

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bf6a_	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
2	c3k2gA_	 Alignment		100.0	32	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
3	c3f4cA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 steartotherophilus strain 10, with glycerol bound
4	c3rhgA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
5	c2vc7A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
6	c2zc1A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
7	c3pnzD_	 Alignment		100.0	29	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase Imo2620 from listeria monocytogenes
8	d2d2ja1	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
9	d1i0da_	 Alignment		100.0	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
10	c1pscA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
11	c2xioA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a

12	c2y1hA_	Alignment		100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
13	c3ipwA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
14	c3e2vA_	Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
15	c3msrA_	Alignment		99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
16	dlxwya1	Alignment		99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
17	dlyixa1	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
18	dlj6oa_	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
19	dlzzma1	Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
20	c2gzxB_	Alignment		99.9	14	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.
21	c3rcmA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
22	c2qabA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: 2-pyrone-4,6-dicarboxylic acid hydrolase; PDBTitle: crystal structure of the 2-pyrone-4,6-dicarboxylic acid2 hydrolase from sphingomonas paucimobilis
23	d2ffia1	Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
24	c3irsB_	Alignment	not modelled	99.9	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
25	c3gg7A_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
26	d2dvta1	Alignment	not modelled	99.9	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
27	c3ij6A_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
28	d2gwga1	Alignment	not modelled	99.9	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like

29	c3guwB	Alignment	not modelled	99.9	15	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
30	c2wm1A	Alignment	not modelled	99.9	14	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
31	c3cjpA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotase family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
32	d2hbva1	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
33	d2f6ka1	Alignment	not modelled	99.8	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
34	c3nurA	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
35	d1xrta2	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
36	d1k1da2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
37	d1nfga2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
38	d1ynya2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
39	d1gkra2	Alignment	not modelled	99.6	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
40	c3pnuA	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
41	d3be7a2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
42	d2icsa2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
43	d1kcx2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
44	d2paja2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
45	d1onwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
46	d2qs8a2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
47	d2uz9a2	Alignment	not modelled	99.5	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
48	d2ftwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
49	c3jzeC	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
50	d2eg6a1	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
51	d2i9ua2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
52	d2r8ca2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
53	c2qpxA	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted metal-dependent hydrolase of the tim-barrel fold; PDBTitle: crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution

54	d1gkpa2	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
55	d2fvka2	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
56	d2p9ba2	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
57	c1xrfA_	Alignment	not modelled	99.3	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
58	d1p1ma2	Alignment	not modelled	99.3	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
59	c2pajA_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
60	d2imra2	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
61	c2ogfB_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
62	c3e0lB_	Alignment	not modelled	99.2	10	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
63	d2bb0a2	Alignment	not modelled	99.1	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
64	c2vr2A_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
65	d2puza2	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
66	c3hpaB_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
67	c2vunC_	Alignment	not modelled	99.1	13	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
68	d2ooda2	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
69	c3gnhA_	Alignment	not modelled	99.1	12	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.
70	c2aqoB_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
71	c3nqbB_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
72	c3dc8B_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
73	d2q09a2	Alignment	not modelled	99.1	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
74	c1p1mA_	Alignment	not modelled	99.1	12	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
75	c3itcA_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
76	c1nfgA_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
77	c3lsbA_	Alignment	not modelled	99.0	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
78	c2ftwA_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
79	c2q09A_	Alignment	not modelled	99.0	13	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 PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
80	c2bb0A_	Alignment	not modelled	99.0	11
81	c2i9uA_	Alignment	not modelled	99.0	12
82	c2gseC_	Alignment	not modelled	99.0	13
83	c1gkpD_	Alignment	not modelled	99.0	13
84	c3d6nA_	Alignment	not modelled	99.0	15
85	c3lnpA_	Alignment	not modelled	99.0	11
86	c1k1dF_	Alignment	not modelled	98.9	15
87	c2icsA_	Alignment	not modelled	98.9	16
88	c2imrA_	Alignment	not modelled	98.9	16
89	c1gkrA_	Alignment	not modelled	98.9	18
90	c2fvmA_	Alignment	not modelled	98.9	16
91	c2gokA_	Alignment	not modelled	98.9	12
92	d1o12a2	Alignment	not modelled	98.9	10
93	d1ra0a2	Alignment	not modelled	98.9	15
94	d4ubpc2	Alignment	not modelled	98.9	13
95	d1itua_	Alignment	not modelled	98.9	13
96	c3be7B_	Alignment	not modelled	98.9	12
97	c3fdgA_	Alignment	not modelled	98.8	12
98	d1m7ja3	Alignment	not modelled	98.8	16
99	c2i5gB_	Alignment	not modelled	98.8	14
100	c3hm7A_	Alignment	not modelled	98.8	12
101	c2ragB_	Alignment	not modelled	98.7	15
102	c3mduA_	Alignment	not modelled	98.7	18
103	c1r9yA_	Alignment	not modelled	98.7	11
104	c2gwnA_	Alignment	not modelled	98.7	14

104	c2gwnA	Alignment	not modelled	98.7	14	PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis. PDB header: hydrolase
105	c3ooqC	Alignment	not modelled	98.7	14	Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
106	c2qs8A	Alignment	not modelled	98.7	11	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
107	c2p50C	Alignment	not modelled	98.7	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
108	c3lu2B	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
109	c3b40A	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
110	c3mpqB	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
111	c2z00A	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
112	c3e74D	Alignment	not modelled	98.6	13	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at2 the metal center
113	c2qt3A	Alignment	not modelled	98.6	8	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
114	c2r8cB	Alignment	not modelled	98.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
115	c3griB	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
116	c2wjeA	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
117	c3feqB	Alignment	not modelled	98.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
118	c2p9bA	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
119	c2oodA	Alignment	not modelled	98.4	11	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
120	dlj5sa	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like