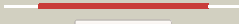



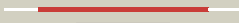

























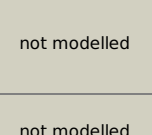


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1215c_(-)_1357765_1359450
Date	Wed Jul 31 22:05:30 BST 2019
Unique Job ID	6d17d1a78780117a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ib3A_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of saco12612 - coce/nond family hydrolase from2 staphylococcus aureus
2	c4pf1D_	 Alignment		100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
3	c2b9vB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
4	c1mpxB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
5	c1l7qA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
6	c1lnsA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: x-prolyl dipeptidyl aminopeptidase; PDBTitle: crystal structure analysis of the x-prolyl dipeptidyl aminopeptidase2 from lactococcus lactis
7	d1lnsa3	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
8	d2b9va2	 Alignment		100.0	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
9	d1mpxa2	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
10	d1ju3a2	 Alignment		100.0	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
11	d1ju3a1	 Alignment		100.0	22	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like

12	d2b9va1	Alignment		100.0	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
13	d1mpxa1	Alignment		100.0	16	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
14	c5oljA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
15	c5l8sD_	Alignment		100.0	17	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
16	c3azqA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
17	d1l7aa_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
18	c2ecfA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
19	c4hxgl_	Alignment		100.0	16	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
20	c5txeA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
21	c5jrlC_	Alignment	not modelled	100.0	17	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)
22	c2hu7A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
23	c2qtbB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
24	c2g5tA_	Alignment	not modelled	100.0	12	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
25	c2jwbB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
26	c1z68A_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
27	d2jwba1	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydroxypseudooxynicotine hydrolase-like
28	c4bp9A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidasse b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently

						bound2 antipain - closed form PDB header: hydrolase
29	c2eepA_	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
30	c4q1vA_	Alignment	not modelled	100.0	15	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
31	c4wj1B_	Alignment	not modelled	100.0	16	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
32	c6eotG_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
33	c2xe4A_	Alignment	not modelled	100.0	15	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
34	c2bklB_	Alignment	not modelled	100.0	19	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
35	c6eosB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
36	c5t88B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
37	c5yznA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
38	c3iumA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
39	c1qfmA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
40	c6eoqC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
41	d1vlqa_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
42	c1yr2A_	Alignment	not modelled	100.0	19	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
43	c5uzwD_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
44	c6eorD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
45	c4ao6A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
46	c4hvtA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
47	c5n4dA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
48	c6agqE_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4
49	c3mveB_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
50	c3h1kB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
51	c3fnbB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
52	c3k2IA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
53	c6fkxD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
						Fold: Galactose-binding domain-like

54	d1lnsa2	Alignment	not modelled	100.0	16	Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
55	c5uw7B_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
56	c5xb6D_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
57	c6grwA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: glucuronoyl esterase from opitutus terrae (au derivative)
58	c3fcyB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
59	c5g59A_	Alignment	not modelled	99.9	15	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
60	c2hdwB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
61	c2o2gA_	Alignment	not modelled	99.9	18	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
62	d1qfma2	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
63	c6gocA_	Alignment	not modelled	99.9	16	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methyltransferase bt1017
64	c1xfdD_	Alignment	not modelled	99.9	17	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
65	c4eziA_	Alignment	not modelled	99.9	14	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
66	c6ehnA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase mz0003; PDBTitle: structural insight into a promiscuous ce15 esterase from the marine2 bacterial metagenome
67	d2hu7a2	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal domain
68	d2i3da1	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
69	c2i3da_	Alignment	not modelled	99.9	19	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
70	c6gu8A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: glucuronoyl esterase from solibacter usitatus
71	c2wtmC_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
72	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
73	c4g4gA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: 4-o-methyl-glucuronoyl methyltransferase; PDBTitle: crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
74	c4wfiA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
75	c3visB_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
76	c5xg0A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
77	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 (bvu_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
78	d2fuka1	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
79	c4z8zA_	Alignment	not modelled	99.9	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
						PDB header: hydrolase

80	c5yalA_	Alignment	not modelled	99.9	24	Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
81	c3trdA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
82	d2bgra2	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
83	d1orva2	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
84	d1jfra_	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
85	c3doiA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
86	c3h2iA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
87	c4zi5A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
88	c4eb0A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: lcc; PDBTitle: crystal structure of leaf-branch compost bacterial cutinase homolog
89	c5cm1A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
90	c3picB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: cip2; PDBTitle: glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina
91	c3nuzF_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: F: PDB Molecule: putative acetyl xylan esterase; PDBTitle: crystal structure of a putative acetyl xylan esterase (bf1801) from2 bacteroides fragilis nctc 9343 at 2.30 a resolution
92	d1hlga_	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
93	d1k8qa_	Alignment	not modelled	99.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
94	c3llcA_	Alignment	not modelled	99.8	11	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
95	c3jw8A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
96	c5oluA_	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol
97	c3qm1A_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: cinnamoyl esterase; PDBTitle: crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
98	c2fx5A_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
99	c3hjuB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
100	c5f2hA_	Alignment	not modelled	99.8	12	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
101	c5hdfB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
102	c3h04A_	Alignment	not modelled	99.8	14	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
103	c5x6sB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: acetylxylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
104	d1dina_	Alignment	not modelled	99.8	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
105	c3f67A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
106	c6eicA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: mycobacterium tuberculosis monoglyceride lipase; PDBTitle: crystal structure of rv0183, a monoglyceride lipase from

					mycobacterium2 tuberculosis
107	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
108	d1xfda2	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
109	c4zv9E_	Alignment	not modelled	99.8	22 PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: 2.00 angstrom resolution crystal structure of an uncharacterized2 protein from escherichia coli o157:h7 str. sakai
110	c5a0aA_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
111	c3bxaA_	Alignment	not modelled	99.8	13 PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
112	c3fcxA_	Alignment	not modelled	99.8	12 PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
113	c3i28A_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
114	c3d59B_	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: B: PDB Molecule: platelet-activating factor acetylhydrolase; PDBTitle: crystal structure of human plasma platelet activating factor2 acetylhydrolase
115	c4zrsA_	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
116	c2veoA_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
117	c4q3kB_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: B: PDB Molecule: mgs-m1; PDBTitle: crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
118	c2q0xA_	Alignment	not modelled	99.8	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
119	c5hc4A_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
120	c1cr6A_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor