Phyre^2

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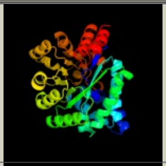
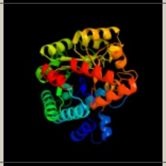
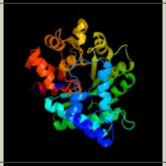
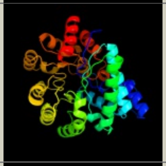
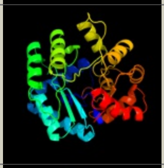
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rysA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
2	d2amxa1	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
3	d1vfla1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
4	d1a4ma_	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
5	c3lggA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase cecr1; **PDBTitle:** crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin
6	c3ou8B_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
7	c3ou8A_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
8	d2a3la1	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
9	c2a3lA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amp deaminase; **PDBTitle:** x-ray structure of adenosine 5'-monophosphate deaminase from2 arabidopsis thaliana in complex with coformycin 5'-phosphate
10	d1p1ma2	Alignment		99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
11	d2i9ua2	Alignment		99.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like

12	d2imra2	Alignment		99.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
13	d2q09a2	Alignment		99.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
14	d1ra0a2	Alignment		99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
15	d2uz9a2	Alignment		99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
16	d2bb0a2	Alignment		99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
17	d2puza2	Alignment		99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
18	c2bb0A_	Alignment		99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis
19	c3e0lB_	Alignment		99.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine deaminase; **PDBTitle:** computationally designed ammelide deaminase
20	c2q09A_	Alignment		99.6	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
21	c2gokA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
22	d2paja2	Alignment	not modelled	99.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
23	d2ooda2	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
24	c1p1mA_	Alignment	not modelled	99.5	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
25	c3hpaB_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
26	c2imrA_	Alignment	not modelled	99.5	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
27	c2pajA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/guanine deaminase; **PDBTitle:** crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
28	c2i9uA_	Alignment	not modelled	99.4	14	**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

29	c3lsbA_	Alignment	not modelled	99.4	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
30	d2r8ca2	Alignment	not modelled	99.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
31	c1r9yA_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine deaminase; **PDBTitle:** bacterial cytosine deaminase d314a mutant.
32	d3be7a2	Alignment	not modelled	99.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
33	d2qs8a2	Alignment	not modelled	99.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
34	c3lnpA_	Alignment	not modelled	99.2	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
35	c3v7pA_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase family protein; **PDBTitle:** crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
36	c3mduA_	Alignment	not modelled	99.2	14	**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
37	c3etkA_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
38	c2oodA_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr3880 protein; **PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum
39	c1xrfA_	Alignment	not modelled	99.0	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	c2vunC_	Alignment	not modelled	99.0	16	**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
41	c3ighX_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
42	c2qt3A_	Alignment	not modelled	98.9	15	**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
43	d2p9ba2	Alignment	not modelled	98.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
44	d1xrta2	Alignment	not modelled	98.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
45	c2vc7A_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
46	c1pscA_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
47	c2vr2A_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
48	c2r8cB_	Alignment	not modelled	98.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eaj56179
49	d2d2ja1	Alignment	not modelled	98.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
50	c3ooqC_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of amidohydrolase from thermotoga maritima msb8
51	d1i0da_	Alignment	not modelled	98.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
52	c3gnhA_	Alignment	not modelled	98.4	18	**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.
						PDB header:hydrolase

53	c2ftwA_	Alignment	not modelled	98.4	16	**Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase; **PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum
54	c2gseC_	Alignment	not modelled	98.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2; **PDBTitle:** crystal structure of human dihydropyrimidinease-like 2
55	c3pnzD_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphotriesterase family protein; **PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes
56	c3f4cA_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
57	c3dc8B_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from sinorhizobium meliloti
58	c3nqbB_	Alignment	not modelled	98.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
59	d1zzma1	Alignment	not modelled	98.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
60	c3rcmA_	Alignment	not modelled	98.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
61	c3gipB_	Alignment	not modelled	98.1	11	**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.
62	c1gkpD_	Alignment	not modelled	98.1	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**hydantoinase; **PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
63	c3msrA_	Alignment	not modelled	98.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
64	d1kcxa2	Alignment	not modelled	98.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
65	c1nfgA_	Alignment	not modelled	97.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-hydantoinase; **PDBTitle:** structure of d-hydantoinase
66	c1k1dF_	Alignment	not modelled	97.9	9	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**d-hydantoinase; **PDBTitle:** crystal structure of d-hydantoinase
67	c3egjA_	Alignment	not modelled	97.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
68	c3be7B_	Alignment	not modelled	97.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase; **PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase
69	c2xioA_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
70	c3k2gA_	Alignment	not modelled	97.8	18	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
71	c2ogjB_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of a dihydroorotase
72	d1gkpa2	Alignment	not modelled	97.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
73	c3ij6A_	Alignment	not modelled	97.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
74	c3hm7A_	Alignment	not modelled	97.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
75	d1xwya1	Alignment	not modelled	97.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
76	c2p50C_	Alignment	not modelled	97.7	12	**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
77	c3guwB_	Alignment	not modelled	97.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_1765; **PDBTitle:** crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121
						PDB header:hydrolase/transferase

78	c3d6nA_	Alignment	not modelled	97.7	14	**Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
79	c1gkrA_	Alignment	not modelled	97.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
80	c3feqB_	Alignment	not modelled	97.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eah89906
81	d2dvta1	Alignment	not modelled	97.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
82	c2zc1A_	Alignment	not modelled	97.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
83	d1j6oa_	Alignment	not modelled	97.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
84	d1bf6a_	Alignment	not modelled	97.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
85	c2qs8A_	Alignment	not modelled	97.4	19	**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
86	c3qy6A_	Alignment	not modelled	97.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe; **PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
87	d2f6ka1	Alignment	not modelled	97.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
88	c2aqoB_	Alignment	not modelled	97.4	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase; **PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
89	c3ipwA_	Alignment	not modelled	97.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
90	d1yixa1	Alignment	not modelled	97.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
91	c3e2vA_	Alignment	not modelled	97.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
92	c3e74D_	Alignment	not modelled	97.2	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of e. coli allantoinase with iron ions at2 the metal center
93	c2p9bA_	Alignment	not modelled	97.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible prolidase; **PDBTitle:** crystal structure of putative prolidase from2 bifidobacterium longum
94	c2wjeA_	Alignment	not modelled	97.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
95	c2vhlB_	Alignment	not modelled	97.1	14	**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
96	d2ffia1	Alignment	not modelled	96.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
97	c2gzxB_	Alignment	not modelled	96.9	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative tatd related dnase; **PDBTitle:** crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
98	c2w9mB_	Alignment	not modelled	96.8	11	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
99	c1rjqA_	Alignment	not modelled	96.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminoacylase; **PDBTitle:** the crystal structure of the d-aminoacylase mutant d366a
100	c3mpgB_	Alignment	not modelled	96.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** dihydroorotase from bacillus anthracis
101	d1onwa2	Alignment	not modelled	96.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
102	d2ftwa2	Alignment	not modelled	96.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
103	d1ynya2	Alignment	not modelled	96.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases

						Family: Hydantoinase (dihydropyrimidinase), catalytic domain
104	c3nurA_	Alignment	not modelled	96.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus
105	c2gwnA_	Alignment	not modelled	96.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis.
106	c2y1hA_	Alignment	not modelled	96.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
107	c3rhgA_	Alignment	not modelled	95.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
108	c2fvmA_	Alignment	not modelled	95.8	7	**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
109	d1k1da2	Alignment	not modelled	95.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
110	c2z00A_	Alignment	not modelled	95.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus
111	d4ubpc2	Alignment	not modelled	94.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
112	c3griB_	Alignment	not modelled	94.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** the crystal structure of a dihydroorotase from staphylococcus aureus
113	c2icsA_	Alignment	not modelled	94.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenine deaminase; **PDBTitle:** crystal structure of an adenine deaminase
114	c2wm1A_	Alignment	not modelled	94.5	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-amino-3-carboxymuconate-6-semialdehyde **PDBTitle:** the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis
115	d2icsa2	Alignment	not modelled	92.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
116	c3cjpA_	Alignment	not modelled	90.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
117	c3irsB_	Alignment	not modelled	90.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bb4693; **PDBTitle:** crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
118	c1o12B_	Alignment	not modelled	90.3	11	**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
119	d2hbva1	Alignment	not modelled	90.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
120	c2ubpC_	Alignment	not modelled	88.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (urease alpha subunit); **PDBTitle:** structure of native urease from bacillus pasteurii