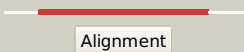

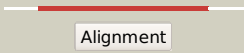

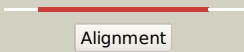

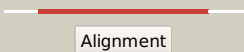

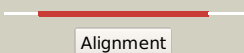

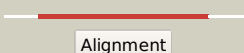

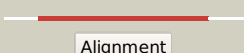





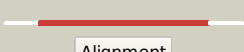

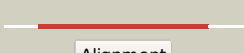



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2054 (-)_2313133_2313846
Date	Mon Aug 5 13:25:16 BST 2019
Unique Job ID	4896294ff019acdd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zv9E_			100.0	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
2	c4zi5A_			100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
3	d1dina_			100.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
4	c3f67A_			100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
5	c3azqA_			100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
6	c2ecfA_			100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia
7	c5oljA_			100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
8	c4hxgl_			100.0	17	PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
9	c5l8sD_			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
10	c2hu7A_			100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
11	c5yznA_			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

12	c4wj1B_	Alignment		100.0	19	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
13	c6eoqC_	Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
14	c2qtbB_	Alignment		99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
15	c2g5tA_	Alignment		99.9	17	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
16	c3h1kB_	Alignment		99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
17	c2eepA_	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
18	c4q1vA_	Alignment		99.9	17	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
19	c3k2iA_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
20	c6eosB_	Alignment		99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
21	c5txeA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
22	c5t88B_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
23	c51rlC_	Alignment	not modelled	99.9	20	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)
24	c6eorD_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
25	c1z68A_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
26	c6eotG_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
27	c2o2gA_	Alignment	not modelled	99.9	20	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
28	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

29	d2i3da1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
30	d2hu7a2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
31	d1l7aa_	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
32	d1qfma2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
33	c3ksrA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative serine hydrolase; PDBTitle: crystal structure of a putative serine hydrolase (xcc3885) from <i>Xanthomonas campestris</i> pv. <i>campestris</i> at 2.69 Å resolution
34	c1xfD_	Alignment	not modelled	99.9	16	PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human α-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
35	d2fuka1	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
36	d1ju3a2	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
37	c2xe4A_	Alignment	not modelled	99.9	16	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from <i>Leishmania major</i>
38	c1qfMA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
39	c4q3kB_	Alignment	not modelled	99.9	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
40	c2bklB_	Alignment	not modelled	99.9	15	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
41	c2c7bA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
42	d1orva2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
43	c3visB_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from <i>Thermobifida alba</i> ahk119
44	c2hdwB_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from <i>Pseudomonas2 aeruginosa</i>
45	c5xb6D_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from <i>E. coli</i>
46	c2wirB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archaeon <i>Pyrobaculum2 caldifontis</i>
47	c3trdA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from <i>Coxiella2 burnetii</i>
48	d1xfda2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
49	d1vlqa_	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
50	c3ga7A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 Å crystal structure of an acetyl esterase from <i>Salmonella2 typhimurium</i>
51	c4bp9A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from <i>Trypanosoma brucei</i> with covalently bound2 antipain - closed form
52	c4krxB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from <i>E. coli</i>
53	c5xg0A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel PET hydrolase from <i>Ideonella sakaiensis2</i> 201-f6
54	d2bgra2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
						PDB header: hydrolase

55	c3aikB	Alignment	not modelled	99.9	16	Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from <i>Sulfolobus</i> 2 tokodaii
56	d1lzlA	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
57	d2b9va2	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
58	c1l7qA	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
59	c4ao6A	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
60	c4ob7A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
61	c2b9vB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
62	c5jd4D	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: lae6; PDBTitle: crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain
63	c2jwbB	Alignment	not modelled	99.9	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.
64	c4xvcG	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
65	c5n4dA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from <i>Galerina marginata</i> bound to 25mer2 macrocyclization substrate - d661a mutant
66	c5oluA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 <i>Bacillus coagulans</i> in complex with glycerol
67	c4ypvA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
68	c5a0aA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, <i>Thermogutta terrifontis</i> , est2-propionate bound
69	c5l2pD	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
70	d2jba1	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
71	c6aaeA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizing enzyme estdl136
72	c3hxB	Alignment	not modelled	99.9	9	PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from <i>Lactococcus lactis</i> ,2 northeast structural genomics consortium target kr108
73	c4wfiA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
74	c3iumA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
75	c3ed1E	Alignment	not modelled	99.9	16	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
76	c6agqE	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from <i>Paenibacillus</i> sp. r4
77	c3fnbB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 <i>Streptococcus mutans</i> ua159
78	d1mpxa2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
79	c4pf1D	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 <i>Thaumarchaeota</i> archaeon
80	c4wy8A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from <i>Rhizomucor miehei</i> 2 explaining their substrate specificity

81	c4v2iB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp
82	d1u4na_	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
83	d1jfra_	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
84	c5jd5A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: mgs-mile3; PDBTitle: 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
85	c4eb0A_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: lcc; PDBTitle: crystal structure of leaf-branch compost bacterial cutinase homolog
86	c5g59A_	Alignment	not modelled	99.8	17	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
87	c4hvtA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
88	c4q05A_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
89	c3bxpA_	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 wcf51 at 1.70 a resolution
90	c3fakA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
91	c3wj2A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
92	c3ib3A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
93	c5cmlA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
94	c3fcyB_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
95	c3dnmA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
96	c5hc4A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
97	c5uzwD_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
98	d1jkma_	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
99	c3mveB_	Alignment	not modelled	99.8	20	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
100	c6a6aA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
101	c3d59B_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B: PDB Molecule: platelet-activating factor acetylhydrolase; PDBTitle: crystal structure of human plasma platelet activating factor2 acetylhydrolase
102	c1mpxB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
103	c2wtmC_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
104	c1yr2A_	Alignment	not modelled	99.8	13	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
105	c6fkxD_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
106	c4zwpD_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase;

106	c4zwnD_	Alignment	not modelled	99.8	12	PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
107	c6gocA_	Alignment	not modelled	99.8	16	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methylesterase bt1017
108	c3qh4A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
109	c5yalA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
110	c5miiD_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
111	d1jja_	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
112	c5dwdB_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of esterase pe8
113	d1fj2a_	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
114	c5uw7B_	Alignment	not modelled	99.8	13	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
115	c3bjrA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
116	c5hdfB_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
117	c2o7vA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
118	c4c87A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
119	c3qm1A_	Alignment	not modelled	99.8	16	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
120	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