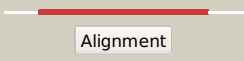

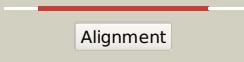

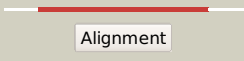

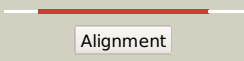

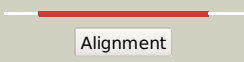

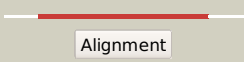

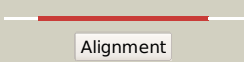

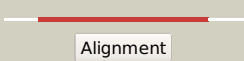

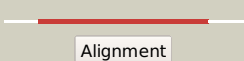

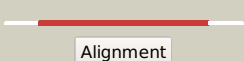

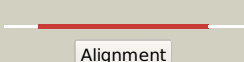

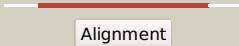

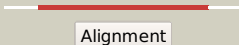

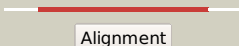



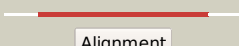

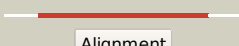

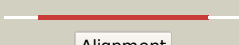






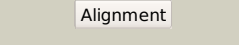

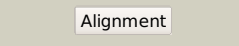



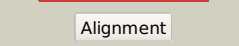


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3438 (- )_3857577_3858419
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	272f48b25a055e9d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3visB_</a>	 Alignment		100.0	20	<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
2	<a href="#">c3d59B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> platelet-activating factor acetylhydrolase; <b>PDBTitle:</b> crystal structure of human plasma platelet activating factor2 acetylhydrolase
3	<a href="#">c5xg0A_</a>	 Alignment		100.0	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
4	<a href="#">d1jfra_</a>	 Alignment		100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Lipase
5	<a href="#">c5yalA_</a>	 Alignment		100.0	20	<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
6	<a href="#">c4eb0A_</a>	 Alignment		100.0	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
7	<a href="#">c4wfiA_</a>	 Alignment		100.0	18	<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
8	<a href="#">c2fx5A_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
9	<a href="#">c2ecfA_</a>	 Alignment		100.0	19	<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
10	<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
11	<a href="#">c3k2iA_</a>	 Alignment		100.0	17	<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

12	<a href="#">c5oljA_</a>	 Alignment		100.0	19	<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
13	<a href="#">c3hikB_</a>	 Alignment		100.0	19	<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)
14	<a href="#">d1l7aa_</a>	 Alignment		99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
15	<a href="#">d2jba1_</a>	 Alignment		99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropseudooxynicotine hydrolase-like
16	<a href="#">c2hu7A_</a>	 Alignment		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
17	<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
18	<a href="#">c6eotG_</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
19	<a href="#">c2jbaB_</a>	 Alignment		99.9	17	<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.
20	<a href="#">c6eosB_</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
21	<a href="#">c2o2gA_</a>	 Alignment	not modelled	99.9	19	<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
22	<a href="#">c4q1vA_</a>	 Alignment	not modelled	99.9	18	<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
23	<a href="#">c3mveB_</a>	 Alignment	not modelled	99.9	19	<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
24	<a href="#">c6eoqC_</a>	 Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
25	<a href="#">c5txeA_</a>	 Alignment	not modelled	99.9	16	<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
26	<a href="#">c4zi5A_</a>	 Alignment	not modelled	99.9	14	<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
27	<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
28	<a href="#">c4hxlj_</a>	 Alignment	not modelled	99.9	18	<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)

29	<a href="#">c2g5tA</a>	Alignment	not modelled	99.9	14	<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
30	<a href="#">c1z68A</a>	Alignment	not modelled	99.9	17	<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
31	<a href="#">c6eorD</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
32	<a href="#">c4wj1B</a>	Alignment	not modelled	99.9	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
33	<a href="#">c2qtB</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
34	<a href="#">c5jrlC</a>	Alignment	not modelled	99.9	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 sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
35	<a href="#">c5xb6D</a>	Alignment	not modelled	99.9	18	<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
36	<a href="#">c5yznA</a>	Alignment	not modelled	99.9	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
37	<a href="#">c1qfmA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
38	<a href="#">c3h04A</a>	Alignment	not modelled	99.9	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
39	<a href="#">d1ju3a2</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
40	<a href="#">c2bklB</a>	Alignment	not modelled	99.9	20	<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
41	<a href="#">c1l7qA</a>	Alignment	not modelled	99.9	16	<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
42	<a href="#">c2hdwB</a>	Alignment	not modelled	99.9	20	<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
43	<a href="#">d1ufoa</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein TT1662
44	<a href="#">c2xe4A</a>	Alignment	not modelled	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
45	<a href="#">c6gocA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> duf3826 domain-containing protein; <b>PDBTitle:</b> methylesterase bt1017
46	<a href="#">c4bp9A</a>	Alignment	not modelled	99.9	14	<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
47	<a href="#">c3fnbB</a>	Alignment	not modelled	99.9	15	<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
48	<a href="#">c5t88B</a>	Alignment	not modelled	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
49	<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
50	<a href="#">c3iumA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
51	<a href="#">c4ao6A</a>	Alignment	not modelled	99.9	18	<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
52	<a href="#">c4d9jl</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> designed 16nm tetrahedral protein cage containing non-haem <b>PDBTitle:</b> structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
53	<a href="#">c5hdfB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
54	<a href="#">c2b9vB</a>	Alignment	not modelled	99.9	16	<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

55	<a href="#">c1xfdD</a>	Alignment	not modelled	99.9	14	<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
56	<a href="#">c6aggE</a>	Alignment	not modelled	99.9	19	<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
57	<a href="#">c5g59A</a>	Alignment	not modelled	99.9	15	<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
58	<a href="#">c3i28A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase 2; <b>PDBTitle:</b> crystal structure of soluble epoxide hydrolase
59	<a href="#">c4zwnD</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
60	<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
61	<a href="#">d2b9va2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
62	<a href="#">c3ksrA</a>	Alignment	not modelled	99.9	17	<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
63	<a href="#">c2wtmC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrivibrio proteoclasticus
64	<a href="#">c5x6sB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylxylan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
65	<a href="#">c4zrsA</a>	Alignment	not modelled	99.9	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
66	<a href="#">d1vlqa</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
67	<a href="#">c1cr6A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
68	<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
69	<a href="#">c3llcA</a>	Alignment	not modelled	99.9	21	<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
70	<a href="#">d1k8qa</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
71	<a href="#">c5uzwD</a>	Alignment	not modelled	99.9	12	<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
72	<a href="#">c2qrUA</a>	Alignment	not modelled	99.9	17	<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
73	<a href="#">c4pf1D</a>	Alignment	not modelled	99.9	13	<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
74	<a href="#">c4z8zA</a>	Alignment	not modelled	99.9	13	<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 ruminiclostridium2 thermocellum atcc 27405
75	<a href="#">d1hlga</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
76	<a href="#">c3jw8A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgll protein; <b>PDBTitle:</b> crystal structure of human mono-glyceride lipase
77	<a href="#">c3fcyB</a>	Alignment	not modelled	99.9	14	<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
78	<a href="#">d2fuka1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
79	<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
80	<a href="#">c6gupB</a>	Alignment	not modelled	99.9	17	<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

81	<a href="#">c3ib3A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coce/nond family hydrolase; <b>PDBTitle:</b> crystal structure of sac02612 - coce/nond family hydrolase from2 staphylococcus aureus
82	<a href="#">d1qfma2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
83	<a href="#">c1mpxB_</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> alpha-amino acid ester hydrolase labeled with selenomethionine
84	<a href="#">c4eziA_</a>	Alignment	not modelled	99.9	20	<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
85	<a href="#">c6fkxD_</a>	Alignment	not modelled	99.9	18	<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
86	<a href="#">c3h2IA_</a>	Alignment	not modelled	99.9	22	<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
87	<a href="#">d1dina_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Dienelactone hydrolase
88	<a href="#">c5f2hA_</a>	Alignment	not modelled	99.9	8	<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
89	<a href="#">c3bxA_</a>	Alignment	not modelled	99.9	11	<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
90	<a href="#">c3f67A_</a>	Alignment	not modelled	99.9	17	<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
91	<a href="#">c3rm3A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable monoacylglycerol lipase; <b>PDBTitle:</b> crystal structure of monoacylglycerol lipase from bacillus sp. h257
92	<a href="#">d2i3da1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
93	<a href="#">c2i3dA_</a>	Alignment	not modelled	99.9	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
94	<a href="#">c3trdA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
95	<a href="#">c4pw0A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from chitinophaga pinensis
96	<a href="#">c3v48B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rutd; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
97	<a href="#">c3g8yA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> susd/ragb-associated esterase-like protein; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bv_u_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
98	<a href="#">d1fj2a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
99	<a href="#">c4q3kB_</a>	Alignment	not modelled	99.9	11	<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
100	<a href="#">c4f0JA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrolytic enzyme; <b>PDBTitle:</b> crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution
101	<a href="#">c3hjuB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of human monoglyceride lipase
102	<a href="#">c3doiA_</a>	Alignment	not modelled	99.9	15	<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
103	<a href="#">c6eicA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis monoglyceride lipase; <b>PDBTitle:</b> crystal structure of rv0183, a monoglyceride lipase from mycobacterium2 tuberculosis
104	<a href="#">c4zv9E_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of an uncharacterized2 protein from escherichia coli o157:h7 str. sakai
105	<a href="#">c2y6vB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
106	<a href="#">c3gm1A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cinnamoyl esterase;

106	<a href="#">c3qmrA</a>	Alignment	not modelled	99.8	14	<b>PDBTitle:</b> crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii <b>PDB header:</b> hydrolase
107	<a href="#">c3bjrA</a>	Alignment	not modelled	99.8	17	<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 <b>PDB header:</b> hydrolase
108	<a href="#">c4l0cA</a>	Alignment	not modelled	99.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> deformylase; <b>PDBTitle:</b> crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16 <b>PDB header:</b> hydrolase
109	<a href="#">c5oluA</a>	Alignment	not modelled	99.8	17	<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 <b>PDB header:</b> transferase
110	<a href="#">c5d6oB</a>	Alignment	not modelled	99.8	11	<b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum <b>PDB header:</b> hydrolase
111	<a href="#">c3dyvA</a>	Alignment	not modelled	99.8	18	<b>Chain:</b> A: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism <b>PDB header:</b> hydrolase
112	<a href="#">c6a6oA</a>	Alignment	not modelled	99.8	18	<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>PDB header:</b> hydrolase
113	<a href="#">c3nuzF</a>	Alignment	not modelled	99.8	14	<b>Chain:</b> F: <b>PDB Molecule:</b> putative acetyl xylan esterase; <b>PDBTitle:</b> crystal structure of a putative acetyl xylan esterase (bf1801) from2 bacteroides fragilis nctc 9343 at 2.30 a resolution <b>PDB header:</b> lyase
114	<a href="#">c5uw7B</a>	Alignment	not modelled	99.8	11	<b>Chain:</b> B: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 y481f variant in complex with follower peptide <b>PDB header:</b> hormone receptor
115	<a href="#">c2zshA</a>	Alignment	not modelled	99.8	24	<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
116	<a href="#">d1uxoa</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
117	<a href="#">c3ed1E</a>	Alignment	not modelled	99.8	22	<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
118	<a href="#">c2qjwA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein xcc1541; <b>PDBTitle:</b> crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
119	<a href="#">c3fcxA</a>	Alignment	not modelled	99.8	20	<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
120	<a href="#">c5esrA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus