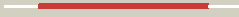























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0129c_fbpC_156576_157598
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	d1d5f26f70c63a0d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dqza_	 Alignment		100.0	100	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
2	d1sfra_	 Alignment		100.0	70	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
3	d1f0na_	 Alignment		100.0	73	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
4	d1r88a_	 Alignment		100.0	42	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
5	c4h18D_	 Alignment		100.0	25	PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
6	d3c8da2	 Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
7	c3fcxA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
8	c3c8dA_	 Alignment		100.0	17	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
9	c3e4dD_	 Alignment		100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
10	d1pv1a_	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
11	c1wb4A_	 Alignment		100.0	18	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

12	c3i6yA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
13	c5cxcC_	Alignment		100.0	11	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
14	c4b6gA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
15	c3ls2D_	Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
16	d1jjfa_	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
17	d1wb4a1	Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
18	c2uz0B_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: tributyryn esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
19	c4rgyA_	Alignment		100.0	24	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
20	c5volA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase
21	c4rotA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of esterase a from streptococcus pyogenes
22	c6qi5A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: ferric enterobactin esterase; PDBTitle: crystal structure of the ferric enterobactin esterase (pfee) from2 pseudomonas aeruginosa in complex with the tris-catechol vector
23	c6guiA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: siderophore esterase iroe-like, putative; PDBTitle: siderophore hydrolase estb mutant h267n from aspergillus fumigatus
24	c2ecfA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
25	c3gffA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: iroe-like serine hydrolase; PDBTitle: crystal structure of iroe-like serine hydrolase (np_718593.1) from2 shewanella oneidensis at 2.12 a resolution
26	c6gunB_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: estb from aspergillus nidulans; PDBTitle: siderophore hydrolase estb from aspergillus nidulans
27	c6guoC_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: putative siderophore-degrading esterase (eurofung); PDBTitle: siderophore hydrolase esta from aspergillus nidulans
28	c3wiaA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: crystal structure of soph native

29	c5l8sD	Alignment	not modelled	99.9	12	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
30	c3doiA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
31	c4q1vA	Alignment	not modelled	99.9	11	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
32	c3azqA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
33	c2qtbB	Alignment	not modelled	99.9	9	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
34	c1z68A	Alignment	not modelled	99.9	8	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
35	c2eepA	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
36	c4wjlB	Alignment	not modelled	99.9	9	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
37	c5oljA	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
38	c2g5tA	Alignment	not modelled	99.9	8	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
39	c4hxgl	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
40	c4w9rA	Alignment	not modelled	99.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein coch_1243 from2 capnocytophaga ochracea dsm 7271
41	c1qfmA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
42	c2bkIB	Alignment	not modelled	99.9	12	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
43	c4bp9A	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
44	c1yr2A	Alignment	not modelled	99.9	17	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
45	c5x6sB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: acetylxy lan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
46	c6eosB	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
47	c5yznA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
48	c6eotG	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
49	c1xfdD	Alignment	not modelled	99.9	11	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
50	c2xe4A	Alignment	not modelled	99.9	15	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
51	c6eoaC	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
52	c6eorD	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
53	c2hu7A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase

54	d2gzsa1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like
55	c5t88B	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
56	c5jrlC	Alignment	not modelled	99.9	15	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)
57	c3iumA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
58	c5n4dA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
59	c4hvtA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
60	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
61	d2h1ia1	Alignment	not modelled	99.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
62	c2qm0B	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
63	c5uw7B	Alignment	not modelled	99.8	14	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
64	d3b5ea1	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
65	c2h1iA	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
66	c5txeA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
67	c3og9A	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
68	c3wydA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1
69	c3d0kA	Alignment	not modelled	99.8	10	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
70	c6avwA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase sober1; PDBTitle: crystal structure of arabidopsis thaliana sober1 l63a
71	c2r8bA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
72	d1qfma2	Alignment	not modelled	99.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
73	c4h0cA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
74	d1orva2	Alignment	not modelled	99.7	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
75	c4fhzA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of a carboxyl esterase at 2.0 angstrom resolution
76	d2bgra2	Alignment	not modelled	99.7	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
77	c4f21G	Alignment	not modelled	99.7	16	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
78	d1xfda2	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
79	d2r8ba1	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
						PDB header: hydrolase

80	c3bxpA	Alignment	not modelled	99.7	11	Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution
81	c5synB	Alignment	not modelled	99.7	18	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: cocrystal structure of the human acyl protein thioesterase 2 with an2 isoform-selective inhibitor, ml349
82	c5f2hA	Alignment	not modelled	99.7	17	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
83	d2jba1	Alignment	not modelled	99.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
84	c2o7vA	Alignment	not modelled	99.6	10	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
85	c2jwbB	Alignment	not modelled	99.6	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.
86	c2o2gA	Alignment	not modelled	99.6	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
87	c4zrsA	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
88	c3u0vA	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lyplal1
89	c5g59A	Alignment	not modelled	99.6	10	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
90	c5hc4A	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
91	c3bjrA	Alignment	not modelled	99.6	10	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
92	d1ufoa	Alignment	not modelled	99.6	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
93	c4q82A	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from haliangium2 ochraceum
94	c3k2iA	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
95	c5dwdB	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of esterase pe8
96	c6avyA	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: crystal structure of zea mays acyl-protein thioesterase 2
97	c3fnbB	Alignment	not modelled	99.5	10	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
98	c5xg0A	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
99	d2hu7a2	Alignment	not modelled	99.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
100	c6a6oA	Alignment	not modelled	99.5	9	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
101	d1fj2a	Alignment	not modelled	99.5	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
102	c3cn9B	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
103	c6grwA	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: glucuronoyl esterase from opitutus terrae (au derivative)
104	c3hkB	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
105	c2zshA	Alignment	not modelled	99.5	13	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
						PDB header: lyase

106	c3mveB_	Alignment	not modelled	99.5	10	Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
107	c2i3dA_	Alignment	not modelled	99.5	13	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
108	d2i3da1	Alignment	not modelled	99.5	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
109	c3ksrA_	Alignment	not modelled	99.5	15	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
110	c5aoaA_	Alignment	not modelled	99.5	13	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
111	c3ed1E_	Alignment	not modelled	99.5	13	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
112	c6gocA_	Alignment	not modelled	99.5	10	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methyltransferase bt1017
113	c1l7qA_	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
114	c4q3kB_	Alignment	not modelled	99.5	15	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
115	d1ju3a2	Alignment	not modelled	99.5	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
116	c4zi5A_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of diene lactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
117	c4wfiA_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
118	c2wtmC_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
119	c3visB_	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
120	c5jd5A_	Alignment	not modelled	99.4	12	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