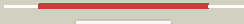



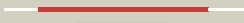














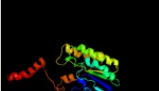




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0518 (-) _610191_610886
Date	Fri Jul 26 01:50:06 BST 2019
Unique Job ID	fb3218c8284b4a18

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2waoA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase e; <b>PDBTitle:</b> structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose
2	<a href="#">c4xvhA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate esterase family 2 (ce2); <b>PDBTitle:</b> crystal structure of a corynascus thermopiles (myceliophthora2 fergusii) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd)
3	<a href="#">c4devE_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> acetyl-xylan esterase est2a; <b>PDBTitle:</b> an acetyl xylan esterase (est2a) from the rumen bacterium butyrivibrio2 proteoclasticus.
4	<a href="#">c2waaA_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylan esterase, putative, axe2c; <b>PDBTitle:</b> structure of a family two carbohydrate esterase from2 cellvibrio japonicus
5	<a href="#">c6iqbA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sgnh-hydrolase family esterase; <b>PDBTitle:</b> esterase aline4 mutant-s13a
6	<a href="#">c4lhsA_</a>	 Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative gdsI-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
7	<a href="#">c2w9xA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyl xylan esterase; <b>PDBTitle:</b> the active site of a carbohydrate esterase displays2 divergent3 catalytic and non-catalytic binding functions
8	<a href="#">c3hp4A_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsI-esterase; <b>PDBTitle:</b> crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
9	<a href="#">c4jggB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase tesa; <b>PDBTitle:</b> crystal structure of tesa
10	<a href="#">c6iq8B_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> esterase crme10 mutant-d178a
11	<a href="#">d1irla_</a>	 Alignment		100.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> TAP-like

12	<a href="#">c2o14A_</a>	Alignment		100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yxim; <b>PDBTitle:</b> x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595
13	<a href="#">c3rjtA_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
14	<a href="#">c4h08A_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
15	<a href="#">c4rw0B_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> crystal structure of a member of the lipolytic protein g-d-s-l family2 from veillonella parvula dsm 2008
16	<a href="#">d3dc7a1</a>	Alignment		100.0	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> BT2961-like
17	<a href="#">c4rshB_</a>	Alignment		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> structure of a putative lipolytic protein of g-d-s-l family from2 desulfitobacterium hafniense dcb-2
18	<a href="#">c3dc7B_</a>	Alignment		99.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein lp_3323; <b>PDBTitle:</b> crystal structure of the protein q88s8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
19	<a href="#">c2vptA_</a>	Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> clostridium thermocellum family 3 carbohydrate esterase
20	<a href="#">d1yzfa1</a>	Alignment		99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> TAP-like
21	<a href="#">c4nrdA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative gds1-like lipase (bacova_04955) from2 bacteroides ovatus atcc 8483 at 2.10 a resolution
22	<a href="#">d1vjga_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Hypothetical protein alr1529
23	<a href="#">c4jhlA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> crystal structure of of axe2, an acetylxylan esterase from geobacillus2 stearothermophilus
24	<a href="#">c5jd3A_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lae5; <b>PDBTitle:</b> crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain
25	<a href="#">c4m8kA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein, gds1-like lipase/acylhydrolase family <b>PDBTitle:</b> crystal structure of a putative gds1-like lipase (bacuni_00748) from2 bacteroides uniformis atcc 8492 at 1.90 a resolution
26	<a href="#">c3milA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamyl acetate-hydrolyzing esterase; <b>PDBTitle:</b> crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae
27	<a href="#">c4q7qA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic protein g-d-s-l family; <b>PDBTitle:</b> the crystal structure of a possible lipase from chitinophaga pinensis2 dsm 2588
						<b>PDB header:</b> hydrolase

28	<a href="#">c3bzwA_</a>	Alignment	not modelled	99.9	17	<b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase; <b>PDBTitle:</b> crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
29	<a href="#">d3bzw1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> BT2961-like
30	<a href="#">c3x0hA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate esterase 1; <b>PDBTitle:</b> crystal structure of a carbohydrate esterase family 1 from talaromyces2 cellulolyticus
31	<a href="#">c5hoeB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> crystal structure of est24, a carbohydrate acetyltransferase from2 sinorhizobium meliloti
32	<a href="#">c4s1pA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> shel_16390 protein, a putative sgnh hydrolase from slackia2 heliotrinireducens
33	<a href="#">c4q9aA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tat pathway signal sequence domain protein; <b>PDBTitle:</b> crystal structure of a putative gdsI-like lipase (parmer_00689) from2 parabacteroides merdae atcc 43184 at 2.86 a resolution
34	<a href="#">c4iyjA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsI-like protein; <b>PDBTitle:</b> crystal structure of a putative acylhydrolase (bacuni_03406) from2 bacteroides uniformis atcc 8492 at 1.37 a resolution
35	<a href="#">c3p94A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsI-like lipase; <b>PDBTitle:</b> crystal structure of a gdsI-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
36	<a href="#">d1k7ca_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Rhamnogalacturonan acetyltransferase
37	<a href="#">d2o14a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> YxiM C-terminal domain-like
38	<a href="#">c6njcB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sialate o-acetyltransferase; <b>PDBTitle:</b> crystal structure of the sialate o-acetyltransferase from bacteroides2 vulgatus
39	<a href="#">c2q0qC_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> aryl esterase; <b>PDBTitle:</b> structure of the native m. smegmatis aryl esterase
40	<a href="#">c5ma1A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase from streptomyces rimosus at2 1.7a resolution
41	<a href="#">c4tx1C_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> the crystal structure of carbohydrate acetyltransferase family member2 from sinorhizobium meliloti
42	<a href="#">c3dc1B_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> arylesterase; <b>PDBTitle:</b> the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58
43	<a href="#">c4hyqA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1; <b>PDBTitle:</b> crystal structure of phospholipase a1 from streptomyces albidoflavus2 na297
44	<a href="#">d1es9a_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
45	<a href="#">d1esca_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Esterase
46	<a href="#">c4k40B_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gdsI-like lipase/acylhydrolase family protein; <b>PDBTitle:</b> peptidoglycan o-acetyltransferase in action, 0 min
47	<a href="#">d1fxwf_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
48	<a href="#">c4hf7A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acylhydrolase; <b>PDBTitle:</b> crystal structure of a gdsI-like lipase (bt0569) from bacteroides2 thetaiotaomicron vpi-5482 at 1.77 a resolution
49	<a href="#">c4c1bC_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> orf1-encoded protein; <b>PDBTitle:</b> esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon
50	<a href="#">d2hsja1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Acetylhydrolase
51	<a href="#">c5ufyA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyltransferase; <b>PDBTitle:</b> structure of streptococcus pneumoniae peptidoglycan o-2 acetyltransferase a (oata) c-terminal catalytic domain
52	<a href="#">c5w78B_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyloxyacyl hydrolase; <b>PDBTitle:</b> human acyloxyacyl hydrolase (aoah), proteolytically processed
53	<a href="#">c6j11A_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermolabile hemolysin; <b>PDBTitle:</b> crystal structure of vvp1pa g389d from vibrio vulnificus

54	<a href="#">c5w7dA_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyloxyacyl hydrolase; <b>PDBTitle:</b> murine acyloxyacyl hydrolase (aoah), s262a mutant
55	<a href="#">c4i8iA_</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4886 family protein (bacuni_01406) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
56	<a href="#">c5xtuA_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gdsl-family esterase; <b>PDBTitle:</b> crystal structure of gdsl esterase of photobacterium sp. j15
57	<a href="#">c3kvnA_</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase esta; <b>PDBTitle:</b> crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
58	<a href="#">d2apia1</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Putative acetylxytan esterase-like
59	<a href="#">c4qn1A_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tail fiber protein; <b>PDBTitle:</b> crystal structure of tail fiber protein gp63.1 from e. coli phage g7c
60	<a href="#">c6pfxB_</a>	Alignment	not modelled	96.2	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecium
61	<a href="#">c6o93A_</a>	Alignment	not modelled	95.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecalis
62	<a href="#">c3bmaC_</a>	Alignment	not modelled	95.4	10	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanyl-lipoteichoic acid synthetase; <b>PDBTitle:</b> crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
63	<a href="#">c3nvbA_</a>	Alignment	not modelled	94.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
64	<a href="#">d1zmba1</a>	Alignment	not modelled	93.9	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> SGNH hydrolase <b>Family:</b> Putative acetylxytan esterase-like
65	<a href="#">c4o8vA_</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alginate biosynthesis protein algJ; <b>PDBTitle:</b> o-acetyltransferase domain of pseudomonas putida algJ
66	<a href="#">c5wb4H_</a>	Alignment	not modelled	90.8	4	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d- <b>PDBTitle:</b> crystal structure of the tara wall teichoic acid glycosyltransferase
67	<a href="#">c5v8eB_</a>	Alignment	not modelled	90.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> bacillus cereus patb1; <b>PDBTitle:</b> structure of bacillus cereus patb1
68	<a href="#">c4kncA_</a>	Alignment	not modelled	83.3	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alginate biosynthesis protein algX; <b>PDBTitle:</b> structural and functional characterization of pseudomonas aeruginosa2 algX
69	<a href="#">c6cciA_</a>	Alignment	not modelled	83.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein eskimo 1; <b>PDBTitle:</b> the crystal structure of xoat1
70	<a href="#">d1luuya</a>	Alignment	not modelled	76.2	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
71	<a href="#">c2pjka_</a>	Alignment	not modelled	73.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 178aa long hypothetical molybdenum cofactor <b>PDBTitle:</b> structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
72	<a href="#">c3pt5A_</a>	Alignment	not modelled	68.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nans (vjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; <b>PDBTitle:</b> crystal structure of nans
73	<a href="#">c5a4aA_</a>	Alignment	not modelled	66.8	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maternal effect protein oskar; <b>PDBTitle:</b> crystal structure of the osk domain of drosophila oskar
74	<a href="#">c2is8A_</a>	Alignment	not modelled	62.1	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis enzyme, moab; <b>PDBTitle:</b> crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
75	<a href="#">c4axnB_</a>	Alignment	not modelled	52.7	6	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> chitinase c1; <b>PDBTitle:</b> hallmarks of processive and non-processive glycoside hydrolases2 revealed from computational and crystallographic studies of the3 serratia marcescens chitinases
76	<a href="#">c2g4rB_</a>	Alignment	not modelled	50.3	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis mog protein; <b>PDBTitle:</b> anomalous substructure of moga
77	<a href="#">d1mkza_</a>	Alignment	not modelled	50.3	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
78	<a href="#">c3menC_</a>	Alignment	not modelled	45.9	7	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl/polyamine aminohydrolase; <b>PDBTitle:</b> crystal structure of acetyl/polyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak <b>PDB header:</b> transcription

79	<a href="#">c3qi7A_</a>	Alignment	not modelled	43.5	11	<b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
80	<a href="#">c1y8aA_</a>	Alignment	not modelled	40.5	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1437; <b>PDBTitle:</b> structure of gene product af1437 from archaeoglobus fulgidus
81	<a href="#">c5a7mA_</a>	Alignment	not modelled	37.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> the structure of hypocrea jecorina beta-xylosidase xyl3a (bxl1)
82	<a href="#">d2csua1</a>	Alignment	not modelled	37.3	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
83	<a href="#">d2f7wa1</a>	Alignment	not modelled	36.2	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
84	<a href="#">d1y5ea1</a>	Alignment	not modelled	35.8	22	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
85	<a href="#">c3rfqC_</a>	Alignment	not modelled	33.8	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
86	<a href="#">c3q9cF_</a>	Alignment	not modelled	32.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> acetylpolyamine amidohydrolase; <b>PDBTitle:</b> crystal structure of h159a apah complexed with n8-acetylspermidine
87	<a href="#">d1jja_</a>	Alignment	not modelled	32.2	22	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
88	<a href="#">c6q7jB_</a>	Alignment	not modelled	27.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-1,4-beta-xylosidase xlnD; <b>PDBTitle:</b> gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
89	<a href="#">d2g2ca1</a>	Alignment	not modelled	26.5	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
90	<a href="#">c1uasA_</a>	Alignment	not modelled	25.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of rice alpha-galactosidase
91	<a href="#">c2qq1A_</a>	Alignment	not modelled	24.8	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
92	<a href="#">d1a9xa3</a>	Alignment	not modelled	24.3	9	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
93	<a href="#">c2yxbA_</a>	Alignment	not modelled	22.6	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
94	<a href="#">c4r3uD_</a>	Alignment	not modelled	19.8	21	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
95	<a href="#">c5yozA_</a>	Alignment	not modelled	19.4	14	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> rab5a; <b>PDBTitle:</b> solution structure of truncated rab5a from leishmania donovani
96	<a href="#">c1hyhA_</a>	Alignment	not modelled	18.9	14	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
97	<a href="#">d1edta_</a>	Alignment	not modelled	18.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase
98	<a href="#">c4yajA_</a>	Alignment	not modelled	17.3	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
99	<a href="#">c5wabD_</a>	Alignment	not modelled	16.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase