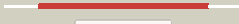



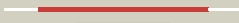






















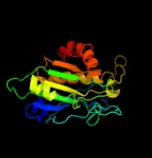





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1104 (- )_1231306_1231995
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	357e93ba3fc6b070

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fg5B_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 alpha-esterase-7 coxylesterase; <b>PDBTitle:</b> crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
2	<a href="#">d1dx4a_</a>	 Alignment		100.0	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
3	<a href="#">c2fj0A_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> crystal structure of juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
4	<a href="#">c4bdtA_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> human acetylcholinesterase in complex with huprine w and fasciculin 2
5	<a href="#">c1f8uA_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
6	<a href="#">d1f8ua_</a>	 Alignment		100.0	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
7	<a href="#">c4qwwA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of the fab410-bfache complex
8	<a href="#">d2h7ca1</a>	 Alignment		100.0	42	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
9	<a href="#">c6i2tC_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
10	<a href="#">c5x61A_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
11	<a href="#">d1k4ya_</a>	 Alignment		100.0	42	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like

12	<a href="#">d2ha2a1</a>	Alignment		100.0	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
13	<a href="#">d1ukca_</a>	Alignment		100.0	32	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
14	<a href="#">c3biwD_</a>	Alignment		100.0	42	<b>PDB header:</b> cell adhesion/cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> neuroligin-1; <b>PDBTitle:</b> crystal structure of the neuroligin-1/neurexin-1beta synaptic adhesion2 complex
15	<a href="#">d1ea5a_</a>	Alignment		100.0	37	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
16	<a href="#">c5w1uA_</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> culex quinquefasciatus carboxylesterase b2
17	<a href="#">d1p0ia_</a>	Alignment		100.0	38	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
18	<a href="#">c2pm8A_</a>	Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> crystal structure of recombinant full length human2 butyrylcholinesterase
19	<a href="#">c2ogsA_</a>	Alignment		100.0	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable carboxylesterase est50; <b>PDBTitle:</b> crystal structure of the geobacillus stearotherophilus2 carboxylesterase est55 at ph 6.2
20	<a href="#">c2w6cX_</a>	Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> ache in complex with a bis-(-)-nor-meptazinol derivative
21	<a href="#">d1thga_</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
22	<a href="#">d1lifa_</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
23	<a href="#">c4be4A_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sterol esterase; <b>PDBTitle:</b> closed conformation of o. piceae sterol esterase
24	<a href="#">d1qe3a_</a>	Alignment	not modelled	100.0	50	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
25	<a href="#">d1crla_</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
26	<a href="#">d1gz7a_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
27	<a href="#">c5a2gB_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
28	<a href="#">d1f6wa_</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
29	<a href="#">d2bcea_</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases

					Family:Acetylcholinesterase-like
30	<a href="#">c5thmA</a>	Alignment	not modelled	100.0	35 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase-6; <b>PDBTitle:</b> esterase-6 from drosophila melanogaster
31	<a href="#">c4j0dB</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tannase; <b>PDBTitle:</b> tannin acyl hydrolase from lactobacillus plantarum (cadmium)
32	<a href="#">c4c87A</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> esterase lpest1 from lactobacillus plantarum wcf51
33	<a href="#">c2zshA</a>	Alignment	not modelled	99.9	27 <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 dela2 recognition by the gibberellin receptor
34	<a href="#">c4q3oB</a>	Alignment	not modelled	99.8	21 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mgs-mt1; <b>PDBTitle:</b> crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
35	<a href="#">c2o7vA</a>	Alignment	not modelled	99.8	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cxe carboxylesterase; <b>PDBTitle:</b> carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
36	<a href="#">c4zrsA</a>	Alignment	not modelled	99.8	31 <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
37	<a href="#">c3bxpA</a>	Alignment	not modelled	99.8	19 <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
38	<a href="#">c3ed1E</a>	Alignment	not modelled	99.8	23 <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
39	<a href="#">c3ga7A</a>	Alignment	not modelled	99.8	17 <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
40	<a href="#">c4n5iX</a>	Alignment	not modelled	99.8	27 <b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
41	<a href="#">c5hc4A</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> structure of esterase est22
42	<a href="#">c5jd5A</a>	Alignment	not modelled	99.8	20 <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
43	<a href="#">c4j7aB</a>	Alignment	not modelled	99.8	27 <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
44	<a href="#">c5miiD</a>	Alignment	not modelled	99.7	19 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxyl esterase 2; <b>PDBTitle:</b> crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
45	<a href="#">c3bjrA</a>	Alignment	not modelled	99.7	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
46	<a href="#">c4q3kB</a>	Alignment	not modelled	99.7	20 <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
47	<a href="#">c3d7rB</a>	Alignment	not modelled	99.7	15 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a putative esterase from staphylococcus aureus
48	<a href="#">d2pbla1</a>	Alignment	not modelled	99.7	19 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
49	<a href="#">c4q05A</a>	Alignment	not modelled	99.7	23 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e25; <b>PDBTitle:</b> crystal structure of an esterase e25
50	<a href="#">d1jkma</a>	Alignment	not modelled	99.7	21 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
51	<a href="#">c4krxB</a>	Alignment	not modelled	99.7	18 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> structure of aes from e. coli
52	<a href="#">c6a6oA</a>	Alignment	not modelled	99.7	20 <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
53	<a href="#">c4v2iB</a>	Alignment	not modelled	99.7	20 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp
54	<a href="#">d1jjia</a>	Alignment	not modelled	99.6	25 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
55	<a href="#">c5id4D</a>	Alignment	not modelled	99.6	23 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> lae6;

55	<a href="#">c5j4bD</a>	Alignment	not modelled	99.6	23	<b>PDBTitle:</b> crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain
56	<a href="#">c5x6sB</a>	Alignment	not modelled	99.6	14	<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
57	<a href="#">c6eoqC</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
58	<a href="#">c4wy5A</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
59	<a href="#">c6eorD</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
60	<a href="#">d1lza</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
61	<a href="#">c6eotG</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
62	<a href="#">c3hxB</a>	Alignment	not modelled	99.6	22	<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
63	<a href="#">c2qruA</a>	Alignment	not modelled	99.6	20	<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
64	<a href="#">c6eosB</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
65	<a href="#">c3doiA</a>	Alignment	not modelled	99.6	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
66	<a href="#">c3dnmA</a>	Alignment	not modelled	99.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> crystal structure hormone-sensitive lipase from a2 metagenome library
67	<a href="#">c4ob7A</a>	Alignment	not modelled	99.6	23	<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
68	<a href="#">c4e14A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
69	<a href="#">c4wjB</a>	Alignment	not modelled	99.6	10	<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
70	<a href="#">c4wy8A</a>	Alignment	not modelled	99.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
71	<a href="#">c3qh4A</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase lipw ; <b>PDBTitle:</b> crystal structure of esterase lipw from mycobacterium marinum
72	<a href="#">c5l2pD</a>	Alignment	not modelled	99.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> arylesterase; <b>PDBTitle:</b> structure of arylesterase
73	<a href="#">c1z68A</a>	Alignment	not modelled	99.6	15	<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
74	<a href="#">c5a0aA</a>	Alignment	not modelled	99.6	28	<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
75	<a href="#">c3azqA</a>	Alignment	not modelled	99.5	16	<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
76	<a href="#">c6aaeA</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of chloramphenicol-metabolizaing enzyme estdl136
77	<a href="#">c4ypvA</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> est8; <b>PDBTitle:</b> high-resolution structure of a metagenome-derived esterase est8
78	<a href="#">c5tXeA</a>	Alignment	not modelled	99.5	17	<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
79	<a href="#">c5oljA</a>	Alignment	not modelled	99.5	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
80	<a href="#">c2qtB</a>	Alignment	not modelled	99.5	12	<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
						<b>PDB header:</b> hydrolase

81	<a href="#">c2ecfA</a>	Alignment	not modelled	99.5	19	<b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from 2 stentrophomonas maltophilia
82	<a href="#">c2g5tA</a>	Alignment	not modelled	99.5	12	<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
83	<a href="#">c2eepA</a>	Alignment	not modelled	99.5	18	<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
84	<a href="#">c3iumA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
85	<a href="#">d1qfma2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
86	<a href="#">c4q1vA</a>	Alignment	not modelled	99.5	17	<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
87	<a href="#">c4bp9A</a>	Alignment	not modelled	99.5	13	<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
88	<a href="#">c5uw7B</a>	Alignment	not modelled	99.5	16	<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
89	<a href="#">c3d0kA</a>	Alignment	not modelled	99.5	19	<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
90	<a href="#">c1xfD</a>	Alignment	not modelled	99.5	17	<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
91	<a href="#">c3fakA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
92	<a href="#">d1vkha</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Putative serine hydrolase Ydr428c
93	<a href="#">c4xvcG</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> esterase e40; <b>PDBTitle:</b> crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
94	<a href="#">c2c7bA</a>	Alignment	not modelled	99.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
95	<a href="#">c5uzwD</a>	Alignment	not modelled	99.5	16	<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 and2 covalent inhibitor zpp
96	<a href="#">c2bkIB</a>	Alignment	not modelled	99.5	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
97	<a href="#">c5l8sD</a>	Alignment	not modelled	99.5	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
98	<a href="#">c1qfma</a>	Alignment	not modelled	99.5	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
99	<a href="#">d1u4na</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
100	<a href="#">c2xe4A</a>	Alignment	not modelled	99.4	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
101	<a href="#">c4hvtA</a>	Alignment	not modelled	99.4	16	<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
102	<a href="#">c3wj2A</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of estfa (fe-lacking apo form)
103	<a href="#">c2hu7A</a>	Alignment	not modelled	99.4	23	<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
104	<a href="#">c5n4dA</a>	Alignment	not modelled	99.4	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
105	<a href="#">c3aikB</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> 303aa long hypothetical esterase; <b>PDBTitle:</b> crystal structure of a hsl-like carboxylesterase from sulfobolus2 tokodaii
						<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> prolyl oligopeptidase;

106	<a href="#">c1yr2A_</a>	Alignment	not modelled	99.4	17	<b>PDBTitle:</b> structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
107	<a href="#">c3h04A_</a>	Alignment	not modelled	99.4	19	<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
108	<a href="#">c3fcxA_</a>	Alignment	not modelled	99.4	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
109	<a href="#">c2wirB_</a>	Alignment	not modelled	99.4	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha/beta hydrolase fold-3 domain protein; <b>PDBTitle:</b> hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
110	<a href="#">c3i6yA_</a>	Alignment	not modelled	99.4	18	<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
111	<a href="#">c4hxgl_</a>	Alignment	not modelled	99.4	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)
112	<a href="#">c5lrC_</a>	Alignment	not modelled	99.4	18	<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)
113	<a href="#">d2bgra2</a>	Alignment	not modelled	99.3	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
114	<a href="#">c5yznA_</a>	Alignment	not modelled	99.3	16	<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
115	<a href="#">c3k2iA_</a>	Alignment	not modelled	99.3	16	<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
116	<a href="#">c3ls2D_</a>	Alignment	not modelled	99.3	15	<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
117	<a href="#">c5cxC_</a>	Alignment	not modelled	99.3	12	<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
118	<a href="#">c4h18D_</a>	Alignment	not modelled	99.3	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
119	<a href="#">c5yalA_</a>	Alignment	not modelled	99.3	19	<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
120	<a href="#">c3wydA_</a>	Alignment	not modelled	99.3	18	<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