

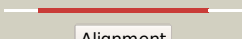













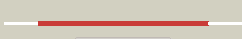











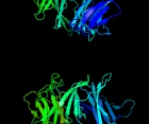




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0457c (-)_547589_549610
Date	Tue Jul 23 14:50:53 BST 2019
Unique Job ID	6a37ff82c1c5cac3

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hvtA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
2	c2xe4A_	 Alignment		100.0	21	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
3	c2bktB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
4	c1qfmA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
5	c1yr2A_	 Alignment		100.0	27	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
6	c4bp9A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
7	c5n4dA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
8	c3iumA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
9	c5uzwD_	 Alignment		100.0	21	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
10	c5uw7B_	 Alignment		100.0	22	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
11	c5t88B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus

12	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
13	c5oljA	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
14	c2g5tA	Alignment		100.0	13	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
15	c2qtbB	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
16	c4hxgl	Alignment		100.0	12	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
17	c2ecfA	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
18	c4wjlb	Alignment		100.0	13	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
19	c1z68A	Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
20	c4q1vA	Alignment		100.0	13	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
21	c2eepA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
22	c3azqA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
23	c6eorD	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
24	c5yznA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
25	c6eogC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
26	c6eotG	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
27	c5txeA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
28	c6eosB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
29	c2hu7A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase

30	c5jrlC_	Alignment	not modelled	100.0	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)
31	c1xfdD_	Alignment	not modelled	100.0	13	PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dpdx, a member of the dipeptidyl aminopeptidase family
32	d1qfma1	Alignment	not modelled	100.0	15	Fold: 7-bladed beta-propeller Superfamily: Peptidase/esterase 'gauge' domain Family: Prolyl oligopeptidase, N-terminal domain
33	d1qfma2	Alignment	not modelled	100.0	34	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
34	c3doiA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
35	d2hu7a2	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
36	c3k2iA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
37	d1orva2	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
38	d2bgra2	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
39	d1vlqa_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
40	c2jwbB_	Alignment	not modelled	100.0	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.
41	d2jbwa1	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
42	c3h1kB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
43	c3fnbB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
44	d2b9va2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
45	c4q3kB_	Alignment	not modelled	99.9	19	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
46	c4pf1D_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
47	c4zi5A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
48	c3ls2D_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
49	d1ju3a2	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
50	d1xfda2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
51	c4b6gA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
52	d1mpxa2	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
53	c1l7qA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
54	c2b9vB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
55	c6gocA_	Alignment	not modelled	99.9	14	PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methylsterase bt1017

56	c5g59A	Alignment	not modelled	99.9	15	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
57	c3e4dD	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
58	c3bxaA	Alignment	not modelled	99.9	14	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
59	d1jka	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
60	c5hc4A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
61	c4h18D	Alignment	not modelled	99.9	12	PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
62	c4eziA	Alignment	not modelled	99.9	16	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
63	d1l7aa	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
64	c3fcxA	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
65	c6agqE	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: E: PDB Molecule: acetyl xylan esterase; PDBTitle: acetyl xylan esterase from paenibacillus sp. r4
66	c4j7aB	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
67	c5x6sB	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: acetylxylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
68	c3i6yA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
69	c6fkxD	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
70	c2o2gA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
71	c1mpxB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
72	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
73	d1lnsa3	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
74	c3ib3A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
75	c5aoaA	Alignment	not modelled	99.9	15	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	c3wlaA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: crystal structure of soph native
77	c5f2hA	Alignment	not modelled	99.9	11	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
78	c4q05A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
79	c3h2iA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
80	c4xvcG	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
81	c4zv9E	Alignment	not modelled	99.9	14	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
82	c5jd5A_	Alignment	not modelled	99.9	18	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
83	c3ksrA_	Alignment	not modelled	99.9	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
84	c5cxcC_	Alignment	not modelled	99.9	12	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
85	d1sfra_	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
86	c4v2iB_	Alignment	not modelled	99.9	16	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
87	c4c87A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcf51
88	c3ed1E_	Alignment	not modelled	99.9	14	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
89	d1lza_	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
90	c6gi5A_	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
91	c4krxB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
92	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
93	c3fcyB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
94	c4q3oB_	Alignment	not modelled	99.9	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
95	c6guiA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: siderophore esterase iroe-like, putative; PDBTitle: siderophore hydrolase estb mutant h267n from aspergillus fumigatus
96	c2veoA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
97	c6aaeA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
98	c4ob7A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
99	c3d0kA_	Alignment	not modelled	99.9	12	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
100	c3qh4A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
101	c4wy8A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
102	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
103	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
104	c3mveB_	Alignment	not modelled	99.9	11	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
105	c3ga7A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
106	c2o7vA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon

107	c6a6oA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
108	c2zshA_	Alignment	not modelled	99.9	17	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
109	c1lnsA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: x-prolyl dipeptidyl aminopeptidase; PDBTitle: crystal structure analysis of the x-prolyl dipeptidyl aminopeptidase2 from lactococcus lactis
110	c5cmlA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: osmc family protein; PDBTitle: crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
111	c4n5iX_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
112	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
113	c5l2pD_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
114	d2i3da1	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
115	c2i3da_	Alignment	not modelled	99.9	15	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
116	d1f0na_	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
117	c2wtmC_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
118	d1pv1a_	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
119	d1dina_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
120	c4e14A_	Alignment	not modelled	99.9	13	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride