



















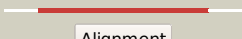





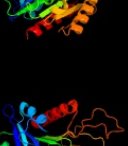
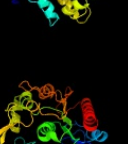


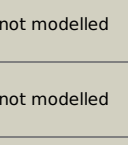


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3298c_(lpqC)_3682107_3683021
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	24ca1665ed4fb898

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ecfA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
2	<a href="#">c5oljA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
3	<a href="#">c3azqA_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
4	<a href="#">c3wiaA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oxidized polyvinyl alcohol hydrolase; <b>PDBTitle:</b> crystal structure of soph native
5	<a href="#">c4hxgl_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> putative uncharacterized protein ph0594; <b>PDBTitle:</b> pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
6	<a href="#">c1z68A_</a>	 Alignment		100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> fibroblast activation protein, alpha subunit; <b>PDBTitle:</b> crystal structure of human fibroblast activation protein alpha
7	<a href="#">c4wjlB_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> inactive dipeptidyl peptidase 10; <b>PDBTitle:</b> structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
8	<a href="#">c2qtbB_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
9	<a href="#">c5x6sB_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> acetylxy lan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
10	<a href="#">c5l8sD_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> amino acyl peptidase; <b>PDBTitle:</b> the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
11	<a href="#">c4q1vA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative dipeptidyl aminopeptidase iv; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution

12	<a href="#">c2g5tA_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
13	<a href="#">c2eepA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl aminopeptidase iv, putative; <b>PDBTitle:</b> prolyl tripeptidyl aminopeptidase complexed with an inhibitor
14	<a href="#">c5yznA_</a>	Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-peptide hydrolase, putative; <b>PDBTitle:</b> crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
15	<a href="#">c6eogC_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
16	<a href="#">c2hu7A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acylamino-acid-releasing enzyme; <b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase
17	<a href="#">c5jrlC_</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like <b>PDBTitle:</b> crystal structure of the shingopyxin i lasso peptide isopeptidase2 spi-isop (native)
18	<a href="#">c5txeA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atxe2; <b>PDBTitle:</b> atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
19	<a href="#">c5t88B_</a>	Alignment		100.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus
20	<a href="#">c1xfdD_</a>	Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> dipeptidyl aminopeptidase-like protein 6; <b>PDBTitle:</b> structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
21	<a href="#">c6eosB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
22	<a href="#">c6eotG_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
23	<a href="#">c6eorD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
24	<a href="#">c1qfmA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
25	<a href="#">c2o2gA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
26	<a href="#">c3doiA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a thermostable esterase complex with2 paraoxon
27	<a href="#">c3e4dD_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
28	<a href="#">c3ls2D_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> s-formylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
						<b>PDB header:</b> hydrolase

29	<a href="#">c3k2IA</a>	Alignment	not modelled	99.9	13	<b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 4; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 4
30	<a href="#">c3fcxA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-formylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of human esterase d
31	<a href="#">c2bkIB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
32	<a href="#">c4bp9A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
33	<a href="#">c4b6gA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> the crystal structure of the neisserial esterase d.
34	<a href="#">c2xe4A</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> structure of oligopeptidase b from leishmania major
35	<a href="#">d1sfra</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
36	<a href="#">c3i6yA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase apc40077; <b>PDBTitle:</b> structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
37	<a href="#">c3hikB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
38	<a href="#">c3d0kA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative poly(3-hydroxybutyrate) depolymerase lpqc; <b>PDBTitle:</b> crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
39	<a href="#">d1dqza</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
40	<a href="#">c4zi5A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> p91; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
41	<a href="#">c5uzwD</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
42	<a href="#">d1f0na</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
43	<a href="#">d1qfma2</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
44	<a href="#">c5n4dA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
45	<a href="#">c5cxcC</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ferulic acid esterase, amce1/fae1a; <b>PDBTitle:</b> structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid
46	<a href="#">c4hvtA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> post-proline cleaving enzyme; <b>PDBTitle:</b> structure of a post-proline cleaving enzyme from rickettsia typhi
47	<a href="#">c3iumA</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
48	<a href="#">d1r88a</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
49	<a href="#">d1pv1a</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical esterase YJL068C
50	<a href="#">c3wydA</a>	Alignment	not modelled	99.9	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lc-est1c; <b>PDBTitle:</b> c-terminal esterase domain of lc-est1
51	<a href="#">d1xfda2</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
52	<a href="#">c4h18D</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cmt1; <b>PDBTitle:</b> three dimensional structure of corynomycoloyl tranferase c
53	<a href="#">c1yr2A</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
54	<a href="#">c3bxpA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase/esterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution

55	<a href="#">d2h1ia1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
56	<a href="#">d2bgra2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
57	<a href="#">d1orva2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
58	<a href="#">c2h1iA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the bacillus cereus carboxylesterase
59	<a href="#">c5uw7B_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 y481f variant in complex with follower peptide
60	<a href="#">d1wb4a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
61	<a href="#">c2uz0B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tributyrin esterase; <b>PDBTitle:</b> the crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
62	<a href="#">c4fhzA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase/carboxylesterase; <b>PDBTitle:</b> crystal structure of a carboxyl esterase at 2.0 angstrom resolution
63	<a href="#">d1jfa_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
64	<a href="#">d2hu7a2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acylamino-acid-releasing enzyme, C-terminal donain
65	<a href="#">c4h0cA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase/carboxylesterase; <b>PDBTitle:</b> crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
66	<a href="#">c3ksrA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine hydrolase; <b>PDBTitle:</b> crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
67	<a href="#">c3fnbB_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylaminoacyl peptidase smu_737; <b>PDBTitle:</b> crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
68	<a href="#">c4q3kB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mgs-m1; <b>PDBTitle:</b> crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
69	<a href="#">c1wb4A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase y; <b>PDBTitle:</b> s954a mutant of the feruloyl esterase module from2 clostridium thermocellum complexed with sinapinate
70	<a href="#">c3mveB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0255 protein vv1_0328; <b>PDBTitle:</b> crystal structure of a novel pyruvate decarboxylase
71	<a href="#">c3f67A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
72	<a href="#">c3hxB_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar hydrolase; <b>PDBTitle:</b> crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
73	<a href="#">c5hc4A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> structure of esterase est22
74	<a href="#">d2i3da1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
75	<a href="#">c2i3dA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu1826; <b>PDBTitle:</b> crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
76	<a href="#">d3b5ea1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
77	<a href="#">c4zrsA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
78	<a href="#">c3ga7A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
79	<a href="#">c3ed1E_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase receptor <b>Chain:</b> E: <b>PDB Molecule:</b> gibberellin receptor gid1; <b>PDBTitle:</b> crystal structure of rice gid1 complexed with ga3
80	<a href="#">c5f2hA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
81	<a href="#">c5volA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase;

						<b>PDBTitle:</b> bacint_04212 ferulic acid esterase
82	<a href="#">c2zshA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> probable gibberellin receptor gid111; <b>PDBTitle:</b> structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
83	<a href="#">c4f21G</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> carboxylesterase/phospholipase family protein; <b>PDBTitle:</b> crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
84	<a href="#">d3c8da2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
85	<a href="#">c1l7qA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cocaine esterase; <b>PDBTitle:</b> ser117ala mutant of bacterial cocaine esterase coce
86	<a href="#">c5a0aA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
87	<a href="#">c4krxB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> structure of aes from e. coli
88	<a href="#">c30g9A</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein yahd a copper inducible hydrolase; <b>PDBTitle:</b> structure of yahd with malic acid
89	<a href="#">d2jbwa1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydrospseudooxynicotine hydrolase-like
90	<a href="#">c5xg0A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(ethylene terephthalate) hydrolase; <b>PDBTitle:</b> crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
91	<a href="#">c4a06A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
92	<a href="#">c6a60A</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase/lipase-like protein; <b>PDBTitle:</b> crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
93	<a href="#">c2jwbB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,6-dihydroxy-pseudo-oxynicotine hydrolase; <b>PDBTitle:</b> crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
94	<a href="#">c4rotA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase a; <b>PDBTitle:</b> crystal structure of esterase a from streptococcus pyogenes
95	<a href="#">c4wfiA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
96	<a href="#">d1mpxa2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
97	<a href="#">d2b9va2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
98	<a href="#">c6gocA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> duf3826 domain-containing protein; <b>PDBTitle:</b> methyltransferase bt1017
99	<a href="#">c3visB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of cutinase est119 from thermobifida alba ahk119
100	<a href="#">c3bjrA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
101	<a href="#">d1ju3a2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
102	<a href="#">c5synB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-protein thioesterase 2; <b>PDBTitle:</b> cocrystal structure of the human acyl protein thioesterase 2 with an2 isoform-selective inhibitor, ml349
103	<a href="#">c2b9vB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amino acid ester hydrolase; <b>PDBTitle:</b> acetobacter turbidans alpha-amino acid ester hydrolase
104	<a href="#">c4ob7A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold-3 domain protein; <b>PDBTitle:</b> crystal structure of esterase rppe mutant w187h
105	<a href="#">c6gunB</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> restb from aspergillus nidulans; <b>PDBTitle:</b> siderophore hydrolase estb from aspergillus nidulans
106	<a href="#">c5jd5A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgs-mile3; <b>PDBTitle:</b> crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy <b>PDB header:</b> hydrolase

107	<a href="#">c4eb0A_</a>	Alignment	not modelled	99.8	16	<b>Chain:</b> A: <b>PDB Molecule:</b> !lcc; <b>PDBTitle:</b> crystal structure of leaf-branch compost bacterial cutinase homolog
108	<a href="#">c6gi5A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ferric enterobactin esterase; <b>PDBTitle:</b> crystal structure of the ferric enterobactin esterase (pfee) from2 pseudomonas aeruginosa in complex with the tris-catechol vector
109	<a href="#">c5g59A_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
110	<a href="#">d2fuka1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
111	<a href="#">c2fx5A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
112	<a href="#">d1dina_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Dienelactone hydrolase
113	<a href="#">c4rgyA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library
114	<a href="#">d1l7aa_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
115	<a href="#">c4pf1D_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> peptidase s15/coce/nond; <b>PDBTitle:</b> crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
116	<a href="#">d1jfra_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Lipase
117	<a href="#">c6avwA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase sober1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana sober1 l63a
118	<a href="#">c5yalA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
119	<a href="#">c2wtmC_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrivibrio proteoclasticus
120	<a href="#">c3c8dA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> enterochelin esterase; <b>PDBTitle:</b> crystal structure of the enterobactin esterase fes from2 shigella flexneri in the presence of 2,3-di-hydroxy-n-3 benzoyl-glycine