

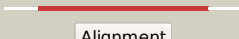

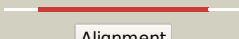











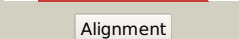






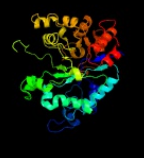






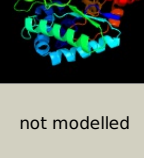


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3313c_(add)_3701258_3702355
Date	Thu Aug 8 16:20:52 BST 2019
Unique Job ID	fc73668579fc82c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ii7A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of plasmodium falciparum adenosine deaminase2 c27q+l227i mutant co-complexed with zn ion, hypoxanthine and inosine
2	d2amxa1	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
3	c6n91A_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of adenosine deaminase from vibrio cholerae2 complexed with pentostatin (deoxycoformycin)
4	c4gxwA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of a cog1816 amidohydrolase (target efi-505188) from2 burkholderia ambifaria, with bound zn
5	d1vfla1	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
6	d1a4ma_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
7	c3rysA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aur1117) from2 arthrobacter aureus
8	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
9	c6iipA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: adenosine/amp deaminase family protein; PDBTitle: the structure of the adal-imp complex
10	c3ou8B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
11	c3ou8A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa

12	d2a3la1	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
13	c2a3la	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: amp deaminase; PDBTitle: x-ray structure of adenosine 5'-monophosphate deaminase from <i>Arabidopsis thaliana</i> in complex with coformycin 5'-phosphate
14	d1p1ma2	Alignment		99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
15	d2i9ua2	Alignment		99.8	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
16	d1ra0a2	Alignment		99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
17	d2imra2	Alignment		99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
18	d2uz9a2	Alignment		99.7	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
19	d2q09a2	Alignment		99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
20	d2bb0a2	Alignment		99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
21	c4dzhA	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from <i>Xanthomonas campestris</i> (target nysgrc-200456) with bound zn
22	d2puza2	Alignment	not modelled	99.5	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
23	c3e0lB	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
24	d2ooda2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
25	c4v1xA	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
26	c4dykB	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from <i>Pseudomonas aeruginosa</i> pao1 (target nysgrc-200449) with bound zn
27	d2paja2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
28	c2bb0A	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from <i>Bacillus subtilis</i> PDB header: hydrolase

29	c2q09A	Alignment	not modelled	99.4	13	Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxoimidazolidin-4-yl)-propionic acid
30	c6ohaA	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: A; PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
31	c1r9yA	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A; PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
32	c2gokA	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
33	c3hpaB	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: B; PDB Molecule: amidohydrolyase; PDBTitle: crystal structure of an amidohydrolyase gi:44264246 from an2 environmental sample of sargasso sea
34	c1p1mA	Alignment	not modelled	99.3	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein tm0936; PDBTitle: structure of thermotoga maritima amidohydrolyase tm09362 bound to ni and methionine
35	c2i9uA	Alignment	not modelled	99.3	10	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
36	c4f0rA	Alignment	not modelled	99.2	12	PDB header: hydrolase Chain: A; PDB Molecule: 5-methylthioadenosine/s-adenosylhomocysteine deaminase; PDBTitle: crystal structure of an adenosine deaminase homolog from2 chromobacterium violaceum (target nysgrc-019589) bound zn and 5'-3 methylthioadenosine (unproductive complex)
37	c2pajA	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A; PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolyase from an environmental sample of2 sargasso sea
38	c4jnrE	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: E; PDB Molecule: putative cytosine deaminase and related metal-dependent PDBTitle: crystal structure of 5-methylcytosine deaminase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 liganded with 5-fluorocytosine
39	c3lsbA	Alignment	not modelled	99.2	12	PDB header: hydrolase Chain: A; PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolyase trzn2 from arthrobacter aureoscens tc1 complexed with zinc and ametrin
40	c3lnpA	Alignment	not modelled	99.2	12	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolyase family protein olei01672_1_465; PDBTitle: crystal structure of amidohydrolyase family protein olei01672_1_4652 from oleispira antarctica
41	c2imrA	Alignment	not modelled	99.2	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolyase dr_0824 from2 deinococcus radiodurans
42	c6ohcB	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: B; PDB Molecule: guanine deaminase; PDBTitle: e. coli guanine deaminase
43	c4f0lB	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: B; PDB Molecule: amidohydrolyase; PDBTitle: crystal structure of amidohydrolyase from brucella melitensis
44	c3mduA	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: A; PDB Molecule: n-formimino-l-glutamate iminohydrolyase; PDBTitle: the structure of n-formimino-l-glutamate iminohydrolyase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
45	d2qs8a2	Alignment	not modelled	99.1	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
46	c3v7pA	Alignment	not modelled	98.9	11	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolyase family protein; PDBTitle: crystal structure of amidohydrolyase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
47	d3be7a2	Alignment	not modelled	98.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
48	c2qt3A	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: A; PDB Molecule: n-isopropylammelide isopropyl amidohydrolyase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolyase atzc2 from pseudomonas sp. strain adp complexed with zn
49	d2r8ca2	Alignment	not modelled	98.7	20	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
50	c2oodA	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: A; PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
51	c6nboA	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: A; PDB Molecule: n-isopropylammelide isopropylaminohydrolyase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolyase from2 burkholderia multivorans atcc 17616
						Fold: TIM beta/alpha-barrel

52	d1xrta2	Alignment	not modelled	98.5	12	Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
53	c1xrfA_	Alignment	not modelled	98.5	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
54	c4c65A_	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
55	c2vunC_	Alignment	not modelled	98.2	13	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
56	c3ooqC_	Alignment	not modelled	98.2	14	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
57	c3f4cA_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
58	d2d2ja1	Alignment	not modelled	98.1	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
59	c3gnhA_	Alignment	not modelled	98.0	13	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.
60	c3etkA_	Alignment	not modelled	98.0	8	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
61	d2p9ba2	Alignment	not modelled	98.0	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
62	d1zzma1	Alignment	not modelled	97.9	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
63	d1i0da_	Alignment	not modelled	97.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
64	c3tn6A_	Alignment	not modelled	97.8	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
65	d1gkpa2	Alignment	not modelled	97.8	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
66	c3nqbB_	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
67	c4l5pD_	Alignment	not modelled	97.8	11	PDB header: lyase Chain: D: PDB Molecule: 5-carboxyvanillate decarboxylase; PDBTitle: crystal structure of 5-carboxyvanillate decarboxylase from2 sphingomonas paucimobilis complexed with 4-hydroxy-3-methoxy-5-3 nitrobenzoic acid
68	d1kcx2	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
69	c3ighX_	Alignment	not modelled	97.7	9	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
70	c4wgxD_	Alignment	not modelled	97.6	13	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
71	c1gkpD_	Alignment	not modelled	97.5	11	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
72	c1k1dF_	Alignment	not modelled	97.4	5	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
73	c1nfgA_	Alignment	not modelled	97.4	9	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
74	c2ogjB_	Alignment	not modelled	97.4	12	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
75	c3msrA_	Alignment	not modelled	97.3	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
76	c2ogjC_	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
77	c3feqB_	Alignment	not modelled	97.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906

78	c1pscA	Alignment	not modelled	97.3	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
79	d1xwya1	Alignment	not modelled	97.2	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
80	c3pnzD	Alignment	not modelled	97.1	10	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
81	c2zc1A	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
82	c3guwB	Alignment	not modelled	97.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_1765; PDBTitle: crystal structure of the tatd-like protein (af1765) from archaeoglobus2 fulgidus, northeast structural genomics consortium target gr121
83	d2ffia1	Alignment	not modelled	97.1	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
84	c2r8cB	Alignment	not modelled	97.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
85	c3be7B	Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
86	c2ftwA	Alignment	not modelled	97.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
87	c3d6nA	Alignment	not modelled	97.0	9	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
88	c1gkrA	Alignment	not modelled	97.0	9	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aureus
89	d1j6oa	Alignment	not modelled	97.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
90	c3k2gA	Alignment	not modelled	97.0	20	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
91	c3ij6A	Alignment	not modelled	96.9	9	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus
92	c4whbC	Alignment	not modelled	96.8	12	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
93	c3qy6A	Alignment	not modelled	96.7	15	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
94	c2vc7A	Alignment	not modelled	96.5	14	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
95	c3dc8B	Alignment	not modelled	96.5	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium melloti
96	c3rcmA	Alignment	not modelled	96.5	11	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
97	c4if2A	Alignment	not modelled	96.5	9	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase homology protein; PDBTitle: structure of the phosphotriesterase from mycobacterium tuberculosis
98	c3hm7A	Alignment	not modelled	96.5	7	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
99	c2qs8A	Alignment	not modelled	96.4	22	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of a xaa-pro dipeptidase with bound methionine in2 the active site
100	c2xioA	Alignment	not modelled	96.4	16	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
101	c2y1hA	Alignment	not modelled	96.4	15	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
102	c2wjeA	Alignment	not modelled	96.3	13	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.

103	c6dxsB	Alignment	not modelled	96.2	12	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: 4-oxalomesaconate hydratase; PDBTitle: crystal structure of the ligj hydratase e284q mutant substrate complex2 with (3z)-2-keto-4-carboxy-3-hexenedioate
104	d1bf6a	Alignment	not modelled	96.2	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
105	d1yixa1	Alignment	not modelled	96.2	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
106	d1ynya2	Alignment	not modelled	96.2	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
107	c2p9bA	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
108	c3dcpB	Alignment	not modelled	96.1	12	PDB header: hydrolase Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
109	c2gzxB	Alignment	not modelled	95.9	15	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.
110	c2vr2A	Alignment	not modelled	95.9	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
111	c2vhlB	Alignment	not modelled	95.9	18	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
112	c4rdzA	Alignment	not modelled	95.9	11	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
113	c2gseC	Alignment	not modelled	95.8	13	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
114	c4c6mA	Alignment	not modelled	95.8	12	PDB header: hydrolase Chain: A: PDB Molecule: cad protein; PDBTitle: crystal structure of the dihydroorotase domain of human cad2 bound to the inhibitor fluoro-orotate at ph 7.0
115	c3e74D	Alignment	not modelled	95.6	12	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at the metal2 center
116	c3umuA	Alignment	not modelled	95.6	16	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of l-histidinol phosphate phosphatase (hisk) from2 lactococcus lactis subsp. lactis il1403 complexed with zn, phosphate3 and l-histidinol
117	c5vn5A	Alignment	not modelled	95.3	11	PDB header: hydrolase Chain: A: PDB Molecule: 2,2',3-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- PDBTitle: crystal structure of ligy from sphingobium sp. strain syk-6
118	d2f6ka1	Alignment	not modelled	95.3	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
119	c4b91B	Alignment	not modelled	95.2	11	PDB header: signaling protein Chain: B: PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5
120	c3mpgB	Alignment	not modelled	94.9	11	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis