

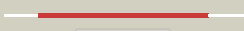





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1076_(lipU)_1200772_1201665
Date	Wed Jul 31 22:05:15 BST 2019
Unique Job ID	7acfc5d510a28ff0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zshA_	 Alignment		100.0	20	PDB header: hormone receptor Chain: A; PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
2	c3ga7A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
3	c3fakA_	 Alignment		100.0	26	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
4	c3dnmA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
5	c5miiD_	 Alignment		100.0	21	PDB header: hydrolase Chain: D; PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
6	c4krxB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
7	c4xvcG_	 Alignment		100.0	26	PDB header: hydrolase Chain: G; PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
8	c3d7rB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
9	c5jd5A_	 Alignment		100.0	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
10	c3ed1E_	 Alignment		100.0	16	PDB header: hydrolase receptor Chain: E; PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
11	c4c87A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1

12	c5jd4D_	Alignment		100.0	19	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
13	c4wy8A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
14	d1lza_	Alignment		100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
15	c4wy5A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
16	c4ypvA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
17	c3qh4A_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
18	c4v2iB_	Alignment		100.0	20	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
19	d1jia_	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
20	c5l2pD_	Alignment		100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
21	c4q05A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
22	c6aaeA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
23	c5hc4A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
24	d1jkma_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
25	c3wj2A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
26	c4q3oB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: mgs-mt1; PDBTitle: crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
27	c3aikB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfobolus2 tokodaii
28	d1u4na_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
29	c4i7eB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: esterase;

29	c4j7aB	Alignment	not modelled	100.0	19	PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library PDB header: hydrolase
30	c2wirB	Alignment	not modelled	100.0	21	Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis PDB header: hydrolase
31	c4ob7A	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h PDB header: hydrolase
32	c2c7bA	Alignment	not modelled	100.0	21	Chain: A: PDB Molecule: carboxylesterase; PDBTitle: the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library PDB header: hydrolase
33	c2o7vA	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon PDB header: hydrolase
34	c4n5iX	Alignment	not modelled	100.0	20	Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis PDB header: hydrolase
35	c4zrsA	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library PDB header: hydrolase
36	c5oljA	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4 PDB header: hydrolase
37	c3azqA	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg PDB header: hydrolase
38	c2ecfA	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia PDB header: lyase
39	c1z68A	Alignment	not modelled	100.0	13	Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha PDB header: hydrolase
40	c5l8sD	Alignment	not modelled	100.0	19	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 PDB header: hydrolase
41	c4q3kB	Alignment	not modelled	100.0	17	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 PDB header: hydrolase
42	c2qtB	Alignment	not modelled	100.0	13	Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor PDB header: hydrolase
43	c2hu7A	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase PDB header: hydrolase
44	c5t88B	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus PDB header: hydrolase
45	c2g5tA	Alignment	not modelled	100.0	13	Chain: A: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag PDB header: hydrolase
46	c4hxgl	Alignment	not modelled	100.0	14	Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form) PDB header: hydrolase/hydrolase inhibitor
47	c4e14A	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride PDB header: hydrolase
48	c2eepA	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor PDB header: hydrolase
49	c5yznA	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1 PDB header: membrane protein
50	c4wjJB	Alignment	not modelled	100.0	15	Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels PDB header: structural genomics, unknown function
51	c2qrUA	Alignment	not modelled	100.0	19	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis PDB header: membrane protein
52	c1xfdD	Alignment	not modelled	100.0	17	Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dpdx, a member of the dipeptidyl aminopeptidase family PDB header: hydrolase
53	c3bxpA	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf1 at 1.70 a resolution PDB header: hydrolase
54	c6eosB	Alignment	not modelled	100.0	17	Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDB header: hydrolase

					PDBTitle: dpp8 - apo, space group 19
55	c6eotG	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: G; PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - srlflyeg, space group 19
56	c6eogC	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
57	c4q1vA	Alignment	not modelled	100.0	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
58	c3hxB	Alignment	not modelled	100.0	16 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
59	c6eorD	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: D; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
60	c1qfmA	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A; PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
61	c5jrlC	Alignment	not modelled	100.0	16 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)
62	c3bjrA	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A; PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
63	d1qfma2	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
64	c5txeA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A; PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
65	c6a6oA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
66	c5aoaA	Alignment	not modelled	99.9	22 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
67	d2pbla1	Alignment	not modelled	99.9	22 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
68	c2bklB	Alignment	not modelled	99.9	22 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
69	c4hvtA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A; PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
70	d1vkha	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
71	c4bp9A	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
72	c5n4dA	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A; PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
73	c2xe4A	Alignment	not modelled	99.9	13 PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
74	d1orva2	Alignment	not modelled	99.9	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
75	c3iumA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A; PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
76	d2bgra2	Alignment	not modelled	99.9	11 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
77	c1yr2A	Alignment	not modelled	99.9	16 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
78	c3h04A	Alignment	not modelled	99.9	15 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
79	c5uzwD	Alignment	not modelled	99.9	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
80	d2hu7a2	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal domain
81	d1xfda2	Alignment	not modelled	99.9	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
82	d1dina_	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
83	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
84	c2i3dA_	Alignment	not modelled	99.9	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
85	d2i3da1	Alignment	not modelled	99.9	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
86	c4zi5A_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
87	c3hkB_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
88	c3k2iA_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
89	c3f67A_	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
90	c4zv9E_	Alignment	not modelled	99.9	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
91	c5f2hA_	Alignment	not modelled	99.9	18 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
92	d1ju3a2	Alignment	not modelled	99.9	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
93	c5g59A_	Alignment	not modelled	99.8	16 PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
94	c3ksrA_	Alignment	not modelled	99.8	18 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
95	c3fnbB_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
96	c3i6yA_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
97	c5cxcC_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: C: PDB Molecule: ferulic acid esterase, amce1/fae1a; PDBTitle: structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid
98	c3doiA_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
99	c4h18D_	Alignment	not modelled	99.8	15 PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
100	d1qe3a_	Alignment	not modelled	99.8	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
101	c3fcxA_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
102	c5volA_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase
103	c1l7qA_	Alignment	not modelled	99.8	12 PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
104	c4b6gA_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
105	c4rgvA_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library

106	c3e4dD_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
107	c2uz0B_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: tributylin esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
108	d2jbwa1	Alignment	not modelled	99.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
109	c2o2gA_	Alignment	not modelled	99.8	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
110	c2jwbB_	Alignment	not modelled	99.8	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.
111	c4eziA_	Alignment	not modelled	99.8	15	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
112	c4rotA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of the esterase a from streptococcus pyogenes
113	c5cmIA_	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
114	d2fuka1	Alignment	not modelled	99.8	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
115	d1vlqa_	Alignment	not modelled	99.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
116	c2wtmC_	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
117	d1l7aa_	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
118	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
119	c5xb6D_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycjy; PDBTitle: crystal structure of ycjy from e. coli
120	c2hdwB_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas aeruginosa