

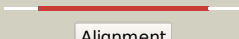

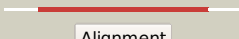
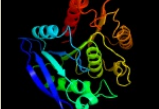


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2765_(-)_3074646_3075383
Date	Wed Aug 7 12:50:42 BST 2019
Unique Job ID	4ca799f91f621658

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zi5A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of diene lactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
2	d1dina_	 Alignment		100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
3	c2ecfA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
4	c3f67A_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative diene lactone hydrolase; PDBTitle: crystal structure of putative diene lactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
5	c5oljA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
6	c3azqA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
7	c2q5tA_	 Alignment		100.0	15	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
8	c5l8sD_	 Alignment		100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase; PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
9	c2qtbB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
10	c4zv9E_	 Alignment		100.0	21	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
11	c1z68A_	 Alignment		100.0	14	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha

12	c5yznA_	Alignment		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
13	c2eepA_	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
14	c4hxgl_	Alignment		100.0	17	PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
15	c2hu7A_	Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
16	c4q1vA_	Alignment		100.0	22	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
17	c3k2iA_	Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
18	c6eoaC_	Alignment		100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
19	c3h1kB_	Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
20	c4wjiB_	Alignment		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
21	c6eorD_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
22	c6eosB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
23	c5t88B_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B; PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
24	c6eotG_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: G; PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slflfyeg, space group 19
25	c5jr1C_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide iso-peptidase2 spi-isop (native)
26	c1qfmA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
27	c5txeA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: atxe2; PDBTitle: atxe2 iso-peptidase - s527a variant with astexin3-dc4 bound
28	c1xfdD_	Alignment	not modelled	100.0	15	PDB header: membrane protein Chain: D; PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family

29	c2bk1B	Alignment	not modelled	100.0	17	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
30	d1qfma2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
31	c2o2gA	Alignment	not modelled	100.0	21	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
32	d1orva2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
33	c4q3kB	Alignment	not modelled	100.0	18	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
34	d1l7aa	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
35	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
36	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
37	d2hu7a2	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
38	d2bgra2	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
39	c5n4dA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
40	c3iumA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
41	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
42	c3ksrA	Alignment	not modelled	100.0	21	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
43	d1vlqa	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
44	c2jwbB	Alignment	not modelled	100.0	15	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	c6agqE	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4
46	d2jbwa1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
47	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
48	c5uzwD	Alignment	not modelled	99.9	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
49	d1ju3a2	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
50	c3trdA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
51	c3mveB	Alignment	not modelled	99.9	18	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
52	d2i3da1	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
53	c2i3dA	Alignment	not modelled	99.9	14	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
54	c1yr2A	Alignment	not modelled	99.9	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

55	c2wirB	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
56	c2c7bA	Alignment	not modelled	99.9	16	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
57	c3ga7A	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
58	c5xb6D	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
59	c4ao6A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
60	c4krxB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
61	c3bxA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfsl at 1.70 a resolution
62	c5g59A	Alignment	not modelled	99.9	16	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
63	d1xfda2	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
64	d2fuka1	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
65	c3fcyB	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
66	c2hdwB	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
67	c3aikB	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
68	c1l7qA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
69	c4ob7A	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
70	c5cmIA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
71	c3hxB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
72	d1lza	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
73	c5jd4D	Alignment	not modelled	99.9	15	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
74	c4ypvA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
75	c5aoaA	Alignment	not modelled	99.9	18	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
76	d1fj2a	Alignment	not modelled	99.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
77	c5jd5A	Alignment	not modelled	99.9	20	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
78	c2b9vB	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
79	c4xvcG	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
						PDB header: hydrolase

80	c5oLuA_	Alignment	not modelled	99.9	17	Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from 2 bacillus coagulans in complex with glycerol
81	c5dwdB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of esterase pe8
82	d2b9va2	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
83	c6fkxD_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
84	c6aaeA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizing enzyme estd136
85	c5l2pD_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
86	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
87	c4q05A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
88	c4wy8A_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
89	c2wtmC_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
90	c3doiA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with 2 paraoxon
91	d1ufoa_	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
92	d1u4na_	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
93	c3ed1E_	Alignment	not modelled	99.9	17	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
94	c3visB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
95	c4pf1D_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
96	c5synB_	Alignment	not modelled	99.9	12	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: cocrystal structure of the human acyl protein thioesterase 2 with an 2 isoform-selective inhibitor, ml349
97	c4v2iB_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a 2 new cold-active and salt tolerant esterase from the marine 3 bacterium thalassospira sp
98	d1mpxa2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
99	c3wj2A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
100	c3bjrA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from 2 lactobacillus plantarum wcf51 at 2.09 a resolution
101	c5f2hA_	Alignment	not modelled	99.9	9	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
102	c5uw7B_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
103	c3u0vA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lypla1
104	c3dnmA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a 2 metagenome library
105	d1jkma_	Alignment	not modelled	99.9	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
106	c5hc4A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22

107	c3i6yA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
108	c3cn9B_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
109	c3fakA_	Alignment	not modelled	99.9	14	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
110	d2h1ia1	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
111	c3ls2D_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
112	c6gocA_	Alignment	not modelled	99.9	18	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methyltransferase bt1017
113	c6a6oA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
114	c3fcxA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
115	d1auoa_	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
116	c3ib3A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
117	c4wfiA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
118	c3llcA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
119	c4zwnD_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
120	c4zrsA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library