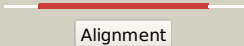

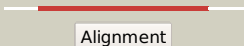

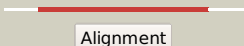







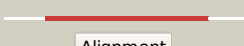

















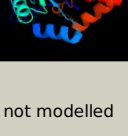


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2303c (- )_2574106_2575029
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	7c59bd8b9697cd8a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4l5pD_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 5-carboxyvanillate decarboxylase; <b>PDBTitle:</b> crystal structure of 5-carboxyvanillate decarboxylase from2 sphingomonas paucimobilis complexed with 4-hydroxy-3-methoxy-5-3 nitrobenzoic acid
2	<a href="#">c6omqA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ptmu3; <b>PDBTitle:</b> crystal structure of ptmu3 complexed with ptm substrate
3	<a href="#">c4hk6D_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil-5-carboxylate decarboxylase; <b>PDBTitle:</b> crystal structure of cordyceps militaris idcase in complex with 5-2 nitro-uracil
4	<a href="#">c4infA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase saro_0799 (target efi-505250) from2 novosphingobium aromaticivorans dsm 12444 with bound calcium
5	<a href="#">c3irsB_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bb4693; <b>PDBTitle:</b> crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
6	<a href="#">c2wm1A_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-carboxymuconate-6-semialdehyde <b>PDBTitle:</b> 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
7	<a href="#">c3nurA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of a putative amidohydrolase from staphylococcus2 aureus
8	<a href="#">d2dvta1</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
9	<a href="#">c4dziD_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative tim-barrel metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase map2389c (target efi-500390) from2 mycobacterium avium subsp. paratuberculosis k-10
10	<a href="#">d2gwga1</a>	 Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
11	<a href="#">d2hbva1</a>	 Alignment		100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like

12	<a href="#">d2f6ka1</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
13	<a href="#">c6dxsB_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalomesaconate hydratase; <b>PDBTitle:</b> crystal structure of the ligj hydratase e284q mutant substrate complex2 with (3z)-2-keto-4-carboxy-3-hexenedioate
14	<a href="#">c3ij6A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus
15	<a href="#">c5vn5A_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,2',3-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- <b>PDBTitle:</b> crystal structure of ligy from sphingobium sp. strain syk-6
16	<a href="#">c2qahA_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-pyrone-4,6-dicarboxylic acid hydrolase; <b>PDBTitle:</b> crystal structure of the 2-pyrone-4,6-dicarboxylic acid hydrolase from2 sphingomonas paucimobills
17	<a href="#">d2ffia1</a>	Alignment		100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
18	<a href="#">c4mupC_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
19	<a href="#">c3cjpA_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted amidohydrolase, dihydroorotase family; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
20	<a href="#">c4i6kA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase family protein; <b>PDBTitle:</b> crystal structure of probable 2-pyrone-4,6-dicarboxylic acid hydrolase2 abaye1769 (target efi-505029) from acinetobacter baumannii with3 citric acid bound
21	<a href="#">c4do7B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase 2; <b>PDBTitle:</b> crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2
22	<a href="#">c2gzxB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative tatd related dnase; <b>PDBTitle:</b> crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
23	<a href="#">d1xwya1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
24	<a href="#">d1j6oa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
25	<a href="#">d1yixa1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
26	<a href="#">d1zzma1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
27	<a href="#">c3rcmA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tatd family hydrolase; <b>PDBTitle:</b> crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
28	<a href="#">c2y1hA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn3; <b>PDBTitle:</b> crystal structure of the human tatd-domain protein 3 (tatdn3)

29	<a href="#">c3gg7A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metalloprotein; <b>PDBTitle:</b> crystal structure of an uncharacterized metalloprotein from 2 deinococcus radiodurans
30	<a href="#">c3guwB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein af_1765; <b>PDBTitle:</b> crystal structure of the tatd-like protein (af1765) from archaeoglobus2 fulgidus, northeast structural genomics consortium target gr121
31	<a href="#">c2qpxA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted metal-dependent hydrolase of the tim-barrel fold; <b>PDBTitle:</b> crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution
32	<a href="#">d1bf6a_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
33	<a href="#">c2vc7A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aryldialkylphosphatase; <b>PDBTitle:</b> structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
34	<a href="#">c3tn6A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
35	<a href="#">c4rdzA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> parathion hydrolase; <b>PDBTitle:</b> crystal structure of vmolac in p64 space group
36	<a href="#">c2xioA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn1; <b>PDBTitle:</b> structure of putative deoxyribonuclease tatdn1 isoform a
37	<a href="#">c4if2A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase homology protein; <b>PDBTitle:</b> structure of the phosphotriesterase from mycobacterium tuberculosis
38	<a href="#">c3f4cA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus hydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
39	<a href="#">d2d2ja1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
40	<a href="#">d1i0da_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
41	<a href="#">c1pscA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> phosphotriesterase from pseudomonas diminuta
42	<a href="#">c3pnzD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphotriesterase family protein; <b>PDBTitle:</b> crystal structure of the lactonase lmo2620 from listeria monocytogenes
43	<a href="#">c3ipwA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase tatd family protein; <b>PDBTitle:</b> crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
44	<a href="#">c2zc1A_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotriesterase; <b>PDBTitle:</b> organophosphorus hydrolase from deinococcus radiodurans
45	<a href="#">c3e2vA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3'-5'-exonuclease; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase from 2 saccharomyces cerevisiae
46	<a href="#">c4i6vA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase 2; <b>PDBTitle:</b> the crystal structure of an amidohydrolase 2 from planctomyces2 limnophilus dsm 3776
47	<a href="#">d1itua_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Renal dipeptidase
48	<a href="#">d1xrta2</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
49	<a href="#">c3fdgA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidase ac. metallo peptidase. merops family m19; <b>PDBTitle:</b> the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
50	<a href="#">d1j5sa_</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Uronate isomerase-like
51	<a href="#">c3rhgA_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphotriesterase; <b>PDBTitle:</b> crystal structure of amidohydrolase pmi1525 (target efi-500319) from 2 proteus mirabilis hi4320
52	<a href="#">c3lu2B_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2462 protein; <b>PDBTitle:</b> structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
53	<a href="#">c5ns5A_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidase glij; <b>PDBTitle:</b> cys-gly dipeptidase glij in complex with cu2+ and zn2+
54	<a href="#">c3k2gA_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase-

						<b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
55	<a href="#">c3itcA</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> renal dipeptidase; <b>PDBTitle:</b> crystal structure of sco3058 with bound citrate and glycerol
56	<a href="#">c2q01A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uronate isomerase; <b>PDBTitle:</b> crystal structure of glucuronate isomerase from caulobacter crescentus
57	<a href="#">c3b40A</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dipeptidase; <b>PDBTitle:</b> crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa
58	<a href="#">c2ragB</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidase; <b>PDBTitle:</b> crystal structure of aminohydrolase from caulobacter crescentus
59	<a href="#">c4fyB</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
60	<a href="#">c2i5gB</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase from pseudomonas aeruginosa
61	<a href="#">d1ynya2</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
62	<a href="#">c3msrA</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolases; <b>PDBTitle:</b> the crystal structure of an amidohydrolase from mycoplasma synoviae
63	<a href="#">c3pnuA</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
64	<a href="#">c5v0gE</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from yersinia pestis in2 complex with zinc and unknown ligand at 2.4 a resolution.
65	<a href="#">d1kcx2</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
66	<a href="#">d1k1da2</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
67	<a href="#">c5vgmA</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from vibrio cholerae in2 complex with zinc at 1.95 a resolution.
68	<a href="#">d2eg6a1</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
69	<a href="#">c3ou8B</a>	Alignment	not modelled	98.5	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
70	<a href="#">d2ftwa2</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
71	<a href="#">d1nfga2</a>	Alignment	not modelled	98.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
72	<a href="#">c3jzeC</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
73	<a href="#">d1gkra2</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
74	<a href="#">c3ou8A</a>	Alignment	not modelled	98.3	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
75	<a href="#">d1p1ma2</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
76	<a href="#">c1xrfA</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution
77	<a href="#">d1a4ma</a>	Alignment	not modelled	98.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
78	<a href="#">c2vunC</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> enamidase; <b>PDBTitle:</b> the crystal structure of enamidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
79	<a href="#">d2paja2</a>	Alignment	not modelled	98.1	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
80	<a href="#">d3be7a2</a>	Alignment	not modelled	98.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like

81	<a href="#">d1ra0a2</a>	Alignment	not modelled	98.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Cytosine deaminase catalytic domain
82	<a href="#">c3nqbB</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine deaminase 2; <b>PDBTitle:</b> crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
83	<a href="#">d2imra2</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> DR0824-like
84	<a href="#">d2qs8a2</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
85	<a href="#">c3ryaA</a>	Alignment	not modelled	97.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase 1; <b>PDBTitle:</b> the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
86	<a href="#">c1r9yA</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine deaminase; <b>PDBTitle:</b> bacterial cytosine deaminase d314a mutant.
87	<a href="#">c1p1mA</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0936; <b>PDBTitle:</b> structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
88	<a href="#">d2bb0a2</a>	Alignment	not modelled	97.8	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
89	<a href="#">c2bb0A</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> structure of imidazolonepropionase from bacillus subtilis
90	<a href="#">d2uz9a2</a>	Alignment	not modelled	97.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
91	<a href="#">c6n91A</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of adenosine deaminase from vibrio cholerae2 complexed with pentostatin (deoxycoformycin)
92	<a href="#">d2fvka2</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
93	<a href="#">d2q09a2</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
94	<a href="#">c4dykB</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an adenosine deaminase from pseudomonas2 aeruginosa pao1 (target nysgrc-200449) with bound zn
95	<a href="#">c2ogjC</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase
96	<a href="#">d2r8ca2</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
97	<a href="#">c6ii7A</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum adenosine deaminase2 c27q+l227i mutant co-complexed with zn ion, hypoxanthine and inosine
98	<a href="#">c4dzhA</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
99	<a href="#">c3mduA</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-formimino-l-glutamate iminohydrolase; <b>PDBTitle:</b> the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
100	<a href="#">c3e0lB</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> guanine deaminase; <b>PDBTitle:</b> computationally designed ammelide deaminase
101	<a href="#">c2q09A</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxoimidazolidin-4-yl)-propionic acid
102	<a href="#">d1vfla1</a>	Alignment	not modelled	97.3	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
103	<a href="#">d2icsa2</a>	Alignment	not modelled	97.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenine deaminase-like
104	<a href="#">d1onwa2</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Isoaspartyl dipeptidase, catalytic domain
105	<a href="#">c4jnrE</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative cytosine deaminase and related metal-dependent <b>PDBTitle:</b> crystal structure of 5-methylcytosine deaminase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 liganded with 5-fluorocytosine <b>PDB header:</b> hydrolase

106	<a href="#">c3hpaB_</a>	Alignment	not modelled	97.2	11	<b>Chain:</b> B; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
107	<a href="#">d2amxa1</a>	Alignment	not modelled	97.2	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Adenosine/AMP deaminase
108	<a href="#">d2puza2</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
109	<a href="#">c2vr2A_</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> human dihydropyrimidinase
110	<a href="#">d1o5ka_</a>	Alignment	not modelled	97.1	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
111	<a href="#">c4gxwA_</a>	Alignment	not modelled	97.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenosine deaminase; <b>PDBTitle:</b> crystal structure of a cog1816 amidohydrolase (target efi-505188) from2 burkhoderia ambifaria, with bound zn
112	<a href="#">c3na8A_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
113	<a href="#">d1gkpa2</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
114	<a href="#">d2i9ua2</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
115	<a href="#">d2qeec1</a>	Alignment	not modelled	96.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Uronate isomerase-like
116	<a href="#">c2ftwA_</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydropyrimidine amidohydrolase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from dictyostelium discoideum
117	<a href="#">c6jpa_</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenosine/amp deaminase family protein; <b>PDBTitle:</b> the structure of the adal-imp complex
118	<a href="#">c2ehhE_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
119	<a href="#">c2pajA_</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative cytosine/guanine deaminase; <b>PDBTitle:</b> crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
120	<a href="#">c3n2xB_</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate