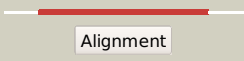

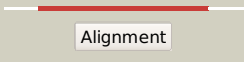

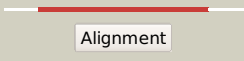

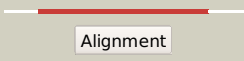

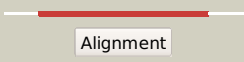
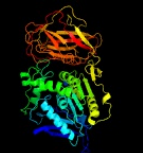
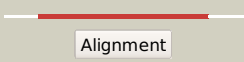

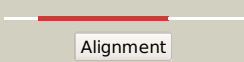
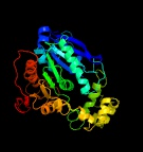
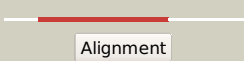

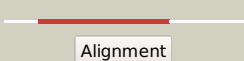

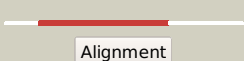

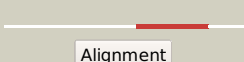
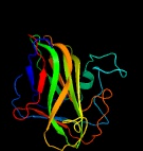










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1835c (-) _2080708_2082594
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	9c67e560fd0b91fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4pf1D_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
2	c2b9vB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
3	c1mpxB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
4	c1l7qA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
5	c3ib3A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sac02612 - coce/nond family hydrolase from2 staphylococcus aureus
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	d2b9va2	 Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
8	d1mpxA2	 Alignment		100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
9	d1lnsa3	 Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
10	d1ju3a2	 Alignment		100.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
11	d1ju3a1	 Alignment		100.0	28	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like

12	d2b9va1	Alignment		100.0	27	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
13	d1mpxa1	Alignment		100.0	26	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
14	c5oljA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
15	c5txeA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
16	d1lnsa2	Alignment		100.0	16	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
17	c5jrlC_	Alignment		100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the shingopyxin i lasso peptide isopeptidase2 spi-isop (native)
18	c3azqA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
19	c2ecfA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
20	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
21	c4bp9A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
22	c2xe4A_	Alignment	not modelled	100.0	19	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
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	c6eotG_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
25	c4q1vA_	Alignment	not modelled	100.0	14	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
26	c2g5tA_	Alignment	not modelled	100.0	14	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
27	c6eosB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
28	c2eepA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor

29	c4hxgl_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
30	c2bklB_	Alignment	not modelled	100.0	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
31	c4wjlb_	Alignment	not modelled	100.0	17	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	c1z68A_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: A; PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
33	c6eoqC_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
34	c5n4dA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
35	c1qfmA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
36	c3iumA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
37	c6eorD_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
38	c4hvtA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
39	c2hu7A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
40	d1l7aa_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
41	c5t88B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B; PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
42	c1yr2A_	Alignment	not modelled	100.0	18	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	c5suzwD_	Alignment	not modelled	100.0	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
44	c2jwbB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
45	c5yznA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
46	d2jbwa1	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
47	c5uw7B_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B; PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
48	c2hdwB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B; PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
49	c3hikB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B; PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
50	c5xb6D_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: D; PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
51	d1vlqa_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
52	c3mveB_	Alignment	not modelled	99.9	13	PDB header: lyase Chain: B; PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
53	c3k2iA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
54	c6aggE_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: E; PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4

55	c1xfdD	Alignment	not modelled	99.9	20	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
56	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
57	d1qfma2	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
58	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
59	c6gocA	Alignment	not modelled	99.9	20	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methylesterase bt1017
60	c6grwA	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: glucuronoyl esterase from opitutus terrae (au derivative)
61	c3fnbB	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
62	c3g8yA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bv_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
63	c5xg0A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
64	d2hu7a2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
65	c6fkxD	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
66	c5g59A	Alignment	not modelled	99.9	14	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
67	c3fcyB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
68	c5yalA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
69	c4wfiA	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
70	c4eziA	Alignment	not modelled	99.9	13	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
71	c3ksrA	Alignment	not modelled	99.8	19	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
72	c3doiA	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
73	c2wtmC	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
74	d1orva2	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
75	d2fuka1	Alignment	not modelled	99.8	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
76	c4zi5A	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
77	d1hlga	Alignment	not modelled	99.8	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
78	d1jfra	Alignment	not modelled	99.8	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
79	c3visB	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
80	c3h2iA	Alignment	not modelled	99.8	13	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
81	d2bgra2	Alignment	not modelled	99.8	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
82	c2i3dA	Alignment	not modelled	99.8	18 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
83	d2i3da1	Alignment	not modelled	99.8	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
84	c4g4gA	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: A: PDB Molecule: 4-o-methyl-glucuronoyl methylesterase; PDBTitle: crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
85	c6ehnA	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase mz0003; PDBTitle: structural insight into a promiscuous ce15 esterase from the marine2 bacterial metagenome
86	c3nuzF	Alignment	not modelled	99.8	13 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
87	c2fx5A	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
88	d1k8qa	Alignment	not modelled	99.8	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
89	c3trdA	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
90	c3picB	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: B: PDB Molecule: cip2; PDBTitle: glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina
91	c4eb0A	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: A: PDB Molecule: lcc; PDBTitle: crystal structure of leaf-branch compost bacterial cutinase homolog
92	c6gu8A	Alignment	not modelled	99.8	19 PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: glucuronoyl esterase from solibacter usitatus
93	d1xfda2	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
94	c4zv9E	Alignment	not modelled	99.7	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
95	c3jw8A	Alignment	not modelled	99.7	15 PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
96	c4z8zA	Alignment	not modelled	99.7	13 PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
97	c3f67A	Alignment	not modelled	99.7	12 PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
98	d1dina	Alignment	not modelled	99.7	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
99	c3i28A	Alignment	not modelled	99.7	11 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
100	c5hdfB	Alignment	not modelled	99.7	19 PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
101	c4zwnD	Alignment	not modelled	99.7	14 PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
102	c3qm1A	Alignment	not modelled	99.7	15 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
103	c3d59B	Alignment	not modelled	99.7	14 PDB header: hydrolase Chain: B: PDB Molecule: platelet-activating factor acetylhydrolase; PDBTitle: crystal structure of human plasma platelet activating factor2 acetylhydrolase
104	c5hc4A	Alignment	not modelled	99.7	15 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
105	c3hjuB	Alignment	not modelled	99.7	15 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
106	c1cr6A	Alignment	not modelled	99.7	11 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
					PDB header: hydrolase Chain: A: PDB Molecule: esterase:

107	c5a0aA_	Alignment	not modelled	99.7	16	PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
108	c3fcxA_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
109	c5cmIA_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
110	c4d9jI_	Alignment	not modelled	99.7	13	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
111	c4q3kB_	Alignment	not modelled	99.7	16	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
112	d1jkma_	Alignment	not modelled	99.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
113	c5f2hA_	Alignment	not modelled	99.7	14	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
114	c3llcA_	Alignment	not modelled	99.7	16	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
115	c2vavL_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
116	d2vata1	Alignment	not modelled	99.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
117	c5oluA_	Alignment	not modelled	99.7	12	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
118	c5x6sB_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: B: PDB Molecule: acetylxytan esterase a; PDBTitle: acetyl xytan esterase from aspergillus awamori
119	c3h04A_	Alignment	not modelled	99.7	11	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
120	c5d6oB_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum