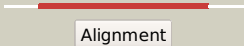

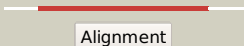

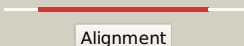







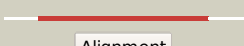











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1400c_(lip)_1575840_1576802
Date	Wed Jul 31 22:05:50 BST 2019
Unique Job ID	0860e516e6d1745e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4v2iB_	 Alignment		100.0	35	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
2	d1lza_	 Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
3	c3ga7A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
4	c5jd4D_	 Alignment		100.0	32	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
5	c4c87A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
6	c4ypvA_	 Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
7	c4ob7A_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
8	c2zshA_	 Alignment		100.0	24	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
9	c4krxB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
10	c6aaeA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
11	d1u4na_	 Alignment		100.0	39	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase

12	c4wy8A_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
13	c3wj2A_	Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
14	c2wirB_	Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
15	c5miiD_	Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
16	d1jja_	Alignment		100.0	35	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
17	c4wy5A_	Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
18	c5l2pD_	Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
19	c5jd5A_	Alignment		100.0	28	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
20	c3dnmA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
21	c5hc4A_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
22	c4xvcG_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
23	c4j7aB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
24	c3ed1E_	Alignment	not modelled	100.0	27	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
25	c4q05A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
26	c2c7bA_	Alignment	not modelled	100.0	35	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
27	c3fakA_	Alignment	not modelled	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
28	d1jkma_	Alignment	not modelled	100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
						PDB header: hydrolase

29	c3qh4A_	Alignment	not modelled	100.0	34	Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
30	c4q3oB_	Alignment	not modelled	100.0	17	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
31	c3aikB_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfobolbus2 tokodaii
32	c3d7rB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
33	c2o7vA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
34	c4zrsA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
35	c4n5iX_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
36	c3bxpA_	Alignment	not modelled	100.0	17	PDB header: hydrolase 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
37	c5oljA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
38	c2ecfA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia
39	c3azqA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
40	c4q3kB_	Alignment	not modelled	100.0	20	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
41	c1z68A_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
42	c2qtbB_	Alignment	not modelled	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
43	c2eepA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
44	c5i8sD_	Alignment	not modelled	100.0	14	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
45	c2q5tA_	Alignment	not modelled	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
46	c4hxxj_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
47	c5txeA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
48	c4wjlB_	Alignment	not modelled	100.0	14	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
49	c6eosB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
50	c5jrlC_	Alignment	not modelled	100.0	12	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)
51	c6eoqC_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
52	c4q1vA_	Alignment	not modelled	100.0	15	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
53	c4e14A_	Alignment	not modelled	100.0	11	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
						PDB header: hydrolase

54	c6eotG	Alignment	not modelled	100.0	17	Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - srlflyeg, space group 19
55	c2hu7A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
56	c1xfdD	Alignment	not modelled	100.0	16	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
57	d1qfma2	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
58	c5yznA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
59	c5t88B	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
60	c6eorD	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
61	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 wcfs1 at 2.09 a resolution
62	c5a0aA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-proprionate bound
63	c6a6oA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
64	c1qfmA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
65	c3hxB	Alignment	not modelled	100.0	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
66	c2bklB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
67	d1orva2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
68	c4hvtA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
69	c2qrUA	Alignment	not modelled	100.0	17	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
70	d2bgra2	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
71	c4bp9A	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
72	c2xe4A	Alignment	not modelled	99.9	12	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
73	d1xfda2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
74	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
75	c3iumA	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
76	c5uzwD	Alignment	not modelled	99.9	10	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
77	d1vkha	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
78	d2hu7a2	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
79	d2pbla1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase

80	c5uw7B	Alignment	not modelled	99.9	10	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
81	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
82	c3k2iA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
83	c1yr2A	Alignment	not modelled	99.9	12	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
84	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
85	c3h1kB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
86	c3f67A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
87	c3h04A	Alignment	not modelled	99.9	17	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
88	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
89	c3ksrA	Alignment	not modelled	99.9	17	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
90	d2i3da1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
91	c2i3dA	Alignment	not modelled	99.9	16	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
92	c3ls2D	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
93	d1dina	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
94	c5cxcC	Alignment	not modelled	99.9	14	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
95	c3doiA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
96	c5volA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase
97	c4b6gA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
98	d1ju3a2	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
99	d1l7aa	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
100	c5xb6D	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: D: PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
101	c2uz0B	Alignment	not modelled	99.9	16	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
102	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
103	c2o2gA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anaabaena variabilis atcc 29413 at 1.92 a resolution
104	c4rotA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of esterase a from streptococcus pyogenes
105	d1vlqa	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like

106	c2hdwB_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
107	c3e4dD_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
108	c3fcxA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
109	c4h18D_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
110	c4rgyA_	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
111	d2fuka1	Alignment	not modelled	99.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
112	c5g59A_	Alignment	not modelled	99.8	13	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
113	d1qe3a_	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
114	c6agqE_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4
115	c1l7qA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
116	c2jwbB_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
117	c5f2hA_	Alignment	not modelled	99.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
118	c4eziA_	Alignment	not modelled	99.8	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
119	c5x6sB_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B: PDB Molecule: acetylxytan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
120	d1jjfa_	Alignment	not modelled	99.8	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase