



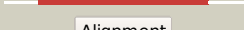

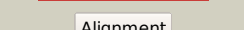

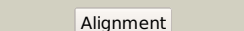


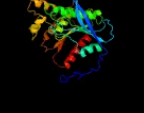






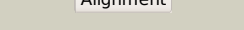

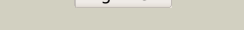








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1592c_(-)_1792407_1793747
Date	Fri Aug 2 13:30:18 BST 2019
Unique Job ID	c604ba428ae2e3bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2veoA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase a; <b>PDBTitle:</b> x-ray structure of candida antarctica lipase a in its closed state.
2	<a href="#">c4eziA_</a>	 Alignment		100.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
3	<a href="#">c3h2iA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
4	<a href="#">c2bkiB_</a>	 Alignment		99.9	21	<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
5	<a href="#">c3azqA_</a>	 Alignment		99.9	18	<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
6	<a href="#">c1qfmA_</a>	 Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
7	<a href="#">c4hvtA_</a>	 Alignment		99.9	14	<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
8	<a href="#">c3iumA_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
9	<a href="#">c5l8sD_</a>	 Alignment		99.9	17	<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
10	<a href="#">c4bp9A_</a>	 Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oligopeptidasse b; <b>PDBTitle:</b> oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
11	<a href="#">c5oljA_</a>	 Alignment		99.9	16	<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

12	<a href="#">c2ecfA_</a>	Alignment		99.9	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
13	<a href="#">c2xe4A_</a>	Alignment		99.9	15	<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
14	<a href="#">c1z68A_</a>	Alignment		99.9	14	<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
15	<a href="#">c5t88B_</a>	Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus
16	<a href="#">c5yznA_</a>	Alignment		99.9	18	<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
17	<a href="#">c4hxgl_</a>	Alignment		99.9	12	<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)
18	<a href="#">c1yr2A_</a>	Alignment		99.9	16	<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
19	<a href="#">c6eosB_</a>	Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
20	<a href="#">c2g5tA_</a>	Alignment		99.9	15	<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
21	<a href="#">c2hu7A_</a>	Alignment	not modelled	99.9	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
22	<a href="#">c2qtbB_</a>	Alignment	not modelled	99.9	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
23	<a href="#">c5n4dA_</a>	Alignment	not modelled	99.9	17	<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
24	<a href="#">c4q1vA_</a>	Alignment	not modelled	99.9	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
25	<a href="#">c4wjJB_</a>	Alignment	not modelled	99.9	17	<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
26	<a href="#">c5uzwD_</a>	Alignment	not modelled	99.9	14	<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
27	<a href="#">c6eotG_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
28	<a href="#">c6eoqC_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo

29	<a href="#">c2eepA</a>	Alignment	not modelled	99.9	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
30	<a href="#">c6eorD</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
31	<a href="#">c1xfdD</a>	Alignment	not modelled	99.9	19	<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
32	<a href="#">c5uw7B</a>	Alignment	not modelled	99.9	13	<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
33	<a href="#">c5jrlC</a>	Alignment	not modelled	99.9	16	<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 sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
34	<a href="#">c5txeA</a>	Alignment	not modelled	99.9	18	<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
35	<a href="#">c3fnbB</a>	Alignment	not modelled	99.9	19	<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
36	<a href="#">c3doiA</a>	Alignment	not modelled	99.8	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
37	<a href="#">d1qfma2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
38	<a href="#">c3bxaA</a>	Alignment	not modelled	99.8	14	<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 wcfs1 at 1.70 a resolution
39	<a href="#">c6agqE</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> acetyl xylan esterase from paenibacillus sp. r4
40	<a href="#">d1l7aa</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
41	<a href="#">d1vlqa</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
42	<a href="#">d2jbwa1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropseudooxynicotine hydrolase-like
43	<a href="#">c5xb6D</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein ycyj; <b>PDBTitle:</b> crystal structure of ycyj from e. coli
44	<a href="#">c2jwbB</a>	Alignment	not modelled	99.8	20	<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.
45	<a href="#">c5f2ha</a>	Alignment	not modelled	99.8	12	<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
46	<a href="#">c4wfiA</a>	Alignment	not modelled	99.8	16	<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
47	<a href="#">d1jfra</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Lipase
48	<a href="#">c3i6yA</a>	Alignment	not modelled	99.8	12	<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
49	<a href="#">c3visB</a>	Alignment	not modelled	99.7	16	<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
50	<a href="#">c3bjrA</a>	Alignment	not modelled	99.7	18	<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 wcfs1 at 2.09 a resolution
51	<a href="#">c3ls2D</a>	Alignment	not modelled	99.7	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
52	<a href="#">c4q3kB</a>	Alignment	not modelled	99.7	16	<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
53	<a href="#">c6fkxD</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> crystal structure of an acetyl xylan esterase from a desert metagenome
54	<a href="#">c3mveB</a>	Alignment	not modelled	99.7	18	<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
55	<a href="#">c4ao6A</a>	Alignment	not modelled	99.7	19	<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
56	<a href="#">c4zi5A</a>	Alignment	not modelled	99.7	18	<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
57	<a href="#">c3fcyB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylan esterase 1; <b>PDBTitle:</b> crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
58	<a href="#">c3k2iA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 4; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 4
59	<a href="#">c2b9vB</a>	Alignment	not modelled	99.7	13	<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
60	<a href="#">c2hdwB</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pa2218; <b>PDBTitle:</b> crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
61	<a href="#">c4eb0A</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lcc; <b>PDBTitle:</b> crystal structure of leaf-branch compost bacterial cutinase homolog
62	<a href="#">d2bgra2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
63	<a href="#">c3hkB</a>	Alignment	not modelled	99.7	15	<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)
64	<a href="#">c5aoaA</a>	Alignment	not modelled	99.7	15	<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
65	<a href="#">c3h04A</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
66	<a href="#">d1hlga</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
67	<a href="#">c4zrsA</a>	Alignment	not modelled	99.7	15	<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
68	<a href="#">c3ga7A</a>	Alignment	not modelled	99.7	18	<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
69	<a href="#">d2b61a1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
70	<a href="#">d2hu7a2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acylamino-acid-releasing enzyme, C-terminal donain
71	<a href="#">d1ju3a2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
72	<a href="#">d2i3da1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
73	<a href="#">c2i3dA</a>	Alignment	not modelled	99.7	14	<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
74	<a href="#">d1orva2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
75	<a href="#">c2o7vA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cxe carboxylesterase; <b>PDBTitle:</b> carboxylesterase aece1 from actinidia eriantha covalently inhibited2 by paraoxon
76	<a href="#">d1k8qa</a>	Alignment	not modelled	99.7	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
77	<a href="#">c3llcA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
78	<a href="#">d1xfda2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
79	<a href="#">c5cxcC</a>	Alignment	not modelled	99.7	18	<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
80	<a href="#">c1l7qA</a>	Alignment	not modelled	99.7	14	<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

81	<a href="#">c3ib3A</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coce/nond family hydrolase; <b>PDBTitle:</b> crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
82	<a href="#">c5x6sB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylxylyan esterase a; <b>PDBTitle:</b> acetyl xylyan esterase from aspergillus awamori
83	<a href="#">c2fx5A</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
84	<a href="#">c2qruA</a>	Alignment	not modelled	99.7	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 an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
85	<a href="#">c3ksrA</a>	Alignment	not modelled	99.7	16	<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
86	<a href="#">c5hdfB</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
87	<a href="#">c5xg0A</a>	Alignment	not modelled	99.7	20	<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
88	<a href="#">c5g59A</a>	Alignment	not modelled	99.6	18	<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
89	<a href="#">c3fcxA</a>	Alignment	not modelled	99.6	12	<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
90	<a href="#">c2wtmC</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrivibrio proteoclasticus
91	<a href="#">c6grwA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyl xylyan esterase; <b>PDBTitle:</b> glucuronoyl esterase from opitutus terrae (au derivative)
92	<a href="#">c4b6gA</a>	Alignment	not modelled	99.6	12	<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.
93	<a href="#">d1mpxa2</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
94	<a href="#">c5oluA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase family protein; <b>PDBTitle:</b> the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol
95	<a href="#">c4krxB</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> structure of aes from e. coli
96	<a href="#">c4pf1D</a>	Alignment	not modelled	99.6	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
97	<a href="#">d2b9va2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
98	<a href="#">d2fuka1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
99	<a href="#">c5hc4A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> structure of esterase est22
100	<a href="#">c3wydA</a>	Alignment	not modelled	99.6	23	<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
101	<a href="#">c2zshA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> probable gibberellin receptor gid11; <b>PDBTitle:</b> structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
102	<a href="#">c6gupB</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> siderophore biosynthesis lipase/esterase, putative; <b>PDBTitle:</b> siderophore hydrolase estb from aspergillus fumigatus
103	<a href="#">c4h18D</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cmt1; <b>PDBTitle:</b> three dimensional structure of corynomycoloyl tranferase c
104	<a href="#">c4z8zA</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the hypothetical protein from ruminclostridium2 thermocellum atcc 27405
105	<a href="#">c6qi5A</a>	Alignment	not modelled	99.6	16	<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
106	<a href="#">c6a6oA</a>	Alignment	not modelled	99.6	14	<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
						<b>Fold:</b> alpha/beta-Hydrolases



107	<a href="#">d2pl5a1</a>	Alignment	not modelled	99.6	13	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
108	<a href="#">c4h0cA</a>	Alignment	not modelled	99.6	18	<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
109	<a href="#">c4q05A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e25; <b>PDBTitle:</b> crystal structure of an esterase e25
110	<a href="#">c3f67A</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dieneactone hydrolase; <b>PDBTitle:</b> crystal structure of putative dieneactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
111	<a href="#">c3hxB</a>	Alignment	not modelled	99.6	17	<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
112	<a href="#">d1lza</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
113	<a href="#">d1jkma</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
114	<a href="#">d1ufoa</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein TT1662
115	<a href="#">d1lnsa3</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
116	<a href="#">c2o2gA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dieneactone hydrolase; <b>PDBTitle:</b> crystal structure of dieneactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
117	<a href="#">c5jkA</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 I374d mutant
118	<a href="#">c6gu8A</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyl xylan esterase; <b>PDBTitle:</b> glucuronoyl esterase from solibacter usitatus
119	<a href="#">c4j7aB</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
120	<a href="#">c1mpxB</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amino acid ester hydrolase; <b>PDBTitle:</b> alpha-amino acid ester hydrolase labeled with selenomethionine