



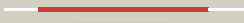



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3egjA_	 Alignment		100.0	62	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
2	c2p50C_	 Alignment		100.0	99	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
3	c2vhlB_	 Alignment		100.0	29	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
4	c1o12B_	 Alignment		100.0	29	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
5	c2bb0A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
6	c2ftwA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
7	c2gseC_	 Alignment		100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
8	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
9	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
10	c2oodA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
11	c2gokA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution

12	c1gkrA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
13	c1k1dF_	Alignment		100.0	16	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
14	c1gkpD_	Alignment		100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
15	c3nqbB_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
16	c2vr2A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
17	c3griB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
18	c2aqoB_	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
19	c3lsbA_	Alignment		100.0	16	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
20	c2pajA_	Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
21	c3lnpA_	Alignment	not modelled	100.0	15	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
22	c3ooqC_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
23	c1nfgA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
24	c2fvmA_	Alignment	not modelled	100.0	14	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
25	c3dc8B_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
26	c3e0lB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammeline deaminase
27	c2gwnA_	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
28	c3gnhA_	Alignment	not modelled	100.0	19	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.
29	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
30	c2p9bA_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
31	c3v7pA_	Alignment	not modelled	100.0	18 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
32	d1yr2a2	Alignment	not modelled	100.0	99 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
33	c3mpgB_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
34	c2z00A_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
35	c3be7B_	Alignment	not modelled	100.0	11 PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
36	c3hm7A_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
37	c1r9yA_	Alignment	not modelled	100.0	12 PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
38	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
39	c1xrfA_	Alignment	not modelled	100.0	17 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	c3hpaB_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
41	c3feqB_	Alignment	not modelled	100.0	18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
42	c2vunC_	Alignment	not modelled	100.0	16 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
43	c3gipB_	Alignment	not modelled	100.0	19 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.
44	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
45	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
46	c1rjqA_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
47	d1un7a2	Alignment	not modelled	100.0	31 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
48	c1p1mA_	Alignment	not modelled	100.0	15 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
49	c2qt3A_	Alignment	not modelled	100.0	14 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
50	c1e9yB_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
51	c2ubpC_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
52	c2icsA_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
53	c1fwcC_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5

54	c3etkA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
55	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)
56	c3mduA	Alignment	not modelled	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
57	c3ighX	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
58	c2ogjB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
59	c2imrA	Alignment	not modelled	99.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
60	d1o12a2	Alignment	not modelled	99.9	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
61	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
62	d2uz9a2	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
63	d1yrra1	Alignment	not modelled	99.7	68	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
64	d2ooda2	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
65	d2i9ua2	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
66	d1gkpa2	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
67	d2bb0a2	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
68	d1kcxa2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
69	d2puza2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
70	d1ra0a2	Alignment	not modelled	99.6	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
71	d2p9ba2	Alignment	not modelled	99.6	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
72	d2q09a2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
73	d2ftwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
74	d2p9ba1	Alignment	not modelled	99.5	27	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
75	d2paja2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
76	d2fvka1	Alignment	not modelled	99.5	16	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
77	d2imra2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
78	d1onwa1	Alignment	not modelled	99.5	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isoaspartyl dipeptidase
79	d1nfga2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
						Fold: TIM beta/alpha-barrel

80	d4ubpc2	Alignment	not modelled	99.5	12	Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
81	c3ggmB_	Alignment	not modelled	99.5	26	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
82	d2r8ca1	Alignment	not modelled	99.5	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
83	d1ejxc1	Alignment	not modelled	99.5	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
84	d1ynya2	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
85	d2qs8a2	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
86	d1k1da2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
87	d3be7a2	Alignment	not modelled	99.4	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
88	d1e9yb1	Alignment	not modelled	99.4	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
89	d1gkra2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
90	d2r8ca2	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
91	d1p1ma2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
92	c3pnuA_	Alignment	not modelled	99.3	7	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
93	d1onwa2	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
94	d2icsa2	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
95	d2fvka2	Alignment	not modelled	99.3	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
96	d1xrta2	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
97	d2ftwa1	Alignment	not modelled	99.2	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
98	d1k1da1	Alignment	not modelled	99.2	19	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
99	d1i0da_	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
100	c3jzeC_	Alignment	not modelled	99.1	9	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
101	d2eg6a1	Alignment	not modelled	99.1	7	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
102	d1ynya1	Alignment	not modelled	99.1	13	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
103	d1gkpa1	Alignment	not modelled	99.1	22	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
104	d1kcxa1	Alignment	not modelled	98.9	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
105	d2bb0a1	Alignment	not modelled	98.9	29	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
106	d1m7ja1	Alignment	not modelled	98.9	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
107	c1pscA_	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase;

					PDBTitle: phosphotriesterase from pseudomonas diminuta
108	d3be7a1	Alignment	not modelled	98.8	11 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
109	d1nfga1	Alignment	not modelled	98.7	15 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
110	d2d2ja1	Alignment	not modelled	98.7	13 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
111	d2paja1	Alignment	not modelled	98.7	21 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
112	d2ooda1	Alignment	not modelled	98.5	27 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
113	c3pnzD_	Alignment	not modelled	98.5	11 PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase Imo2620 from listeria monocytogenes
114	c3ou8B_	Alignment	not modelled	98.5	13 PDB header: hydrolase Chain: B: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
115	c2zc1A_	Alignment	not modelled	98.4	13 PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
116	d1m7ja3	Alignment	not modelled	98.4	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
117	c3f4cA_	Alignment	not modelled	98.3	11 PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
118	d1bf6a_	Alignment	not modelled	98.3	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
119	d1gkra1	Alignment	not modelled	98.3	28 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
120	d1xrta1	Alignment	not modelled	98.3	29 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)