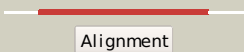

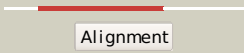







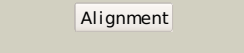

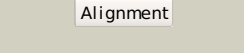

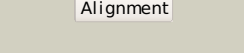



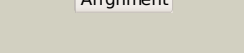

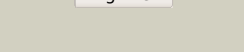






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3nqbB_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> adenine deaminase 2; <b>PDBTitle:</b> crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
2	<a href="#">c2aqoB_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> isoaspartyl dipeptidase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
3	<a href="#">c2pajA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative cytosine/guanine deaminase; <b>PDBTitle:</b> crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
4	<a href="#">c2ubpC_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> protein (urease alpha subunit); <b>PDBTitle:</b> structure of native urease from bacillus pasteurii
5	<a href="#">c1xrfA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution
6	<a href="#">c2ftwA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydropyrimidine amidohydrolase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from dictyostelium discoideum
7	<a href="#">c3lsbA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> triazine hydrolase; <b>PDBTitle:</b> crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureuscs tc1 complexed with zinc and ametrin
8	<a href="#">c2gseC_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dihydropyrimidinase-related protein 2; <b>PDBTitle:</b> crystal structure of human dihydropyrimidinease-like 2
9	<a href="#">c2vunC_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> enamidase; <b>PDBTitle:</b> the crystal structure of amidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
10	<a href="#">c2p50C_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
11	<a href="#">c3be7B_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> zn-dependent arginine carboxypeptidase; <b>PDBTitle:</b> crystal structure of zn-dependent arginine carboxypeptidase

12	<a href="#">c2vr2A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> human dihydropyrimidinase
13	<a href="#">c3hpaB_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
14	<a href="#">c2gokA_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
15	<a href="#">c2q09A_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxo-imidazolidin-4-yl)-propionic acid
16	<a href="#">c2vhlB_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis
17	<a href="#">c2icsA_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenine deaminase; <b>PDBTitle:</b> crystal structure of an adenine deaminase
18	<a href="#">c2bb0A_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> structure of imidazolonepropionase from bacillus subtilis
19	<a href="#">c1fwcC_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> urease; <b>PDBTitle:</b> klebsiella aerogenes urease, c319a variant at ph 8.5
20	<a href="#">c3dc8B_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from sinorhizobium meliloti
21	<a href="#">c1gkrA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-atp dependent l-selective hydantoinase; <b>PDBTitle:</b> l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aureus
22	<a href="#">c1gkpD_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> hydantoinase; <b>PDBTitle:</b> d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
23	<a href="#">c3gipB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acyl-d-glutamate deacylase; <b>PDBTitle:</b> crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
24	<a href="#">c3gnhA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine, l-arginine carboxypeptidase cc2672; <b>PDBTitle:</b> crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.
25	<a href="#">c1e9yB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> urease subunit beta; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
26	<a href="#">c3la4A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease; <b>PDBTitle:</b> crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
27	<a href="#">c3d6nA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase

28	<a href="#">c2fvmA</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
29	<a href="#">c2r8cB</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative amidohydrolase; <b>PDBTitle:</b> crystal structure of uncharacterized protein eaj56179
30	<a href="#">c2gwnA</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the structure of putative dihydroorotase from porphyromonas2 gingivalis.
31	<a href="#">c1k1dF</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> d-hydantoinase; <b>PDBTitle:</b> crystal structure of d-hydantoinase
32	<a href="#">c3lnpA</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase family protein olei01672_1_465; <b>PDBTitle:</b> crystal structure of amidohydrolase family protein2 olei01672_1_465 from oleispira antarctica
33	<a href="#">c1nfgA</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-hydantoinase; <b>PDBTitle:</b> structure of d-hydantoinase
34	<a href="#">c1rjqA</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-aminoacylase; <b>PDBTitle:</b> the crystal structure of the d-aminoacylase mutant d366a
35	<a href="#">c3egjA</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
36	<a href="#">c2p9bA</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible prolidase; <b>PDBTitle:</b> crystal structure of putative prolidase from2 bifidobacterium longum
37	<a href="#">c1o12B</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-6-phosphate2 deacetylase (tm0814) from thermotoga maritima at 2.5 a3 resolution
38	<a href="#">c3feqB</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative amidohydrolase; <b>PDBTitle:</b> crystal structure of uncharacterized protein eah89906
39	<a href="#">c1p1mA</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0936; <b>PDBTitle:</b> structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
40	<a href="#">c3hm7A</a>	 Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allantoinase; <b>PDBTitle:</b> crystal structure of allantoinase from bacillus halodurans c-125
41	<a href="#">c2qt3A</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-isopropylammelide isopropyl amidohydrolase; <b>PDBTitle:</b> crystal structure of n-isopropylammelide isopropylaminohydrolase atzc2 from pseudomonas sp. strain adp complexed with zn
42	<a href="#">c2z00A</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase from thermus thermophilus
43	<a href="#">c3ooqC</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase from thermotoga maritima msb8
44	<a href="#">c3griB</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the crystal structure of a dihydroorotase from staphylococcus aureus
45	<a href="#">c3mpgB</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> dihydroorotase from bacillus anthracis
46	<a href="#">c3e74D</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> allantoinase; <b>PDBTitle:</b> crystal structure of e. coli allantoinase with iron ions at2 the metal center
47	<a href="#">c2ogjB</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase
48	<a href="#">c2i9uA</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine/guanine deaminase related protein; <b>PDBTitle:</b> crystal structure of guanine deaminase from c. acetobutylicum with2 bound guanine in the active site
49	<a href="#">c3e0lB</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> guanine deaminase; <b>PDBTitle:</b> computationally designed ammeline deaminase
50	<a href="#">c2qs8A</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of a xaa-pro dipeptidase with bound2 methionine in the active site
51	<a href="#">c3v7pA</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase family protein; <b>PDBTitle:</b> crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
52	<a href="#">c2oodA</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> blr3880 protein;

52	<a href="#">c200uA</a>	Alignment	not modelled	100.0	17	<b>PDBTitle:</b> crystal structure of guanine deaminase from bradyrhizobium japonicum
53	<a href="#">c1r9yA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine deaminase; <b>PDBTitle:</b> bacterial cytosine deaminase d314a mutant.
54	<a href="#">c3mduA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-formimino-l-glutamate iminohydrolase; <b>PDBTitle:</b> the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
55	<a href="#">c3ighX</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
56	<a href="#">c3etkA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
57	<a href="#">c2imrA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dr_0824; <b>PDBTitle:</b> crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
58	<a href="#">d2icsa2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenine deaminase-like
59	<a href="#">c3msrA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolases; <b>PDBTitle:</b> the crystal structure of an amidohydrolase from mycoplasma synoviae
60	<a href="#">d1onwa2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Isoaspartyl dipeptidase, catalytic domain
61	<a href="#">d1o12a2</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
62	<a href="#">d2paja2</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
63	<a href="#">d1xrta2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
64	<a href="#">d1kcxa2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
65	<a href="#">d4ubpc2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> alpha-subunit of urease, catalytic domain
66	<a href="#">d1ynya2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
67	<a href="#">d3be7a2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
68	<a href="#">d2p9ba2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
69	<a href="#">d2ftwa2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
70	<a href="#">d1gkpa2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
71	<a href="#">d1un7a2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
72	<a href="#">c3pnuA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
73	<a href="#">d1e9yb1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
74	<a href="#">d2ooda2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
75	<a href="#">d2bb0a2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
76	<a href="#">d1yrra2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
77	<a href="#">d1k1da2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
78	<a href="#">d2qs8a2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like

79	<a href="#">d1ejxc1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
80	<a href="#">d2i9ua2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
81	<a href="#">d2uz9a2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
82	<a href="#">dli0da_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
83	<a href="#">d2puza2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
84	<a href="#">d1nfga2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
85	<a href="#">c3ggmB_</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bt9727_2919; <b>PDBTitle:</b> crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
86	<a href="#">d2r8ca2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
87	<a href="#">d2eg6a1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
88	<a href="#">d1ra0a2</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Cytosine deaminase catalytic domain
89	<a href="#">d2q09a2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
90	<a href="#">d1onwa1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Isoaspartyl dipeptidase
91	<a href="#">c3jzeC_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. It2
92	<a href="#">d2fvka1</a>	Alignment	not modelled	99.6	28	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
93	<a href="#">c1pscA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> phosphotriesterase from pseudomonas diminuta
94	<a href="#">d2d2ja1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
95	<a href="#">d1gkra2</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
96	<a href="#">d2imra2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> DR0824-like
97	<a href="#">d2r8ca1</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
98	<a href="#">c2zc1A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> organophosphorus hydrolase from deinococcus radiodurans
99	<a href="#">dlyxa1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
100	<a href="#">d2fvka2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
101	<a href="#">c3pnzD_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphotriesterase family protein; <b>PDBTitle:</b> crystal structure of the lactonase Imo2620 from listeria monocytogenes
102	<a href="#">d1yrra1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA
103	<a href="#">d2p9ba1</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
104	<a href="#">d1plma2</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
105	<a href="#">d1bf6a_</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like



106	<a href="#">dlzzma1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
107	<a href="#">c3f4cA</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus hydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus hydrolase from geobacillus2 steaerothermophilus strain 10, with glycerol bound
108	<a href="#">c2vc7A</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aryldialkylphosphatase; <b>PDBTitle:</b> structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
109	<a href="#">dlm7ja1</a>	Alignment	not modelled	99.4	29	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> D-aminoacylase
110	<a href="#">d2ftwa1</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
111	<a href="#">dlk1da1</a>	Alignment	not modelled	99.3	23	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
112	<a href="#">c3rcmA</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tatd family hydrolase; <b>PDBTitle:</b> crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
113	<a href="#">dlxwya1</a>	Alignment	not modelled	99.2	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
114	<a href="#">c2y1hA</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyri bonuclease tatdn3; <b>PDBTitle:</b> crystal structure of the human tatd-domain protein 3 (tatdn3)
115	<a href="#">dlgkpa1</a>	Alignment	not modelled	99.2	28	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
116	<a href="#">dlj6oa</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
117	<a href="#">dlynay1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
118	<a href="#">dlm7ja3</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> D-aminoacylase, catalytic domain
119	<a href="#">dlkcxa1</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
120	<a href="#">c3rhgA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphotriesterase; <b>PDBTitle:</b> crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320