







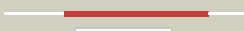














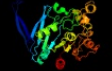


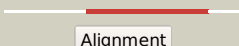

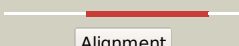

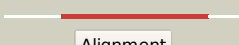

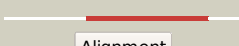







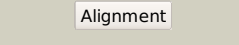

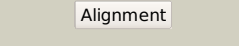
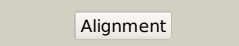
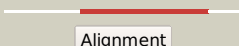

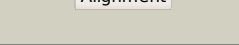



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2627c (-)_2953517_2954758
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	303c1246b8f1419f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fnbB_	 Alignment		100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
2	c4z8zA_	 Alignment		100.0	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminclostridium2 thermocellum atcc 27405
3	c2jwbB_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
4	d2jbwa1	 Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydrospseudooxynicotine hydrolase-like
5	c3azqA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
6	c2hu7A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
7	c2ecfA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
8	c5l8sD_	 Alignment		100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase; PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
9	c5yznA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
10	c5oljA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
11	c4hxgl_	 Alignment		100.0	18	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)

12	c6eorD_	 Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
13	c6eosB_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
14	c5t88B_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
15	c1z68A_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
16	c6eoqC_	 Alignment		100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
17	c6eotG_	 Alignment		100.0	17	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyg, space group 19
18	c5txeA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
19	c4q1vA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative dipeptidyl aminopeptidase iv; PDBTitle: crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution
20	c2g5tA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
21	c2eepA_	 Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
22	c5jrlC_	 Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
23	c3mveB_	 Alignment	not modelled	99.9	10	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
24	c2qtbB_	 Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
25	c4wjlb_	 Alignment	not modelled	99.9	15	PDB header: membrane protein Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
26	c1xfdD_	 Alignment	not modelled	99.9	15	PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
27	c1qfmA_	 Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
28	d1l7aa_	 Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like

29	c5g59A	Alignment	not modelled	99.9	18	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
30	c4ao6A	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
31	c4bp9A	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
32	c2bkB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
33	c2xe4A	Alignment	not modelled	99.9	15	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
34	c1yr2A	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
35	c6agqE	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4
36	c5n4dA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
37	d1vlqa	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
38	c6fkxD	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
39	c3iumA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
40	c3fcyB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
41	c5uzwD	Alignment	not modelled	99.9	14	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
42	c2o2gA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
43	d1hlga	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
44	c4hvtA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
45	c3hikB	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
46	c3k2IA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
47	c2qjwA	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
48	c5f2hA	Alignment	not modelled	99.9	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
49	c2wtmC	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
50	d2fuka1	Alignment	not modelled	99.9	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
51	c3g8yA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bv_u_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
52	d1k8qa	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
53	c4eziA	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution

54	c2q0xA_	Alignment	not modelled	99.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
55	c2vavL_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
56	c5uw7B_	Alignment	not modelled	99.9	13	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
57	c3ksrA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative serine hydrolase; PDBTitle: crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
58	c2i3dA_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
59	d2i3da1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
60	d2vata1	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
61	d1ufoa_	Alignment	not modelled	99.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
62	c5d6oB_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum
63	c4d9jl_	Alignment	not modelled	99.8	16	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
64	c3trdA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
65	c1l7qA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
66	d1ju3a2	Alignment	not modelled	99.8	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
67	c3llcA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
68	c3h04A_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
69	c3ib3A_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
70	c5cmlA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
71	c4fleA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
72	c5hdfB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
73	c3jw8A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
74	d2hu7a2	Alignment	not modelled	99.8	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
75	c3i28A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
76	c2hdwB_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
77	c5efzC_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
78	c3rm3A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from bacillus sp. h257
79	c4zrsA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library

80	c5oluA	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from <i>Bacillus coagulans</i> in complex with glycerol
81	d2b61a1	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
82	c1cr6A	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
83	c3bxA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from <i>Bacillus plantarum</i> wcf51 at 1.70 Å resolution
84	c3doiA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with 2 paraoxon
85	c3qm1A	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: cinnamoyl esterase; PDBTitle: crystal structure of the <i>Bacillus johnsonii</i> cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
86	c2qruA	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha/beta hydrolase superfamily protein from <i>Enterococcus faecalis</i>
87	c2rauA	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from <i>Sulfolobus solfataricus</i> at 1.85 Å resolution
88	c5w8pA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from <i>Mycobacterium abscessus</i>
89	c4pf1D	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon 2 thaumararchaeota archaeon
90	c4h0cA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from <i>Dyadobacter fermentans</i> dsm 18053
91	c3vvlA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
92	c3om8A	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from <i>Pseudomonas aeruginosa</i> pa01
93	c6eicA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: <i>Mycobacterium tuberculosis</i> monoglyceride lipase; PDBTitle: crystal structure of rv0183, a monoglyceride lipase from <i>Mycobacterium tuberculosis</i>
94	c2veoA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
95	c2r11D	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from <i>Bacillus subtilis</i> at 1.96 Å resolution
96	c6gocA	Alignment	not modelled	99.8	15	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methyltransferase bt1017
97	c3fcxA	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
98	c4qloA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from <i>Staphylococcus aureus</i>
99	c5uroA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in <i>Trichoderma reesei</i>
100	c2y6vB	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from <i>Saccharomyces cerevisiae</i> (crystal form i)
101	c4c87A	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpe1 from <i>Bacillus plantarum</i> wcf51
102	c5yhpB	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast <i>Glaciozyma antarctica</i>
103	c6gupB	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from <i>Aspergillus fumigatus</i>
104	c4zi5A	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of diene lactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
105	c3v48B	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd

					from2 e.coli
106	d1vkha_	Alignment	not modelled	99.8	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
107	d1qfma2	Alignment	not modelled	99.8	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
108	c3hjuB_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
109	c4b6gA_	Alignment	not modelled	99.8	10 PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
110	c3i1iA_	Alignment	not modelled	99.8	16 PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
111	d2pbla1	Alignment	not modelled	99.8	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
112	c5xb6D_	Alignment	not modelled	99.8	11 PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
113	d1mtza_	Alignment	not modelled	99.8	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
114	c4wfiA_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
115	d2h1ia1	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
116	c4zwnD_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
117	c6avyA_	Alignment	not modelled	99.8	12 PDB header: hydrolase Chain: A: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: crystal structure of zea mays acyl-protein thioesterase 2
118	c2xuaH_	Alignment	not modelled	99.8	13 PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
119	c5jkjA_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
120	c5xksB_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: B: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from thermophilic2 geobacillus sp. 12amor