Phyre2

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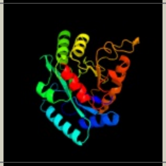
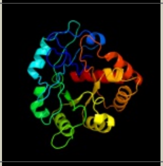
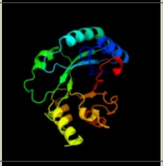
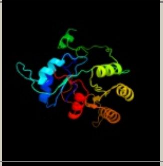
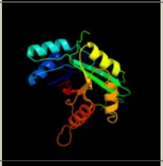
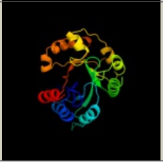
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m65a_	Alignment		100.0	100	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
2	c2w9mB_	Alignment		100.0	19	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
3	c2yz5B_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol phosphatase; **PDBTitle:** histidinol phosphate phosphatase complexed with phosphate
4	c3qy6A_	Alignment		100.0	16	**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
5	c2wjeA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
6	c3dcpB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol-phosphatase; **PDBTitle:** crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141.
7	c3e0fA_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase; **PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
8	c2yb1A_	Alignment		99.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
9	d2anua1	Alignment		99.9	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
10	c2anuA_	Alignment		99.9	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm0559; **PDBTitle:** crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
11	c3e0dA_	Alignment		99.9	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit

12	c3e38A_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**two-domain protein containing predicted php-like metal- **PDBTitle:** crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
13	c2hnhA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
14	c3f2cA_	Alignment		99.8	22	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
15	d1v77a_	Alignment		98.3	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30
16	d1bf6a_	Alignment		97.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
17	c3rcmA_	Alignment		97.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
18	d1yixa1	Alignment		97.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
19	d1xrta2	Alignment		97.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
20	c3rysA_	Alignment		97.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
21	d1xwya1	Alignment	not modelled	97.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
22	c2xioA_	Alignment	not modelled	96.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
23	c2y1hA_	Alignment	not modelled	96.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
24	d1zzma1	Alignment	not modelled	96.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
25	c3f4cA_	Alignment	not modelled	96.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
26	d1j6oa_	Alignment	not modelled	96.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
27	c3rhgA_	Alignment	not modelled	96.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
28	c3ou8A_	Alignment	not modelled	96.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
						PDB header:hydrolase

29	c2vc7A_	Alignment	not modelled	95.9	16	**Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
30	c3ou8B_	Alignment	not modelled	95.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
31	d2icsa2	Alignment	not modelled	95.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
32	c3ipwA_	Alignment	not modelled	95.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
33	d2amxa1	Alignment	not modelled	94.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
34	c3gg7A_	Alignment	not modelled	94.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
35	c3msrA_	Alignment	not modelled	94.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
36	d1vfla1	Alignment	not modelled	94.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
37	d1i0da_	Alignment	not modelled	94.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
38	d1onwa2	Alignment	not modelled	93.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
39	c2zc1A_	Alignment	not modelled	93.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
40	d1ynya2	Alignment	not modelled	93.3	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
41	c3k2gA_	Alignment	not modelled	93.2	10	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
42	c1pscA_	Alignment	not modelled	93.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
43	d2f6ka1	Alignment	not modelled	92.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
44	d2imra2	Alignment	not modelled	92.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
45	d2i9ua2	Alignment	not modelled	92.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
46	d1p1ma2	Alignment	not modelled	91.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
47	c3ij6A_	Alignment	not modelled	90.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
48	d1k1da2	Alignment	not modelled	90.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
49	c3guwB_	Alignment	not modelled	90.3	11	**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
50	d1gkra2	Alignment	not modelled	90.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
51	c3nqbB_	Alignment	not modelled	89.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
52	d2ffia1	Alignment	not modelled	89.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
53	d2paja2	Alignment	not modelled	88.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
54	d2d2ja1	Alignment	not modelled	87.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
55	c3pnzD_	Alignment	not modelled	87.1	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphotriesterase family protein;

		Alignment				**PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes
56	c2wm1A_	Alignment	not modelled	86.3	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
57	d2fvka2	Alignment	not modelled	85.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
58	d2bb0a2	Alignment	not modelled	85.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
59	c2gzxB_	Alignment	not modelled	85.6	9	**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.
60	c3e2vA_	Alignment	not modelled	84.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
61	d2puza2	Alignment	not modelled	84.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
62	d1nfga2	Alignment	not modelled	82.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
63	d2q09a2	Alignment	not modelled	80.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
64	d2ftwa2	Alignment	not modelled	79.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
65	d2uz9a2	Alignment	not modelled	77.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
66	d1kcxa2	Alignment	not modelled	77.3	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
67	c3cprB_	Alignment	not modelled	71.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
68	c2yxgD_	Alignment	not modelled	70.1	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
69	c2qahA_	Alignment	not modelled	69.6	18	**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
70	c3daqB_	Alignment	not modelled	65.0	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
71	c1xrfA_	Alignment	not modelled	62.7	12	**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
72	c3cjpA_	Alignment	not modelled	61.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
73	c3irsB_	Alignment	not modelled	60.8	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
74	c2bb0A_	Alignment	not modelled	57.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis
75	d2p9ba2	Alignment	not modelled	54.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
76	c3lggA_	Alignment	not modelled	54.4	17	**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
77	c1o12B_	Alignment	not modelled	54.3	24	**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
78	d1ra0a2	Alignment	not modelled	52.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
79	c3nurA_	Alignment	not modelled	52.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus

80	d1xxxa1	Alignment	not modelled	51.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
81	d1yara1	Alignment	not modelled	51.0	24	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
82	d1x92a_	Alignment	not modelled	50.6	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
83	d1iruf_	Alignment	not modelled	49.0	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
84	c1iruF_	Alignment	not modelled	49.0	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**20s proteasome; **PDBTitle:** crystal structure of the mammalian 20s proteasome at 2.75 a2 resolution
85	d3be7a2	Alignment	not modelled	48.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
86	c3pnuA_	Alignment	not modelled	48.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
87	c3noeA_	Alignment	not modelled	45.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
88	d1a4ma_	Alignment	not modelled	45.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
89	d1rypb_	Alignment	not modelled	45.0	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
90	d1o12a2	Alignment	not modelled	44.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
91	c3hm7A_	Alignment	not modelled	43.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
92	c3si9B_	Alignment	not modelled	42.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
93	d1irug_	Alignment	not modelled	41.9	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
94	c2xhzC_	Alignment	not modelled	41.4	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
95	d1vkya_	Alignment	not modelled	41.4	18	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
96	d4ubpc2	Alignment	not modelled	40.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
97	c2i5gB_	Alignment	not modelled	39.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
98	d1rypg_	Alignment	not modelled	39.4	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
99	c3bdmF_	Alignment	not modelled	39.4	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome component c1; **PDBTitle:** yeast 20s proteasome:glidobactin a-complex
100	c3lu2B_	Alignment	not modelled	39.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
101	d1irua_	Alignment	not modelled	38.5	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
102	d1yrra2	Alignment	not modelled	38.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
103	d1hl2a_	Alignment	not modelled	37.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
104	c3fxaA_	Alignment	not modelled	37.8	25	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
105	d1f6ya_	Alignment	not modelled	37.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases

106	c3trjC_	Alignment	not modelled	36.8	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
107	d2q02a1	Alignment	not modelled	36.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
108	d1irud_	Alignment	not modelled	35.9	24	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
109	c3h4pB_	Alignment	not modelled	35.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus2 jannaschii
110	d1un7a2	Alignment	not modelled	34.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
111	d1iruc_	Alignment	not modelled	34.2	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
112	c1gkrA_	Alignment	not modelled	34.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
113	d1rypf_	Alignment	not modelled	33.5	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
114	d1rypd_	Alignment	not modelled	33.1	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
115	c2q09A_	Alignment	not modelled	32.9	12	**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
116	d1gkpa2	Alignment	not modelled	32.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
117	c2vr2A_	Alignment	not modelled	32.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
118	d1irue_	Alignment	not modelled	32.2	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
119	d2bz1a1	Alignment	not modelled	31.7	19	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
120	c3bd0D_	Alignment	not modelled	31.5	12	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii