hm7A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
17	c1gkpD_	Alignment		100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
18	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.
19	c1k1dF_	Alignment		100.0	16	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
20	c1gkrA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
21	c1xrfA_	Alignment	not modelled	100.0	16	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
22	c3be7B_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
23	c3e0lB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammeline deaminase
24	c3mpgB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
25	c1nfgA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
26	c2fvmA_	Alignment	not modelled	100.0	16	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
27	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.
28	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

29	c2aqoB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
30	c2qs8A	Alignment	not modelled	100.0	15	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
31	c2vunC	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
32	c2z00A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
33	c3feqB	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
34	c3d6nA	Alignment	not modelled	100.0	17	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
35	c3gipB	Alignment	not modelled	100.0	16	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.
36	c2r8cB	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
37	c3mduA	Alignment	not modelled	100.0	16	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
38	c3e74D	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at2 the metal center
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	c2oodA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
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	c1rjqA	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
43	c3ooqC	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
44	c1e9yB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
45	c2p9bA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
46	c2ubpC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
47	c3la4A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
48	c2p50C	Alignment	not modelled	100.0	13	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
49	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
50	c3egjA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
51	d1ra0a2	Alignment	not modelled	100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
52	c3etkA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
						PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent

53	c3ighX	Alignment	not modelled	100.0	18	hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
54	c2icsA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
55	c1o12B	Alignment	not modelled	100.0	14	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
56	c2ogjB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
57	c2imrA	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
58	d2uz9a2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
59	d2i9ua2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
60	d1p1ma2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
61	d2bb0a2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
62	d2q09a2	Alignment	not modelled	99.8	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
63	d1gkpa2	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
64	d2ooda2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
65	d2imra2	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
66	d2puza2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
67	c3msrA	Alignment	not modelled	99.7	9	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
68	d2paja2	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
69	d1kcxa2	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
70	d2ftwa2	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
71	d1ynya2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
72	d1xrta2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
73	d3be7a2	Alignment	not modelled	99.6	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
74	c3pnuA	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
75	d2qs8a2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
76	d1k1da2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
77	c3jzeC	Alignment	not modelled	99.6	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. It2
78	d4ubpc2	Alignment	not modelled	99.6	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
79	d2eg6a1	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase

80	d2r8ca2	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
81	d1gkra2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
82	d1i0da	Alignment	not modelled	99.5	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
83	d1nfga2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
84	d2p9ba2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
85	d2fvka2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
86	d1ejxc1	Alignment	not modelled	99.4	22	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
87	d1yrra1	Alignment	not modelled	99.4	12	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
88	d1e9yb1	Alignment	not modelled	99.4	19	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
89	d1onwa2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
90	d1onwa1	Alignment	not modelled	99.4	14	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isoaspartyl dipeptidase
91	d2d2ja1	Alignment	not modelled	99.4	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
92	c3ggmB	Alignment	not modelled	99.4	20	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
93	d2fvka1	Alignment	not modelled	99.4	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
94	c3ou8B	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: B: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
95	c1pscA	Alignment	not modelled	99.3	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
96	d2p9ba1	Alignment	not modelled	99.3	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
97	d1un7a2	Alignment	not modelled	99.3	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
98	c3ou8A	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
99	d2r8ca1	Alignment	not modelled	99.2	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
100	c2zc1A	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
101	d1yrra2	Alignment	not modelled	99.2	9	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
102	d1m7ja3	Alignment	not modelled	99.1	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
103	c3pnzD	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
104	c3f4cA	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearrowtherophilus strain 10, with glycerol bound
105	d2icsa2	Alignment	not modelled	99.1	9	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
106	d1a4ma	Alignment	not modelled	99.0	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
						Fold: Composite domain of metallo-dependent hydrolases

107	d1k1da1	Alignment	not modelled	99.0	22	Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
108	d1vfla1	Alignment	not modelled	99.0	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
109	d2ftwa1	Alignment	not modelled	99.0	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
110	d1ynya1	Alignment	not modelled	99.0	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
111	c2vc7A	Alignment	not modelled	99.0	10	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
112	c3rysa	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
113	d1bf6a	Alignment	not modelled	98.9	8	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
114	d1gkpa1	Alignment	not modelled	98.9	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
115	d3be7a1	Alignment	not modelled	98.8	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
116	d1o12a2	Alignment	not modelled	98.8	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
117	d1yixa1	Alignment	not modelled	98.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
118	d2amxa1	Alignment	not modelled	98.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
119	d1kcxa1	Alignment	not modelled	98.7	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
120	d1m7ja1	Alignment	not modelled	98.7	12	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase