Phyre2

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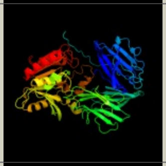
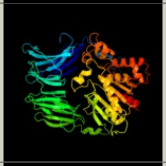
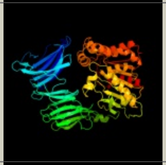
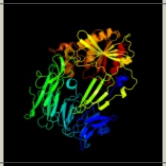
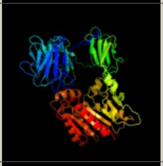
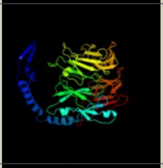
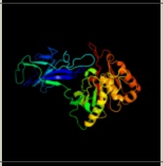
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xe4A_	Alignment		100.0	37	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major
2	c1yr2A_	Alignment		100.0	22	**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
3	c2bklB_	Alignment		100.0	26	**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
4	c3iumA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
5	c1qfmA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
6	c2ecfA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
7	c2g5tA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** crystal structure of human dipeptidyl peptidase iv (dppiv)2 complexed with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
8	c2eepA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
9	c2qtbB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
10	c1z68A_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
11	c3azqA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg

12	c2hu7A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
13	c1xfdD_	Alignment		100.0	13	**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
14	d1qfma1	Alignment		100.0	19	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
15	d1qfma2	Alignment		100.0	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Prolyl oligopeptidase, C-terminal domain
16	c3doiA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
17	d2hu7a2	Alignment		99.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
18	d1orva2	Alignment		99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
19	d2bgra2	Alignment		99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
20	c3k2iA_	Alignment		99.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
21	d2jbwa1	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
22	c2jbwB_	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-oxynicotine2 hydrolase.
23	d1vlqa_	Alignment	not modelled	99.9	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
24	d2b9va2	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
25	c3fnbB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
26	d1xfda2	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
27	c3hlkB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
28	d1mpxa2	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like

29	c2b9vB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
30	d1ju3a2	Alignment	not modelled	99.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
31	c1l7qA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
32	c3ls2D_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
33	d1l7aa_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
34	c3h2iA_	Alignment	not modelled	99.8	15	**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
35	c3bxpA_	Alignment	not modelled	99.8	9	**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
36	c2o2gA_	Alignment	not modelled	99.8	17	**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
37	d1lnsa3	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
38	c2veoA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its2 closed state.
39	c3ib3A_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
40	c3i6yA_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase apc40077; **PDBTitle:** structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
41	c1mpxB_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
42	d1jkma_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
43	c3fcxA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
44	c3mveB_	Alignment	not modelled	99.8	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
45	c3ksrA_	Alignment	not modelled	99.8	14	**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
46	c2zshA_	Alignment	not modelled	99.7	15	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**probable gibberellin receptor gid1l1; **PDBTitle:** structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
47	c3ed1E_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
48	c2o7vA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cxe carboxylesterase; **PDBTitle:** carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
49	c3f67A_	Alignment	not modelled	99.7	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
50	c3fcyB_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xylan esterase 1; **PDBTitle:** crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
51	d1sfra_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
52	c2i3dA_	Alignment	not modelled	99.7	17	**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
53	d2i3da1	Alignment	not modelled	99.7	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
54	c3e4dD_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
						PDB header:hydrolase

55	c3qh4A_	Alignment	not modelled	99.7	18	**Chain:** A: **PDB Molecule:**esterase lipw; **PDBTitle:** crystal structure of esterase lipw from mycobacterium marinum
56	c3d0kA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative poly(3-hydroxybutyrate) depolymerase lpqc; **PDBTitle:** crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
57	c3ga7A_	Alignment	not modelled	99.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
58	c2wtmC_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
59	d1pv1a_	Alignment	not modelled	99.7	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
60	d1lzla_	Alignment	not modelled	99.7	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
61	d1jjfa_	Alignment	not modelled	99.7	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
62	d1dina_	Alignment	not modelled	99.7	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Dienelactone hydrolase
63	d1f0na_	Alignment	not modelled	99.7	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
64	d1dqza_	Alignment	not modelled	99.7	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
65	d2fuka1	Alignment	not modelled	99.7	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
66	c1lnsA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**x-prolyl dipeptidyl aminopetidase; **PDBTitle:** crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
67	d2gzsa1	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**IroE-like
68	c3trdA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
69	c3hxkB_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sugar hydrolase; **PDBTitle:** crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108
70	c3d7rB_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a putative esterase from staphylococcus aureus
71	c3dnmA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase/lipase; **PDBTitle:** crystal structure hormone-sensitive lipase from a2 metagenome library
72	c2qm0B_	Alignment	not modelled	99.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bes; **PDBTitle:** crystal structure of bes protein from bacillus cereus
73	c3fakA_	Alignment	not modelled	99.6	15	**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
74	d2pbla1	Alignment	not modelled	99.6	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
75	c3bjrA_	Alignment	not modelled	99.6	11	**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
76	c2c7bA_	Alignment	not modelled	99.6	18	**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
77	c3llcA_	Alignment	not modelled	99.6	14	**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
78	d1jfra_	Alignment	not modelled	99.6	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Lipase
79	c3qm1A_	Alignment	not modelled	99.6	13	**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
80	d1vkha_	Alignment	not modelled	99.6	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
						Fold:alpha/beta-Hydrolases

81	d1u4na_	Alignment	not modelled	99.6	15	**Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
82	c3h04A_	Alignment	not modelled	99.6	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
83	d1wb4a1	Alignment	not modelled	99.6	9	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
84	d1jjia_	Alignment	not modelled	99.6	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
85	c2wirB_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein; **PDBTitle:** hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
86	c2qruA_	Alignment	not modelled	99.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
87	c3c8dA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**enterochelin esterase; **PDBTitle:** crystal structure of the enterobactin esterase fes from2 shigella flexneri in the presence of 2,3-di-hydroxy-n-3 benzoyl-glycine
88	c2hdwB_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
89	d1ufoa_	Alignment	not modelled	99.5	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
90	c3aikB_	Alignment	not modelled	99.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**303aa long hypothetical esterase; **PDBTitle:** crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
91	c2q0xA_	Alignment	not modelled	99.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
92	c2gopB_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trilobed protease; **PDBTitle:** the beta-propeller domain of the trilobed protease from pyrococcus2 furiosus reveals an open velcro topology
93	d1r88a_	Alignment	not modelled	99.5	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
94	c2uz0B_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tributyrin esterase; **PDBTitle:** the crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
95	d1hlga_	Alignment	not modelled	99.5	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
96	c3g8yA_	Alignment	not modelled	99.5	12	**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
97	c2fx5A_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** pseudomonas mendocina lipase
98	d3c8da2	Alignment	not modelled	99.5	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
99	c2h1iA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
100	d1fj2a_	Alignment	not modelled	99.5	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
101	c1wb4A_	Alignment	not modelled	99.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase y; **PDBTitle:** s954a mutant of the feruloyl esterase module from2 clostridium thermocellum complexed with sinapinate
102	d2h1ia1	Alignment	not modelled	99.4	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
103	d1k8qa_	Alignment	not modelled	99.4	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
104	c3u0vA_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysophospholipase-like protein 1; **PDBTitle:** crystal structure analysis of human lyplal1
105	c3jw8A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
106	c3nuzF_	Alignment	not modelled	99.4	12	**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
						Fold:alpha/beta-Hydrolases

107	d3b5ea1	Alignment	not modelled	99.4	15	**Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
108	c3hjuB_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
109	c2w8bB_	Alignment	not modelled	99.4	8	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
110	c3og9A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
111	c3dyvA_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase d; **PDBTitle:** snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
112	c3cn9B_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
113	d2bgra1	Alignment	not modelled	99.3	10	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
114	c3picB_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cip2; **PDBTitle:** glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina
115	d1k32a2	Alignment	not modelled	99.3	9	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
116	d1orva1	Alignment	not modelled	99.3	11	**Fold:**8-bladed beta-propeller **Superfamily:**DPP6 N-terminal domain-like **Family:**DPP6 N-terminal domain-like
117	d2d81a1	Alignment	not modelled	99.3	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
118	c3d59B_	Alignment	not modelled	99.3	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**platelet-activating factor acetylhydrolase; **PDBTitle:** crystal structure of human plasma platelet activating2 factor acetylhydrolase
119	c3pe7A_	Alignment	not modelled	99.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese
120	d2b61a1	Alignment	not modelled	99.3	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase